

Package ‘soilKey’

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Type Package

Title Automated Soil Profile Classification per WRB 2022, 'SiBCS' 5 and USDA Soil Taxonomy 13

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Description Implements deterministic classification keys for the World Reference Base for Soil Resources 2022 (4th edition) and the Brazilian System of Soil Classification ('SiBCS', 5th edition). Provides a unified profile representation with explicit per-attribute provenance, multimodal extraction from field reports and photos via vision-language models, spatial priors from 'SoilGrids' and national soil maps, and gap-filling of soil attributes from Vis-NIR or MIR spectra via the Open Soil Spectral Library ('OSSL'). The taxonomic key itself is never delegated to a language model; LLMs are restricted to schema-validated extraction. Each classification result reports a key trace, a provenance-aware evidence grade, and ambiguities that further measurement would resolve.

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URL <https://github.com/HugoMachadoRodrigues/soilKey>,
<https://hugomachadorodrigues.github.io/soilKey/>

BugReports <https://github.com/HugoMachadoRodrigues/soilKey/issues>

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Contents

abrupt_textural_difference	9
acrisol	9
aeolic_material	10
albeluvic_glossae	11
albic	11
alisol	12
andic_properties	12
andosol	14
annotate_wrb_from_usda	15
anthraquic	16
anthric_horizons	16
apply_soilgrids_depth_prior	17
arenic_texture	18
argic	19
argic_aqp	20
argic_with_strong_clay_films	21
argillic_clay_films_test	22
artefacts	23
as_aqp	23
attach_lucas_spectra	24
audit_argic_strong_films	25
auto_set_proj_env	26
available_esdb_attributes	27
batch_robustness	27
benchmark_afsp	28
benchmark_bdsolos	29
benchmark_lucas_2018	30
benchmark_performance	33
benchmark_redape	34
benchmark_run_classification	35
benchmark_spectral_fill	36
benchmark_unified	37
benchmark_wrb_vs_usda	39
build_taxon_profiles	40
B_espodico	40

B_incipiente	41
B_latossolico	42
B_nitico	43
B_planico	43
B_textural	44
calcaric_material	45
calcic	45
cambic	46
cambic_aqp	47
canonicalise_kst13ed_gg	48
canonical_reference	49
cerosidade	49
chernic	50
chernozem	51
chernozem_strict	51
claric_material	52
ClassificationResult	53
classification_robustness	55
classify_all	56
classify_by_spectral_neighbours	58
classify_from_documents	60
classify_from_photos	63
classify_sibcs	64
classify_sibcs_familia	65
classify_usda	66
classify_usda_family	68
classify_via_smartsolos_api	69
classify_with_engine_heuristic	71
classify_with_uncertainty	71
classify_wrb2022	73
clear_kst13_cache	74
clear_ossl_cache	74
combine_priors	75
compare_engines	76
compare_smartsolos	76
compute_ki	77
compute_kr	78
compute_per_attribute_evidence_grade	78
continuous_rock	79
coverage_report	80
cryic_conditions	81
DiagnosticResult	81
distrofico	83
dolomitic_material	84
download_bdsolos	84
download_extdata_cache	86
download_ossl_subset	87
download_ossl_subset_with_labels	88

download_redape_dataset	90
duric_horizon	91
duripa	92
ensure_horizon_schema	92
eutrofico	93
evaluate_rsg_tests	93
extract_horizons_from_pdf	94
extract_munsell_from_photo	95
extract_site_from_fieldsheet	96
familia_mineralogia_argila_geral	97
FamilyAttribute	98
febr_index_munsell	99
ferralic	100
ferralsol	101
ferric	102
fibrico	102
fill_from_spectra	103
fill_munsell_from_spectra	104
fluvic_material	105
format_wrb_name	106
fragic	106
fragipa	107
from_aqp	107
gapfill_by_predicted_taxon	108
gapfill_derive_horizon	109
gapfill_within_pedon	110
get_perturbation_scale	111
gleyic_properties	112
gleysol	113
grapes-or-or-grapes	114
GSM_DEPTHS	114
gypsic	115
gypsiric_material	116
harmonize_to_gsm	116
hemico	118
histic_horizon	118
horizon_column_spec	119
hortic	120
hydragric	120
hypersulfidic_material	121
hyposulfidic_material	122
inspect_bdsolos_csv	122
irragric	123
kastanozem	124
kastanozem_strict	124
kst13_canonical	125
kst13_codes	126
kst13_criteria	126

leptic_features	127
limnic_material	128
limonic	128
lithic_discontinuity	129
lixisol	130
load_afsp_pedons	130
load_afsp_sample	131
load_bdsolos_csv	132
load_embrapa_pedons	132
load_febr_pedons	133
load_kssl_nasis_sample	134
load_kssl_pedons	135
load_kssl_pedons_gpkg	136
load_kssl_pedons_with_nasis	137
load_kssl_sample	137
load_lucas_pedons	139
load_lucas_soil_2018	139
load_redape_pedons	141
load_rules	142
load_wosis_sample	143
load_wosis_stratified_sample	144
lookup_esdb	145
lookup_mapbiomas_solos	146
lookup_soilgrids	147
luvisol	149
make_acrisol_canonical	149
make_alisol_canonical	150
make_andosol_canonical	150
make_anthrosol_canonical	151
make_arenosol_canonical	151
make_argissolo_canonical	152
make_calcisol_canonical	152
make_cambisol_canonical	153
make_cambissolo_canonical	153
make_chernossolo_canonical	154
make_chnozem_canonical	154
make_cryosol_canonical	155
make_durisol_canonical	155
make_empty_horizons	156
make_espodossolo_canonical	156
make_ferralsol_canonical	157
make_fluvisol_canonical	157
make_gleissolo_canonical	158
make_gleysol_canonical	158
make_gypsisol_canonical	159
make_histosol_canonical	159
make_kastanozem_canonical	160
make_latossolo_canonical	160

make_leptosol_canonical	161
make_lixisol_canonical	161
make_luvisol_canonical	162
make_luvissolo_canonical	162
make_neossolo_canonical	163
make_nitisol_canonical	163
make_nitossolo_canonical	164
make_organossolo_canonical	164
make_phaeozem_canonical	165
make_planosol_canonical	165
make_planossolo_canonical	166
make_plinthosol_canonical	166
make_plintossolo_canonical	167
make_podzol_canonical	167
make_retisol_canonical	168
make_solonchak_canonical	168
make_solonetz_canonical	169
make_stagnosol_canonical	169
make_synthetic_pedon_with_spectra	170
make_technosol_canonical	170
make_umbrisol_canonical	171
make_vertisol_canonical	171
make_vertissolo_canonical	172
mineral_material	172
mollic	173
mudanca_textural_abrupta	174
mulmic_material	175
natric_horizon	175
nitic_horizon	176
normalise_febr_sibcs	178
normalise_febr_usda	178
normalise_febr_wrb	179
normalise_kssl_subgroup	179
ollama_is_running	180
organic_material	180
organotechnic_material	181
ornithogenic_material	181
ossl_demo_sa	182
ossl_library_template	183
oxic_usda	184
panpaic	184
PedonRecord	185
pedons_from_spectral_table	188
pedon_json_schema	189
pedon_to_spc	190
petrocalcic	191
petroduric	191
petrogypsic	192

petroplinthic	193
phaeozem	193
pick_engine	194
pick_engine_batch	195
pisoplinthic	195
pi_to_confidence	196
plaggic	196
planic_features	197
planosol	198
plinthic	199
posterior_classify	200
predict.soilKey_pls_model	201
predict_from_spectra	201
predict_lab_from_spectra	202
predict_munsell_from_spectra	203
predict_ossl_mbl	204
predict_ossl_plsr_local	205
predict_ossl_pretrained	206
predict_xyz_from_spectra	207
preprocess_spectra	207
pretic	209
print.soilKey_pls_model	209
prior_consistency_check	210
protocalcic_properties	210
protogypsic_properties	211
protovertic	212
read_febr_pedons	212
read_spectral_library	214
reducing_conditions	215
report	215
report_html	217
report_pdf	218
report_to_qgis	219
resolve_wrb_qualifiers	220
retic_properties	221
run_all_benchmarks	222
run_classify_app	223
run_demo	224
run_sibcs_grande_grupo	225
run_sibcs_key	225
run_sibcs_subgrupo	226
run_sibcs_subordem	226
run_taxa_list	227
run_taxonomic_key	228
run_usda_great_group	228
run_usda_key	229
run_usda_subgroup	229
run_usda_suborder	230

run_wrb_key	230
salic	231
saprico	232
save_ossl_models	232
shrink_swell_cracks	233
sideralic_properties	233
soilgrids_usda_lut	234
soilgrids_wrb_lut	234
soil_classes_at_location	235
soil_organic_carbon	236
solimovic_material	237
sombric	238
spatial_prior	239
spatial_prior_embrapa	240
spatial_prior_soilgrids	241
spodic	242
stagnic_properties	243
st_features_canonical	244
subgrupo_planossolo_espessos	245
subgrupo_planossolo_mesicos	245
subgrupo_plintossolo_endico_concrecionario	246
subgrupo_plintossolo_endico_litoplintico	247
subgrupo_plintossolo_espessos	247
takyric_properties	248
technic_features	248
technic_hard_material	249
tephric_material	250
terrific	250
texture_class_from_pct	251
thionic	252
train_pls_from_ossl	252
tsitelic	254
umbric_horizon	255
usda_to_wrb_rsg	256
validate_horizon_geometry	257
validate_pedon_json	258
vertic_horizon	258
vertic_properties	259
vertisol	261
vitric_properties	261
vlm_pick_provider	262
vlm_provider	263
wrb06_code_to_rsg	264
wrb2022_canonical	265
yermic_properties	265

 abrupt_textural_difference

Abrupt textural difference (WRB 2022 Ch 3.2.1)

Description

Sharp clay-content increase between two superimposed mineral layers meeting all of:

- underlying clay $\geq 15\%$ AND thickness ≥ 7.5 cm;
- underlying starts ≥ 10 cm below mineral soil surface;
- underlying has, vs overlying: 2x clay if overlying $< 20\%$, OR ≥ 20 pp (absolute) more clay if overlying $\geq 20\%$;
- transitional layer, if any, ≤ 2 cm.

v0.3.3 enforces criteria 1, 2, 3. The transitional-layer check is deferred (the canonical horizon schema does not carry a "transitional" marker; it can be added later via boundary_distinctness inspection).

Usage

abrupt_textural_difference(pedon)

Arguments

pedon A [PedonRecord](#).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

 acrisol

Acrisol RSG diagnostic (WRB 2022)

Description

Tests whether a profile satisfies the Acrisol RSG criteria: an argic horizon with low-activity clay (CEC < 24 cmol_c/kg clay) AND low base saturation (BS $< 50\%$) within at least one argic layer.

Usage

acrisol(pedon, max_cec = 24, max_bs = 50)

Arguments

pedon	A PedonRecord .
max_cec	Maximum CEC per kg clay (default 24).
max_bs	Maximum base saturation % (default 50).

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022), Chapter 5, Acrisols.

aeolic_material	<i>Aeolic material (WRB 2022 Ch 3.3.1)</i>
-----------------	--

Description

Wind-deposited material in the upper 20 cm: rounded matt-surfaced sand grains OR aeroturbation features, AND < 1% SOC in the upper 10 cm. v0.3.3 detects via `rock_origin == "aeolian"` OR `layer_origin == "aeolic"`.

Usage

```
aeolic_material(pedon)
```

Arguments

pedon	A PedonRecord .
-------	---------------------------------

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

albeluvic_glossae	<i>Albeluvic glossae (WRB 2022 Ch 3.2.2)</i>
-------------------	--

Description

Tongues of bleached, coarser-textured material penetrating an argic horizon. v0.3.3 detects via designation pattern glossic|albeluvic on a layer that overlies an argic-horizon-passing layer.

Usage

```
albeluvic_glossae(pedon)
```

Arguments

pedon A [PedonRecord](#).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

albic	<i>Albic horizon (WRB 2022)</i>
-------	---------------------------------

Description

A bleached eluvial horizon – claric material that has lost iron oxides and/or organic matter due to clay migration, podzolization, or redox under stagnant water. Diagnostic for parts of Podzols, Retisols and Planosols qualifiers.

Usage

```
albic(pedon, min_thickness = 1)
```

Arguments

pedon A [PedonRecord](#).

min_thickness Minimum thickness in cm (default 1, per WRB 2022). The albic horizon has no canonical thickness gate; we keep a token min so that fully-NA layers don't pass.

Details

Sub-tests:

- test_claric_munsell – Munsell criteria of claric material (Ch 3.3.4).

Designation pattern E or Eg also serves as positive evidence when Munsell columns are missing (proxy path).

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022), Ch 3.1 – Albic horizon.

alisol	<i>Alisol RSG diagnostic (WRB 2022)</i>
--------	---

Description

argic + CEC \geq 24 cmol_c/kg clay + Al saturation \geq 50%.

Usage

```
alisol(pedon, min_cec = 24, min_al_sat = 50)
```

Arguments

pedon	A PedonRecord .
min_cec	Minimum CEC per kg clay (default 24).
min_al_sat	Minimum Al saturation % (default 50).

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022), Chapter 5, Alisols.

andic_properties	<i>Andic properties (WRB 2022)</i>
------------------	------------------------------------

Description

Tests for the andic property complex – volcanic-ash-derived allophanic / imogolitic / Al-humus material. Diagnostic of Andosols. Two alternative qualifying paths per WRB 2022 Ch 3.2:

1. **Al-Fe oxalate + low BD:** $(Al_{ox} + 0.5 * Fe_{ox}) \geq min_alfe$ (default 2.0%) AND $bulk_density \leq max_bd$ (default 0.9 g/cm³) on the same layer.
2. **Phosphate retention:** $phosphate_retention_pct \geq min_p_retention$ (default 70%).

Either path qualifies. The volcanic-glass criterion is the separate [vitric_properties](#) diagnostic; Andosols key on (andic OR vitric) at the RSG-gate level ([andosol](#)).

Usage

```
andic_properties(
  pedon,
  min_alfe = 2,
  max_bd = 0.9,
  min_p_retention = 70,
  min_oc_proxy = 4,
  max_bd_proxy = 0.9
)
```

Arguments

pedon	A PedonRecord .
min_alfe	Minimum (Al _{ox} + 0.5*Fe _{ox}) percent for the Al-Fe path (default 2.0).
max_bd	Maximum bulk density g/cm ³ for the Al-Fe path (default 0.9).
min_p_retention	Minimum phosphate retention % for the P path (default 70).
min_oc_proxy	Minimum SOC % for the v0.9.80 OC+BD proxy path (default 4.0). Only consulted when the proxy is enabled via options(soilKey.andic_oc_bd_proxy = TRUE).
max_bd_proxy	Maximum bulk density g/cm ³ for the v0.9.80 OC+BD proxy path (default 0.9). Only consulted when the proxy is enabled.

Value

A [DiagnosticResult](#).

v0.9.80 OC + BD proxy (opt-in)

Field-described volcanic-ash soils (e.g.\ AfSP, KSSL/NASIS, SOTER) routinely lack oxalate Al/Fe and phosphate retention measurements, so the canonical paths return NA and Andosols cascade to other RSGs. The genetic signature is still detectable from coarser data: very high SOC (>= 4-5%) plus low bulk density (<= 0.9 g/cm³) typical of allophanic / Al-humus complexation.

With options(soilKey.andic_oc_bd_proxy = TRUE) the function adds a third path that fires when both canonical paths fail and the surface horizon shows oc_pct >= min_oc_proxy AND bulk_density_g_cm3 <= max_bd_proxy (or OC alone >= 5% when BD is missing). Default is FALSE (canonical behaviour preserved).

v0.9.85 proxy contiguous-layer extension (opt-in)

When options(soilKey.andic_oc_bd_proxy_extend = TRUE) (only meaningful with soilKey.andic_oc_bd_proxy = TRUE), iteratively extend the proxy layers to include contiguous deeper layers whose oc_pct >= min_oc_proxy / 2 AND whose bulk_density_g_cm3 is missing OR <= max_bd_proxy + 0.15. The extension stops at the first horizon failing either constraint, so a ferralic / argic subsoil cannot accidentally inflate the andic thickness. Default is FALSE – canonical proxy behaviour preserved.

References

IUSS Working Group WRB (2022), Chapter 3, Andic properties.

andosol

Andosol RSG gate (WRB 2022 Ch 4, p 104)

Description

WRB-canonical: layer(s) with *andic* OR *vitric* properties, combined thickness ≥ 30 cm within 100 cm starting ≤ 25 cm; OR $\geq 60\%$ of the entire soil thickness when a limiting layer starts 25-50 cm. Plus: no argic, ferralic, petroplinthic, pisoplinthic, plinthic or spodic horizon ≤ 100 cm (unless buried below 50 cm).

Usage

```
andosol(
  pedon,
  min_thickness = 30,
  max_top_cm = 25,
  buried_below_cm = 50,
  strict = NULL
)
```

Arguments

pedon	A PedonRecord .
min_thickness	Numeric threshold or option (see Details).
max_top_cm	Numeric threshold or option (see Details).
buried_below_cm	Numeric: layers of the exclusion diagnostics whose top_cm \geq this depth are treated as buried and do NOT exclude the Andosol (default 50, per WRB 2022 Ch 4 p 104).
strict	Logical or NULL. When NULL (default) it resolves via <code>getOption("soilKey.rsg_strict", FALSE)</code> . TRUE disables the buried-exclusion tolerance.

Details

v0.3.4 enforces (1) andic OR vitric AND (2) combined thickness ≥ 30 cm starting in the upper 25 cm AND (3) the negative-list exclusions on argic / ferralic / plinthic / spodic.

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

v0.9.85 buried-exclusion fix

WRB 2022 Ch 4 p 104 specifies the Andosol exclusion list (argic / ferralic / petroplinthic / piso-plinthic / plinthic / spodic) as " ≤ 100 cm *unless buried below 50 cm*". The earlier implementation excluded an Andosol whenever any of those diagnostics passed anywhere in the profile, including on layers starting deeper than 50 cm – which mis-fires on AfSP Andosol references like CM W3_0047, where an argic layer at 56-72 cm wrongly excluded the andic surface stack. v0.9.85 restricts the exclusion check to layers starting ≤ 50 cm: a buried argic / ferralic / plinthic / spodic at deeper levels no longer disqualifies the surface andic stack from Andosol.

Tier-3 strict mode (v0.9.98)

With `strict = TRUE` the v0.9.85 buried-exclusion tolerance is switched off: *any* argic / ferralic / plinthic / spodic horizon anywhere in the profile excludes the Andosol, regardless of depth.

annotate_wrb_from_usda

Annotate KSSL/NASIS pedons with a derived WRB Reference Soil Group

Description

Applies `usda_to_wrb_rsg` to each pedon's USDA classification (preserved as `site$reference_usda + site$reference_usda_suborder` by `load_kssl_pedons_gpkg`) and writes the result to `site$reference_wrb_from_usda` – a "best-guess" expected WRB label for benchmark comparison.

Usage

`annotate_wrb_from_usda(pedons)`

Arguments

`pedons` List of `PedonRecord` objects.

Details

Pedons that already have `site$reference_wrb` populated (e.g.\ from external sources) are left untouched.

Value

The same list, with `site$reference_wrb_from_usda` populated where USDA classification is present.

anthraquic	<i>Anthraquic horizon (WRB 2022): puddled-rice / paddy plough layer. v0.3.3 detects via designation pattern Ap1 Ap Hh.</i>
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Description

Anthraquic horizon (WRB 2022): puddled-rice / paddy plough layer. v0.3.3 detects via designation pattern Ap1|Ap|Hh.

Usage

```
anthraquic(pedon, min_thickness = 20, max_top_cm = 50)
```

Arguments

pedon	A PedonRecord .
min_thickness	Numeric threshold or option (see Details).
max_top_cm	Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

anthric_horizons	<i>Anthric horizons (WRB 2022)</i>
------------------	------------------------------------

Description

Tests for any of five anthropogenic surface horizons recognised by WRB 2022 (hortic, irragric, plaggic, pretic, terric). Diagnostic of Anthrosols. Two alternative paths qualify:

1. **Designation:** any layer's designation contains one of hortc|irragric|plaggic|prectic|terric.
2. **Property-based:** a surface layer (top_cm <= 5) at least min_thickness_cm cm thick (default 20) with elevated dark colour (Munsell value moist <= max_munsell_value, default 4) AND elevated plant-available P (p_mehlich3_mg_kg >= min_p_mg_kg, default 50).

Either path qualifies.

Usage

```
anthric_horizons(
  pedon,
  min_thickness_cm = 20,
  min_p_mg_kg = 50,
  max_munsell_value = 4
)
```

Arguments

pedon	A PedonRecord .
min_thickness_cm	Minimum thickness for the property-based path (default 20).
min_p_mg_kg	Minimum plant-available P (Mehlich 3, mg/kg) for the property-based path (default 50).
max_munsell_value	Maximum Munsell value moist for the property-based path (default 4).

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022), Chapter 5, Anthrosols.

apply_soilgrids_depth_prior

Fill missing horizon attributes from a SoilGrids depth prior

Description

For each horizon and each requested attribute, interpolates the value at the horizon's mid-depth from the six standard SoilGrids 2.0 depth slices (0-5, 5-15, 15-30, 30-60, 60-100, 100-200 cm) and writes it into the pedon with source = "inferred_prior". Existing values are preserved unless overwrite = TRUE; the [PedonRecord](#) authority order means a SoilGrids prior can never silently displace a measured, spectra-predicted or VLM-extracted value.

Usage

```
apply_soilgrids_depth_prior(
  pedon,
  attrs = NULL,
  depth_profiles = NULL,
  overwrite = FALSE
)
```

Arguments

pedon	A PedonRecord with at least one horizon. For the live fetch it must also carry site\$lat and site\$lon.
attrs	Character vector of horizon columns to fill. Defaults to all SoilGrids-backed attributes: clay_pct, sand_pct, silt_pct, ph_h2o, oc_pct, cec_cmol.

- `depth_profiles` Optional named list mapping an attribute to a numeric vector of six slice values (0-5 ... 100-200 cm). When supplied the SoilGrids network call is skipped entirely – this is the path the test suite and offline users take.
- `overwrite` If FALSE (default) only NA cells are filled. If TRUE, every requested cell is overwritten (subject to the provenance authority order).

Details

This is the depth-resolved companion to [spatial_prior_soilgrids](#) (which returns a site-level RSG probability vector, not horizon attributes), and the attribute-fill stage of [classify_from_photos](#).

Value

Invisibly, the mutated pedon. An attribute "soilgrids_depth_fill" on the return value records how many cells were filled.

Examples

```
## Not run:
p <- make_cambisol_canonical()
p$horizons$clay_pct <- NA_real_
# Offline: supply the six-slice profiles directly.
apply_soilgrids_depth_prior(
  p, attrs = "clay_pct",
  depth_profiles = list(clay_pct = c(18, 20, 24, 28, 30, 30)))

## End(Not run)
```

arenic_texture	<i>Arenic texture (WRB 2022)</i>
----------------	----------------------------------

Description

Tests whether the upper 100 cm is uniformly coarser than sandy loam (i.e., $\text{silt} + 2 * \text{clay} < 30$ in every layer). Diagnostic of Arenosols.

Usage

```
arenic_texture(pedon, max_top_cm = 100, engine = NULL)
```

Arguments

- `pedon` A [PedonRecord](#).
- `max_top_cm` Maximum top depth (cm) of layers to be tested (default 100, per WRB 2022).
- `engine` One of "soilkey" (default; strict WRB sand threshold via `test_coarse_texture_throughout`) or "aqp" (LUCAS-friendly fallback: passes when $\text{sand} \geq 70$ reads `getOption("soilKey.diagnostic_`

Details

Sub-test: test_coarse_texture_throughout.

v0.3 limitations: WRB 2022 Arenosol also requires that no other diagnostic horizon (argic, ferralic, etc.) is present, but those exclusions happen at the key level via canonical RSG order.

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022), Chapter 5, Arenosols.

argic	<i>Argic horizon (WRB 2022)</i>
-------	---------------------------------

Description

Tests whether any horizon meets the argic horizon criteria per Chapter 3 of the WRB 2022 (4th edition). Argic is a subsurface horizon with distinctly higher clay content than the overlying horizon, qualified by three depth-conditional clay-increase rules; it must also have texture of sandy loam or finer, satisfy a minimum thickness, and not exhibit albeluvic glossic features (which would direct the profile to the Retisol path).

Usage

```
argic(
  pedon,
  min_thickness = 7.5,
  system = c("wrb2022", "usda"),
  engine = NULL,
  require_t = NULL
)
```

Arguments

pedon	A PedonRecord .
min_thickness	Minimum thickness in cm (default 7.5).
system	One of "wrb2022" (default) or "usda". Selects the clay-increase threshold set: WRB uses 6/1.4/20 pp/ratio/pp; KST 13ed uses 3/1.2/8 (looser). See test_clay_increase_argic for the table.
engine	v0.9.63+. One of "soilkey" (the hand-coded path, default for back-compat) or "aqp" (canonical NRCS dispatch via aqp::getArgillicBounds). When NULL (the new default) the function reads getOption("soilKey.diagnostic_engine", "soilkey") so a global options(soilKey.diagnostic_engine = "aqp") flips every argic() call without modifying call sites. See argic_aqp .

require_t v0.9.63+. Forwarded to `aqp::getArgillicBounds` when engine = "aqp": TRUE requires a "t" suffix in the horizon designation (the strict KST 13ed text); FALSE accepts argic by clay-increase alone (more permissive on data-sparse profiles). NULL (default) auto-picks: TRUE for system = "usda", FALSE for system = "wrb2022". Ignored when engine = "soilkey".

Details

Sub-tests called (each a list with passed, layers, missing, details, notes):

- test_clay_increase_argic – the three-pronged WRB 2022 clay-increase rule.
- test_minimum_thickness – thickness ≥ 7.5 cm (configurable via min_thickness).
- test_texture_argic – texture of sandy loam or finer ($\text{silt} + 2 * \text{clay} \geq 30$).
- test_not_albeluvisc – excludes profiles with glossic tongues (Retisol path).

v0.1 limitations: clay-increase distance (≤ 30 cm vertical, or ≤ 15 cm with abrupt textural change) is not yet enforced; that is scheduled for v0.2 and depends on horizon boundary descriptions.

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022). *World Reference Base for Soil Resources*, 4th edition. International Union of Soil Sciences, Vienna. Chapter 3 – Argic horizon.

argic_aqp	<i>Argic / argillic horizon via aqp::getArgillicBounds()</i>
-----------	--

Description

Wraps `aqp::getArgillicBounds()` (Beaudette et al.) in soilKey's [DiagnosticResult](#) contract. The aqp implementation is the canonical NRCS R port and uses the tiered USDA-NRCS clay-increase thresholds:

- Eluvial clay $< 15\%$
- Eluvial clay 15-40%
- Eluvial clay $\geq 40\%$

(vs. soilKey's hand-coded [argic](#) which uses the WRB 6/1.4/20 thresholds). For BDsolos / FEBR / KSSL profiles the aqp rule is closer to KST 13ed and BDsolos field practice.

Usage

```
argic_aqp(pedon, require_t = FALSE, ...)
```

Arguments

pedon	A PedonRecord .
require_t	Whether to require an explicit "t" suffix in the horizon designation (default FALSE for BDsolos / FEBR; TRUE matches the strict KST 13ed text).
...	Reserved for future arguments.

Details

By default aqp requires a "t" suffix in the horizon designation (`require_t = TRUE`); we expose this so callers can be permissive on datasets where designation is missing or non-conforming (BDsolos exports often drop the "t").

Value

A [DiagnosticResult](#) with name = "argic_aqp". \$layers are the row indices of horizons in the argillic / argic depth interval. \$evidence carries the raw aqp c(ubound, lbound) bounds for traceability.

See Also

[argic](#) (soilKey hand-coded; WRB 6/1.4/20), `aqp::getArgillicBounds`.

argic_with_strong_clay_films

Test whether a pedon's argic horizon has strong clay films

Description

Wraps [argic\(\)](#) and inspects the `clay_films_amount` field at the argic-passing layers. Returns a structured result that [B_latossolico\(\)](#) uses to decide whether the SiBCS Cap 18 strong-films exclusion fires.

Usage

```
argic_with_strong_clay_films(pedon)
```

Arguments

pedon	A PedonRecord .
-------	---------------------------------

Value

A list with:

- passed – logical, TRUE only when argic passes AND at least one argic-passing layer has a strong (*comum / abundante*) film qualifier.
- layers – integer vector of argic-passing layer indices (empty when passed is FALSE).
- argic – the underlying [DiagnosticResult](#) from [argic\(\)](#).
- films – character vector of the clay_films_amount values at the argic-passing layers.

argillic_clay_films_test

Test for clay-illuviation evidence (KST 13ed Ch 3 p 4)

Description

KST 13ed argillic horizon requires "evidence of illuvial accumulation of clay" alongside the clay-increase rule. Acceptable evidence:

- oriented clays bridging sand grains in $\geq 1\%$ of the horizon;
- clay films lining pores or coating ped faces;
- lamellae more than 5 mm thick.

Usage

```
argillic_clay_films_test(pedon)
```

Arguments

pedon A [PedonRecord](#).

Details

This test reads three complementary slots, in order of evidence strength:

1. pedon\$site\$nasid_diagnostic_features – the NASIS peddiagfeatures.featkind vector. The surveyor's explicit "Argillic horizon" entry directly confirms clay-illuviation evidence (~13 500 entries in the 2021 NASIS snapshot). Strongest evidence.
2. pedon\$horizons\$clay_films_amount – per-horizon clay-film abundance derived from NASIS phpvfsf. Values: "few", "common", "many", "continuous". Direct measurement.
3. pedon\$horizons\$designation containing a 't' master suffix (e.g. Bt, Btk, Btx, Bt1, 2Bt). v0.9.28: the pedologist who wrote that designation explicitly identified the horizon as clay-illuvial – per KST 13ed Ch 18, the 't' suffix means "accumulation of silicate clay" – so it counts as positive evidence even when NASIS records are absent. This unlocks the KST 13ed argillic thresholds for the ~47 peddiagfeatures and phpvfsf records.

Any of the three sources counts as positive evidence (logical OR). passed = NA when none is populated AND no horizon designation field is present at all (lab-only loaders without horizon descriptions). passed = FALSE when designations exist but none has a 't' suffix and NASIS slots are empty.

Value

A [DiagnosticResult](#).

References

Soil Survey Staff (2022), Keys to Soil Taxonomy 13th ed., Ch. 3, argillic horizon (clay-illuviation criteria, p. 4); Ch. 18, master horizon symbols (t: silicate-clay accumulation, p. 332).

artefacts	<i>Artefacts (WRB 2022 Ch 3.3.2)</i>
-----------	--------------------------------------

Description

Per the canonical definition: human-made / human-altered / human- excavated material. v0.3.3 returns the layers where artefacts_pct >= 1.

Usage

```
artefacts(pedon, min_pct = 1)
```

Arguments

pedon	A PedonRecord .
min_pct	Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

as_aqp	<i>Convert one or more PedonRecord objects to an aqp SoilProfileCollection</i>
--------	--

Description

Builds a `aqp::SoilProfileCollection` from one `PedonRecord` or a list of them. Standard `soilKey` columns (`top_cm`, `bottom_cm`, `designation`, `clay_pct`, `sand_pct`, `silt_pct`) are renamed to `aqp`'s canonical convention (`top`, `bottom`, `name`, `clay`, `sand`, `silt`). All other columns are passed through unchanged. Site-level slots (`lat`, `lon`, `country`, `parent_material`, `reference_*`, `nasis_diagnostic_features`, etc.) are attached to the SPC's site table.

Usage

```
as_aqp(x)
```

Arguments

x A [PedonRecord](#) or a list of them.

Details

Requires the aqp package, listed in Suggests; the function raises a clear error if aqp is not installed.

Value

A `aqp::SoilProfileCollection`.

See Also

[from_aqp](#), the inverse conversion.

Examples

```
## Not run:
library(soilKey)
library(aqp)

pedons <- list(make_ferralsol_canonical(), make_luvisol_canonical())
spc <- as_aqp(pedons)
length(spc)            # 2 profiles
aqp::horizons(spc)    # one row per horizon, aqp-named columns

## End(Not run)
```

`attach_lucas_spectra` *Attach LUCAS 2018 Vis-NIR spectra to a list of PedonRecord objects*

Description

Joins the LUCAS Soil 2018 Spectral Library (separate ESDAC release, ~83 GB) onto the pedons returned by [load_lucas_soil_2018](#), by matching the LUCAS POINT_ID of the spectra against pedon\$site\$id. Each matched pedon gets \$spectra\$vnir populated as a numeric matrix (rows = horizons, cols = wavelengths).

Usage

```
attach_lucas_spectra(
  pedons,
  spectra,
  point_id_col = "POINT_ID",
  verbose = TRUE
)
```

Arguments

pedons	List of PedonRecord objects.
spectra	A wide or long data.frame as described above.
point_id_col	Name of the LUCAS point-id column in spectra. Default "POINT_ID".
verbose	If TRUE (default), reports the join hit rate.

Details

Two input shapes are accepted:

- A wide data.frame keyed by an integer POINT_ID column with one column per wavelength (column names parseable as numeric nm). One row per LUCAS point.
- A long data.frame with columns POINT_ID, wavelength_nm, reflectance.

Spectra are attached only to the topsoil horizon (row 1); the subsoil horizon (if any) is left without spectra. After this call, `benchmark_lucas_2018(..., fill_topsoil_from = "spectra", ossl_models = ...)` feeds the spectra through [predict_from_spectra](#) (v0.9.46) to fill any chemistry / texture gap not already populated by SoilGrids.

Value

The list of pedons (mutated in place; returned invisibly).

See Also

[predict_from_spectra](#), [predict_munsell_from_spectra](#), [load_lucas_soil_2018](#).

audit_argic_strong_films

Audit the strong-clay-films exclusion across a list of pedons

Description

Applies [argic_with_strong_clay_films\(\)](#) to every pedon in pedons and returns a per-pedon table summarising how the v0.9.61 [B_latossolico\(\)](#) latossolic-vs-argic rule resolves on the benchmark sample.

Usage

```
audit_argic_strong_films(pedons, reference_filter = NULL)
```

Arguments

pedons	List of PedonRecord objects.
reference_filter	Optional regex applied to <code>p\$site\$reference_sibcs</code> to keep only pedons whose reference matches (case-sensitive, ICU). Default NULL keeps every pedon.

Details

Useful for empirical validation of the SiBCS Cap 18 precedence rule on field-described datasets such as Bdsolos and Redape, where clay-film qualifiers are recorded in mixed Portuguese / English tokenisation. The audit is read-only and never invokes `classify_sibcs()`.

Value

A data.frame with columns `id`, `reference_sibcs`, `argic_passed`, `has_films_at_argic`, `strong_films_at_argic`, and `would_exclude_from_latossolo`.

Examples

```
## Not run:
peds <- load_bdsolos_csv("RJ.csv")
a <- audit_argic_strong_films(peds, reference_filter = "LATOSSOLO")
table(a$would_exclude_from_latossolo)

## End(Not run)
```

auto_set_proj_env *Auto-detect PROJ_LIB and GDAL_DATA directories*

Description

Probes the common system locations for PROJ `proj.db` and GDAL data directories, on macOS Homebrew (Apple silicon and Intel), Linuxbrew, conda / mamba environments, and Debian / Ubuntu / Fedora apt or dnf installs. Sets the corresponding environment variables only when they are not already set, so a user-provided value always wins. Idempotent: safe to call repeatedly.

Usage

```
auto_set_proj_env(verbose = FALSE)
```

Arguments

`verbose` If TRUE, emits a cli message confirming what was detected.

Details

Called automatically from `.onLoad`; call manually after installing PROJ / GDAL via Homebrew if you want to refresh the env without restarting R.

Value

Invisibly, a named list with `PROJ_LIB` and `GDAL_DATA` (the values that were set, or `NA_character_` if a value was already present or no candidate was found).

 available_esdb_attributes

List ESDB Raster Library attributes available at a given root

Description

Walks ‘raster_root’ and returns the folder names that contain a valid ‘<NAME>.tif’ raster. Useful for discovery before calling [lookup_esdb](#).

Usage

```
available_esdb_attributes(raster_root)
```

Arguments

raster_root Path to the unpacked ESDB raster directory (typically ‘<some>/ESDB-Raster-Library-1k-GeoTIFF-...’).

Value

A character vector of attribute names (sorted).

Examples

```
## Not run:
available_esdb_attributes("~/data/ESDB-Raster-Library-1k-GeoTIFF-20240507")
#> [1] "AGLI1NNI" "AGLI2NNI" "AGLIM1" "AGLIM2" "ALT" "ATC" "AWC_SUB" ...
#>   [continued: 71 attributes]

## End(Not run)
```

 batch_robustness

Batch robustness across many pedons

Description

Runs [classification_robustness](#) on each pedon in a list and returns a tidy data.frame with one row per pedon. Useful for paper-grade claims like "85 to a 5

Usage

```
batch_robustness(pedons, ...)
```

Arguments

pedons List of [PedonRecord](#) objects.
 ... Passed to [classification_robustness](#).

Value

A data.frame with columns id, baseline, robustness, n_flipped.

Examples

```
## Not run:
pedons <- list(make_ferralsol_canonical(),
               make_luvisol_canonical(),
               make_chernozem_canonical())
batch_robustness(pedons, system = "wrb2022", n = 50)
#>      id baseline robustness n_flipped
#> 1 FR-canon-01 Ferralsols      0.96      2
#> 2 LV-canon-01 Luvisols      1.00      0
#> 3 CH-canon-01 Chernozems    0.94      3

## End(Not run)
```

benchmark_afsp

Benchmark soilKey WRB predictions against AfSP ground truth

Description

Benchmark soilKey WRB predictions against AfSP ground truth

Usage

```
benchmark_afsp(pedons, verbose = TRUE)
```

Arguments

pedons List of [PedonRecord](#) from [load_afsp_pedons](#) or [load_afsp_sample](#).
verbose Print progress.

Value

List with accuracy, n_compared, confusion, per_class_recall.

benchmark_bdsolos	<i>Benchmark soilKey classifiers against BDsolos national reference labels</i>
-------------------	--

Description

Runs `classify_wrb2022`, `classify_sibcs`, and `classify_usda` on each `PedonRecord` loaded from a BDsolos CSV via `load_bdsolos_csv`, then compares each predicted classification against the corresponding BDsolos reference label (`reference_sibcs`, `reference_wrb`, `reference_st`) and reports per-system accuracy, per-class recall, and a confusion matrix.

Usage

```
benchmark_bdsolos(
  pedons,
  systems = c("wrb2022", "sibcs", "usda"),
  sibcs_level = c("order", "subordem"),
  max_n = NULL,
  verbose = TRUE
)
```

Arguments

pedons	A list of <code>PedonRecord</code> objects, typically produced by <code>load_bdsolos_csv</code> .
systems	Character vector. Any subset of <code>c("wrb2022", "sibcs", "usda")</code> . Default runs all three.
sibcs_level	One of "order" (default) or "subordem". Forwarded to <code>normalise_febr_sibcs</code> .
max_n	Optional integer; cap classification at the first <code>max_n</code> pedons. NULL (default) classifies every pedon.
verbose	If TRUE (default), emits cli progress messages.

Value

A list with elements:

- `per_system` – named list (one entry per requested system) of `list(accuracy, n_compared, n_correct, n_errors, confusion, per_class)` (or `list(accuracy = NA_real_, message)` when no reference labels were present).
- `coverage` – named list of `list(n_with_ref, n_total, pct)` per system.
- `config` – named list capturing `n_pedons`, `systems`, `sibcs_level`, `soilKey_version`, `timestamp`.

Reference label coverage

BDsolos densely populates `reference_sibcs` (~82 of the v0.9.59 audit) but sparsely populates `reference_wrb` and `reference_st` (UF-dependent; ~5 states). The function always reports the per-system label coverage (`$coverage`) so the caller can judge how representative each accuracy figure is.

Comparison level

SiBCS comparison is at level = "order" by default, which converts the Bdsolos all-caps Portuguese label (e.g. "ARGISSOLO VERMELHO Tb EUTROFICO ...") to the soilKey plural Title Case form ("Argissolos") via `normalise_febr_sibcs`. Set `sibcs_level = "subordem"` to compare the first two SiBCS tokens (Ordem + Subordem).

WRB and USDA comparisons are at the Reference Soil Group / Order level: `normalise_febr_wrb()` strips qualifier parens and pluralises the bare RSG ("Xanthic Ferralsol" -> "Ferralsols"); `normalise_febr_usda()` maps the suffix of the last subgroup token to the USDA Order ("Typic Haplorthox" -> "Oxisols").

Errors and missing-label handling

Pedons without a reference label for a given system are silently excluded from THAT system's comparison (but still classified for the other two systems). If a system has zero pedons with a reference label, the corresponding `$per_system` entry has `accuracy = NA_real_` and `message = "no_reference_labels"`. Classifier errors are caught per-pedon and recorded in `n_errors`; they do not abort the run.

See Also

[load_bdsolos_csv](#), [benchmark_lucas_2018](#), [classify_all](#), [normalise_febr_sibcs](#), [normalise_febr_wrb](#), [normalise_febr_usda](#).

Examples

```
## Not run:
# Single UF -- typical SiBCS-dense slice
peds <- load_bdsolos_csv("RJ.csv")
bench <- benchmark_bdsolos(peds, systems = c("sibcs", "wrb2022", "usda"))
bench$coverage      # how many pedons had each reference label
bench$per_system$sibcs$accuracy
bench$per_system$sibcs$confusion

# Subordem level
bench2 <- benchmark_bdsolos(peds, systems = "sibcs",
                           sibcs_level = "subordem")

## End(Not run)
```

benchmark_lucas_2018 *Run the LUCAS Soil 2018 / ESDB WRB benchmark*

Description

For each pedon in pedons, attaches the canonical Reference Soil Group at its coordinate via [lookup_esdb](#), runs [classify_wrb2022](#) (or [classify_sibcs](#)), and tabulates predicted vs reference. Optionally fills missing texture from ISRIC SoilGrids 250m before classifying so that WRB diagnostic horizons that depend on clay (argic, ferralic, nitic) are reachable.

Usage

```
benchmark_lucas_2018(
  pedons,
  esdb_root,
  attribute = "WRBLV1",
  fill_texture_from = NULL,
  fill_topsoil_from = c("none", "soilgrids", "spectra"),
  fill_subsoil_from = c("none", "soilgrids"),
  fill_properties = c("clay", "sand", "silt", "phh2o", "soc", "cec", "bdod", "nitrogen",
    "cfvo"),
  ossl_models = NULL,
  classify_with = c("wrb2022", "sibcs"),
  max_n = NULL,
  soilgrids_lookup_fn = lookup_soilgrids,
  verbose = TRUE
)
```

Arguments

pedons	List of PedonRecord objects, typically from load_lucas_soil_2018 .
esdb_root	Path to the unpacked ESDB raster directory (containing the WRBLV1 / sub-folder).
attribute	ESDB attribute to use as reference. Default "WRBLV1" (Reference Soil Group, 31 codes). Other sensible choices: "FA090LV1" (legacy FAO 1990).
fill_texture_from	Deprecated alias for fill_topsoil_from (v0.9.49 signature). When "soilgrids", treated as fill_topsoil_from = "soilgrids" with fill_properties = c("clay", "sand", "silt") and fill_subsoil_from = "none".
fill_topsoil_from	One of "none" (default), "soilgrids" (fills topsoil 0-20 cm from SoilGrids 250m at 0-5 cm), or "spectra" (runs predict_from_spectra with the supplied ossl_models; pedons must have \$spectra\$vnir attached, e.g. via attach_lucas_spectra).
fill_subsoil_from	One of "none" (default) or "soilgrids" (synthesises a 30-60 cm B horizon from SoilGrids 250m). Unlocks WRB diagnostic horizons that depend on sub-soil features (cambic, argic, mollic).
fill_properties	Character vector of SoilGrids properties to fill when fill_topsoil_from = "soilgrids" or fill_subsoil_from = "soilgrids". Default uses all 9 properties: clay, sand, silt, phh2o, soc, cec, bdod, nitrogen, cfvo. Set to c("clay", "sand", "silt") to recover the v0.9.49 behaviour. cfvo is mapped to coarse_fragments_pct, which drives the Leptosols diagnostic (≥ 90 within 25 cm).
ossl_models	Required when fill_topsoil_from = "spectra". A list of soilKey_pls_model objects from train_pls_from_ossl (v0.9.46).
classify_with	One of "wrb2022" (default) or "sibcs".
max_n	Optional integer cap on the number of pedons benchmarked. Useful for quick development runs.

soilgrids_lookup_fn
 Internal: SoilGrids lookup function (defaults to [lookup_soilgrids](#)). Override for unit tests to inject a deterministic stub.

verbose
 If TRUE (default), prints progress.

Details

This closes Route B of the v0.9.27 EU-LUCAS roadmap end-to-end: v0.9.44 [lookup_esdb](#) provides the reference label; v0.9.49 (this) provides the loader and the comparison loop; v0.9.48 [lookup_soilgrids](#) fills texture; v0.9.46 [predict_from_spectra](#) and v0.9.47 [predict_munsell_from_spectra](#) can fill the chemistry / Munsell gaps when Vis-NIR is available.

Value

A list with elements:

predictions data.frame with one row per pedon: point_id, lon, lat, country, predicted, reference_code, reference_name, agree.

confusion Confusion table (predicted vs reference) over in-scope rows.

accuracy Overall fraction of correct classifications among in-scope rows.

per_rsg Per-RSG recall data.frame.

n_in_scope Number of pedons with both predicted and reference set.

n_total Total pedons benchmarked.

n_errors Number of pedons where the classifier errored out.

errors List of (i, id, error) tuples for classifier errors.

config Recap of arguments used.

See Also

[load_lucas_soil_2018](#), [lookup_esdb](#), [lookup_soilgrids](#).

Examples

```
## Not run:
pedons <- load_lucas_soil_2018(
  "soil_data/eu_lucas/LUCAS-SOIL-2018-data-report-readme-v2/LUCAS-SOIL-2018-v2",
  countries = c("ES"), max_n = 50)
bench <- benchmark_lucas_2018(
  pedons,
  esdb_root = "soil_data/eu_lucas/ESDB-Raster-Library-1k-GeoTIFF-20240507",
  fill_texture_from = "soilgrids")
bench$accuracy
bench$per_rsg

## End(Not run)
```

benchmark_performance *Run the soilKey performance benchmark*

Description

Generates n synthetic pedons (5 horizons each, with the chemistry / morphology populated for typical Argissolo / Latossolo / Cambissolo cases), calls each classifier on each pedon, and reports per-call latency + total throughput.

Usage

```
benchmark_performance(
  n = 100L,
  systems = c("wrb2022", "sibcs", "usda"),
  include_familia = FALSE,
  seed = 42L,
  verbose = TRUE
)
```

Arguments

<code>n</code>	Integer. Number of synthetic pedons to generate. Default 100; pass 1000 or higher for batch-level measurements.
<code>systems</code>	Character vector. Which classifiers to time. Default <code>c("wrb2022", "sibcs", "usda")</code> (all three).
<code>include_familia</code>	Pass-through to <code>classify_sibcs</code> when "sibcs" is in <code>systems</code> . Default FALSE.
<code>seed</code>	RNG seed for reproducibility. Default 42.
<code>verbose</code>	If TRUE (default), prints a per-system summary line.

Details

Designed to be a one-shot reproducible benchmark: the synthetic pedons use a fixed RNG seed so timings on the same machine are comparable across releases.

Value

A list with elements:

`summary` data.frame: `system`, `n_pedons`, `total_seconds`, `mean_seconds`, `median_seconds`, `pedons_per_minute`.

`per_pedon` data.frame with one row per (pedon, system) call: `i`, `system`, `seconds`, `status`.

`config` list with `n`, `seed`, `soilKey_version`, `R_version`, `platform`.

Examples

```
## Not run:
bench <- benchmark_performance(n = 100)
bench$summary
#>   system n_pedons total_seconds mean_seconds median_seconds pedons_per_minute
#> 1 wrb2022     100      ~ 5-12      0.05-0.12      ~              ~
#> 2 sibcs      100      ~ 5-15      0.05-0.15      ~              ~
#> 3 usda       100      ~ 4-10      0.04-0.10      ~              ~

## End(Not run)
```

benchmark_redape	<i>Benchmark soilKey SiBCS predictions against the Redape gold standard</i>
------------------	---

Description

Runs [classify_sibcs](#) on each pedon and compares against the curator-validated reference label (Order / Suborder / Great Group / Subgroup). Returns per-level accuracy and the confusion matrix at the requested granularity.

Usage

```
benchmark_redape(
  pedons,
  level = c("order", "subordem", "gde_grupo", "subgrupo"),
  verbose = TRUE
)
```

Arguments

pedons	List of PedonRecord objects (typically from load_redape_pedons).
level	One of "order" (default), "subordem", "gde_grupo", or "subgrupo".
verbose	Print progress (default TRUE).

Value

A list with accuracy, n_compared, confusion, per_class_recall, and the per-pedon predictions table. predictions now also includes columns ref_norm and pred_norm – the canonical comparison keys – for downstream auditing.

v0.9.81 level-aware comparison

Earlier versions accepted the level argument but always used rsg_or_order for the prediction and the order field for the reference, so all four levels reported identical accuracy. v0.9.81 reads the level-specific slots from res\$trace (subordem, grande_grupo, subgrupo) and concatenates the matching reference fields, applying SiBCS-aware Portuguese pluralisation so the comparison key matches the predictor's plural Title Case form.

 benchmark_run_classification

Run a benchmark across one of the loaded pedon lists

Description

Classifies each pedon in pedons against the named system, compares against the published reference (e.g. site\$reference_wrb), and returns a confusion matrix + top-1 / top-3 accuracy + bootstrap CI on top-1.

Usage

```
benchmark_run_classification(
  pedons,
  system = c("wrb2022", "sibcs", "usda"),
  level = c("order", "subgroup", "subordem", "great_group", "suborder"),
  boot_n = 1000L
)
```

Arguments

pedons	List of PedonRecord objects (output of one of the load_* functions).
system	One of "wrb2022", "sibcs", "usda".
level	Granularity of the comparison: <ul style="list-style-type: none"> • "order" (default) – the top-level RSG / Ordem / Order, compared against cls\$rsg_or_order; • "subgroup" – the full classified name (Subgroup in USDA, Subgrupo in SiBCS, RSG + qualifiers in WRB), compared against cls\$name after case-insensitive token normalisation; • "subordem" – SiBCS-only, the 2nd-level "Ordem + Subordem" (e.g. "Latosso-los Vermelhos"). Comparison via the first two normalised tokens of the predicted name vs the reference; • "great_group" (USDA, v0.9.24) – the LAST token of the subgroup name (e.g. "typic hapludalfs" -> "hapludalfs"). Isolates whether the Great Group machinery is correct independent of subgroup modifiers (Typic / Aquic / Vertic / Cumulic / Pachic / etc.). Reads site\$reference_usda_grtgroup; • "suborder" (USDA, v0.9.24) – maps the Great Group prediction to its canonical Suborder suffix ("hapludalfs" -> "udalfs") using the KST 13ed Ch 4 ~70-Suborder list. Reads site\$reference_usda_suborder.
boot_n	Bootstrap replicates for CI (default 1000).

Value

A list with elements accuracy_top1, accuracy_ci, confusion, and per_pedon (one row per pedon with predicted vs reference).

 benchmark_spectral_fill

Benchmark the accuracy lift of spectral gap-fill (ON vs OFF), k-fold

Description

The honest measurement that has been data-blocked until a spectra-bearing, labelled dataset exists. For each cross-validation fold it calibrates a spectral library on the training profiles, then classifies the held-out profiles twice – **OFF** (spectra-only pedon, no lab attributes) and **ON** ([fill_from_spectra](#) predicts the lab attributes from the scan first) – and scores both against the reference label. Non-circular: the calibration library never includes a test profile.

Usage

```
benchmark_spectral_fill(
  reflectance,
  metadata,
  id_col = "id",
  system = c("sibcs", "wrb2022", "usda"),
  profile_col = NULL,
  folds = 5L,
  properties = NULL,
  method = c("mbl", "plsr_local", "pretrained"),
  wavelengths = NULL,
  resample_to = NULL,
  property_map = NULL,
  label_map = NULL,
  normalize = c("auto", "none", "percent"),
  fold_id = NULL,
  verbose = TRUE
)
```

Arguments

reflectance	Reflectance data: a matrix / data.frame with rows = samples and columns named by wavelength (nm); OR a long data.frame with id_col, wavelength_nm, reflectance; OR a path to a CSV in either form.
metadata	A data.frame with one row per sample carrying id_col plus lab attributes and optional taxonomic labels and lat/ lon. Rows are aligned to reflectance by id_col.
id_col	Sample identifier column shared by both tables (default "id").
system	One of "sibcs" (default), "wrb2022", "usda".
profile_col	Column grouping samples into profiles (default id_col).
folds	Number of CV folds (default 5).
properties	Attributes to predict from spectra (default the fill_from_spectra set).

method	Spectral model: "mbl", "plsr_local" or "pretrained" (passed to fill_from_spectra).
wavelengths	Optional explicit wavelength vector (nm) when the reflectance columns are not wavelength-named.
resample_to	Optional target wavelength grid (nm) to linearly resample every spectrum onto (e.g. 350:2500); default keeps the native grid.
property_map, label_map	Optional named lists overriding the alias auto-detection, e.g. property_map = list(clay_pct = "ARGILA").
normalize	One of "auto" (divide by 100 when values look like percent), "percent", or "none".
fold_id	Optional integer vector (one per profile, in sorted-id order) to use fixed folds instead of the deterministic modulo split.
verbose	Print a one-line summary (default TRUE).

Value

A list with accuracy_off, accuracy_on, delta, n, per-fold rows, and the per-profile predictions frame.

See Also

[read_spectral_library](#), [fill_from_spectra](#)

benchmark_unified *Unified cross-dataset benchmark across SiBCS / WRB / USDA*

Description

Runs a system's soilKey classifier on every dataset that has reference labels for that system, then pools the results into a single nation-/world-wide accuracy estimate.

Usage

```
benchmark_unified(
  systems = c("all", "wrb2022", "sibcs", "usda"),
  datasets = c("all", "bdsolos", "febr", "kssl", "lucas_esdb"),
  paths = NULL,
  max_n_per_dataset = NULL,
  engine = c("soilkey", "aqp", "both"),
  harmonize = FALSE,
  gapfill = FALSE,
  verbose = TRUE
)
```

Arguments

systems	Character vector. Any subset of c("wrb2022", "sibcs", "usda"). Default "all" runs all three.
datasets	Character vector. Any subset of c("bdsolos", "febr", "kssl", "lucas_esdb"). Default "all" pools every dataset that has reference labels for the requested systems. Datasets without reference labels for a system are silently excluded from that system's pooled result.
paths	Named list of dataset paths. Element names should match those in datasets. If NULL (default), soilKey looks for canonical paths under "~/soil_data/".
max_n_per_dataset	Optional integer to cap per-dataset sample size (useful for development / debugging). NULL (default) classifies every available pedon.
engine	Currently forwarded to Phase-1 aqp wiring. One of "soilkey" (default), "aqp", "both". When "aqp", sets options(soilkey.diagnostic_engine = "aqp") for the duration of the benchmark, which routes argic() / cambic() through the canonical aqp::getArgillicBounds / getCambicBounds.
harmonize	If TRUE (default FALSE), applies harmonize_to_gsm to each dataset's pedons before classification, putting all chemistry/texture on the GSM depth grid (0-5 / 5-15 / 15-30 / 30-60 / 60-100 / 100-200 cm). Required for cross-dataset pooling integrity (Phase 2.3) but slow (~1-2 min for 1k pedons) and may degrade per-dataset accuracy slightly because the splined depths are approximations.
gapfill	If not FALSE (the default), applies gapfill_within_pedon to each dataset's pedons before classification, filling interior NA cells of the continuous depth-trending attributes by within-pedon linear interpolation. Accepts the same values as the gapfill argument of classify_all (TRUE, a character vector of attributes, or a named list). Lets you measure the ON/OFF accuracy lift of gap-fill reproducibly through the harness.
verbose	If TRUE (default), emits cli progress.

Value

A list with elements:

- per_system – per-system pooled list(accuracy, n_compared, n_correct, confusion, per_class).
- per_system_per_dataset – per-(system, dataset) same shape, for breakdown.
- coverage – per-(system, dataset) sample sizes and label coverage.
- config – captures systems, datasets, engine, soilKey_version, timestamp.

Datasets and their reference labels

Dataset	Systems with reference labels
BDsolos	SiBCS (dense), WRB (sparse), USDA (sparse)
FEBR superconjunto	SiBCS, WRB, USDA (most rows have all 3)
KSSL+NASIS	USDA only (samp_taxsubgrp universal)

LUCAS + ESDB raster WRB (via lookup_esdb on coords)

For each (system, dataset) pair, this function:

1. Loads pedons via the appropriate load_* helper.
2. Filters to pedons with a populated reference label for the requested system.
3. Normalises both reference and predicted labels via normalise_febr_*() / KSSL canonicalisation helpers.
4. Calls the system's classifier and records pred-vs-ref.

Then pools per-system results across datasets.

Engine selection (Phase 1 wiring)

For datasets with morphological data (BDSolos / FEBR), the diagnostics that pivot Argissolos / Latossolos / Cambissolos classification can be run with two engines:

- engine = "soilkey" (default) – the hand-coded WRB 6/1.4/20 thresholds.
- engine = "aqp" – aqp::getArgillicBounds / getCambicBounds (KST 13ed 3/1.2/8 thresholds).

On the v0.9.62 RJ benchmark (722 perfis), aqp was 14.8 pp stricter on argic and 40.6 pp more permissive on cambic; the SiBCS Argissolos / Latossolos / Cambissolos boundary is sensitive to both. engine is currently forwarded to a future v0.9.63 wired argic() / cambic(); for now, benchmark_unified() reports separately per engine when engine = "both".

See Also

[benchmark_bdsolos](#), [benchmark_lucas_2018](#), [benchmark_run_classification](#), [harmonize_to_gsm](#).

benchmark_wrb_vs_usda *Benchmark soilKey WRB predictions against a USDA-derived ground truth*

Description

Convenience wrapper: applies [annotate_wrb_from_usda](#) to attach derived WRB labels, runs [classify_wrb2022](#) on each pedon, and returns top-1 accuracy + per-RSG recall.

Usage

```
benchmark_wrb_vs_usda(pedons, verbose = TRUE)
```

Arguments

pedons	List of PedonRecord objects with site\$reference_usda populated (typically from load_kssl_pedons_gpkg).
verbose	Print progress.

Value

A list with accuracy, n_compared, confusion, per_class_recall.

build_taxon_profiles *Build per-taxon mean depth profiles for predicted-taxon gap-fill*

Description

For each taxon (the first word of the reference label at the requested level), averages each attribute across the calibration pedons into the six standard depth slices (0-5 ... 100-200 cm). The result feeds [gapfill_by_predicted_taxon](#). Calibrate on a set DISJOINT from the pedons you will fill (e.g. a train split) to keep the fill non-circular.

Usage

```
build_taxon_profiles(pedons, ref_field = "reference_sibcs", attrs = NULL)
```

Arguments

pedons	A list of PedonRecord with a reference label.
ref_field	Site field holding the reference label (default "reference_sibcs"; e.g. "reference_usda" / "reference_wrb").
attrs	Attributes to profile (default the continuous gap-fill set).

Value

A named list taxon -> attr -> numeric(6) (NA where a taxon has no measured value in a slice).

See Also

[gapfill_by_predicted_taxon](#)

B_espodico *Horizonte B espodico (SiBCS Cap 2, p 62-65; v0.7)*

Description

Subsuperficial com acumulo iluvial de Al + Fe + materia organica; espessura \geq 2.5 cm. Tipos: Bs, Bhs, Bh, ortstein. Reuso de [spodic](#) (WRB) que ja codifica criterios essencialmente identicos.

Usage

```
B_espodico(pedon, ...)
```

Arguments

pedon A [PedonRecord](#).
 ... Reserved for future arguments.

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

B_incipiente	<i>Horizonte B incipiente (SiBCS Cap 2, p 59-61; v0.7)</i>
--------------	--

Description

Subsuperficial sob A/Ap/AB com alteracao fisica e quimica incipiente, NAO satisfazendo a B textural / latossolico / nitico / espodico / planico, com:

- espessura \geq 10 cm;
- textura francoarenosa ou mais fina;
- < 50% estrutura da rocha original;
- evidencias de pedogenese (cor mais viva OR remocao de carbonatos OR designation Bw/Bi);
- NAO satisfaz: argic, ferralic, espodic, planic, e nao tem duripa/etrocalcico/fragipa.

Usage

```
B_incipiente(pedon, min_thickness = 10)
```

Arguments

pedon A [PedonRecord](#).
 min_thickness Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

B_latossolico

*Horizonte B latossolico (SiBCS Cap 2, p 57-59; v0.7 strict)***Description**

Adicionalmente a [ferralic](#) (WRB), o B latossolico SiBCS exige:

- Espessura minima de 50 cm;
- Textura francoarenosa ou mais fina;
- Estrutura granular muito pequena/pequena ou em blocos subangulares fraco/moderado;
- < 5% volume mostrando estrutura da rocha original;
- $K_i \leq 2.2$ (geralmente ≤ 2.0);
- Cerosidade no maximo pouca e fraca.

v0.7 enforce thickness, texture, e ausencia de estrutura primaria herdada via designation e clay; K_i/K_r quantitativos sao v0.8 (precisa de SiO_2/Al_2O_3 lab-data nao no schema).

Usage

```
B_latossolico(
  pedon,
  min_thickness = 50,
  max_cec_per_clay = NULL,
  engine = NULL,
  ...
)
```

Arguments

pedon	A PedonRecord .
min_thickness	Numeric threshold or option (see Details).
max_cec_per_clay	Numeric threshold or option (see Details). Defaults to NULL (engine-aware): 17 in soilkey engine (the SiBCS-loose threshold, slightly more permissive than strict WRB ferralic 16) or 20 in aqp engine (v0.9.68 regional tolerance for Embrapa lab methodology offset).
engine	One of "soilkey" (default) or "aqp"; NULL reads <code>getOption("soilKey.diagnostic_engine")</code> . Forwarded to ferralic .
...	Reserved for future arguments.

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

B_nitico

*Horizonte B nitico (SiBCS Cap 2, p 61-62; v0.7)***Description**

Subsuperficial nao hidromorfico, textura argilosa/muito argilosa (clay $\geq 35\%$ desde a superficie), com pequeno incremento de argila (B/A ≤ 1.5), estrutura em blocos sub/angulares ou prismatica grau moderado/forte, cerosidade no minimo comum + moderada, espessura ≥ 30 cm. Argila ativ baixa OR ativ alta + carater aluminico.

Usage

```
B_nitico(
  pedon,
  min_thickness = 30,
  min_clay_pct = 35,
  max_b_a_ratio = 1.5,
  min_cerosidade = c("common", "many", "abundant", "strong")
)
```

Arguments

pedon A [PedonRecord](#).

min_thickness Numeric threshold or option (see Details).

min_clay_pct Numeric threshold or option (see Details).

max_b_a_ratio Numeric threshold or option (see Details).

min_cerosidade Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

B_planico

*Horizonte B planico (SiBCS Cap 2, p 65-66; v0.7)***Description**

Tipo especial de B textural com mudanca textural abrupta + permeabilidade lenta + cores neutras/escurecidas + cromas baixos.

Usage

```
B_planico(pedon)
```

Arguments

pedon A [PedonRecord](#).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

B_textural

Horizonte B textural (SiBCS Cap 2, p 54-57; v0.7 strict)

Description

Horizonte mineral subsuperficial com incremento de argila + cerosidade OR aumento gradativo, satisfazendo criterios de espessura e relacao textural B/A. v0.7 enforce as alternativas (a)-(j) do SiBCS por delegacao parcial ao WRB [argic](#) (criterios de clay-increase essencialmente identicos) acrescidos de:

- espessura ≥ 7.5 cm OR $\geq 10\%$ da soma das espessuras dos sobrejacentes; e
- textura \geq francoarenosa.

Refinamentos pendentes para v0.8: cerosidade obrigatoria sob certas estruturas (criterio i.1 / i.2 / i.3); lamelas ≥ 15 cm combinadas.

Usage

B_textural(pedon, ...)

Arguments

pedon A [PedonRecord](#).
 ... Reserved for future arguments.

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

calcaric_material	<i>Calcaric material (WRB 2022 Ch 3.3.3): $\geq 2\%$ CaCO₃ throughout the fine earth, primary carbonates from the parent material.</i>
-------------------	--

Description

Calcaric material (WRB 2022 Ch 3.3.3): $\geq 2\%$ CaCO₃ throughout the fine earth, primary carbonates from the parent material.

Usage

```
calcaric_material(pedon, min_caco3_pct = 2)
```

Arguments

pedon A [PedonRecord](#).
min_caco3_pct Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

calcic	<i>Calcic horizon (WRB 2022)</i>
--------	----------------------------------

Description

Tests whether any horizon meets the calcic horizon criteria. The calcic horizon is a horizon of secondary carbonate accumulation, diagnostic for Calcisols and qualifying many other RSGs.

Usage

```
calcic(pedon, min_thickness = 15, min_caco3_pct = 15)
```

Arguments

pedon A [PedonRecord](#).
min_thickness Minimum thickness in cm (default 15).
min_caco3_pct Minimum CaCO₃ percent in fine earth (default 15).

Details

Sub-tests called:

- test_caco3_concentration – CaCO₃ >= 15%.
- test_minimum_thickness – thickness >= 15 cm.

v0.2 limitations: the WRB criterion of "5% absolute or relative more CaCO₃ than the underlying horizon" is not enforced; this captures true calcic horizons but may also mark uniformly carbonate-rich substrates that are not pedologically calcic. Cementation (petrocalcic) is not yet detected. Both refinements are scheduled for v0.3.

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022). *World Reference Base for Soil Resources*, 4th edition. International Union of Soil Sciences, Vienna. Chapter 3 – Calcic horizon.

cambic	<i>Cambic horizon (WRB 2022)</i>
--------	----------------------------------

Description

Tests whether any horizon meets the cambic horizon criteria. The cambic horizon is a subsurface horizon with evidence of pedological alteration that does not meet the criteria for any stronger diagnostic horizon. It is the diagnostic of Cambisols.

Usage

```
cambic(pedon, min_thickness = 15, min_top_cm = 5, engine = NULL)
```

Arguments

pedon	A PedonRecord .
min_thickness	Minimum thickness in cm (default 15).
min_top_cm	Minimum top depth (cm) for a horizon to be considered cambic-eligible (default 5). Anchors the candidate set to subsurface layers.
engine	v0.9.63+. One of "soilkey" (hand-coded path, default for back-compat) or "aqp" (canonical NRCS dispatch via <code>aqp::getCambicBounds</code>). When NULL (the new default) the function reads <code>getOption("soilkey.diagnostic_engine", "soilkey")</code> , so a <code>globalOptions(soilkey.diagnostic_engine = "aqp")</code> flips every <code>cambic()</code> call without modifying call sites. The aqp engine fired 40.6 soilkey 0 v0.9.50 LUCAS WRB benchmark from 0 100 cambic_aqp .

Details

v0.2 implementation tests three conditions:

- thickness \geq 15 cm (`test_minimum_thickness`)
- texture sandy loam or finer (`test_texture_argic`)
- NOT `argic` AND NOT `ferralic`

v0.2 limitations: WRB 2022 also excludes profiles with spodic, calcic, gypsic, plinthic, vertic, and several other diagnostic horizons. Those exclusions, plus the WRB criteria of "evidence of alteration" (color/structure differences from parent material, carbonate removal), are scheduled for v0.3.

Value

A `DiagnosticResult`.

References

IUSS Working Group WRB (2022), Chapter 3, Cambic horizon.

cambic_aqp

Cambic horizon via `aqp::getCambicBounds()`

Description

Wraps `aqp::getCambicBounds()` in `soilKey`'s `DiagnosticResult` contract. The `aqp` test enforces the KST 13ed cambic criteria:

- Texture finer than loamy fine sand (i.e. NOT in the sandy-texture pattern).
- Soil structure or absence of rock structure.
- Evidence of pedogenic alteration (chroma / value / clay).
- NOT meeting `argic` / `oxic` / `spodic` / `mollic` criteria.

`soilKey`'s `cambic` (and the SiBCS proxy `B_incipiente`) implements similar logic but with SiBCS / WRB-flavoured exclusions; the `aqp` engine here is an independent canonical reference.

Usage

```
cambic_aqp(pedon, argi_bounds = NULL, ...)
```

Arguments

<code>pedon</code>	A <code>PedonRecord</code> .
<code>argi_bounds</code>	Optional <code>c(ubound, lbound)</code> for argillic bounds (forwarded to <code>aqp</code>). <code>NULL</code> (default) means the <code>aqp</code> internals re-detect.
<code>...</code>	Reserved for future arguments.

Value

A `DiagnosticResult` with name = "cambic_aqp".

See Also

`cambic` (soilKey hand-coded), `aqp::getCambicBounds`.

canonicalise_kst13ed_gg

Canonicalise a USDA Great Group label to a KST 13ed-compatible key

Description

Maps both obsolete (pre-KST 13ed) and modern Great Group names to a single canonical key, so that direct equality between predicted and reference Great Group names ignores edition-driven renaming. Names that have no known mapping pass through unchanged.

Usage

```
canonicalise_kst13ed_gg(gg)
```

Arguments

`gg` Character vector of Great Group names (lower case, no whitespace).

Details

Examples of the canonicalisation (each pair is rendered equivalent):

- "haplaquolls" (KST 8) === "endoaquolls" (KST 13ed)
- "pellusterts" (KST 8) === "hapluderts" (KST 13ed)
- "camborthids" (KST 8) === "haplocambids" (KST 13ed)
- "vitrandepts" (KST 8) === "vitrudands" (KST 13ed)

Value

Character vector of canonical keys. Unmapped names pass through. NA stays NA. Empty input returns empty vector.

References

Soil Survey Staff (2022), Keys to Soil Taxonomy 13ed, Ch 4 (Order keys); previous editions for the obsolete names.

canonical_reference *Load a canonical reference dataset from soilKey or SoilTaxonomy*

Description

Resolution order:

1. If the SoilTaxonomy package is installed AND the prefer_pkg argument is TRUE (default), load the dataset from the installed package (always fresh).
2. Otherwise, load from the vendored copy at inst/extdata/canonical/<name>.rda.

Usage

```
canonical_reference(
  name = c("WRB_4th_2022", "ST_criteria_13th", "ST_features"),
  prefer_pkg = TRUE
)
```

Arguments

name	One of "WRB_4th_2022", "ST_criteria_13th", "ST_features".
prefer_pkg	If TRUE (default), prefer the installed SoilTaxonomy package over the vendored copy. Set to FALSE to force the vendored copy (e.g. for reproducibility of a specific soilKey release).

Value

The dataset as the original R object (list or data.frame).

See Also

[wrb2022_canonical](#), [kst13_canonical](#), [st_features_canonical](#).

cerosidade *Cerosidade quantitativa (SiBCS Cap 13, p 207; Cap 1)*

Description

Diagnostico parametrizado quantidade x intensidade de cerosidade (clay films / cutans). Consume as colunas v0.7.2 clay_films_amount (ordinal: few/pouca, common/comum, many/abundante, continuous/continua) e clay_films_strength (ordinal: weak/fraca, moderate/moderada, strong/forte; "shiny" mapeado a "strong"), introduzidas em substituicao ao legado clay_films.

Usage

```
cerosidade(pedon, min_amount = "common", min_strength = "moderate")
```

Arguments

pedon	A PedonRecord .
min_amount	Quantidade minima: "few", "common", "many", "continuous" (ou equivalentes em PT-BR). Default "common".
min_strength	Intensidade minima: "weak", "moderate", "strong". Default "moderate". Pass NULL para ignorar a dimensao de intensidade.

Details

Discriminante critico Nitossolos vs Argissolos no Cap 13: Nitossolos exigem cerosidade \geq comum + \geq moderada (defaults).

Value

[DiagnosticResult](#); passed = TRUE se ao menos um horizonte B atende ambos os limiares.

References

Embrapa (2018), SiBCS 5a ed., Cap 13 (Nitossolos), p 207; Cap 1 (atributos diagnosticos).

chernic	<i>Chernic horizon (WRB 2022): the cherozemic-style mollic with very high biological activity (worm holes, casts, coprolites). v0.3.3: delegates to mollic + worm_holes_pct \geq 50 (proxy for "biological homogenization").</i>
---------	---

Description

Chernic horizon (WRB 2022): the cherozemic-style mollic with very high biological activity (worm holes, casts, coprolites). v0.3.3: delegates to mollic + worm_holes_pct \geq 50 (proxy for "biological homogenization").

Usage

```
chernic(pedon, min_worm_pct = 50)
```

Arguments

pedon	A PedonRecord .
min_worm_pct	Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

chernozem	<i>Chernozem RSG diagnostic (WRB 2022)</i>
-----------	--

Description

Tests whether a profile satisfies the Chernozem RSG criteria: a mollic horizon plus secondary carbonates somewhere in the profile, plus chroma (moist) ≤ 2 in at least one layer of the upper 20 cm.

Usage

```
chernozem(pedon, max_chroma_upper = 2)
```

Arguments

pedon	A PedonRecord .
max_chroma_upper	Maximum moist chroma in the upper part (default 2, per WRB 2022).

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022), Chapter 5, Chernozems.

chernozem_strict	<i>Chernozem RSG gate (strengthened, WRB 2022 Ch 4, p 111)</i>
------------------	--

Description

WRB-canonical: chernic horizon AND, starting ≤ 50 cm below the lower limit of the mollic horizon and (if a petrocalcic horizon is present) above it, a layer with protocalcic properties ≥ 5 cm thick OR a calcic horizon AND base saturation $\geq 50\%$ from the surface to the protocalcic / calcic layer throughout.

Usage

```
chernozem_strict(pedon, min_bs = 50, max_top_cm = 50, strict = NULL)
```

Arguments

pedon	A PedonRecord .
min_bs	Numeric threshold or option (see Details).
max_top_cm	Numeric threshold or option (see Details).
strict	Logical or NULL. When NULL (default) it resolves via <code>getOption("soilKey.rsg_strict", FALSE)</code> . TRUE raises the base-saturation floor to 80%.

Details

v0.3.4 strengthens the previous v0.2 chernozem (which only required mollic + chernic_color) by adding the protocalcic / calcic gate and the BS \geq 50% requirement.

Note: the v0.2 chernozem() diagnostic remains available as a less-strict variant; chernozem_strict() is what the v0.3.4 key.yaml uses for the CH RSG.

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

Tier-3 strict mode (v0.9.98)

With `strict = TRUE` the base-saturation floor above the carbonate-bearing layer is raised from 50% to 80%, in line with the very high base status expected of a textbook Chernozem.

claric_material	<i>Claric material (WRB 2022 Ch 3.3.4): light-coloured fine earth with Munsell criteria.</i>
-----------------	--

Description

Claric material (WRB 2022 Ch 3.3.4): light-coloured fine earth with Munsell criteria.

Usage

```
claric_material(pedon)
```

Arguments

pedon	A PedonRecord .
-------	---------------------------------

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

ClassificationResult *ClassificationResult: structured outcome of running a key*

Description

ClassificationResult: structured outcome of running a key

ClassificationResult: structured outcome of running a key

Details

Returned by `classify_wrb2022` (and the future `classify_sibcs`). Carries the full decision trace — which RSGs were tested, which passed, which failed, which were indeterminate because of missing data — plus the assigned class, qualifiers, ambiguities (RSGs that nearly satisfied), missing data that would refine the result, the provenance-aware evidence grade, and any biogeographical or prior-based warnings.

Public fields

`system` Character. "WRB 2022" or "SiBCS 5".

`name` Character. Full classification name with qualifiers (e.g. "Rhodic Ferralsol (Clayic, Humic, Dystric)").

`rsg_or_order` Character. Bare RSG (WRB) or order (SiBCS), e.g. "Ferralsols".

`qualifiers` List. Principal and supplementary qualifiers in canonical order.

`trace` List. One element per RSG tested (in key order), each with code, name, passed, evidence, missing.

`ambiguities` List. RSGs that came close to passing — useful hints for follow-up measurements.

`missing_data` Character vector. Attributes whose measurement would refine or resolve the result.

`evidence_grade` Character. "A" (measured), "B" (spectra-predicted), "C" (prior-inferred), "D" (VLM-extracted), "E" (user-assumed), or `NA_character_`.

`prior_check` List or NULL. Result of the spatial-prior sanity check (consistent / inconsistent / not run).

`warnings` Character vector. Free-form warnings.

Methods

Public methods:

- `ClassificationResult$new()`
- `ClassificationResult$print()`
- `ClassificationResult$summary()`
- `ClassificationResult$report()`
- `ClassificationResult$clone()`

Method `new()`: Build a ClassificationResult.

Usage:

```
ClassificationResult$new(
  system,
  name,
  rsg_or_order = NA_character_,
  qualifiers = list(),
  trace = list(),
  ambiguities = list(),
  missing_data = character(0),
  evidence_grade = NA_character_,
  prior_check = NULL,
  warnings = character(0)
)
```

Arguments:

system System name.
 name Classification name.
 rsg_or_order RSG (WRB) or order (SiBCS).
 qualifiers List of qualifier names.
 trace List of per-RSG test entries.
 ambiguities List of close-call RSGs.
 missing_data Character vector.
 evidence_grade Single character A/B/C/D or NA.
 prior_check List or NULL.
 warnings Character vector.

Method print(): Pretty-print the result with key trace, ambiguities, and warnings.

Usage:

```
ClassificationResult$print(...)
```

Arguments:

... Ignored (S3 print signature compatibility).

Method summary(): Compact summary list.

Usage:

```
ClassificationResult$summary(...)
```

Arguments:

... Ignored (S3 summary signature compatibility).

Method report(): Render this classification as a self-contained report (delegates to the package-level [report](#) generic). HTML output is dependency-free; PDF requires rmarkdown and a working LaTeX engine.

Usage:

```
ClassificationResult$report(
  file,
  format = c("auto", "html", "pdf"),
  pedon = NULL,
  ...
)
```

Arguments:

file Output path. Format is inferred from the extension.
 format One of "html" or "pdf" (defaults to "auto", which infers from the extension).
 pedon Optional PedonRecord whose horizons / provenance are added to the report.
 ... Forwarded to [report_html](#) or [report_pdf](#).

Method clone(): The objects of this class are cloneable with this method.

Usage:

```
ClassificationResult$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

classification_robustness

Robustness of classification under input perturbation

Description

For a given [PedonRecord](#), perturb a chosen list of horizon attributes by a configured fractional amount, re-classify under the requested system, and report how often the classification \$rsg_or_order (or full \$name) matches the unperturbed baseline.

Usage

```
classification_robustness(  
  pedon,  
  system = c("wrb2022", "sibcs", "usda"),  
  level = c("order", "name"),  
  n = 50L,  
  perturbations = NULL,  
  provenance_aware = FALSE,  
  seed = 42L  
)
```

Arguments

pedon	A PedonRecord .
system	One of "wrb2022", "sibcs", "usda".
level	Either "order" (compare \$rsg_or_order) or "name" (compare full classification name).
n	Number of Monte-Carlo perturbed runs (default 50).
perturbations	Named list. Each name is a horizon column; each element is a function taking the original value and returning a perturbed value. NA-tolerant. Ignored when provenance_aware = TRUE.

provenance_aware	If FALSE (default) every cell is perturbed by the fixed perturbations panel – the exact v0.9.42 behaviour. If TRUE, each (horizon, attribute) cell is perturbed by an amount scaled to its provenance evidence grade, and perturbations is ignored. See classify_with_uncertainty for the full provenance-weighted posterior.
seed	Random seed for reproducibility.

Details

Default perturbation panel:

- clay_pct: ± 5
- sand_pct: ± 5
- silt_pct: ± 5
- ph_h2o: ± 0.2 absolute
- oc_pct: ± 10

Value

A list with elements baseline (the unperturbed classification name), n (number of MC runs), robustness (fraction of perturbed runs matching baseline), flipped_to (table of alternative classifications when the perturbation flipped the result).

Examples

```
## Not run:
p <- make_ferralsol_canonical()
classification_robustness(p, system = "wrb2022", n = 50)
#> $baseline      : "Ferralsols"
#> $robustness     : 0.96 (48 / 50 perturbed runs landed on Ferralsols)
#> $flipped_to    : table(c("Cambisols" = 1, "Acrisols" = 1))

## End(Not run)
```

classify_all

Classify a pedon across all three taxonomic systems

Description

Convenience wrapper that runs [classify_wrb2022](#), [classify_sibcs](#), and [classify_usda](#) on the same [PedonRecord](#) and returns a single named list with one entry per system (plus a summary table that's handy for reports).

Usage

```

classify_all(
  pedon,
  systems = "all",
  on_missing = c("warn", "silent", "error"),
  include_familia = TRUE,
  include_family = FALSE,
  specifiers = FALSE,
  gapfill = FALSE,
  ...
)

```

Arguments

pedon	A PedonRecord .
systems	Character vector. Any subset of <code>c("wrb2022", "sibcs", "usda")</code> , or the literal "all" (default) to run every system.
on_missing	One of "warn" (default), "silent", "error". Forwarded verbatim to each classifier.
include_familia	Forwarded to classify_sibcs (default TRUE). Has no effect on the other systems.
include_family	Forwarded to classify_usda (default FALSE) to derive the USDA 5th-level family. No effect on the other systems.
specifiers	Forwarded to classify_wrb2022 (default FALSE) to auto-attach WRB depth specifiers. No effect on the other systems.
gapfill	Forwarded to all three classifiers (default FALSE => byte-identical). Opt-in within-pedon depth gap-fill; see gapfill_within_pedon . Applied independently per system on a deep copy, so the caller's pedon is never mutated.
...	Additional named arguments are silently ignored.

Details

Each classifier still produces its own [ClassificationResult](#) with the full key trace and evidence grade – nothing is collapsed or homogenised. The wrapper exists for ergonomics, not abstraction.

Value

A named list with elements:

- wrb – [ClassificationResult](#) from `classify_wrb2022()` (or NULL if the system was skipped or errored).
- sibcs – as above, from `classify_sibcs()`.
- usda – as above, from `classify_usda()`.
- summary – a 1-row data.frame with one column per system, holding the resulting \$name (or NA when the system was skipped / errored). Useful for tabulating many pedons in one shot.

Selecting a subset of systems

Pass `systems = c("wrb2022", "sibcs")` (or any other subset) to skip systems you don't need. Default `systems = "all"` runs all three.

Errors and partial results

If a single classifier raises an error, the corresponding slot of the returned list is set to NULL and a one-line warning is emitted (so you can rerun the offender on its own to see the full traceback). The other classifiers still run and their results are returned. This matches the spirit of `on_missing = "warn"` on the individual classifiers.

Side effects

None. The classifiers do not mutate pedon; the wrapper does not attach any side-channel state.

See Also

[classify_wrb2022](#), [classify_sibcs](#), [classify_usda](#).

Examples

```
pr <- make_ferralsol_canonical()
all_three <- classify_all(pr)
all_three$summary

# WRB + USDA only (skip SiBCS):
classify_all(pr, systems = c("wrb2022", "usda"))$summary
```

`classify_by_spectral_neighbours`

Classify a soil by spectral similarity to OSSL reference profiles

Description

Given a Vis-NIR (or MIR) spectrum and an OSSL reference library enriched with WRB / SiBCS / USDA labels, returns the K most spectrally similar profiles plus a probabilistic class prediction aggregated from their labels.

Usage

```
classify_by_spectral_neighbours(
  spectrum,
  ossl_library,
  system = c("wrb2022", "sibcs", "usda"),
  k = 25L,
  preprocess = "snv+sg1",
  region = NULL,
  verbose = TRUE
)
```

Arguments

spectrum	Numeric vector or 1-row matrix (the query spectrum). Must align (after preprocessing) with the column space of <code>ossl_library\$Xr</code> .
ossl_library	A list with <code>Xr</code> (numeric matrix, rows = OSSL training profiles, cols = wavelengths) and <code>Yr</code> (data frame keyed by property; <i>must include</i> a column named <code>wrb_rsg</code> and / or <code>sibcs_orderm</code> / <code>usda_order</code> for the labels to aggregate over). <code>ossl_library</code> may also carry <code>lat</code> and <code>lon</code> columns in <code>Yr</code> for the regional filter.
system	One of "wrb2022" (default), "sibcs", "usda". Controls which label column of <code>Yr</code> is aggregated.
k	Number of nearest neighbours (default 25).
preprocess	Pre-processing pipeline; passed to <code>preprocess_spectra</code> . Default "snv+sg1".
region	Optional <code>list(lat, lon, radius_km)</code> for a regional filter on <code>ossl_library\$Yr\$lat / lon</code> .
verbose	Emit a cli summary.

Details

This is the **spectral analogy** classifier. It does not replace the deterministic key in `classify_wrb2022` / `classify_sibcs` / `classify_usda`; instead it provides a high-prior "expected class" before the user has lab data, reducing the search space when collecting confirming attributes.

Value

A list with three elements:

`distribution` A data.table with columns `class`, `n_neighbours`, `probability` (= `n_neighbours / k`), sorted by probability.

`neighbours` A data.table with one row per neighbour (top K), columns `rank`, `distance`, `class`, plus any other columns present in `ossl_library$Yr`.

`query` The query metadata (`system`, `k`, `region filter`, `n_library_rows`, `n_filtered`).

Distance metric

By default we compute distances on PLS scores (matching the resemble / OSSL recipe), with PLS components fit on the OSSL reference `Yr` matrix. When `resemble` is unavailable, we fall back to PCA scores from `stats::prcomp` on the preprocessed `Xr` – a defensible-but-simpler heuristic.

Region filter

Optional `lat / lon / radius_km` arguments filter the OSSL library to profiles within `radius_km` (great-circle) of the query location before computing distances. This implements the "biome-aware" use case the architecture document calls for: a Cerrado profile shouldn't have its class inferred from spectral neighbours in the Boreal taiga.

See Also

`predict_ossl_mbl` (predicts attributes), `classify_wrb2022` (the deterministic key).

Examples

```
## Not run:
# Toy run against the bundled demo library (synthetic):
data(ossl_demo_sa)
# Inject a fake label column for the demo (real OSSL has it):
ossl_demo_sa$Yr$wrb_rsg <- sample(c("FR", "AC", "LX", "AL"),
                                nrow(ossl_demo_sa$Yr),
                                replace = TRUE)

query <- ossl_demo_sa$Xr[1, ]
res <- classify_by_spectral_neighbours(query, ossl_demo_sa,
                                     k = 10)

res$distribution # ranked classes
res$neighbours  # the 10 most similar profiles

## End(Not run)
```

classify_from_documents

Build a fully-classified 'PedonRecord' from documents in one call

Description

Highest-level entry point of the soilKey VLM pipeline. Given a soil-description PDF and / or a profile-wall photograph, this function:

Usage

```
classify_from_documents(
  pdf = NULL,
  image = NULL,
  fieldsheet = NULL,
  pedon = NULL,
  provider = "auto",
  model = NULL,
  systems = c("wrb", "sibcs", "usda"),
  report = NULL,
  overwrite = FALSE,
  verbose = TRUE
)
```

Arguments

pdf	Optional path to a soil-description PDF.
image	Optional path to a profile-wall image (JPG / PNG); if supplied, Munsell extraction is attempted with the configured provider.
fieldsheet	Optional path to a site-metadata field sheet (image or PDF).

pedon	Optional existing PedonRecord ; when supplied, the function fills only the fields VLM extraction can fill (subject to the provenance-authority order).
provider	Either a provider name passed to vlm_provider (default "ollama") OR a pre-built ellmer chat object (when you want full control over system_prompt, api_key, ...).
model	Optional model identifier; passed through to vlm_provider() when provider is a string. Defaults to the per-provider default from default_model .
systems	Character vector listing which classification systems to run; subset of <code>c("wrb", "sibcs", "usda")</code> . Default: all three.
report	Optional output path for a self-contained report (.html or .pdf). When supplied, report is called on the classification results + pedon. Default NULL (no report file).
overwrite	When merging extracted values into an existing pedon, allow VLM-extracted attributes to clobber already-recorded ones. Default FALSE – the provenance authority order (measured > extracted_vlm) is enforced by <code>PedonRecord\$add_measurement()</code> .
verbose	Emit cli progress messages. Default TRUE.

Details

1. Constructs a vision-language provider chat object via [vlm_provider](#) (defaults to local Ollama with Gemma 4 edge for institutional independence and data sovereignty).
2. Extracts horizons from pdf via [extract_horizons_from_pdf](#), Munsell colours from image via [extract_munsell_from_photo](#), and site metadata from fieldsheet via [extract_site_from_fieldsheet](#). Every extracted attribute is stamped source = "extracted_vlm" in the PedonRecord's provenance log.
3. Runs the three deterministic keys ([classify_wrb2022](#), [classify_sibcs](#), [classify_usda](#)). The VLM never classifies – the package's architectural invariant is preserved.
4. Optionally renders a one-pager HTML / PDF report via [report](#).

At least one of pdf, image or fieldsheet must be supplied; you can also pass an existing partially-filled PedonRecord via pedon and let this function fill the gaps.

Value

A list with elements:

pedon The (mutated) [PedonRecord](#).

classifications Named list with up to three [ClassificationResult](#) objects keyed by wrb, sibcs, usda.

report Path to the rendered report file (if report = ... was supplied), else NULL.

provider The chat-provider object actually used (useful for downstream debugging or cost accounting).

Why local-first by default

The default provider = "ollama" runs the entire VLM pipeline on the user's machine via Gemma 4 (edge variant, ~3 GB, multimodal text+image). No part of the soil description, photograph or field sheet ever leaves the local network. This is the recommended configuration for governmental surveys, indigenous land studies, and unpublished research data; it also makes the pipeline reproducible without an internet connection. Cloud providers ("anthropic", "openai", "google") remain one argument away when they are the right call.

Architectural invariants preserved

- The VLM never classifies. Every extracted value carries source = "extracted_vlm"; the deterministic keys consume the resulting PedonRecord unaware of how each value was obtained.
- Provenance is preserved end-to-end. The evidence_grade on each ClassificationResult reflects whether decisive attributes came from measured, predicted_spectra, extracted_vlm, inferred_prior, or user_assumed – so a caller always knows how robust the classification is.
- Authority order is enforced. A pre-existing measured value is never silently overwritten by a later extracted_vlm value (unless overwrite = TRUE).

See Also

[vlm_provider](#), [extract_horizons_from_pdf](#), [classify_wrb2022](#), [report](#).

Examples

```
## Not run:
# The simplest possible end-to-end call -- local Gemma 4 edge.
res <- classify_from_documents(
  pdf      = "perfil_042_descricao.pdf",
  image    = "perfil_042_parede.jpg",
  report   = "perfil_042.html"
)
res$classifications$wrb$name
#> "Geric Ferric Rhodic Chromic Ferralsol (Clayic, Humic, Dystric, Ochric, Rubic)"

# Cloud provider for a one-shot, production run
res <- classify_from_documents(
  pdf      = "perfil_042_descricao.pdf",
  provider = "anthropic"
)

# Different Gemma 4 size on Ollama
res <- classify_from_documents(
  pdf      = "perfil_042_descricao.pdf",
  provider = "ollama",
  model    = "gemma4:31b"
)

## End(Not run)
```

classify_from_photos *Classify a soil profile from field photographs alone*

Description

A no-lab-data pipeline: profile photographs are sent to a vision-language model for Munsell-colour and (optionally) site-metadata extraction; the missing horizon attributes are back-filled from a SoilGrids depth prior; and the WRB 2022, SiBCS 5 and USDA Soil Taxonomy keys are run on the assembled [PedonRecord](#).

Usage

```
classify_from_photos(
  images,
  lat = NULL,
  lon = NULL,
  country = NULL,
  provider = NULL,
  systems = c("wrb", "sibcs", "usda"),
  soilgrids = TRUE,
  depth_profiles = NULL,
  on_missing = "silent"
)
```

Arguments

images	Either a character vector of profile-photo paths, or a named list with elements profile (character vector, required) and fieldsheet (character vector, optional).
lat, lon	Optional decimal-degree coordinates. When supplied they seed pedon\$site and are used for the SoilGrids fetch; a field sheet can also supply them through extraction.
country	Optional ISO-2 country code; passed through to the constructed pedon's site metadata.
provider	A vision-language provider: an ellmer chat object for live use, or a <code>MockVLMProvider</code> for testing and offline demos. Required – there is no default, so a real classification is never produced from canned data by accident.
systems	Character vector, any subset of <code>c("wrb", "sibcs", "usda")</code> .
soilgrids	If TRUE (default) missing horizon attributes are back-filled from a SoilGrids depth prior via apply_soilgrids_depth_prior .
depth_profiles	Optional named list of six-slice SoilGrids depth profiles, forwarded to apply_soilgrids_depth_prior . Supplying it skips the network call.
on_missing	Forwarded to the classifiers; default "silent".

Details

Because every value originates from a photograph or a spatial prior, the classification's evidence grade is low by construction (D for VLM-extracted attributes, C where a SoilGrids prior contributed). The result is a screening estimate, not a substitute for a described and sampled profile.

Value

A named list with one `ClassificationResult` per requested system (`$wrb`, `$sibcs`, `$usda`), the constructed `$pedon`, its `$provenance` ledger, and a one-row `$summary` data frame. If extraction yields no horizons the list instead carries `$error` and a NULL pedon.

See Also

[extract_munsell_from_photo](#), [apply_soilgrids_depth_prior](#), [compute_per_attribute_evidence_grade](#).

Examples

```
## Not run:
# Live use with an ellmer chat:
res <- classify_from_photos(
  images = list(profile = "profile.jpg", fieldsheet = "sheet.jpg"),
  lat = -22.7, lon = -43.6, country = "BR",
  provider = ellmer::chat_anthropic())
res$wrb$name
res$wrb$evidence_grade # "D" or "C"

## End(Not run)
```

classify_sibcs	<i>Classifica um pedon segundo o SiBCS 5a edicao (1o + 2o + 3o + 4o niveis)</i>
----------------	---

Description

v0.7 ligou as 13 ordens; v0.7.1 desce ao 2o nivel (subordens) via `run_sibcs_subordem`; v0.7.3 desce ao 3o nivel (Grandes Grupos) via `run_sibcs_grande_grupo` para as ordens progressivamente viradas em `inst/rules/sibcs5/grandes-grupos/<ordem>.yaml` (Cap 14 Organossolos primeiro). Quando a subordem ainda nao tem bloco de Grandes Grupos, ou quando nenhum Grande Grupo passa (e nao ha catch-all default), a classificacao para no 2o nivel.

Usage

```
classify_sibcs(
  pedon,
  rules = NULL,
  on_missing = c("warn", "silent", "error"),
  include_familia = FALSE,
  gapfill = FALSE
)
```

Arguments

pedon	A PedonRecord .
rules	Conjunto de regras pre-carregado.
on_missing	Um de "warn" (default), "silent", "error".
include_familia	Quando TRUE (default FALSE), adiciona o 5o nivel categorico (Familia) via classify_sibcs_familia . O label textual da Familia aparece em <code>\$trace\$familia_label</code> , e a lista de FamilyAttributes em <code>\$trace\$familia</code> .
gapfill	Preenchimento opcional de lacunas por interpolacao intra-perfil, default FALSE (no-op; classificacao byte-identica). TRUE preenche celulas NA interiores dos atributos continuos por profundidade; um vetor de caracteres restringe aos atributos citados; uma lista nomeada e repassada a gapfill_within_pedon . Celulas preenchidas recebem proveniencia <code>inferred_prior</code> , baixando o grau de evidencia para "C". Opera sobre copia profunda – o pedon do chamador nunca e modificado.

Value

Um [ClassificationResult](#) cujo name eh o nome completo da classe atribuida no nivel mais profundo (Grande Grupo > Subordem > Ordem) e `rsg_or_order` eh o nome da ordem (e.g. "Organos-solos"). Os codigos de cada nivel e o trace ficam em `$trace`.

Examples

```
pedon <- make_latossolo_canonical()
res <- classify_sibcs(pedon)
res$name
```

classify_sibcs_familia

Classifica um perfil no 5o nivel categorico do SiBCS (Familia)

Description

Aplica as dimensoes pertinentes a ordem do solo e devolve uma lista nomeada de [FamilyAttribute](#). O label textual da Familia eh formado adicionando-se cada value nao-nulo apos a designacao do 4o nivel, separados por virgulas (Cap 18, p 281).

Usage

```
classify_sibcs_familia(
  pedon,
  ordem_code = NULL,
  sg_code = NULL,
  max_depth_cm = 200
)
```

Arguments

pedon	A PedonRecord .
ordem_code	Codigo da ordem (1 letra: "P", "L", ...). Se NULL, sera derivado de sg_code.
sg_code	Codigo do subgrupo do 4o nivel (e.g. "PVdAr"). Opcional; usado para ajustes especificos por SG (e.g. forcar subgrupamento textural em arenicos/espessarenicos).
max_depth_cm	Profundidade da secao de controle (default 200 cm).

Details

Esta funcao NAO eh uma chave determinista: cada perfil recebe SIMULTANEAMENTE todos os adjetivos pertinentes (multi-rotulo).

Value

Lista nomeada de [FamilyAttribute](#).

Status v0.7.14.A

Implementadas 5 dimensoes – grupamento textural, subgrupamento textural, distribuicao de cascalhos, constituicao esquelética, tipo de horizonte superficial. Outras dimensoes (prefixos epi/meso/endo, saturacao de bases, alico, mineralogia, atividade da argila, oxidos de ferro, andico, especificos de Organossolos) adicionadas em sub-commits subsequentes.

References

Embrapa (2018), SiBCS 5a ed., Cap 18, pp 281-288.

classify_usda

Classify a pedon under USDA Soil Taxonomy (13th edition)

Description

Walks the canonical USDA key (Order -> Suborder -> Great Group -> Subgroup) using YAML rule files at:

- inst/rules/usda/key.yaml: Order key (12 entries)
- inst/rules/usda/suborders/<order>.yaml
- inst/rules/usda/great-groups/<order>.yaml
- inst/rules/usda/subgroups/<order>.yaml

Usage

```

classify_usda(
  pedon,
  rules = NULL,
  on_missing = c("warn", "silent", "error"),
  include_family = FALSE,
  infer_temperature = TRUE,
  gapfill = FALSE
)

```

Arguments

pedon	A PedonRecord .
rules	Optional pre-loaded rule set.
on_missing	One of "warn" (default), "silent", "error".
include_family	If TRUE, derive and prepend the 5th-level family modifiers. Default FALSE (output byte-identical to earlier versions).
infer_temperature	When deriving the family, infer the soil temperature regime from latitude/elevation if site\$soil_temperature_regime is absent (default TRUE). See family_temperature_regime_usda .
gapfill	Opt-in within-pedon depth gap-fill, default FALSE (no-op, classification stays byte-identical). TRUE fills interior NA cells of the continuous depth-trending attributes by linear interpolation from the profile's own measured horizons; a character vector restricts it to those attributes; a named list is passed to gapfill_within_pedon . Filled cells carry <code>inferred_prior</code> provenance, so the evidence grade drops to "C". Runs on a deep copy – the caller's pedon is never mutated.

Details

With `include_family = TRUE` it additionally derives the 5th category, the **family** – a set of class modifiers (particle-size, mineralogy, CEC-activity, reaction, temperature regime, depth) PREPENDED to the subgroup name, e.g. *"fine, kaolinitic, isohyperthermic Rhodic Hapludox"*. See [classify_usda_family](#).

Value

A [ClassificationResult](#) with deepest-level taxon name. Each level's trace is in `$trace`; the family attributes are in `$trace$family`.

References

Soil Survey Staff (2022). Keys to Soil Taxonomy, 13th edition. USDA Natural Resources Conservation Service.

Examples

```

pedon <- make_ferralsol_canonical()
res <- classify_usda(pedon)
res$name

```

```
# include the 5th (family) level:  
classify_usda(pedon, include_family = TRUE)$name
```

classify_usda_family *Classify the USDA family (5th level) of a pedon*

Description

Runs the applicable family-modifier dimensions and returns them as a named list of [FamilyAttribute](#) objects (multi-label; each dimension is orthogonal). Mirrors [classify_sibcs_familia](#).

Usage

```
classify_usda_family(  
  pedon,  
  order_code = NULL,  
  subgroup_code = NULL,  
  infer_temperature = TRUE  
)
```

Arguments

pedon	A PedonRecord .
order_code	Optional USDA order code (selects applicable dimensions).
subgroup_code	Optional subgroup code (reserved for refinements).
infer_temperature	Passed to <code>family_temperature_regime_usda</code> .

Value

Named list of [FamilyAttribute](#) objects.

References

Soil Survey Staff (2022), KST 13th ed., Ch. 16–17.

See Also

[family_label_usda](#), [classify_usda](#).

```
classify_via_smartsolos_api
```

Classify a PedonRecord via Embrapa's SmartSolosExpert REST API

Description

Sends a soilKey [PedonRecord](#) to the SmartSolosExpert REST endpoint maintained by Embrapa (Glauber Vaz's PROLOG-based implementation of the SiBCS classifier) and returns the resulting four-level classification (Ordem / Subordem / Grande Grupo / Subgrupo) wrapped in a soilKey [ClassificationResult](#).

Usage

```
classify_via_smartsolos_api(
    pedon,
    api_key = Sys.getenv("AGROAPI_TOKEN"),
    endpoint = c("classification", "verification"),
    drenagem = NULL,
    reference_sibcs = NULL,
    base_url = "https://api.cnptia.embrapa.br/smartsolos/expert/v1",
    timeout_seconds = 30,
    post_fn = NULL,
    verbose = TRUE
)
```

Arguments

pedon	A PedonRecord .
api_key	Bearer token. Defaults to Sys.getenv("AGROAPI_TOKEN"). Required unless post_fn is supplied (test injection).
endpoint	One of "classification" (default; classify only) or "verification" (classify + compare against user-supplied reference_sibcs).
drenagem	Optional drainage class. Integer 1..8 or Portuguese string ("bem drenado" etc.).
reference_sibcs	Optional named list (ordem, subordem, gde_grupo, subgrupo) used by the "verification" endpoint as the user's reference.
base_url	Override base URL. Default "https://api.cnptia.embrapa.br/smartsolos/expert/v1".
timeout_seconds	HTTP timeout (default 30).
post_fn	Internal: function with signature function(payload) -> response_list for unit tests. When supplied, the network is bypassed.
verbose	If TRUE (default), emits a one-line summary.

Details

This is an **external classifier** – the package does not host or replicate the PROLOG rules. The function exists so soilKey users can cross-validate the local classifier against an authoritative Embrapa-hosted reference. Use the "verification" endpoint to compare against your own user-supplied reference classification (the API returns a per-level match summary with counters L0..L4).

Authentication: register a free AgroAPI account at <https://www.agroapi.cnptia.embrapa.br/portal/>, subscribe to the SmartSolosExpert API and generate an access token. Pass it via the AGROAPI_TOKEN environment variable or the api_key argument.

Value

A `ClassificationResult` with system = "SiBCS 5a edicao (SmartSolosExpert API)" and the four taxonomic levels in rsg_or_order (Ordem) and qualifiers (Subordem / GdeGrupo / Subgrupo). Verification-mode responses additionally carry trace\$smartsolos_summary (the per-level match counters L0..L4).

References

Vaz, G. J., Silva Neto, L. de F. da, & Barbedo, J. G. A. (2025). SmartSolos Expert: an expert system for Brazilian soil classification. *Smart Agricultural Technology*, 10, 100735. doi:10.1016/j.atech.2024.100735.

Vaz, G. J., Silva Neto, L. de F. da, Lima, R. N., & Oliveira, S. R. de M. (2019). Uma API para a classificacao de solos do Brasil. In *Anais do 12 Congresso Brasileiro de Agroinformatica (SBIAGRO 2019)*, pp. 63-72. Ponta Grossa.

Vaz, G. J., Silva Jr, A. F., & Silva Neto, L. de F. da (2023). Brazilian soil data for taxonomic classification. *Redape*, V1. doi:10.48432/PYKKA7.

See Also

`classify_sibcs` for the local PROLOG-free classifier; `compare_smartsolos` for a side-by-side comparison helper; `benchmark_redape` for the gold-standard curated dataset published by the same authors.

Examples

```
## Not run:
Sys.setenv(AGROAPI_TOKEN = "<your token>")
res <- classify_via_smartsolos_api(make_argissolo_canonical())
res$rsg_or_order      # "ARGISSOLO"
res$qualifiers
#> $subordem "VERMELHO"
#> $gde_grupo "Distrofico"
#> $subgrupo "tipico"

## End(Not run)
```

```
classify_with_engine_heuristic
```

Classify a pedon with the engine chosen by 'pick_engine()'

Description

Convenience wrapper that routes [classify_wrb2022](#) / [classify_sibcs](#) / [classify_usda](#) through whichever engine the heuristic recommends for the specific pedon.

Usage

```
classify_with_engine_heuristic(  
  pedon,  
  system = c("wrb2022", "sibcs", "usda"),  
  min_score = 3L,  
  ...  
)
```

Arguments

pedon	A PedonRecord .
system	One of "wrb2022", "sibcs", "usda".
min_score	Forwarded to pick_engine.
...	Forwarded to the underlying classifier.

Value

The result of the chosen classifier (a [ClassificationResult](#)). The chosen engine is captured in `$trace$engine_used`.

```
classify_with_uncertainty
```

Posterior distribution over classification outcomes

Description

Runs n Monte-Carlo perturbations of a pedon and tallies the resulting classes into an empirical posterior. Unlike [classification_robustness](#), the perturbation magnitude of every (horizon, attribute) cell is scaled by its provenance evidence grade (see [get_perturbation_scale](#)): an A-grade measurement is nudged by a few percent, an E-grade assumption by a third of its value. The posterior therefore reflects not just how close the profile sits to a key boundary, but how trustworthy the inputs that placed it there actually are.

Usage

```

classify_with_uncertainty(
  pedon,
  n = 200L,
  system = c("wrb2022", "sibcs", "usda"),
  level = c("rsg", "name"),
  scales = NULL,
  sensitivity = TRUE,
  seed = 42L
)

```

Arguments

pedon	A PedonRecord .
n	Number of Monte-Carlo draws (default 200).
system	One of "wrb2022", "sibcs", "usda".
level	"rsg" (default; compare the RSG / order) or "name" (compare the full classification name, qualifiers included – strictly more uncertain).
scales	Optional named list overriding the default per-grade magnitudes; each element has the shape returned by get_perturbation_scale , keyed by grade letter.
sensitivity	If TRUE (default) also computes a leave-one-attribute-out sensitivity ranking. Set FALSE to skip that extra pass when only the posterior is needed.
seed	Random seed for reproducibility.

Value

A list of class "soilkey_uncertainty" with elements: posterior (named numeric vector summing to 1, sorted descending), top1 (the modal class), entropy (Shannon entropy of the posterior, natural log), sensitivity (a data.table of attribute / importance, or NULL), n_runs, n_success, baseline, system and level.

See Also

[classification_robustness](#), [get_perturbation_scale](#), [compute_per_attribute_evidence_grade](#).

Examples

```

p <- make_ferralsol_canonical()
u <- classify_with_uncertainty(p, n = 50, system = "wrb2022")
u$posterior # P(RSG = x)
u$entropy # near 0 for a robust profile

```

classify_wrb2022	Classify a pedon under WRB 2022
------------------	---------------------------------

Description

High-level classification entry point. Pre-computes the implemented diagnostic horizons (argic, ferralic, mollic) for transparent reporting, runs the key, and assembles a [ClassificationResult](#) with the trace, ambiguities, missing-data hints, evidence grade, and (in future) prior sanity check.

Usage

```
classify_wrb2022(
  pedon,
  prior = NULL,
  prior_threshold = 0.01,
  on_missing = c("warn", "silent", "error"),
  rules = NULL,
  strict = NULL,
  specifiers = FALSE,
  gapfill = FALSE
)
```

Arguments

pedon	A PedonRecord .
prior	Optional spatial prior – a <code>data.table</code> with columns <code>rsg_code</code> and <code>probability</code> , typically the return value of spatial_prior . If supplied, the result records a <code>prior_check</code> entry from prior_consistency_check ; an inconsistent prior also emits a warning. The deterministic key is NEVER overridden by the prior.
prior_threshold	Probability below which the prior triggers an "inconsistent" warning (default 0.01).
on_missing	One of "warn" (default), "silent", "error". Behaviour when the trace reports missing attributes.
rules	Optional pre-loaded rule set.
strict	Logical or NULL. Controls WRB Tier-3 strict mode for the per-RSG numerical gates (Vertisols, Andosols, Gleysols, Planosols, Ferralsols, Chernozems, Kastanozems). When NULL (default) the gates follow <code>getOption("soilKey.rsg_strict", FALSE)</code> . Passing TRUE or FALSE forces strict mode on or off for the duration of this call; see the individual RSG-gate help pages (e.g. ferralsol) for the strengthened thresholds.
specifiers	Logical. When TRUE, auto-attach WRB 2022 Ch 5 depth specifiers (Epi-/Endo-/Bathy-/Amphi-/Panto-/Kato-) to depth-anchored qualifiers based on the diagnostic feature's actual depth – e.g. a gleyic feature confined to 50–100 cm yields Endogleyic instead of Gleyic. Default FALSE keeps the canonical names byte-identical. Surface / epipedon qualifiers are excluded (their depth is definitional).

`gapfill` Opt-in within-pedon depth gap-fill, default FALSE (no-op, classification stays byte-identical). TRUE fills interior NA cells of the continuous depth-trending attributes by linear interpolation from the profile's own measured horizons; a character vector restricts it to those attributes; a named list is passed to `gapfill_within_pedon`. Filled cells carry `inferred_prior` provenance, so the evidence grade drops to "C". Runs on a deep copy – the caller's pedon is never mutated.

Value

A `ClassificationResult`.

Examples

```
pedon <- make_ferralsol_canonical()
res <- classify_wrb2022(pedon)
res$name
```

`clear_kst13_cache` *Clear the in-memory KST13 cache*

Description

Useful when the vendored JSON files are updated mid-session. Frees ~3.1 MB.

Usage

```
clear_kst13_cache()
```

Value

NULL, invisibly. Called for its side effect of emptying the KST 13th-edition lookup cache.

`clear_oss1_cache` *Clear the soilKey OSS1 cache*

Description

Removes the per-region cache files written by `download_oss1_subset`. Useful when a stale cache is suspected or when disk space is tight.

Usage

```
clear_oss1_cache(region = NULL, cache_dir = NULL, verbose = TRUE)
```

Arguments

region	Optional character vector of regions to clear; the default NULL clears every cached file under 'tools::R_user_dir("soilKey", "cache")'.
cache_dir	Cache directory (defaults to the soilKey user-cache dir).
verbose	If TRUE, prints which files were removed.

Value

Invisibly, the character vector of files that were removed.

combine_priors	<i>Combine multiple spatial priors via weighted geometric mean</i>
----------------	--

Description

Given a list of priors (each a `data.table` with `rsg_code`, `probability`), pools them into a single distribution using a weighted geometric mean and renormalises to sum to 1.

Usage

```
combine_priors(priors, weights = NULL, epsilon = 1e-06)
```

Arguments

priors	A list of <code>data.table</code> s with columns <code>rsg_code</code> and <code>probability</code> .
weights	Optional non-negative numeric vector of length <code>length(priors)</code> . Defaults to equal weights. Will be renormalised to sum to 1.
epsilon	Smoothing floor for classes missing from a prior (default 1e-6). Must be > 0 – otherwise any class missing from a single prior is suppressed entirely.

Details

Geometric pooling has two desirable properties for soil-class priors:

1. externally Bayesian (the pooled posterior under any common likelihood matches what one would get by individual updates), and
2. zero-preserving: a class assigned probability 0 by any prior is suppressed in the pooled distribution. To avoid that, classes absent from a given prior are imputed with the smoothing constant `epsilon`.

Value

A `data.table` with columns `rsg_code`, `probability`, sorted by descending probability.

compare_engines	<i>Side-by-side comparison of soilKey vs aqp diagnostic engines</i>
-----------------	---

Description

Runs the soilKey hand-coded diagnostic and the aqp wrapper on the same pedon, returns both results plus an agreement flag. Useful for A/B benchmarks and for choosing which engine to use per dataset.

Usage

```
compare_engines(pedon, diagnostic = c("argic", "cambic"))
```

Arguments

pedon	A PedonRecord .
diagnostic	One of "argic" or "cambic".

Value

A list with soilkey, aqp, agree.

compare_smartsolos	<i>Cross-validate the local SiBCS classifier against the SmartSolosExpert API</i>
--------------------	---

Description

Runs both [classify_sibcs](#) (local) and [classify_via_smartsolos_api](#) (remote PROLOG via Embrapa AgroAPI) on the same [PedonRecord](#) and tabulates agreement at each of the four SiBCS categorical levels.

Usage

```
compare_smartsolos(pedon, ...)
```

Arguments

pedon	A PedonRecord .
...	Forwarded to classify_via_smartsolos_api .

Value

A list with local and remote ClassificationResults plus a one-row agreement data.frame with columns ordem, subordem, gde_grupo, subgrupo, n_match.

Examples

```
## Not run:  
Sys.setenv(AGROAPI_TOKEN = "<your token>")  
cmp <- compare_smartsolos(make_argissolo_canonical())  
cmp$agreement  
  
## End(Not run)
```

`compute_ki`*Ki (silica:alumina molar) – SiBCS Cap 1, p 32*

Description

Calcula o índice molar $Ki = SiO_2 / Al_2O_3$ a partir de teores percentuais por ataque sulfúrico-NaOH (Embrapa Manual de Métodos). Massas molares: 60.08 (SiO₂), 101.96 (Al₂O₃):

Usage

```
compute_ki(sio2_pct, al2o3_pct)
```

Arguments

sio2_pct	Teor de SiO ₂ por ataque sulfúrico (%).
al2o3_pct	Teor de Al ₂ O ₃ por ataque sulfúrico (%).

Details
$$Ki \text{ (molar)} = (\% SiO_2 / 60.08) / (\% Al_2O_3 / 101.96) \approx 1.6973 \times (\% SiO_2 / \% Al_2O_3)$$
Value

Ki molar (numeric); NA se algum input for NA ou $Al_2O_3 \leq 0$.

References

Embrapa (2018), SiBCS 5a ed., Cap 1, p 32; Embrapa Manual de Métodos de Análise de Solo (3a ed., 2017).

Examples

```
compute_ki(sio2_pct = 18, al2o3_pct = 20) # ~1.53, abaixo do limite latossolico
```

compute_kr *Kr (silica:sesquioxidos molar) – SiBCS Cap 1, p 32*

Description

Calcula o índice molar $Kr = SiO_2 / (Al_2O_3 + Fe_2O_3)$ usando massas molares 60.08 (SiO₂), 101.96 (Al₂O₃) e 159.69 (Fe₂O₃):

Usage

```
compute_kr(sio2_pct, al2o3_pct, fe2o3_pct)
```

Arguments

sio2_pct	Teor de SiO ₂ por ataque sulfurico (%).
al2o3_pct	Teor de Al ₂ O ₃ por ataque sulfurico (%).
fe2o3_pct	Teor de Fe ₂ O ₃ por ataque sulfurico (%).

Details

$$Kr \text{ (molar)} = (\% SiO_2 / 60.08) / (\% Al_2O_3 / 101.96 + \% Fe_2O_3 / 159.69)$$

Value

Kr molar (numeric); NA se algum input for NA ou denominador ≤ 0 .

References

Embrapa (2018), SiBCS 5a ed., Cap 1, p 32.

Examples

```
compute_kr(sio2_pct = 18, al2o3_pct = 20, fe2o3_pct = 12)
```

compute_per_attribute_evidence_grade
Per-attribute provenance-aware evidence grade

Description

Resolves the evidence grade of every (horizon, attribute) cell that carries a provenance entry. Where a cell has more than one entry (a value re-sourced over the profile's lifetime) the most authoritative source wins, mirroring [PedonRecord](#)'s own authority order.

Usage

```
compute_per_attribute_evidence_grade(pedon)
```

Arguments

pedon A [PedonRecord](#).

Details

Grades: A measured, B predicted from spectra, C inferred from a spatial prior, D extracted by a vision-language model, E user-assumed.

Value

A data.table with columns horizon_idx, attribute and grade, sorted by horizon then attribute. A pedon with no provenance entries yields a zero-row table.

See Also

[classify_from_photos](#), the global evidence grade reported on every [ClassificationResult](#).

Examples

```
p <- make_ferralsol_canonical()
compute_per_attribute_evidence_grade(p) # all-measured -> all grade A
```

continuous_rock	<i>Continuous rock (WRB 2022 Ch 3.2.5)</i>
-----------------	--

Description

Consolidated material below the soil. v0.3.3: detects via designation R or Cr on the lowermost (or any) layer.

Usage

```
continuous_rock(pedon)
```

Arguments

pedon A [PedonRecord](#).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

coverage_report	<i>Honest taxonomic-completeness report</i>
-----------------	---

Description

Measures, by NAME, exactly which canonical taxa/qualifiers the package's deterministic rule base registers, replacing hand-maintained coverage claims with an auditable, reproducible diff. For "usda_subgroup" the canonical reference is the Soil Taxonomy 13th-edition subgroup set from [kst13_codes](#); for "wrb_qualifiers" it is the WRB 2022 principal + supplementary qualifier set from [wrb2022_canonical](#).

Usage

```
coverage_report(
  system = c("usda_subgroup", "usda_great_group", "usda_suborder", "wrb_qualifiers",
            "sibcs"),
  write = FALSE,
  report_dir = NULL
)
```

Arguments

system	Which axis to measure. USDA taxon levels against the Soil Taxonomy 13th-edition code set (kst13_codes): "usda_subgroup" (default), "usda_great_group", "usda_suborder". WRB 2022 qualifiers against wrb2022_canonical : "wrb_qualifiers" – here "covered" means the qual_* function exists <i>and</i> is a genuine implementation (not an unconditional passed = NA stub), and the inert ones are returned in \$stubs. "sibcs" has no external canonical class list, so it honestly reports registered class counts per level only (no percentage).
write	If TRUE, also write a Markdown summary to report_dir. Default FALSE.
report_dir	Directory for the Markdown report when write = TRUE. Defaults to inst/benchmarks/reports inside the installed package.

Value

Invisibly, a list with \$overall (one-row data frame: system, level, canonical_n, registered_n, covered_n, missing_n, pct), \$by_group (per order, or per principal/supplementary), \$missing (canonical names not registered), \$extra (registered names absent from the canonical set), and – for "wrb_qualifiers" – \$stubs (functions that exist but are inert). A compact summary is printed as a side effect.

Examples

```
cov <- coverage_report("usda_subgroup")
cov$overall
head(cov$missing)
```

cryic_conditions	<i>Cryic conditions (WRB 2022)</i>
------------------	------------------------------------

Description

Tests whether continuous frozen / permafrost material occurs within the upper max_top_cm. Two alternative paths qualify per WRB 2022:

1. **Permafrost temperature:** a layer at top_cm ≤ max_top_cm (default 100) with permafrost_temp_C ≤ max_temp_C (default 0 C).
2. **Designation pattern:** a layer at top_cm ≤ max_top_cm with designation containing suffix "f" (frozen) or matching "^Cf" / "perma". Used as a fallback when the temperature field is not in the pedon (typical of legacy survey data).

Either path qualifies. Diagnostic of Cryosols.

Usage

```
cryic_conditions(pedon, max_top_cm = 100, max_temp_C = 0)
```

Arguments

pedon	A PedonRecord .
max_top_cm	Maximum top depth (cm) (default 100).
max_temp_C	Maximum mean annual permafrost-zone temperature (deg C) for the temperature path (default 0).

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022), Chapter 5, Cryosols.

DiagnosticResult	<i>DiagnosticResult: structured outcome of a diagnostic test</i>
------------------	--

Description

DiagnosticResult: structured outcome of a diagnostic test

DiagnosticResult: structured outcome of a diagnostic test

Details

Returned by every WRB or SiBCS diagnostic function (e.g. `argic`, `ferralic`, `mollic`). A `DiagnosticResult` never reduces to a bare TRUE/FALSE — it always carries (a) which layers satisfied the criteria, (b) the per-sub-test evidence, (c) which attributes would have been required but are missing, and (d) the literature reference for the diagnostic definition.

passed is TRUE/FALSE/NA; NA means the test could not be evaluated because critical attributes were missing. This three-valued semantics propagates through the rule engine — an indeterminate test does not silently fail.

Public fields

`name` Character. Name of the diagnostic (e.g. "argic").

`passed` Logical. TRUE, FALSE, or NA.

`layers` Integer vector. Indices of horizons that satisfy the diagnostic.

`evidence` Named list. Sub-test results, each itself a list with at least `passed`, `layers`, and `missing`.

`missing` Character vector. Attribute names that would have been needed but were NA.

`reference` Character. Literature citation for this diagnostic.

`notes` Character. Free-form notes (interpretation choices, edge cases hit).

Methods

Public methods:

- `DiagnosticResult$new()`
- `DiagnosticResult$print()`
- `DiagnosticResult$as_list()`
- `DiagnosticResult$clone()`

Method `new()`: Build a `DiagnosticResult`.

Usage:

```
DiagnosticResult$new(
  name,
  passed = NA,
  layers = integer(0),
  evidence = list(),
  missing = character(0),
  reference = NA_character_,
  notes = NA_character_
)
```

Arguments:

`name` Diagnostic name.

`passed` TRUE/FALSE/NA.

`layers` Integer vector of horizon indices that satisfied.

`evidence` Named list of sub-test results.

`missing` Character vector of missing attribute names.

reference Citation string.

notes Free-form notes.

Method `print()`: Pretty-print the result with sub-test breakdown.

Usage:

```
DiagnosticResult$print(...)
```

Arguments:

... Ignored (S3 print signature compatibility).

Method `as_list()`: Return the result as a plain list (for serialization).

Usage:

```
DiagnosticResult$as_list()
```

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
DiagnosticResult$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

distrofico

Solo distrofico (SiBCS Cap 1, p 30)

Description

Negacao operacional de [eutrofico](#): $V < 50\%$ no horizonte diagnostico subsuperficial.

Usage

```
distrofico(pedon, max_v = 50)
```

Arguments

pedon A [PedonRecord](#).

max_v Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

dolomitic_material	<i>Dolomitic material (WRB 2022 Ch 3.3.5): $\geq 2\%$ Mg-rich carbonate, $\text{CaCO}_3/\text{MgCO}_3 < 1.5$. v0.3.3: detects via designation pattern kdo do magn as proxy when ratio data missing.</i>
--------------------	--

Description

Dolomitic material (WRB 2022 Ch 3.3.5): $\geq 2\%$ Mg-rich carbonate, $\text{CaCO}_3/\text{MgCO}_3 < 1.5$. v0.3.3: detects via designation pattern kdo|do|magn as proxy when ratio data missing.

Usage

```
dolomitic_material(pedon)
```

Arguments

pedon A [PedonRecord](#).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

download_bdsolos	<i>Download the BDsolos consulta-publica CSV (experimental, requires chromote)</i>
------------------	--

Description

Drives the Embrapa BDsolos web form via headless Chrome (chromote) to produce a CSV of all profiles + all attributes. Marked **experimental**: heavy queries (no UF filter) frequently overload the Embrapa server. Prefer filter_uf = batches of one or two states at a time and stitch the resulting CSVs.

Usage

```
download_bdsolos(
  out_path,
  accept_terms = FALSE,
  filter_uf = NULL,
  attributes = "default",
  timeout_seconds = 600,
  chromote_session = NULL,
  verbose = TRUE
)
```

Arguments

out_path	File path for the downloaded CSV.
accept_terms	Logical. Must be TRUE to proceed; the function aborts otherwise. Documents informed consent to the BDSolos terms (personal/academic use, ABNT citation).
filter_uf	Optional 2-letter UF code (e.g. "RJ", "SC"). Strongly recommended – the full-table query often times out.
attributes	Character vector. Which attribute groups to request. Defaults to the full SiBCS-classification-relevant set (Identificacao + Localizacao + Classificacao for Pontos de Amostragem, Identificacao + Morfológicas + Físicas + Químicas for Horizontes; Mineralógicas excluded for performance). Pass "all" to include Mineralógicas.
timeout_seconds	Total timeout for the AJAX query. Default 600 (10 min).
chromote_session	Optional pre-built chromote::ChromoteSession. Useful to share a session across calls.
verbose	If TRUE (default), prints progress.

Details

Per the Embrapa terms-of-use, the data is licensed for personal / academic use and publications must cite the source per ABNT. **Set** `accept_terms = TRUE` **to acknowledge this and let the function click "Concordo" on your behalf.**

Value

File path to the downloaded CSV (invisible).

See Also

[load_bdsolos_csv](#), [inspect_bdsolos_csv](#).

Examples

```
## Not run:
# Single UF (fast, recommended)
download_bdsolos("soil_data/bdsolos/RJ.csv",
  accept_terms = TRUE,
  filter_uf    = "RJ")

# Stitch multiple UFs
for (uf in c("RJ", "SP", "MG", "ES")) {
  download_bdsolos(file.path("soil_data/bdsolos",
    paste0(uf, ".csv")),
    accept_terms = TRUE, filter_uf = uf)
}

# Then load all of them
```

```

csvs <- list.files("soil_data/bdsolos", "\\*.csv$", full.names = TRUE)
all_pedons <- unlist(lapply(csvs, load_bdsolos_csv), recursive = FALSE)
length(all_pedons)

## End(Not run)

```

download_extdata_cache

Download one or more soilKey lazy-fetch caches from GitHub Release

Description

soilKey ships four large benchmark caches (KSSL, KSSL+NASIS, AfSP, WoSIS stratified) that are too large to embed in the CRAN source tarball. Since v0.9.94 they are pinned to a versioned GitHub Release and downloaded on demand into the user cache directory at `tools::R_user_dir("soilKey", "data")`.

Usage

```

download_extdata_cache(
  which = "all",
  release = .SOILKEY_LAZY_FETCH_RELEASE,
  overwrite = FALSE,
  verbose = TRUE
)

```

Arguments

which	Character vector of cache names to download. "all" (default) downloads every lazy-fetch cache. Valid names: "afsp_sample", "kssl_sample", "kssl_nasis_sample", "wosis_stratified_sample".
release	GitHub Release tag to pull from (default "v0.9.94-data"). Override only if you maintain a local mirror.
overwrite	If TRUE, redownload even if the file is already present in the user cache (default FALSE).
verbose	Print progress (default TRUE).

Details

On first call to any of `load_kssl_sample()`, `load_kssl_nasis_sample()`, `load_afsp_sample()`, or `load_wosis_stratified_sample()`, soilKey checks for the file in the user cache. If missing, the loader prompts (interactive sessions only) to download. Use `download_extdata_cache()` to eagerly populate the cache without prompting.

Value

Invisibly, a named character vector of local paths to the downloaded files.

Examples

```
## Not run:
# Download every lazy-fetch cache once, ahead of any benchmark run:
download_extdata_cache()

# Or just the WRB AfSP sample:
download_extdata_cache("afsp_sample")

## End(Not run)
```

download_oss1_subset *Download an OSSL subset and return an 'oss1_library' artefact*

Description

Fetches a region-filtered subset of the Open Soil Spectral Library (Sanderman et al. 2024) and assembles it into the 'list(Xr, Yr, metadata)' shape consumed by [predict_oss1_mbl](#) and [predict_oss1_plsr_local](#). The result is cached under 'tools::R_user_dir("soilKey", "cache")' so subsequent calls in the same session (or future R sessions) skip the network.

Usage

```
download_oss1_subset(
  region = c("global", "south_america", "north_america", "europe", "africa", "asia",
            "oceania"),
  properties = c("clay_pct", "sand_pct", "silt_pct", "cec_cmol", "bs_pct", "ph_h2o",
                "oc_pct", "fe_dcb_pct", "caco3_pct"),
  wavelengths = 350:2500,
  endpoint = NULL,
  cache_dir = NULL,
  force = FALSE,
  verbose = TRUE
)
```

Arguments

region	One of "global", "south_america", "north_america", "europe", "africa", "asia", "oceania". Filters the OSSL training rows by their site coordinates' continent.
properties	Character vector of OSSL property names to keep in 'Yr' (drops other reference columns to keep the artefact small). Defaults to the WRB-relevant set used by fill_from_spectra .
wavelengths	Integer vector of wavelengths (nm) the returned Xr matrix will be interpolated to. Defaults to Vis-NIR/SWIR (350-2500 nm at 1-nm resolution, 2151 columns).
endpoint	OSSL HTTP endpoint serving the JSON manifest; overrideable via options(soilKey.oss1_endpoint = ...) for testing or for using a private mirror. The default is the public Soil Spectroscopy GG bucket.

cache_dir	Cache directory; defaults to <code>tools::R_user_dir("soilKey", "cache")</code> .
force	If TRUE, re-fetches even when a cached subset exists.
verbose	If TRUE, emits a 'cli' summary of the fetch.

Details

This function intentionally does **not** fall back to the synthetic predictor on network failure – a missing OSSL artefact is a real condition that the caller must handle, and silent fallback would make benchmarks meaningless.

Value

A list with elements `Xr` (numeric matrix, rows = training profiles, columns = wavelengths in nm), `Yr` (data.frame with the requested property columns, rows aligned to `Xr`), and metadata (snapshot date, region, n profiles, source URL, and the SHA-256 of the cache file). Pass it as the `oss1_library` argument to `fill_from_spectra` or `predict_oss1_mbl`.

References

Sanderman, J., Savage, K., Dangal, S.R.S., Duran, G., Rivard, C., Cardona, M.T., Sandzhieva, A., Aramian, A. & Safanelli, J.L. (2024). Soil Spectroscopy for Global Good – the Open Soil Spectral Library (OSSL). <https://soilspectroscopy.org/>.

download_oss1_subset_with_labels

Download an OSSL subset and attach WRB / SiBCS / USDA labels

Description

Fetches a region-filtered slice of the Open Soil Spectral Library via `download_oss1_subset` and post-joins WRB Reference Soil Group labels from WoSIS GraphQL by spatial nearest-neighbour. The resulting artefact has the canonical `list(Xr, Yr, metadata)` shape – with extra columns in `Yr`: `wrb_rsg`, `wrb_label_source`, `wrb_label_distance_km`, plus optionally `sibcs_order` and `usda_order` when `translate_systems = TRUE`.

Usage

```
download_oss1_subset_with_labels(
  region = c("global", "south_america", "north_america", "europe", "africa", "asia",
            "oceania"),
  max_distance_km = 5,
  wosis_endpoint = NULL,
  translate_systems = TRUE,
  max_to_label = Inf,
  verbose = TRUE,
  query_fn = NULL,
  ...
)
```

Arguments

region	OSSL region filter; one of "global", "south_america", "north_america", "europe", "africa", "asia", "oceania".
max_distance_km	WoSIS spatial-join tolerance in kilometres (default 5). Profiles whose nearest WRB-labeled WoSIS neighbour is farther than this are left unlabeled.
wosis_endpoint	Override for the WoSIS GraphQL endpoint (default <code>getOption("soilKey.wosis_graphql")</code>). The canonical value is <code>"https://graphql.isric.org/wosis/graphql"</code> .
translate_systems	If TRUE (default), also adds <code>sibcs_ordem</code> and <code>usda_order</code> columns derived from the WRB label via the Schad (2023) Annex Table 1 / SiBCS 5 ^a ed. Annex A correspondence. Those translations are 1:N for some classes; we pick the most-common partner and tag rows where the translation is genuinely ambiguous.
max_to_label	Maximum number of profiles to query against WoSIS (default Inf). WoSIS throttles aggressive queries; cap this when running interactive demos.
verbose	Emit cli progress messages.
query_fn	Optional injection of the per-coordinate WoSIS query function. Default uses <code>.query_nearest_wosis_wrb</code> . Tests pass a stub here to exercise the join logic without network.
...	Forwarded to download_ossl_subset .

Value

A list with `Xr` (numeric matrix), `Yr` (data frame with the labels attached), and metadata (list with the OSSL fetch metadata + the join statistics: number of profiles labeled, average / max distance, WoSIS endpoint, snapshot date).

Why this function exists

OSSL stores Vis-NIR / MIR spectra and lab data but typically lacks WRB Reference Soil Group labels on most profiles (KSSL data is USDA-flavoured; non-US contributions are inconsistent). WoSIS, by contrast, archives ~228 000 profiles with WRB labels but no spectra. This function bridges the two so the user can run [classify_by_spectral_neighbours](#) on a real-data OSSL library without having to do the spatial join themselves.

Caveats and provenance

WRB labels obtained via spatial join are **weak labels**. The same physical location may have been classified differently across surveys (different WRB editions, different interpretations). Each row carries:

- `wrb_label_source = "wosis_spatial_join"`: label inherited from a WoSIS neighbour within `max_distance_km`.
- `wrb_label_distance_km`: the distance to that neighbour (NA when no neighbour was found within tolerance).

- wrb_label_source = "ossl_native": label was already present in OSSL Yr (rare; preserved verbatim).
- wrb_label_source = "missing": no neighbour within tolerance; the row stays unlabeled and will be skipped downstream.

Treat the labels as priors, not ground truth.

See Also

[download_ossl_subset](#), [classify_by_spectral_neighbours](#).

Examples

```
## Not run:
# Real OSSL South-America subset with WRB labels:
lib <- download_ossl_subset_with_labels(
  region      = "south_america",
  max_distance_km = 10
)
table(lib$Yr$wrb_rsg, useNA = "always")
table(lib$Yr$wrb_label_source)

# Drop into the spectral analogy classifier:
res <- classify_by_spectral_neighbours(
  spectrum      = my_query_spectrum,
  ossl_library  = lib,
  k             = 25,
  region       = list(lat = -22.7, lon = -43.7,
                      radius_km = 500)
)

## End(Not run)
```

download_redape_dataset

Download the curated Redape GeoTab dataset (Vaz et al 2023)

Description

Enumerates the dataset via the Dataverse API and downloads all JSON profile files (the structured / interoperable format used by the curators) into `dest_dir`. Skips files already present unless `overwrite = TRUE`.

Usage

```
download_redape_dataset(
  dest_dir,
  dataset_doi = .REDAPE_GEOTAB_DOI,
  include_rtf = FALSE,
```

```

    overwrite = FALSE,
    verbose = TRUE
  )

```

Arguments

`dest_dir` Destination directory for the JSON files.

`dataset_doi` DOI of the dataset (default: the Vaz 2023 dataset).

`include_rtf` If TRUE, also download the original RTF profile sheets (default FALSE; the JSON files alone are enough for classification).

`overwrite` If TRUE, re-download files that already exist locally.

`verbose` Print progress (default TRUE).

Value

Character vector of paths to the downloaded files.

References

Vaz, G. J., Silva Jr, A. F., & Silva Neto, L. de F. da (2023). Brazilian soil data for taxonomic classification. Redape, V1. doi:10.48432/PYKKA7.

duric_horizon	<i>Duric horizon (WRB 2022)</i>
---------------	---------------------------------

Description

Tests for $\geq 10\%$ volume of duripan nodules (Si-cemented) within a horizon at least 10 cm thick. Diagnostic of Durisols.

Usage

```
duric_horizon(pedon, min_thickness = 10, min_duripan_pct = 10)
```

Arguments

`pedon` A [PedonRecord](#).

`min_thickness` Minimum thickness (cm; default 10 per WRB 2022).

`min_duripan_pct` Minimum duripan volume % (default 10 per WRB 2022).

Value

A [DiagnosticResult](#).

v0.3.1: thresholds aligned with WRB 2022 Ch 3.1.7 (10%, 10 cm) – previous v0.3 used 15%/15 cm. Petroduric (cemented continuous duripan) detection still deferred and will be added in v0.4.

References

IUSS Working Group WRB (2022), Chapter 3.1.7 – Duric horizon (p. 41).

duripa	<i>Duripa (SiBCS Cap 2, p 74; v0.7)</i>
--------	---

Description

Reuso de [duric_horizon](#) (WRB Ch 3.1): subsuperficial cimentado por silica, continuo ou em \geq 50% volume.

Usage

```
duripa(pedon, ...)
```

Arguments

pedon	A PedonRecord .
...	Reserved for future arguments.

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

ensure_horizon_schema	<i>Coerce a horizons-like data.frame to the canonical schema</i>
-----------------------	--

Description

Adds any missing canonical columns as NAs of the right type and reorders canonical columns first. Extra user-supplied columns are preserved at the end. Coerces character values to numeric where the schema requires it.

Usage

```
ensure_horizon_schema(h)
```

Arguments

h	Input data.frame or data.table.
---	---------------------------------

Value

A data.table with the canonical horizon columns present, in canonical order, with extra columns preserved at the end.

Examples

```
h <- ensure_horizon_schema(data.frame(top_cm = 0, bottom_cm = 20))
"designation" %in% names(h)
```

eutrofico	<i>Solo eutrofico (SiBCS Cap 1, p 30)</i>
-----------	---

Description

Returns TRUE se a saturacao por bases (V%) \geq 50% no horizonte diagnostico subsuperficial (B ou C). 65% para A chernozemico.

Usage

```
eutrofico(pedon, min_v = 50)
```

Arguments

pedon A [PedonRecord](#).
min_v Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

evaluate_rsg_tests	<i>Evaluate the test block of a single RSG</i>
--------------------	--

Description

Given a parsed tests block from a YAML key entry, evaluates the appropriate combinator and returns a list with passed, evidence, missing, and (optionally) notes.

Usage

```
evaluate_rsg_tests(pedon, tests)
```

Arguments

pedon A [PedonRecord](#).
tests A tests block from the YAML.

Value

A list summarising the test outcome.

```
extract_horizons_from_pdf
```

Extract horizons from a soil description PDF

Description

Reads a PDF (typically a soil survey chapter, field-sheet scan, or thesis appendix), prompts the configured VLM to extract horizon attributes against `inst/schemas/horizon.json`, and merges the result into pedon. Every extracted attribute is recorded with `source = "extracted_vlm"` and the model's reported confidence and verbatim source quote.

Usage

```
extract_horizons_from_pdf(
    pedon,
    pdf_path = NULL,
    provider,
    max_retries = 3L,
    overwrite = FALSE,
    prompt_name = "extract_horizons",
    schema_name = "horizon",
    pdf_text = NULL
)
```

Arguments

<code>pedon</code>	A PedonRecord to merge into. Mutated in place AND returned invisibly.
<code>pdf_path</code>	Path to the PDF file. Either <code>pdf_path</code> or <code>pdf_text</code> must be supplied.
<code>provider</code>	A chat provider from vlm_provider (or a <code>MockVLMProvider</code> for testing).
<code>max_retries</code>	Integer; how many times to re-prompt on validation failure. Default 3.
<code>overwrite</code>	If TRUE, lower-authority values are allowed to clobber higher-authority ones. Default FALSE.
<code>prompt_name</code>	Override the default prompt template ("extract_horizons").
<code>schema_name</code>	Override the default schema ("horizon").
<code>pdf_text</code>	Optional alternative to <code>pdf_path</code> : the already-extracted description text. Useful for smoke tests, unit tests without <code>pdftools</code> , and for already-OCR'd field-sheet text.

Details

The `PedonRecord`'s authority order guarantees that values already tagged "measured" are never silently overwritten by VLM extraction unless `overwrite = TRUE`.

If the PDF is long (more than ~30,000 characters), it is chunked page-by-page and each page is sent independently. This is a conservative-but-simple strategy; for very long surveys callers should pre-chunk and call this function once per profile.

Value

Invisibly, the (mutated) pedon. Carries a "vlm_extraction" attribute with the parsed response, number of attempts, and number of provenance entries added.

Failure modes

- If pdftools is not installed -> error.
- If the PDF cannot be read -> error.
- If the VLM response fails JSON parse / schema validation after max_retries + 1 attempts -> error from validate_or_retry.

extract_munsell_from_photo

Extract Munsell color from a profile photo

Description

Sends the photo to a multimodal VLM with a prompt that asks the model to estimate Munsell hue / value / chroma per visible horizon (when a Munsell reference card is in frame). Recorded as extracted_vlm with the model's self-reported confidence; photos without a reference card should yield confidence below 0.5 per the prompt specification.

Usage

```
extract_munsell_from_photo(
  pedon,
  image_path,
  provider,
  max_retries = 3L,
  overwrite = FALSE,
  prompt_name = "extract_munsell_from_photo",
  schema_name = "horizon"
)
```

Arguments

pedon	A PedonRecord .
image_path	Path to the image file (JPG / PNG).
provider	A chat provider from vlm_provider (or a MockVLMProvider for testing).
max_retries	Integer; how many times to re-prompt on validation failure. Default 3.
overwrite	If TRUE, lower-authority values are allowed to clobber higher-authority ones. Default FALSE.
prompt_name	Override the default prompt template ("extract_horizons").
schema_name	Override the default schema ("horizon").

Details

Quantitative non-color attributes (clay %, CEC, pH, etc.) are **never** extracted from photos, by prompt-level instruction. If the model returns one anyway, it is silently dropped.

Value

Invisibly, the mutated pedon, with the photo added to pedon\$images.

```
extract_site_from_fieldsheet
```

Extract site metadata from a field-sheet image

Description

Sends a photographed / scanned field sheet to a multimodal VLM and merges the extracted site-level metadata (lat, lon, elevation, parent material, land use, etc.) into pedon\$site. Existing fields are preserved unless overwrite = TRUE; only NULL fields are filled.

Usage

```
extract_site_from_fieldsheet(  
  pedon,  
  image_path,  
  provider,  
  max_retries = 3L,  
  overwrite = FALSE,  
  prompt_name = "extract_site_metadata",  
  schema_name = "site"  
)
```

Arguments

pedon	A PedonRecord .
image_path	Path to the field-sheet image.
provider	A chat provider from vlm_provider (or a MockVLMProvider for testing).
max_retries	Integer; how many times to re-prompt on validation failure. Default 3.
overwrite	If TRUE, lower-authority values are allowed to clobber higher-authority ones. Default FALSE.
prompt_name	Override the default prompt template ("extract_horizons").
schema_name	Override the default schema ("horizon").

Value

Invisibly, the mutated pedon.

familia_mineralogia_argila_geral

Familia: mineralogia da fracao argila (geral, nao-Latossolos)

Description

Classifica a mineralogia da argila para Argissolos, Cambissolos, Plintossolos, Luvisolos, Nitossolos, Vertissolos, Chernossolos, Planossolos, Gleissolos quando ha informacao quantitativa de atividade da argila e/ou Ki/Kr. Cobre as classes nao endereçadas por familia_mineralogia_argila_latossolo:

- esmectitica: $T_{argila} \geq ta_threshold$ (default 27 cmolc/kg argila), indicando dominancia de argilas 2:1 expansivas (esmectita / vermiculita / micas hidratadas).
- caulinitica: $Ki \geq ki_caulinitico_min$ (default 0.75) e $Kr \geq kr_caulinitico_min$ (default 0.75), alem de $T_{argila} < ta_threshold$.
- oxidica: $Kr < kr_caulinitico_min$, indicando predominancia de oxihidroóxidos de Fe e Al.
- mista: nenhum dos outros gates fechou conclusivamente – evidencia heterogenea ou incompleta.

Quando os tres atributos (T_{argila} , Ki , Kr) estiverem ausentes, o resultado fica NULL e os atributos faltantes sao reportados.

Usage

```
familia_mineralogia_argila_geral(
  pedon,
  max_depth_cm = 200,
  ta_threshold = 27,
  ki_caulinitico_min = 0.75,
  kr_caulinitico_min = 0.75
)
```

Arguments

pedon	A PedonRecord .
max_depth_cm	Profundidade da secao de controle (default 200).
ta_threshold	Limite cmolc/kg argila para esmectitica (default 27).
ki_caulinitico_min	Limite Ki para caulinitica (default 0.75).
kr_caulinitico_min	Limite Kr para caulinitica vs oxidica (default 0.75).

Value

[FamilyAttribute](#).

References

Embrapa (2018), SiBCS 5a ed., Cap 18, p 286-287.

FamilyAttribute *Classe S4-like para atributos de Familia (5o nivel SiBCS)*

Description

Classe S4-like para atributos de Familia (5o nivel SiBCS)

Classe S4-like para atributos de Familia (5o nivel SiBCS)

Details

Estrutura categorica (em vez de booleana) que representa um adjetivo composto da Familia. value eh o adjetivo atribuido (string) ou NULL quando a dimensao nao se aplica ou nao foi possivel determinar.

Public fields

name Nome da dimensao (e.g. "grupamento_textural").

value Adjetivo atribuido (e.g. "argilosa") ou NULL.

evidence Lista nomeada com valores intermediarios.

missing Vetor de colunas necessarias mas indisponiveis.

reference String com referencia bibliografica.

Methods

Public methods:

- [FamilyAttribute\\$new\(\)](#)
- [FamilyAttribute\\$print\(\)](#)
- [FamilyAttribute\\$clone\(\)](#)

Method new(): Build a FamilyAttribute.

Usage:

```
FamilyAttribute$new(
  name,
  value = NULL,
  evidence = list(),
  missing = character(0),
  reference = ""
)
```

Arguments:

name Nome da dimensao (e.g. "grupamento_textural").

value Adjetivo atribuido (e.g. "argilosa") ou NULL.

evidence Lista nomeada com valores intermediarios.
 missing Vetor de colunas necessarias mas indisponiveis.
 reference String com referencia bibliografica.

Method print(): Pretty-print the attribute.

Usage:

```
FamilyAttribute$print(...)
```

Arguments:

... Ignored (S3 print signature compatibility).

Method clone(): The objects of this class are cloneable with this method.

Usage:

```
FamilyAttribute$clone(deep = FALSE)
```

Arguments:

deep Whether to make a deep clone.

febr_index_munsell *Curated index of FEBR datasets that carry Munsell colors*

Description

Returns a data.frame listing FEBR dataset IDs that have at least one Munsell-related column populated in their camada table, with metadata: n_horizons, n_finite_munsell, coverage, column_pattern.

Usage

```
febr_index_munsell(min_coverage = 0.1, refresh = FALSE, verbose = TRUE)
```

Arguments

min_coverage	Drop datasets whose Munsell coverage (fraction of horizons with non-NA hue) is below this. Default 0.1.
refresh	Logical. If TRUE, re-scan FEBR over the network instead of using the bundled May-2026 cache.
verbose	If TRUE (default), prints a one-line summary.

Details

Backed by a precomputed cache shipped in R/sysdata.rda (.FEBR_MUNSELL_INDEX; results of the May 2026 scan over 249 datasets). On first call after install, returns the cache instantly. Pass refresh = TRUE to re-scan FEBR live (slow, network-dependent; updates the in-memory copy but does not modify the bundled cache).

Value

A data.frame sorted by n_finite_munsell descending.

See Also

[read_febr_pedons](#).

ferralic	<i>Ferralic horizon (WRB 2022)</i>
----------	------------------------------------

Description

Tests whether any horizon meets the ferralic horizon criteria. The ferralic horizon is a subsurface horizon resulting from long and intense weathering, characterized by very low cation exchange capacity per unit clay – the canonical "low-activity clay" signal that defines the Ferralsol RSG.

Usage

```
ferralic(pedon, min_thickness = 30, max_cec = NULL, engine = NULL)
```

Arguments

pedon	A PedonRecord .
min_thickness	Minimum thickness in cm (default 30).
max_cec	Maximum CEC (1M NH ₄ OAc, pH 7) per kg clay (default NULL = 16 in soilkey engine, 20 in aqp engine; see engine).
engine	One of "soilkey" (default; strict 16 cmol _c /kg-clay threshold per WRB 2022) or "aqp" (relaxed 20 cmol _c /kg-clay – a regional tolerance that accommodates Brazilian / SOTERLAC Latossolos data, where Embrapa-style Mehlich/Ca+Mg+K+Al sum often reads ~17-20 on profiles that the canonical NRCS / WRB definition would accept as ferralic). NULL reads <code>getOption("soilkey.diagnostic_engine")</code> . The numeric threshold can also be overridden directly via <code>options(soilkey.ferralic_max_cec = ...)</code> .

Details

Sub-tests called:

- test_ferralic_texture – texture sandy loam or finer.
- test_cec_per_clay – CEC / clay ≤ 16 (or 20 under engine = "aqp") cmol_c/kg clay.
- test_ferralic_thickness – thickness ≥ 30 cm.

v0.3.1 alignment with WRB 2022 Ch 3.1.10 (p. 44): the older "ECEC ≤ 12 cmol_c/kg clay" gate was removed because it is not in the canonical text – only CEC (1M NH₄OAc, pH 7) ≤ 16 is required.

v0.9.67 regional tolerance: BDsolos RJ benchmark (n=722 perfis) showed 88/115 Latossolos failing the strict 16-cmol gate because Embrapa lab methodology often reads CEC at 17-20 on profiles that are unambiguously Latossolos by every other criterion. The engine = "aqp" threshold of 20 closes that gap without redefining the WRB threshold itself; users targeting strict WRB 2022 fidelity should keep engine = "soilkey".

The weatherable-mineral test ($\leq 10\%$ by volume), water-dispersible-clay test, and stratification / rock-structure exclusions remain deferred (they need mineralogical data outside the canonical horizon schema) and are refinements rather than gates.

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022). *World Reference Base for Soil Resources*, 4th edition. International Union of Soil Sciences, Vienna. Chapter 3.1.10 – Ferralic horizon (p. 44).

ferralsol

Ferralsol RSG gate (WRB 2022 Ch 4, p 110)

Description

WRB-canonical: ferralic horizon ≤ 150 cm AND no argic horizon starting above (or at the upper limit of) the ferralic, UNLESS the argic in its upper 30 cm or throughout has one or more of:

- $< 10\%$ water-dispersible clay; OR
- $\Delta\text{pH} (\text{pH}_{\text{KCl}} - \text{pH}_{\text{water}}) \geq 0$; OR
- $\geq 1.4\%$ soil organic carbon.

v0.3.4 enforces all three exception paths. The ΔpH check uses `ph_kcl` and `ph_h2o`; the WDC check uses `water_dispersible_clay_pct` (introduced in v0.3.3 schema).

Usage

```
ferralsol(pedon, strict = NULL)
```

Arguments

<code>pedon</code>	A PedonRecord .
<code>strict</code>	Logical or NULL. When NULL (default) it resolves via <code>getOption("soilKey.rsg_strict", FALSE)</code> . TRUE requires two of the three argic exception paths.

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

Tier-3 strict mode (v0.9.98)

When an argic horizon sits above the ferralic, the default gate keeps the profile as a Ferralsol if *any one* of the three exception paths (WDC $< 10\%$, $\Delta\text{pH} \geq 0$, SOC $\geq 1.4\%$) holds. With `strict = TRUE` the gate requires *at least two* of the three – a single weak indicator no longer rescues a profile with a translocated-clay argic from being keyed out of Ferralsols.

ferric	<i>Ferric horizon (WRB 2022)</i>
--------	----------------------------------

Description

A horizon of iron accumulation that does not reach the cementation / redness levels of plinthic. Diagnostic for the Ferric qualifier.

Usage

```
ferric(pedon, min_thickness = 15, min_fe_dith_pct = 5)
```

Arguments

pedon	A PedonRecord .
min_thickness	Minimum thickness (cm; default 15).
min_fe_dith_pct	Minimum dithionite-extractable iron percent (default 5).

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022), Chapter 3.1, Ferric horizon.

fibrico	<i>Material organico fibrico (SiBCS Cap 14)</i>
---------	---

Description

Material organico pouco decomposto: >= 40% de fibras esfregadas OU indice de von Post H1-H4. Discrimina Organossolos Fibricos no 3o nivel.

Usage

```
fibrico(pedon)
```

Arguments

pedon	A PedonRecord .
-------	---------------------------------

Value

[DiagnosticResult](#).

References

Embrapa (2018), SiBCS 5a ed., Cap 14 (Organossolos), pp 224-226.

fill_from_spectra *Fill missing soil attributes from spectra via OSSSL*

Description

Given a [PedonRecord](#) carrying a `spectra$vnir` matrix (rows = horizons, columns = wavelengths in nm), pre-processes the spectra, predicts the requested soil properties using the chosen OSSSL-backed method, and writes the predictions into the pedon's horizons table via `pedon$add_measurement(..., source = "predicted_spectra")`. Each call updates the pedon's provenance log so that downstream classification can derive an evidence grade.

Usage

```
fill_from_spectra(
  pedon,
  library = "ossl",
  region = c("global", "south_america", "north_america", "europe", "africa"),
  properties = c("clay_pct", "sand_pct", "silt_pct", "cec_cmol", "bs_pct", "ph_h2o",
    "oc_pct", "fe_dcb_pct", "caco3_pct"),
  method = c("mb1", "plsr_local", "pretrained"),
  preprocess = "snv+sg1",
  k_neighbors = 100L,
  overwrite = FALSE,
  ossl_library = NULL,
  ossl_models = NULL,
  verbose = TRUE
)
```

Arguments

pedon	A PedonRecord with a <code>spectra\$vnir</code> matrix.
library	Currently only "ossl" is supported.
region	One of "global", "south_america", "north_america", "europe", "africa". Used to subset the OSSSL training data when supported by the underlying back-end.
properties	Character vector of OSSSL-supported property names to predict. Default covers the most-requested WRB/SiBCS-relevant attributes.
method	One of "mb1", "plsr_local", "pretrained".
preprocess	Pre-processing pipeline; passed to preprocess_spectra .
k_neighbors	Number of neighbours for memory-based methods.
overwrite	If FALSE (default), only fill cells whose existing provenance is weaker than <code>predicted_spectra</code> .

ossl_library	Optional OSSL library object (see predict_ossl_mbl).
ossl_models	Optional named list of pretrained models (see predict_ossl_pretrained).
verbose	If TRUE, prints a cli summary.

Details

By default, predicted values do **not** overwrite measured values (the `add_measurement()` authority logic protects them). Setting `overwrite = TRUE` forces overwrite of any non-measured value.

Value

The mutated pedon, invisibly. Provenance entries with `source = "predicted_spectra"` are added per (horizon, property).

See Also

[preprocess_spectra](#), [predict_ossl_mbl](#), [predict_ossl_plsr_local](#), [predict_ossl_pretrained](#), [pi_to_confidence](#).

fill_munsell_from_spectra

Fill missing Munsell colors on a PedonRecord from Vis-NIR spectra

Description

High-level helper that runs [predict_munsell_from_spectra](#) per horizon over the Vis-NIR spectra in `pedon$spectra$vnir` and writes the resulting hue / value / chroma back to the matching horizon rows via `pedon$add_measurement(..., source = "predicted_spectra")`.

Usage

```
fill_munsell_from_spectra(pedon, overwrite = FALSE, verbose = TRUE)
```

Arguments

pedon	A PedonRecord that has <code>\$spectra\$vnir</code> populated (rows = horizons, cols = wavelengths).
overwrite	If TRUE, overwrite existing Munsell measurements. Default FALSE (only fills horizons whose Munsell is currently NA).
verbose	If TRUE (default), prints a per-horizon summary.

Details

This is the operational answer to the v0.9.35 Argissolo color confusion: when surveyor Munsell colors are missing and the user has Vis-NIR (e.g. from OSSL), call this helper, then re-run [classify_sibcs](#) – the v0.9.45 "color-undetermined" fallback will lift, and the classification will descend to `subordem / grande grupo / subgrupo` with proper `evidence_grade`.

Value

The pedon, invisibly. Provenance entries with source = "predicted_spectra" are appended.

fluvic_material	<i>Fluvic material (WRB 2022)</i>
-----------------	-----------------------------------

Description

Tests whether the profile shows fluvic material features: alternating textures across consecutive horizons within the upper 100 cm AND an irregular (non-monotone) organic carbon pattern with depth. Diagnostic of Fluvisols.

Usage

```
fluvic_material(pedon, max_top_cm = 100, min_clay_swing = 8)
```

Arguments

pedon	A PedonRecord .
max_top_cm	Maximum top depth (cm) considered (default 100).
min_clay_swing	Minimum absolute clay-percent change between consecutive layers required to count as alternation (default 8 percentage points).

Details

Sub-test: test_fluvic_stratification.

v0.3 limitations: WRB 2022 fluvic material also requires age (typically <100 years for sediment freshness), which v0.3 does not check (no temporal fields in the schema). The stratification proxy is conservative – truly heterogeneous floodplain profiles with dramatic texture swings will pass; subtle alluvial sequences may miss. v0.4 will refine.

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022), Chapter 3, Fluvic material.

format_wrb_name	<i>Format a WRB 2022 soil name with qualifiers</i>
-----------------	--

Description

Format a WRB 2022 soil name with qualifiers

Usage

```
format_wrb_name(
  rsg_name,
  principal = character(0),
  supplementary = character(0)
)
```

Arguments

rsg_name	Full RSG name (e.g. "Ferralsols").
principal	Character vector of principal-qualifier names.
supplementary	Character vector of supplementary-qualifier names (default empty in v0.9).

Value

Formatted string per Ch 6 p 154 ("Rhodic Ferralsol (Clayic, Humic, Dystric)").

fragic	<i>Fragic horizon (WRB 2022): a high-bulk-density horizon with restricted rooting. v0.3.3: detects via bulk_density_g_cm3 >= 1.65 AND structure grade massive/very firm OR designation pattern x/Bx.</i>
--------	---

Description

Fragic horizon (WRB 2022): a high-bulk-density horizon with restricted rooting. v0.3.3: detects via bulk_density_g_cm3 >= 1.65 AND structure grade massive/very firm OR designation pattern x/Bx.

Usage

```
fragic(pedon, min_thickness = 15, min_bd = 1.65)
```

Arguments

pedon	A PedonRecord .
min_thickness	Numeric threshold or option (see Details).
min_bd	Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

fragipa	<i>Fragipa (SiBCS Cap 2, p 73-74; v0.7)</i>
---------	---

Description

Reuso de [fragipic](#) (WRB v0.3.3): horizonte subsuperficial endurecido quando seco, baixa MO, BD elevada, quebradicidade.

Usage

```
fragipa(pedon, ...)
```

Arguments

pedon	A PedonRecord .
...	Reserved for future arguments.

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

from_aqp	<i>Convert an aqp SoilProfileCollection back to a list of PedonRecord</i>
----------	---

Description

Inverse of [as_aqp](#). Walks each profile in the SPC, renames aqp's canonical horizon column names back to soilKey's (top -> top_cm, name -> designation, clay -> clay_pct, ...), assembles a [PedonRecord](#) per profile, and returns the list.

Usage

```
from_aqp(spc)
```

Arguments

spc	A <code>aqp::SoilProfileCollection</code> .
-----	---

Details

Round-trip property: `from_aqp(as_aqp(pedon))` reproduces pedon modulo column ordering.

Value

A list of [PedonRecord](#) objects (length = length(spc)).

See Also

[as_aqp](#), the forward conversion.

Examples

```
## Not run:
pedons <- list(make_ferralsol_canonical(), make_luvisol_canonical())
spc <- as_aqp(pedons)
pedons2 <- from_aqp(spc)
identical(pedons[[1]]$horizons$clay_pct, pedons2[[1]]$horizons$clay_pct)
#> [1] TRUE

## End(Not run)
```

gapfill_by_predicted_taxon

Fill missing horizon attributes from the predicted taxon's mean profile

Description

Classifies pedon with NO fill to get a provisional taxon, then fills its missing cells from `taxon_profiles[[<that taxon>]]` (built by [build_taxon_profiles](#)). Non-circular: the fill is keyed on the model's own prediction, not the reference. Each fill is written with `source = "inferred_prior"` (grade C). Reachable via `gapfill = list(method = "taxon", taxon_profiles = <...>)`.

Usage

```
gapfill_by_predicted_taxon(
  pedon,
  taxon_profiles,
  system = c("sibcs", "wrb2022", "usda"),
  attrs = NULL,
  confidence = 0.55
)
```

Arguments

pedon	A PedonRecord .
taxon_profiles	Output of build_taxon_profiles .
system	One of "sibcs" (default), "wrb2022", "usda".
attrs	Attributes to fill (default: those present in the matched profile).
confidence	Provenance confidence (default 0.55, below a coordinate prior).

Value

Invisibly, the mutated pedon; attribute "gapfill_by_predicted_taxon" records the taxon + cells filled.

See Also

[build_taxon_profiles](#), [apply_soilgrids_depth_prior](#)

gapfill_derive_horizon

Fill horizon attributes derivable BY DEFINITION from the same horizon

Description

Recovers cells that are exact closures of other measured columns in the same horizon (not statistical estimates): the texture third (clay/silt/sand) when the other two are present and sum to ≤ 100 ; effective CEC as $\text{sum}(\text{bases}) + a1$; aluminium saturation as $100 * a1 / \text{ecec}$; and base saturation as $100 * \text{sum}(\text{bases}) / \text{cec}$. Every fill is written with source = "inferred_prior" so the [PedonRecord](#) authority order keeps it from displacing a measured value and the evidence grade drops to "C". Companion to [gapfill_within_pedon](#) (depth interpolation) and [apply_soilgrids_depth_prior](#) (external prior); reachable via the `gapfill = list(method = "derive")` argument of the classifiers.

Usage

```
gapfill_derive_horizon(pedon, overwrite = FALSE)
```

Arguments

pedon	A PedonRecord .
overwrite	If FALSE (default) only NA target cells are filled.

Value

Invisibly, the mutated pedon; attribute "gapfill_derive_horizon" records the count filled.

See Also

[gapfill_within_pedon](#), [apply_soilgrids_depth_prior](#)

gapfill_within_pedon *Fill interior missing horizon attributes by within-pedon depth interpolation*

Description

For each requested attribute, builds a depth profile from the horizons in which that attribute is *measured* (non-NA) and linearly interpolates the value at the mid-depth of every horizon where it is missing – but only for horizons whose mid-depth falls strictly between the shallowest and deepest measured layer. Cells above the top or below the bottom measured layer are left NA: the function interpolates, it never extrapolates. Each fill is written with source = "inferred_prior", so the [PedonRecord](#) authority order keeps it from displacing a measured, spectra-predicted or VLM-extracted value, and any downstream `compute_evidence_grade` call reports grade "C".

Usage

```
gapfill_within_pedon(pedon, attrs = NULL, confidence = 0.6, overwrite = FALSE)
```

Arguments

pedon	A PedonRecord with at least two horizons.
attrs	Character vector of horizon columns to fill. Defaults to the continuous depth-trending attributes a linear interpolation can reasonably estimate (clay/silt/sand, pH, organic carbon, CEC/ECEC, base/aluminium saturation, bulk density).
confidence	Numeric in $[0, 1]$ recorded as the provenance confidence of each interpolated cell. Defaults to 0.6 – below a measured value but anchored on the profile's own data, hence above the 0.5 used for an external SoilGrids prior.
overwrite	If FALSE (default) only NA cells are filled. If TRUE, non-measured cells are re-interpolated (measured cells are still never overwritten, and the provenance authority order is always respected).

Details

This is the within-pedon companion to [apply_soilgrids_depth_prior](#) (which fills from an external SoilGrids profile rather than from the profile's own measured layers). It is the mechanism behind the opt-in `gapfill` argument of [classify_wrb2022](#), [classify_sibcs](#), [classify_usda](#) and [classify_all](#).

Note that this mutates `pedon` in place (as [apply_soilgrids_depth_prior](#) does). The `gapfill` argument of the classifiers operates on a deep copy instead, so a classification call never alters the caller's `pedon`.

Value

Invisibly, the mutated `pedon`. An attribute "gapfill_within_pedon" on the return value records how many cells were filled and for which attributes.

See Also

[apply_soilgrids_depth_prior](#), [classify_all](#)

Examples

```
h <- data.frame(
  top_cm    = c(0, 20, 40, 60),
  bottom_cm = c(20, 40, 60, 90),
  clay_pct  = c(15, NA, 35, 40)
)
p <- PedonRecord$new(horizons = h)
gapfill_within_pedon(p, attrs = "clay_pct")
p$horizons$clay_pct # second horizon filled to ~25 by interpolation
```

get_perturbation_scale

Monte-Carlo perturbation scale for an evidence grade

Description

Returns the noise magnitudes used by [classify_with_uncertainty](#) for a cell of the given evidence grade. A measurement (grade A) is perturbed only slightly; a user-assumed value (grade E) is perturbed heavily, reflecting how little is actually known about it.

Usage

```
get_perturbation_scale(grade = c("A", "B", "C", "D", "E"))
```

Arguments

grade	One of "A" (measured), "B" (spectra-predicted), "C" (prior-inferred), "D" (VLM-extracted) or "E" (user-assumed).
-------	--

Value

A list with three elements: pct (the half-width of the multiplicative perturbation, applied to most numeric attributes), ph_abs (the half-width of the additive perturbation applied to pH columns) and munsell_abs (the additive half-width for Munsell value / chroma columns).

Examples

```
get_perturbation_scale("A")$pct # 0.03 -- measured values barely move
get_perturbation_scale("E")$pct # 0.30 -- assumptions move a lot
```

gleyic_properties *Gleyic properties (WRB 2022)*

Description

Tests whether the profile shows gleyic properties – evidence of prolonged saturation by groundwater – within the upper 50 cm. Gleyic properties are diagnostic for Gleysols and qualify many other RSGs (Endogleyic, Epigleyic qualifiers).

Usage

```
gleyic_properties(
  pedon,
  max_top_cm = 50,
  min_redox_pct = 5,
  stagnic_decay_factor = 3
)
```

Arguments

pedon	A PedonRecord .
max_top_cm	Maximum top depth (cm) of a candidate layer (default 50, per WRB 2022).
min_redox_pct	Minimum redoximorphic_features_pct (default 5).
stagnic_decay_factor	Numeric threshold or option (see Details).

Details

Sub-test: test_gleyic_features – requires explicit redoximorphic_features_pct $\geq 5\%$ within the upper 50 cm.

v0.2 deliberately does NOT use the Munsell-based shortcut (chroma $\leq 2 + \text{value} \geq 4$) as a primary criterion: that pattern fits albic / bleached horizons of Podzols just as well as truly reduced gleyic horizons. v0.3 will add reductimorphic / oxidimorphic feature discrimination once we model field-described mottle properties. v0.9.72 adds the designation-suffix path (opt-in).

Value

A [DiagnosticResult](#).

v0.9.72 designation morphological inference (opt-in)

Field-described Brazilian Gleissolos profiles (e.g. the Embrapa Redape curated dataset) routinely encode gleyic properties via the designation suffix g (e.g. Cg, Cg1, Cgn, Apg) plus low-chroma Munsell colours (chroma ≤ 2), without recording redoximorphic_features_pct as a numeric percent. The strict canonical test then returns NA on every horizon and Gleissolos cascade to other Orders.

With options(soilKey.gleyic_designation_inference = TRUE) the function accepts a layer as gleyic when:

1. the canonical redoximorphic_features_pct test is NA for that layer, AND
2. the designation matches [A-Z]+g[0-9a-z]? (a horizon name with a g suffix in the master letter sequence, e.g.\ Cg, Bg2, Apg, Cgn), AND
3. the layer has munsell_chroma_moist <= 2 (low-chroma reduced colour) when Munsell is recorded; if Munsell is missing on the layer the suffix alone is sufficient (designation suffix is the most direct signal of pedologist field judgment).

This is conservative: the suffix g is a master-letter modifier in the FAO/Embrapa horizon nomenclature that explicitly means "gleyic-affected" – the curator already made the call. Default is FALSE (canonical behaviour preserved).

References

IUSS Working Group WRB (2022), Chapter 3, Gleyic properties.

gleysol

Gleysol RSG gate (WRB 2022 Ch 4, p 103)

Description

WRB-canonical (multi-path):

1. Layer ≥ 25 cm starting ≤ 40 cm with gleyic properties throughout AND reducing conditions in some parts of every sublayer; OR
2. Mollic/umbric > 40 cm thick with reducing conditions some parts of every sublayer 40 cm below mineral surface to lower limit, AND directly underneath a layer ≥ 10 cm with lower limit ≥ 65 cm having gleyic properties + reducing conditions; OR
3. Permanent saturation by water ≤ 40 cm.

v0.3.4 enforces path 1 (the dominant path) and path 3 via designation (W / saturated marker). Path 2 is deferred (requires a depth-of- saturation column that's not standard).

Usage

```
gleysol(pedon, strict = NULL)
```

Arguments

pedon	A PedonRecord .
strict	Logical or NULL. When NULL (default) it resolves via <code>getOption("soilKey.rsg_strict", FALSE)</code> . TRUE tightens path 1 and disables path 3.

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

Tier-3 strict mode (v0.9.98)

With `strict = TRUE` the path-1 gleyic+reducing layer must start within the upper 25 cm (instead of 40 cm), and the path-3 designation-only fallback (a “W” / aquic marker) is disabled: strict mode requires measured gleyic and reducing evidence.

grapes-or-or-grapes *Default-value-for-NULL operator*

Description

Returns the left-hand side if it is non-NULL, otherwise the right-hand side. Re-exported so that downstream code can use the same idiom `soilKey` itself uses internally.

Usage

`a %||% b`

Arguments

`a` The candidate value.
`b` The fallback used when `a` is NULL.

Value

Either `a` or `b`.

GSM_DEPTHS *Default GlobalSoilMap depth intervals (cm)*

Description

GSM standard per Arrouays et al. (2014) "GlobalSoilMap: Toward a fine-resolution global grid of soil properties". Boundaries: 0-5, 5-15, 15-30, 30-60, 60-100, 100-200 cm.

Usage

`GSM_DEPTHS`

Format

An object of class `numeric` of length 7.

gypsic	<i>Gypsic horizon (WRB 2022)</i>
--------	----------------------------------

Description

Tests whether any horizon meets the gypsic horizon criteria. The gypsic horizon is a horizon of secondary gypsum accumulation, diagnostic for Gypsisols.

Usage

```
gypsic(pedon, min_thickness = 15, min_gypsum_pct = 5)
```

Arguments

pedon A [PedonRecord](#).
min_thickness Minimum thickness in cm (default 15).
min_gypsum_pct Minimum gypsum percent in fine earth (default 5).

Details

Sub-tests called:

- test_caso4_concentration – gypsum \geq 5%.
- test_minimum_thickness – thickness \geq 15 cm.

v0.2 limitations: the WRB rule that gypsum content must exceed the underlying horizon by 1% (absolute) is not enforced. Petrogypsic (cemented) horizons are not yet detected. Both deferred to v0.3.

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022). *World Reference Base for Soil Resources*, 4th edition. International Union of Soil Sciences, Vienna. Chapter 3 – Gypsic horizon.

gypsiric_material	<i>Gypsic material (WRB 2022 Ch 3.3.7): $\geq 5\%$ gypsum that is primary (not secondary). Without a "secondary fraction" schema column, v0.3.3 treats any layer with caso4_pct ≥ 5 as gypsiric unless it explicitly carries gypsic-horizon designation.</i>
-------------------	---

Description

Gypsic material (WRB 2022 Ch 3.3.7): $\geq 5\%$ gypsum that is primary (not secondary). Without a "secondary fraction" schema column, v0.3.3 treats any layer with caso4_pct ≥ 5 as gypsiric unless it explicitly carries gypsic-horizon designation.

Usage

```
gypsiric_material(pedon, min_caso4_pct = 5)
```

Arguments

pedon	A PedonRecord .
min_caso4_pct	Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

harmonize_to_gsm	<i>Harmonise pedons to GlobalSoilMap depth intervals</i>
------------------	--

Description

Runs `mpspline2::mpspline_tidy()` on each requested numeric horizon attribute, producing a new `PedonRecord` per input pedon whose horizons table covers the canonical GSM intervals (`GSM_DEPTHS`). Categorical attributes (designation, Munsell hue) are propagated by mode-over-depth-overlap.

Usage

```
harmonize_to_gsm(
  pedons,
  attributes = c("clay_pct", "silt_pct", "sand_pct", "ph_h2o", "oc_pct", "cec_cmol",
    "base_saturation_pct", "munsell_value_moist", "munsell_chroma_moist",
    "redoximorphic_features_pct"),
  depths = GSM_DEPTHS,
  lam = 0.1,
  verbose = TRUE
)
```

Arguments

pedons	A list of PedonRecord objects.
attributes	Character vector of numeric horizon column names to harmonise. Default covers the chemistry / texture / Munsell numeric columns the soilKey diagnostics use.
depths	Numeric vector of GSM depth boundaries (n+1 values for n intervals). Default GSM_DEPTHS .
lam	Smoothing parameter for the spline (default 0.1, per Bishop et al. 1999 recommendation).
verbose	If TRUE (default), emits cli progress.

Value

A list of new [PedonRecord](#) objects with harmonised horizons.

Why mass-preserving

The Bishop et al. (1999) spline conserves the integral of the attribute over depth: if the original pedon has 30 g/kg OC over 0-15 cm, the harmonised pedon will report 30 g/kg integrated over 0-15 cm (split between 0-5 and 5-15 in proportion to the spline-implied gradient). This is a critical property for benchmark integrity: simple linear interpolation does not preserve mass and biases means upward / downward systematically.

Categorical handling

designation and munsell_hue_moist (and other character columns in the horizon schema) cannot be splined. Instead, for each target GSM interval, we pick the modal value weighted by the depth-overlap fraction with the input horizons. Ties broken by uppermost-input-horizon precedence.

References

Bishop, T.F.A., McBratney, A.B., Laslett, G.M. (1999). "Modelling soil attribute depth functions with equal-area quadratic smoothing splines." *Geoderma* 91: 27-45.

Arrouays, D. et al. (2014). "GlobalSoilMap: Toward a fine-resolution global grid of soil properties." *Advances in Agronomy* 125: 93-134.

See Also

`mpspline2::mpspline_tidy`, [GSM_DEPTHS](#).

hemico	<i>Material organico hemico (SiBCS Cap 14)</i>
--------	--

Description

Material organico em decomposicao intermediaria: 17-40% de fibras esfregadas OU indice de von Post H5-H6. Discrimina Organossolos Hemicos no 3o nivel.

Usage

hemico(pedon)

Arguments

pedon A [PedonRecord](#).

Value

[DiagnosticResult](#).

References

Embrapa (2018), SiBCS 5a ed., Cap 14 (Organossolos), pp 224-226.

histic_horizon	<i>Histic horizon (WRB 2022)</i>
----------------	----------------------------------

Description

A surface (or near-surface, after drainage) horizon of organic material; diagnostic of Histosols. Two alternative qualifying paths per WRB 2022:

- **Contiguous:** a single layer of organic material (OC % \geq min_oc) reaching the surface and at least min_thickness cm thick (default 10 cm).
- **Cumulative:** organic material totalling cumulative_min_cm cm (default 40) within the upper cumulative_max_depth_cm (default 80). Relevant for folic / mossy Histosols on slopes.

Either path qualifies. The "after drainage" qualifier (recently drained organic soils) is treated as implicit since the same OC and thickness criteria apply.

Usage

```

histic_horizon(
  pedon,
  min_thickness = 10,
  min_oc = 12,
  surface_top_cm = 0,
  cumulative_min_cm = 40,
  cumulative_max_depth_cm = 80
)

```

Arguments

pedon	A PedonRecord .
min_thickness	Minimum thickness (cm) for the contiguous path (default 10).
min_oc	Minimum organic carbon % (default 12, WRB 2022; equivalent to >= 20% organic matter).
surface_top_cm	Maximum top depth (cm) for a layer to be considered "surface-related" in the contiguous path (default 0).
cumulative_min_cm	Minimum cumulative thickness (cm) for the cumulative path (default 40).
cumulative_max_depth_cm	Depth window (cm) for the cumulative path (default 80).

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022), Chapter 3, Histic horizon and organic material.

horizon_column_spec *Canonical horizon column specification*

Description

Returns the schema for the horizons data.table carried by a [PedonRecord](#): an ordered named list mapping column names to their R type ("numeric" or "character"). Adding a new attribute means editing this single function.

Usage

```
horizon_column_spec()
```

Value

Named list of column types in canonical order.

Examples

```
spec <- horizon_column_spec()
head(names(spec))
```

hortic	<i>Hortic horizon (WRB 2022): garden / kitchen-midden topsoil. Diagnostic criteria: thickness \geq 20 cm, dark colour (mollic-like), high P (Mehlich-3 P \geq 100 mg/kg or P2O5_1pct_citric \geq 175 mg/kg), high SOC.</i>
--------	---

Description

Hortic horizon (WRB 2022): garden / kitchen-midden topsoil. Diagnostic criteria: thickness \geq 20 cm, dark colour (mollic-like), high P (Mehlich-3 P \geq 100 mg/kg or P2O5_1pct_citric \geq 175 mg/kg), high SOC.

Usage

```
hortic(pedon, min_thickness = 20, min_oc = 1, min_p_mehlich3 = 100)
```

Arguments

pedon	A PedonRecord .
min_thickness	Numeric threshold or option (see Details).
min_oc	Numeric threshold or option (see Details).
min_p_mehlich3	Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

hydragric	<i>Hydragric horizon (WRB 2022): subsoil hydric horizon under anthraquic. v0.3.3 detects via designation pattern Bg Brg immediately below an anthraquic-like topsoil.</i>
-----------	---

Description

Hydragric horizon (WRB 2022): subsoil hydric horizon under anthraquic. v0.3.3 detects via designation pattern Bg|Brg immediately below an anthraquic-like topsoil.

Usage

```
hydragric(pedon, min_thickness = 20)
```

Arguments

- pedon A [PedonRecord](#).
- min_thickness Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

hypersulfidic_material

Hypersulfidic material (WRB 2022 Ch 3.3.8): $\geq 0.01\%$ inorganic sulfidic S, pH ≥ 4 , capable of severe acidification on aerobic incubation.

Description

Hypersulfidic material (WRB 2022 Ch 3.3.8): $\geq 0.01\%$ inorganic sulfidic S, pH ≥ 4 , capable of severe acidification on aerobic incubation.

Usage

```
hypersulfidic_material(pedon, min_s_pct = 0.01, min_pH = 4)
```

Arguments

- pedon A [PedonRecord](#).
- min_s_pct Numeric threshold or option (see Details).
- min_pH Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

`hyposulfidic_material` *Hyposulfidic material (WRB 2022 Ch 3.3.9): same inorganic sulfidic S and field pH as hypersulfidic but does NOT consist of hypersulfidic (criterion 3 – does not acidify to pH < 4 on aerobic incubation, usually self-neutralised by carbonate). Reachable from v0.9.128: when incubation_ph is measured, a sulfidic + pH ≥ 4 layer that stays ≥ 4 on incubation is the set-complement of [hypersulfidic_material](#) and is reported here. Without an incubation pH the two cannot be told apart, so this returns empty (the layer is reported as potential hypersulfidic instead).*

Description

Hyposulfidic material (WRB 2022 Ch 3.3.9): same inorganic sulfidic S and field pH as hypersulfidic but does NOT consist of hypersulfidic (criterion 3 – does not acidify to pH < 4 on aerobic incubation, usually self-neutralised by carbonate). Reachable from v0.9.128: when incubation_ph is measured, a sulfidic + pH ≥ 4 layer that stays ≥ 4 on incubation is the set-complement of [hypersulfidic_material](#) and is reported here. Without an incubation pH the two cannot be told apart, so this returns empty (the layer is reported as potential hypersulfidic instead).

Usage

```
hyposulfidic_material(pedon, min_s_pct = 0.01, min_ph = 4)
```

Arguments

<code>pedon</code>	A PedonRecord .
<code>min_s_pct</code>	Numeric threshold or option (see Details).
<code>min_ph</code>	Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

`inspect_bdsolos_csv` *Diagnostic inspection of a Bdsolos CSV before loading*

Description

Reads the CSV header, attempts to map each column to the soilKey horizon schema via `.bdsolos_match_column`, and prints three sections:

Usage

```
inspect_bdsolos_csv(path, sep = NULL)
```

Arguments

path	Path to the CSV downloaded from BDsolos.
sep	Field separator (default ", "; some BDsolos exports use "; " or tab).

Details

- **Mapped columns** – BDsolos name -> soilKey name
- **Unmapped columns** – columns the loader will ignore (review these before running `load_bdsolos_csv` to make sure no critical attribute is silently dropped)
- **Munsell coverage** – whether matiz / valor / cromax are present in either umido or seco variants

Run this before `load_bdsolos_csv` on any new CSV from BDsolos, especially if the export schema looks unfamiliar (BDsolos has shipped multiple schema versions over the years).

Value

Invisibly, a list with mapped, unmapped, munsell_present, taxon_column.

irragric	<i>Irragric horizon (WRB 2022): topsoil thickened by irrigation deposits. v0.3.3: thickness >= 20 cm + sediment-derived structure proxied via designation Apk Apg Au.</i>
----------	--

Description

Irragric horizon (WRB 2022): topsoil thickened by irrigation deposits. v0.3.3: thickness >= 20 cm + sediment-derived structure proxied via designation Apk|Apg|Au.

Usage

```
irragric(pedon, min_thickness = 20)
```

Arguments

pedon	A PedonRecord .
min_thickness	Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

kastanozem	<i>Kastanozem RSG diagnostic (WRB 2022)</i>
------------	---

Description

Tests whether a profile satisfies the Kastanozem RSG criteria: a mollic horizon plus secondary carbonates plus NOT-Chernozem colour (chroma (moist) > 2 in the upper 20 cm).

Usage

```
kastanozem(pedon, max_chroma_upper = 2)
```

Arguments

pedon	A PedonRecord .
max_chroma_upper	Maximum moist chroma to qualify as Chernozem (default 2). Kastanozem requires the upper-20-cm chroma to EXCEED this value.

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022), Chapter 5, Kastanozems.

kastanozem_strict	<i>Kastanozem RSG gate (strengthened, WRB 2022 Ch 4, p 112)</i>
-------------------	---

Description

Same structure as [chernozem_strict](#) but using the mollic horizon (no chernic gate) and starting \<= 70 cm of mineral soil surface.

Usage

```
kastanozem_strict(pedon, min_bs = 50, max_top_cm = 70, strict = NULL)
```

Arguments

pedon	A PedonRecord .
min_bs	Numeric threshold or option (see Details).
max_top_cm	Numeric threshold or option (see Details).
strict	Logical or NULL. When NULL (default) it resolves via <code>getOption("soilKey.rsg_strict", FALSE)</code> . TRUE raises the base-saturation floor to 75%.

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

Tier-3 strict mode (v0.9.98)

With `strict = TRUE` the base-saturation floor above the carbonate-bearing layer is raised from 50% to 75%. The 70 cm carbonate-depth window is left unchanged.

kst13_canonical	<i>Keys to Soil Taxonomy 13th edition canonical reference</i>
-----------------	---

Description

Convenience wrapper for `canonical_reference("ST_criteria_13th")`. Returns a nested list of 3,153 parsed Keys-to-Soil-Taxonomy clauses per chapter / page / key / taxon / code / clause / logic.

Usage

```
kst13_canonical(prefer_pkg = TRUE)
```

Arguments

<code>prefer_pkg</code>	If TRUE (default), prefer the installed SoilTaxonomy package over the vendored copy. Set to FALSE to force the vendored copy (e.g. for reproducibility of a specific soilKey release).
-------------------------	--

Details

Source: NCSS-tech SoilTaxonomy R package. Original: [USDA-NRCS \(2022\). *Keys to Soil Taxonomy*, 13th edition.](#)

Value

The canonical *Keys to Soil Taxonomy* (13th ed.) criteria reference (a list / data.frame).

kst13_codes

Load the canonical KST 13ed code -> taxon-name lookup table

Description

Returns the 3,153-row data.frame from `inst/rules/usda/canonical/2022_KST_codes.json`, vendored from NCSS-tech/SoilKnowledgeBase. Each row is a (code, name) pair.

Usage

```
kst13_codes()
```

Details

Code structure:

- Single letter ("A"- "L"): Soil Order (Gelisols, Histosols, ..., Entisols)
- Two letters ("AB", "AC", ...): Suborder
- Three letters: Great Group
- Four letters: Subgroup

Value

A data.frame with columns `code`, `name`.

See Also

[kst13_criteria](#), [kst13_canonical](#).

kst13_criteria

Load the canonical KST 13ed criteria for a single taxon code

Description

Returns the parsed clause data.frame for one code (e.g. "A" for Gelisols, "ABA" for Histels.Folistels, etc.). Each row is one clause of the diagnostic text with content, chapter, page columns.

Usage

```
kst13_criteria(code)
```

Arguments

`code` Character. Taxon code in the KST 13ed code system (e.g. "A" for Gelisols, "ABCD" for the Lithic Folistels subgroup).

Details

For the full 3,153-element nested list (all codes), use [kst13_canonical](#) (which loads the SoilTaxonomy R-package RDA equivalent).

Value

A data.frame with the parsed clauses for that code, or NULL if the code is not present.

See Also

[kst13_codes](#), [kst13_canonical](#).

leptic_features	<i>Leptic features (WRB 2022)</i>
-----------------	-----------------------------------

Description

Tests whether continuous rock or rock-like material occurs within max_depth cm of the surface. Two alternative paths qualify per WRB 2022:

1. **Designation:** a layer at depth \leq max_depth with designation matching "^R" or "^{Cr}" (continuous rock or weathered rock-like substrate).
2. **Coarse fragments:** a layer at depth \leq max_depth with coarse_fragments_pct \geq min_coarse_pct (default 90% by volume), interpreted as rock-dominated even when not R / Cr-designated.

Either path qualifies.

Usage

```
leptic_features(pedon, max_depth = 25, min_coarse_pct = NULL, engine = NULL)
```

Arguments

pedon	A PedonRecord .
max_depth	Maximum depth (cm) at which continuous rock or rock-dominated material must appear (default 25).
min_coarse_pct	Minimum coarse-fragment percent for the coarse-fragments path (default 90 in soilkey engine, 50 in aqp engine; NULL picks a default per engine).
engine	One of "soilkey" (default; strict 90\ cfvo threshold) or "aqp" (LUCAS-friendly relaxed 50\ requiring positive evidence of rock contact – v0.9.66 tightening). The thin-topsoil path fires only when a horizon ending within max_depth also satisfies <i>at least one</i> of: (a) designation contains "R" (e.g.\ AR, BR, Cr, R, Rk), (b) coarse_fragments_pct \geq 30 (gravelly), or (c) a deeper horizon is R/Cr-designated. Users with a strong external prior (e.g.\ a parent-material survey that documents rock < 25 cm but did not record it in the horizon table) can opt back into the original v0.9.65 loose behaviour with options(soilkey.leptic_assume_rock_below = TRUE). NULL (the default) reads getOption("soilkey.diagnostic_engine").

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022), Chapter 5, Leptosols.

limnic_material	<i>Limnic material (WRB 2022 Ch 3.3.10): subaquatic deposits (coprogenous earth, diatomaceous earth, marl, gyttja). v0.3.3: detects via rock_origin %in% c("lacustrine", "marine") or designation pattern.</i>
-----------------	--

Description

Limnic material (WRB 2022 Ch 3.3.10): subaquatic deposits (coprogenous earth, diatomaceous earth, marl, gyttja). v0.3.3: detects via rock_origin %in% c("lacustrine", "marine") or designation pattern.

Usage

```
limnic_material(pedon)
```

Arguments

pedon A [PedonRecord](#).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

limonic	<i>Limonic horizon (WRB 2022 Ch 3.1)</i>
---------	--

Description

From Greek *leimon* = meadow. A subaqueous / wet-meadow horizon showing accumulation of secondary Fe/Mn (oxi)hydroxides from fluctuating redox cycles. Distinct from *limnic material* (Ch 3.3.10), which is the parent material; the limonic horizon is the *soil* horizon derived from such material plus subsequent pedogenesis.

Usage

```
limonic(pedon, min_thickness = 5, min_redox_pct = 5)
```

Arguments

pedon	A PedonRecord .
min_thickness	Numeric threshold or option (see Details).
min_redox_pct	Numeric threshold or option (see Details).

Details

v0.3.5 detection: redoximorphic_features_pct ≥ 5 AND designation pattern Bm / Bjm / m as proxy for past meadow wetness.

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

lithic_discontinuity *Lithic discontinuity (WRB 2022 Ch 3.2.7)*

Description

Significant abrupt change in parent material between two layers. v0.3.3 simplified: detects via large discontinuity in coarse_fragments_pct (≥ 10 pp absolute jump) OR rock_origin difference between consecutive layers.

Usage

```
lithic_discontinuity(pedon)
```

Arguments

pedon	A PedonRecord .
-------	---------------------------------

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

lixisol	<i>Lixisol RSG diagnostic (WRB 2022)</i>
---------	--

Description

argic + CEC < 24 cmol_c/kg clay + BS >= 50%.

Usage

```
lixisol(pedon, max_cec = 24, min_bs = 50)
```

Arguments

pedon	A PedonRecord .
max_cec	Maximum CEC per kg clay (default 24).
min_bs	Minimum base saturation % (default 50).

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022), Chapter 5, Lixisols.

load_afsp_pedons	<i>Load Africa Soil Profiles (AfSP) v1.2 as PedonRecord objects</i>
------------------	---

Description

Reads the AfSP DBase tables shipped inside AF-AfSP1.2.zip (downloadable from <https://files.isric.org/public/afsp>) and converts each profile + its horizons to a soilKey [PedonRecord](#). Filters to profiles with a populated WRB 2006 RSG code (i.e. \ classifiable; AfSP has ~7000 of these of the total 18,533).

Usage

```
load_afsp_pedons(
  afsp_dir,
  max_n = NULL,
  countries = NULL,
  wrb_codes = NULL,
  verbose = TRUE
)
```

Arguments

afsp_dir	Directory containing the extracted AfSP DBase tables (AfSP012Qry_Profiles.dbf, AfSP012Qry_Layers.dbf).
max_n	Optional integer; take a random sample of this size from the classifiable profiles.
countries	Optional character vector of ISO country codes to keep (e.g. c("MW", "ET", "TZ")).
wrb_codes	Optional character vector of WRB 2006 RSG codes to keep (e.g. c("VR", "FR", "AC")).
verbose	Print progress.

Value

A list of [PedonRecord](#) objects.

References

Leenaars, J. G. B., van Oostrum, A. J. M., & Ruiperez Gonzalez, M. (2014). Africa Soil Profiles Database, Version 1.2. ISRIC Report 2014/01. ISRIC – World Soil Information, Wageningen. Project page: <https://isric.org/projects/africa-soil-profiles-database-afsp>.

load_afsp_sample	<i>Load the bundled AfSP stratified sample (v0.9.77)</i>
------------------	--

Description

Returns a 130-profile snapshot from AfSP v1.2 stratified by WRB RSG (5 profiles per RSG x 26 RSGs), pre-built so users can run the African WRB benchmark offline without the 35 MB ZIP download.

Usage

```
load_afsp_sample()
```

Details

This is the African analogue of [load_wosis_stratified_sample](#) (global WoSIS) and [load_kssl_nasis_sample](#) (US KSSL+NASIS).

Value

A list with pedons, pulled_on, source, filter.

Reference

Leenaars, J. G. B., van Oostrum, A. J. M., & Ruiperez Gonzalez, M. (2014). Africa Soil Profiles Database, Version 1.2. ISRIC Report 2014/01.

load_bdsolos_csv	<i>Load a BDSolos CSV export as a list of PedonRecord objects</i>
------------------	---

Description

Reads the long-format BDSolos CSV (one row per horizon, with a profile-id key) and returns a list of [PedonRecord](#) objects. Auto-detects the column-name convention via [inspect_bdsolos_csv](#) and maps to the soilKey horizon schema. Texture (argila / silte / areia) is converted from g/kg to percent (BDSolos canonical unit).

Usage

```
load_bdsolos_csv(path, sep = NULL, verbose = TRUE)
```

Arguments

path	Path to the BDSolos CSV.
sep	Field separator. Default ", "; BDSolos sometimes exports with ";" or tab – pass it explicitly.
verbose	If TRUE (default), prints a one-line summary.

Details

Profile-id columns are auto-detected: looks for any column whose normalised name matches "id_perfil|profile_id|cod_ falls back to the first column when none match.

Value

A list of [PedonRecord](#) objects. Each pedon has site\$id from the profile-id column, the taxonomic reference (when present) at site\$reference_sibcs, and one horizon row per CSV row matching the profile id.

See Also

[inspect_bdsolos_csv](#), [download_bdsolos](#).

load_embrapa_pedons	<i>Load Embrapa dadosolos pedons with reference SiBCS classification</i>
---------------------	--

Description

Reads the Embrapa BDSolos CSV export (or the dadosolos R package data frame, if present). Assembles a list of [PedonRecord](#) objects with the SiBCS classification attached as pedon\$site\$reference_sibcs.

Usage

```
load_embrapa_pedons(csv_path, head = NULL, verbose = TRUE)
```

Arguments

csv_path	Path to the BDsolos CSV (long format: one row per horizon, with a profile-id key and per-profile classification).
head	Optional integer for parser validation.
verbose	If TRUE (default), emits a summary.

Details

The dadosolos / BDsolos archive ships with ~5k profiles in PT-BR with full SiBCS classification, lab data, and horizon morphology – the primary validation set for Brazilian-context use. Available from <https://www.bdsolos.cnptia.embrapa.br/>.

Value

A list of [PedonRecord](#) objects.

load_febr_pedons	<i>Load the Embrapa FEBR superconjunto into a list of PedonRecords</i>
------------------	--

Description

Reads the FEBR febr-superconjunto.txt export (one row per camada / horizon, with the profile-level classification denormalised onto every row), groups rows by (dataset_id, observacao_id), and returns a list of [PedonRecord](#) objects with all three reference taxa attached on \$site: reference_sibcs (raw FEBR string, e.g. "LATOSSOLO VERMELHO"), reference_usda, reference_wrb.

Usage

```
load_febr_pedons(
  path,
  head = NULL,
  require_classification = c("sibcs", "any", "wrb", "usda"),
  verbose = TRUE
)
```

Arguments

path	Path to febr-superconjunto.txt.
head	Optional integer; if not NULL, return only the first head unique profiles after grouping.

require_classification	One of c("any", "sibcs", "wrb", "usda"). Default "sibcs": drop profiles whose chosen classification is NA. "any" keeps profiles with at least one of the three.
verbose	If TRUE (default), summarises the load.

Details

Drops profiles whose taxon_sibcs is NA (no usable reference). Drops camadas with no horizon-depth information (no profund_sup / profund_inf).

Value

A list of [PedonRecord](#) objects.

load_kssl_nasis_sample
Load the bundled KSSL + NASIS morphological-enriched sample (v0.9.75)

Description

Returns a 99-profile snapshot built by joining the NCSS Lab Data Mart (ncss_labdata.gpkg) with the companion NASIS Morphological sqlite (NASIS_Morphological_*.sqlite) via [load_kssl_pedons_with_nasis](#). Pre-annotated with derived WRB Reference Soil Group via [usda_to_wrb_rsg](#).

Usage

```
load_kssl_nasis_sample()
```

Details

Compared to [load_kssl_sample](#) (KSSL lab tables only), this sample carries the morphological evidence that several WRB diagnostic horizons need:

```
| Field | KSSL-only | KSSL + NASIS | |-----|-----:|-----:| | munsell_hue_moist | 0 | munsell_value_moist | 0 | munsell_chroma_moist | 0 | munsell_hue_dry | 0 | structure_grade | 0 | structure_type | 0 | clay_films_amount | 0 | slickensides | 0
```

First-ever benchmark on this enriched sample (soilKey v0.9.75, full v0.9.69-72 fallback stack):

- Top-1 baseline: 19.1\ **+3.5pp lift purely from NASIS morphology**)
- Top-1 full stack: 20.6\
- Phaeozem: 1/33 -> 2/33 (Munsell-driven mollic detection)
- Podzol: 0/15 -> 1/15

Remaining ceiling driven by attributes neither dataset preserves: Solonetz needs Na/ESP, Vertisols need slickensides + cracks (NASIS records 1.7 on subsoil samples NASIS often lacks).

Value

A list with pedons, pulled_on, source, join_helper, cross_walk.

Reference

Beaudette, D., Skovlin, J., Roecker, S., Brown, A. (2024). aqp: Algorithms for Quantitative Pedology. R package version 2.x. <https://github.com/ncss-tech/aqp>.

Examples

```
## Not run:
s <- load_kssl_nasis_sample()
length(s$pedons)
#> 99
# Munsell now populated (KSSL-only sample had 0%):
mean(vapply(s$pedons,
            function(p) any(!is.na(p$horizons$munsell_hue_moist)),
            logical(1)))
#> 0.99

## End(Not run)
```

load_kssl_pedons	<i>Load NCSS / KSSL pedons with reference USDA Soil Taxonomy classification</i>
------------------	---

Description

Reads the KSSL pedon CSV export (typically named NCSS_Pedon_Layer.csv or similar) plus the lab-data CSV, joins on pedon_key, and assembles a list of PedonRecord objects. The published USDA Soil Taxonomy classification (from the Series or Subgroup field) is attached as pedon\$site\$reference_usda.

Usage

```
load_kssl_pedons(pedon_csv, layer_csv, head = NULL, verbose = TRUE)
```

Arguments

pedon_csv	Path to the pedon-level CSV (one row per profile, with site-level metadata + classification).
layer_csv	Path to the layer-level CSV (one row per horizon, with horizon properties).
head	Optional integer; if not NULL, returns only the first head pedons (useful for parser validation).
verbose	If TRUE (default), emits a summary of the load.

Details

KSSL is the de-facto standard for validating USDA Soil Taxonomy keys (~50k profiles, lab-grade analytical data, professional pedon descriptions). Get the export from the USDA-NRCS NCSS Lab Data Mart (ncsslabdatamart.sc.egov.usda.gov).

Value

A list of [PedonRecord](#) objects.

load_kssl_pedons_gpkg *Load KSSL / NCSS pedons from the ncsslabdata GeoPackage*

Description

Reads the 'lab_combine_nasis_ncss' / 'lab_site' / 'lab_layer' / 'lab_chemical_properties' / 'lab_physical_properties' views from the NCSS Lab Data Mart GeoPackage and assembles a list of [PedonRecord](#) objects. Each pedon has its USDA Soil Taxonomy Order attached as `site$reference_usda`, normalised to match 'classify_usda()' output ("Mollisols", "Alfisols", ...).

Usage

```
load_kssl_pedons_gpkg(
  gpkg,
  head = NULL,
  require_b_horizon = TRUE,
  verbose = TRUE
)
```

Arguments

gpkg	Path to <code>ncsslabdata.gpkg</code> .
head	Optional integer; load only the first N classified pedons. Useful for parser validation.
require_b_horizon	If TRUE (default), drops pedons whose deepest horizon's <code>bottom_cm</code> < 30. Most non-Entisol Order gates need a B horizon.
verbose	If TRUE (default), emits progress messages.

Value

A list of [PedonRecord](#) objects.

 load_kssl_pedons_with_nasis

Load KSSL pedons enriched with NASIS morphology

Description

Joins the NCSS Lab Data Mart GeoPackage with the NASIS Morphological SQLite to produce PedonRecord objects whose horizons table has BOTH lab chemistry + physics AND field morphology (Munsell, structure, clay films, slickensides, cracks). Required for the morphological-evidence diagnostics ([argic](#) clay-films, [vertic_horizon](#) slickensides, mollic_epipedon_usda Munsell, etc.) to fire on KSSL profiles – the lab gpkg alone has none of those.

Usage

```
load_kssl_pedons_with_nasis(
  gpkg,
  sqlite,
  head = NULL,
  require_b_horizon = TRUE,
  verbose = TRUE
)
```

Arguments

gpkg	Path to ncss_labdata.gpkg.
sqlite	Path to NASIS_Morphological_*.sqlite.
head	Optional integer; load only the first N classified pedons. Useful for parser validation / scaling.
require_b_horizon	If TRUE (default), drops pedons whose deepest horizon's bottom_cm < 30.
verbose	If TRUE (default), emits progress messages.

Value

A list of [PedonRecord](#) objects.

 load_kssl_sample

Load the bundled KSSL/NCSS lab-data sample (v0.9.74)

Description

Returns a 100-profile snapshot from the NCSS Lab Data Mart (KSSL gpkg, head = 100) pre-annotated with derived WRB Reference Soil Group via [usda_to_wrb_rsg](#).

Usage

```
load_kssl_sample()
```

Details

This is the bundled offline counterpart to `load_kssl_pedons_gpkg` – use this for tests and demos when the 5.5 GB `gpkg` is not available locally.

Each pedon has BOTH:

- `site$reference_usda` (Order, Suborder, Greatgroup, Subgroup) – the canonical KSSL classification.
- `site$reference_wrb_from_usda` – the derived WRB RSG via the IUSS WRB 2022 Annex 6 cross-walk.

First-ever KSSL WRB benchmark (soilKey v0.9.74, full v0.9.69-72 fallback stack):

- Top-1 accuracy: 20.1%
- Calcisol 69%
- Phaeozem / Kastanozem / Solonetz 0% data not in KSSL lab tables (in companion NASIS).

Value

A list with pedons, `pulled_on`, `source`, `cross_walk`.

Reference

Beaudette, D., Skovlin, J., Roecker, S., Brown, A. (2024). `aqp`: Algorithms for Quantitative Pedology. R package version 2.x. <https://github.com/ncss-tech/aqp>.

Examples

```
## Not run:
s <- load_kssl_sample()
length(s$pedons)
#> 100
table(vapply(s$pedons, function(p) p$site$reference_wrb_from_usda,
             character(1)))

## End(Not run)
```

load_lucas_pedons	<i>Load EU-LUCAS / ESDB pedons with reference WRB classification</i>
-------------------	--

Description

Reads the EU-LUCAS topsoil dataset joined with the ESDB profile archive (the v3 release produced by JRC). Assembles a list of PedonRecord objects with the WRB Reference Soil Group attached as pedon\$site\$reference_wrb.

Usage

```
load_lucas_pedons(lucas_csv, head = NULL, verbose = TRUE)
```

Arguments

lucas_csv	Path to the LUCAS topsoil CSV.
head	Optional integer for parser validation.
verbose	If TRUE (default), emits a summary.

Details

LUCAS is harvested every 3-6 years on a regular grid; the ESDB classification is updated synchronously. ~28k profile cells with WRB labels in the 2015-2018 release.

Value

A list of [PedonRecord](#) objects.

load_lucas_soil_2018	<i>Load the LUCAS Soil 2018 Topsoil release as a list of PedonRecord objects</i>
----------------------	--

Description

Reads the canonical European Soil Data Centre (ESDAC) release of LUCAS Soil 2018 Topsoil chemistry as published in the JRC report (ESDAC dataset <https://esdac.jrc.ec.europa.eu/content/lucas-2018-topsoil>). The release ships ~18,984 European topsoil samples at 0-20 cm with pH (H2O and CaCl2), EC, OC, CaCO3, P, N, K and oxalate-extractable Al / Fe; a separate BulkDensity_2018_final-2.csv carries bulk density at 0-10 / 10-20 / 20-30 / 0-20 cm for ~6,272 of those points and is joined automatically when present.

Usage

```
load_lucas_soil_2018(
  path,
  attach_bulk_density = TRUE,
  countries = NULL,
  max_n = NULL,
  verbose = TRUE
)
```

Arguments

path	Folder containing LUCAS-SOIL-2018.csv (typically <root>/LUCAS-SOIL-2018-data-report-readme-
attach_bulk_density	If TRUE (default), joins the BulkDensity_2018_final-2.csv sister file on POINTID when present.
countries	Optional character vector of NUTS_0 codes (e.g. c("ES", "FR")) to filter pedons. Default NULL (all countries).
max_n	Optional integer cap on the number of pedons returned (after country filter). Useful for development.
verbose	If TRUE (default), prints a summary line.

Details

What's NOT in the release (and how to fill it):

- **Texture (clay / sand / silt)** – not in this CSV. Pass `benchmark_lucas_2018(..., fill_texture_from = "soilgrids")` to fill from ISRIC SoilGrids 250m via [lookup_soilgrids](#).
- **Munsell colors** – not collected by LUCAS Soil 2018. If the user has Vis-NIR spectra (release separate ~83 GB), use [predict_munsell_from_spectra](#) (v0.9.47).
- **Vis-NIR spectra** – distributed separately by ESDAC. Once downloaded and attached to the pedon's \$spectra, [predict_from_spectra](#) (v0.9.46) fills clay / sand / silt / pH / OC / CEC.
- **Taxonomic reference** – not in the LUCAS release; [benchmark_lucas_2018](#) attaches the canonical WRB Reference Soil Group via [lookup_esdb](#) (v0.9.44) at the pedon's coordinates.

Unit conversions applied (LUCAS -> soilKey schema):

- OC, N, CaCO₃, Ox_Al, Ox_Fe: g/kg ->
- EC: mS/m -> dS/m (* 0.01)
- P, K: mg/kg unchanged
- pH: unitless

Special LUCAS string values "< LOD", "<LOD", empty cells and "n.d." / "ND" are converted to NA before numeric coercion.

Value

A list of [PedonRecord](#) objects (one per LUCAS point). Each pedon has a `site$id` matching the LUCAS POINTID, `site$lat` / `site$lon` in WGS84, and either one or two horizons (the second being 20-30 cm when the subsoil OC / CaCO3 columns are populated). Provenance entries from the loader use `source = "measured"`.

See Also

[benchmark_lucas_2018](#), [lookup_esdb](#), [lookup_soilgrids](#).

Examples

```
## Not run:
path <- "soil_data/eu_lucas/LUCAS-SOIL-2018-data-report-readme-v2/LUCAS-SOIL-2018-v2"
pedons <- load_lucas_soil_2018(path, countries = c("ES", "PT"),
                             max_n = 100)

length(pedons)
pedons[[1]]

## End(Not run)
```

load_redape_pedons *Load curated soil profiles from the Embrapa Redape GeoTab dataset*

Description

Reads the structured JSON files (one profile per file) published by Vaz et al. 2023 at the Embrapa Redape repository (DOI 10.48432/PYKKA7) and converts each one to a soilKey [PedonRecord](#).

Usage

```
load_redape_pedons(json_dir, max_n = NULL, verbose = TRUE)
```

Arguments

<code>json_dir</code>	Directory containing the GeoTab JSON files (or a character vector of file paths).
<code>max_n</code>	If non-NULL, take a random sample of this size.
<code>verbose</code>	Print progress (default TRUE).

Details

The dataset is unique in two ways:

- Every profile was hand-reviewed by experienced pedologists (the curation note and author list are preserved on each pedon site record), so it is suitable as a gold-standard benchmark.
- Unlike BDsolos, all profiles ship the full exchange complex (Ca, Mg, K, Na, Al *and* H), so `cec_cmol` (Valor T = S + H + Al) is computed directly without any fallback option.

Value

A list of [PedonRecord](#) objects.

Reference

Vaz, G. J., Silva Jr, A. F., & Silva Neto, L. de F. da (2023). Brazilian soil data for taxonomic classification. Redape, V1. doi:[10.48432/PYKKA7](https://doi.org/10.48432/PYKKA7).

See Also

[download_redape_dataset](#), [benchmark_redape](#).

load_rules	<i>Load a soilKey rule set (YAML)</i>
------------	---------------------------------------

Description

Load a soilKey rule set (YAML)

Usage

```
load_rules(system = c("wrb2022", "usda", "sibcs5"), package = "soilKey")
```

Arguments

system	One of "wrb2022" (full WRB 2022 key, v0.2 wires 16/32 RSGs), "usda" (USDA Soil Taxonomy, v0.2 scaffold with one delegating diagnostic), or "sibcs5" (SiBCS 5th edition, v0.2 scaffold with one delegating diagnostic).
package	Package owning the rule files (default "soilKey").

Value

A parsed YAML list with elements version, source, and a system-specific taxa list (rsgs, orders, or ordens).

load_wosis_sample	<i>Load the bundled WoSIS South-America sample</i>
-------------------	--

Description

Returns a 40-profile snapshot of WoSIS GraphQL data pulled on 2026-05-03 with continent = "South America". The data is a frozen artefact – do NOT use it for current paper-grade benchmarks (the WoSIS database is updated periodically; the bundled snapshot is for reproducible tests and offline development only).

Usage

```
load_wosis_sample()
```

Details

For up-to-date benchmarks, call `run_wosis_benchmark_graphql()` directly against the live ISRIC GraphQL endpoint.

Value

A list as described above.

Returned data

A list with elements:

- `profiles_raw` – the parsed GraphQL response (one element per profile; nested layer arrays).
- `pedons` – PedonRecord objects ready for classification (one per profile).
- `pulled_on` – Date of the snapshot.
- `endpoint`, `filter`, `n_pulled` – metadata.

Examples

```
## Not run:  
sample <- load_wosis_sample()  
length(sample$pedons)  
#> 40  
classify_wrb2022(sample$pedons[[1]])$rsg_or_order  
  
## End(Not run)
```

load_wosis_stratified_sample

Load the bundled WoSIS stratified RSG-balanced sample (v0.9.73)

Description

Returns a 130-profile snapshot of WoSIS GraphQL data pulled on 2026-05-09 with ****stratified sampling by WRB Reference Soil Group****: 5 profiles per RSG across 26 RSGs (Acrisol, Andosol, Arenosol, Calcisol, Cambisol, Chernozem, Cryosol, Ferralsol, Fluvisol, Gleysol, Gypsisol, Histosol, Kastanozem, Leptosol, Luvisol, Nitisol, Phaeozem, Planosol, Plinthosol, Podzol, Regosol, Solonchak, Solonetz, Stagnosol, Umbrisol, Vertisol).

Usage

```
load_wosis_stratified_sample()
```

Details

This is the recommended cache for global WRB benchmarking. Compared to `load_wosis_sample()` (40 SA-only profiles, mostly Solonetz and Phaeozem from Argentina), the stratified sample provides:

- Even coverage across the 26 most important RSGs.
- Richer analytical attributes – CEC available on 26 ECEC on 37 in the SA snapshot).
- Geographic diversity (Angola, Brazil, USA, China, Russia, South Africa, Indonesia, Argentina, etc.).

First-ever benchmark on this sample (soilKey v0.9.73, full v0.9.69-72 fallback stack):

- Overall top-1 accuracy: 16.2%
- Histosol 100% from 20% Cambisol 60%
- 18 RSGs at 0% expose (Munsell colours, base saturation, sodium for Solonetz, slickensides for Vertisols, etc.). Documented data ceiling.

For the live API, call `run_wosis_benchmark_graphql()` or the `read_wosis_profiles_graphql(wrb_rsg = "...", n_max = N)` helper (small RSG-filtered queries are tractable; large unfiltered pulls time out as of 2026-05).

Value

A list with:

- `pedons`: list of 130 `PedonRecord` objects.
- `meta`: named integer vector of profiles per RSG.
- `pulled_on`: pull date.
- `endpoint`: ISRIC GraphQL endpoint URL.
- `filter`: pull strategy metadata.
- `n_pulled`: 130.

Reference

Batjes, N. H., Ribeiro, E., van Oostrum, A. (2020). Standardised soil profile data to support global mapping and modelling (WoSIS snapshot 2019). *Earth System Science Data*, 12, 299-320. [doi:10.5194/essd122992020](https://doi.org/10.5194/essd122992020).

Examples

```
## Not run:
s <- load_wosis_stratified_sample()
length(s$pedons)
#> 130
table(vapply(s$pedons, function(p) p$site$wosis_rsg, character(1)))
#> 5 of each: Acrisol, Andosol, ... Vertisol

## End(Not run)
```

lookup_esdb

Look up an ESDB raster value at WGS84 coordinates

Description

Loads the requested attribute raster, reprojects WGS84 lat/lon input to the raster's native CRS (typically LAEA Europe, EPSG:3035), and extracts the value(s). When a Value Attribute Table ('.vat.dbf') is available, the integer raster value is decoded to its coded string (e.g. '21' -> "LV" -> Luvisol).

Usage

```
lookup_esdb(coords, attribute, raster_root, decode = TRUE)
```

Arguments

coords	A two-column matrix or data.frame with 'lon' and 'lat' (WGS84 decimal degrees) – in that order. A single c(lon, lat) vector is also accepted.
attribute	Name of the ESDB attribute folder, e.g. "WRBLV1" or "WRBFU". See available_esdb_attributes .
raster_root	Path to the unpacked ESDB raster directory.
decode	If TRUE (default), decode the integer raster value to the VAT-coded string (e.g. "21" -> "LV"). If FALSE, return the raw integer.

Details

Coordinates outside the European raster footprint return 'NA' silently (rather than erroring) so vectorised calls degrade gracefully.

Value

Character vector (decoded codes) or numeric vector (raw values) of the same length as `nrow(coords)`.
NA for points outside the raster footprint.

See Also

[available_esdb_attributes](#)

Examples

```
## Not run:
root <- "~/data/ESDB-Raster-Library-1k-GeoTIFF-20240507"

# Single point: Wageningen, Netherlands (5.66 E, 51.97 N)
lookup_esdb(c(5.66, 51.97), "WRBLV1", root)
#> [1] "GL" # Gleysol per the ESDB 1km raster

# Vector: Lisbon + Berlin + Helsinki
coords <- rbind(c(-9.14, 38.72), c(13.40, 52.52), c(24.94, 60.17))
lookup_esdb(coords, "WRBLV1", root)
#> [1] "CM" "LV" "PZ" # Cambisol, Luvisol, Podzol

## End(Not run)
```

lookup_mapbiomas_solos

Look up a MapBiomas Solos raster value at WGS84 coordinates

Description

MapBiomas Solos (Project MapBiomas, Brazil) distributes a national raster of SiBCS classes at 30 m, downloadable from <https://mapbiomas.org/en/produtos>. This helper mirrors the shape of [lookup_esdb](#) but is local-file only: pass the path of the unpacked GeoTIFF and the function reprojects the user's WGS84 lat/lon to the raster's native CRS, extracts the pixel and (optionally) decodes the integer class code via a user-supplied legend.

Usage

```
lookup_mapbiomas_solos(coords, raster_path, legend = NULL)
```

Arguments

<code>coords</code>	A 2-column matrix or <code>data.frame</code> with lon, lat (WGS84 decimal degrees), or a length-2 numeric vector for a single query.
<code>raster_path</code>	Path to the unpacked MapBiomas Solos GeoTIFF.
<code>legend</code>	Optional two-column <code>data.frame</code> (first column = numeric value, second = SiBCS class name). When provided, the integer raster value is decoded; when <code>NULL</code> , the raw integer is returned.

Details

MapBiomass does not bundle a `.vat.dbf`; the canonical legend is published as a CSV / dictionary on their website. Pass it via `legend` as a two-column `data.frame` (`value`, `class_name`) to enable decoding.

Value

Character vector of decoded class names (when legend is supplied) or numeric vector of raster values. Same length as `nrow(coords)`. NA for points outside the raster footprint.

See Also

[lookup_esdb](#), [lookup_soilgrids](#).

Examples

```
## Not run:
tif <- "~/data/mapbiomas_solos_collection2_2023.tif"
legend <- data.frame(
  value = c(1L, 2L, 3L, 4L, 5L, 6L, 7L, 8L, 9L, 10L, 11L, 12L, 13L),
  class_name = c("Latossolo Vermelho-Amarelo",
                 "Latossolo Amarelo",
                 "Argissolo Vermelho-Amarelo",
                 "Argissolo Amarelo",
                 "Neossolo Quartzarenico",
                 "Cambissolo Haplico",
                 "Espodosolo",
                 "Gleissolo",
                 "Nitossolo",
                 "Planossolo",
                 "Plintossolo",
                 "Vertisol",
                 "Outros")
)
lookup_mapbiomas_solos(c(-43.0, -22.0), tif, legend)

## End(Not run)
```

lookup_soilgrids

Look up a SoilGrids 250m soil property at WGS84 coordinates

Description

Reads ISRIC SoilGrids 250m (Hengl et al. 2017, 2021) directly from the ISRIC Cloud-Optimized GeoTIFF (COG) endpoint at <https://files.isric.org/soilgrids/latest/data/> – no download required, only the pixel under each query coordinate is transferred over HTTPS.

Usage

```
lookup_soilgrids(
  coords,
  property = c("clay", "sand", "silt", "phh2o", "soc", "cec", "bdod", "nitrogen", "ocd",
    "ocs", "cfvo"),
  depth = c("0-5cm", "5-15cm", "15-30cm", "30-60cm", "60-100cm", "100-200cm"),
  quantile = c("mean", "Q0.05", "Q0.5", "Q0.95", "uncertainty"),
  baseurl = "https://files.isric.org/soilgrids/latest/data",
  raw = FALSE
)
```

Arguments

coords	A 2-column matrix or data.frame with lon, lat (WGS84 decimal degrees), or a length-2 numeric vector for a single query.
property	One of the SoilGrids 250m predicted properties: "clay", "sand", "silt", "phh2o", "soc", "cec", "bdod", "nitrogen", "ocd", "ocs", "cfvo".
depth	Depth interval. One of "0-5cm", "5-15cm", "15-30cm", "30-60cm", "60-100cm", "100-200cm".
quantile	Output quantile. One of "mean" (default), "Q0.05", "Q0.5", "Q0.95", "uncertainty".
baseurl	Base URL of the SoilGrids COG endpoint. Default is the canonical ISRIC location; override only for a local mirror.
raw	If TRUE, returns the integer raster value without scaling. Default FALSE (returns the value in conventional units).

Details

SoilGrids stores integer rasters scaled per property; this helper applies the canonical conversion factor so the returned value is in conventional soil units (% , pH, g/kg, cmol(c)/kg, g/cm³).

Value

Numeric vector of length nrow(coords). NA outside the SoilGrids footprint or on network errors.

See Also

[lookup_esdb](#), [lookup_mapbiomas_solos](#).

Examples

```
## Not run:
# Single point
lookup_soilgrids(c(-43.0, -22.0),
  property = "phh2o",
  depth = "0-5cm",
  quantile = "mean")

# Vector + multiple properties
```

```

coords <- rbind(c(-43.0, -22.0), c(-9.14, 38.72))
lookup_soilgrids(coords, "clay", "0-5cm", "mean")
lookup_soilgrids(coords, "phh2o", "0-5cm", "mean")

## End(Not run)

```

luvisol

Luvisol RSG diagnostic (WRB 2022)

Description

argic + CEC \geq 24 cmol_c/kg clay + Al saturation < 50%.

Usage

```
luvisol(pedon, min_cec = 24, max_al_sat = 50)
```

Arguments

pedon	A PedonRecord .
min_cec	Minimum CEC per kg clay (default 24).
max_al_sat	Maximum Al saturation % (default 50).

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022), Chapter 5, Luvisols.

make_acrisol_canonical

Build the canonical Acrisol fixture

Description

Synthetic tropical-humid Acrisol on weathered gneiss: argic horizon at Bt1 with low-activity clay (CEC/clay ~ 17 cmol_c/kg clay) and low base saturation (BS ~ 25%). By construction:

- [argic](#): PASSES on Bt1.
- [acrisol](#): PASSES (CEC low, BS low).
- [lixisol](#), [alisol](#), [luvisol](#): FAIL.
- Other diagnostics: FAIL.

Usage

```
make_acrisol_canonical()
```

Value

A [PedonRecord](#).

```
make_alisol_canonical Build the canonical Alisol fixture
```

Description

Synthetic humid-tropical Alisol on weathered shale: argic horizon at Bt1 with high-activity clay (CEC/clay ~ 34) AND high Al saturation (Al sat ~ 70%); the canonical "young weathering on a 2:1 clay parent that has not yet released enough Al into the precipitate-stabilised pool". By construction:

- [argic](#): PASSES on Bt1.
- [alisol](#): PASSES (CEC high, Al sat high).
- [acrisol](#), [lixisol](#), [luvisol](#): FAIL.

Usage

```
make_alisol_canonical()
```

Value

A [PedonRecord](#).

```
make_andosol_canonical  
Build the canonical Andosol fixture
```

Description

Synthetic Andosol on volcanic tephra: very dark surface with low bulk density (0.7 g/cm³) and high active Al + Fe (Al_{ox} + 0.5 * Fe_{ox} = 2.25%). By construction [andic_properties](#) passes.

Usage

```
make_andosol_canonical()
```

Value

A [PedonRecord](#).

`make_anthrosol_canonical`*Build the canonical Anthrosol fixture*

Description

Synthetic Anthrosol with a hortic horizon – a long-cultivated dark surface from sustained organic-matter additions (typical of centuries-old kitchen-garden / homegarden soils). By construction [anthric_horizons](#) passes via the designation pattern.

Usage`make_anthrosol_canonical()`**Value**

A [PedonRecord](#).

`make_arenosol_canonical`*Build the canonical Arenosol fixture*

Description

Synthetic coastal-dune Arenosol: sandy throughout the upper 100 cm (silt + 2*clay < 30). By construction [arenic_texture](#) passes uniformly while every clay-dependent diagnostic fails.

Usage`make_arenosol_canonical()`**Value**

A [PedonRecord](#).

`make_argissolo_canonical`*Perfil canonico de Argissolo (SiBCS 5a ed., Cap 5)*

Description

B textural com gradiente significativo, argila ativ baixa ou alta + V baixa. Catch-all final na chave – tipica do Brasil tropical.

Usage`make_argissolo_canonical()`**Value**

A [PedonRecord](#) populated with the canonical horizons and site metadata for this reference profile.

`make_calcisol_canonical`*Build the canonical Calcisol fixture*

Description

Synthetic semi-arid Calcisol on calcareous loess: A horizon with modest secondary carbonate; a thick Bk1 with the diagnostic calcic horizon (35% CaCO₃ over 40 cm); deepening accumulation in Bk2. By construction:

- `calcic`: PASSES on Bk1 and Bk2.
- `gypsic`, `salic`: FAIL.
- `argic`, `ferralic`, `mollic`: FAIL.

Usage`make_calcisol_canonical()`**Value**

A [PedonRecord](#).

`make_cambisol_canonical`*Build the canonical Cambisol fixture*

Description

Synthetic temperate-zone Cambisol on weathered colluvium: modest subsurface alteration in Bw without meeting argic clay-increase or ferralic CEC criteria. By construction:

- [cambic](#): PASSES on Bw (thickness 35 cm, sandy clay loam, no argic / no ferralic).
- [argic](#), [ferralic](#), [mollic](#), [calcic](#), [gypsic](#), [salic](#): FAIL.

Usage`make_cambisol_canonical()`**Value**

A [PedonRecord](#).

`make_cambissolo_canonical`*Perfil canonico de Cambissolo (SiBCS 5a ed., Cap 6)*

Description

Reusa fixture WRB Cambisol – B incipiente sem ser plintico, vertico, planico, etc.

Usage`make_cambissolo_canonical()`**Value**

A [PedonRecord](#) populated with the canonical horizons and site metadata for this reference profile.

`make_chnossolo_canonical`*Perfil canonico de Chernossolo (SiBCS 5a ed., Cap 7)*

Description

Reusa fixture WRB Chernozem – A chernozemico + Bk com argila Ta + V alta. SiBCS strictos exigem (a) Bi/Bt + Ta + V alta, OR (b) calcico/petrocalcico/carbonatico + A chernozemico.

Usage`make_chnossolo_canonical()`**Value**

A [PedonRecord](#) populated with the canonical horizons and site metadata for this reference profile.

`make_chnozem_canonical`*Build the canonical Chernozem fixture*

Description

Synthetic Ukrainian / Russian steppe Chernozem on loess: thick dark Ah, granular structure, secondary carbonates accumulating in the Bk. By construction:

- [mollic](#): PASSES on horizon Ah1 (moist value 2, chroma 1, dry value 3; SOC 4%; BS 89%; thickness 30 cm; strong granular structure).
- [argic](#): FAILS (essentially no clay differentiation; ratios all close to 1).
- [ferralic](#): FAILS (CEC/clay ~ 120 cmol_c/kg clay – high-activity 2:1 clay).

Usage`make_chnozem_canonical()`**Value**

A [PedonRecord](#).

`make_cryosol_canonical`*Build the canonical Cryosol fixture*

Description

Synthetic Arctic Cryosol on weathered shale with permafrost at 50 cm: thawed A horizon over a frozen Bf horizon. By construction [cryic_conditions](#) passes via the designation pattern.

Usage`make_cryosol_canonical()`**Value**

A [PedonRecord](#).

`make_durisol_canonical`*Build the canonical Durisol fixture*

Description

Synthetic semi-arid Durisol with a Si-cemented subsurface horizon (35% duripan nodules over 45 cm). By construction [duric_horizon](#) passes on Bdu.

Usage`make_durisol_canonical()`**Value**

A [PedonRecord](#).

make_empty_horizons *Build an empty horizons data.table with the canonical schema*

Description

Build an empty horizons data.table with the canonical schema

Usage

```
make_empty_horizons(n = 0L)
```

Arguments

n Number of rows (default 0).

Value

A data.table with all canonical horizon columns filled with NAs of the correct type.

Examples

```
h <- make_empty_horizons(3)
nrow(h)
```

make_espodossolo_canonical
Perfil canonico de Espodossolo (SiBCS 5a ed., Cap 8)

Description

Reusa fixture WRB Podzol – B espodico imediatamente abaixo de E.

Usage

```
make_espodossolo_canonical()
```

Value

A [PedonRecord](#) populated with the canonical horizons and site metadata for this reference profile.

`make_ferralsol_canonical`*Build the canonical Ferralsol fixture*

Description

Synthetic but realistic Brazilian Latossolo Vermelho (Ferralsol per WRB 2022): deeply weathered, kaolinitic / oxidic, with the canonical "low-activity clay" signature. Diagnostic outcomes are deterministic by construction:

- **ferralic**: PASSES on horizons Bw1 and Bw2 (CEC/clay = 8.3 cmol_c/kg clay; ECEC/clay = 3.6 cmol_c/kg clay; texture sandy clay / clay; thickness \geq 30 cm).
- **argic**: FAILS (gradual clay increase, all pairwise ratios $<$ 1.2; absolute increment too small for the \geq 40% rule).
- **mollic**: FAILS (chroma $>$ 3, BS $<$ 50%, A horizon $<$ 20 cm thick).

Usage`make_ferralsol_canonical()`**Value**

A [PedonRecord](#).

`make_fluvisol_canonical`*Build the canonical Fluvisol fixture*

Description

Synthetic floodplain Fluvisol: stratified textures across consecutive C horizons, OC pattern non-monotone with depth (because C2 is more recently deposited, OC-richer than C1). By construction [fluvic_material](#) passes.

Usage`make_fluvisol_canonical()`**Value**

A [PedonRecord](#).

`make_gleissolo_canonical`*Perfil canonico de Gleissolo (SiBCS 5a ed., Cap 9)*

Description

Reusa fixture WRB Gleysol – horizonte glei dentro de 50 cm.

Usage`make_gleissolo_canonical()`**Value**

A [PedonRecord](#) populated with the canonical horizons and site metadata for this reference profile.

`make_gleysol_canonical`*Build the canonical Gleysol fixture*

Description

Synthetic Gleysol from a high-water-table floodplain: A with low chroma but no explicit redox features (so gleyic test is anchored on Bg); Bg with diagnostic redoximorphic features (35% by volume) within the upper 50 cm. By construction:

- `gleyic_properties`: PASSES on Bg.
- `argic, ferralic, mollic, cambic, plinthic, spodic, calcic, gypsic, salic`: FAIL.

Usage`make_gleysol_canonical()`**Value**

A [PedonRecord](#).

`make_gypsisol_canonical`*Build the canonical Gypsisol fixture*

Description

Synthetic Gypsisol on gypsiferous parent material: shallow A; gypsum accumulation rising sharply in the By1 horizon (35% gypsum over 50 cm) – the diagnostic gypsic horizon. By construction:

- [gypsic](#): PASSES on By1 and By2.
- [calcic](#), [salic](#): FAIL.
- [argic](#), [ferralic](#), [mollic](#): FAIL.

Usage`make_gypsisol_canonical()`**Value**

A [PedonRecord](#).

`make_histosol_canonical`*Build the canonical Histosol fixture*

Description

Synthetic boreal-mire Histosol: thick (50 cm) surface organic horizon with OC ~ 35%, low chroma, no exchangeable-base data reported (typical of histic profiles where laboratory chemistry on organic material is reported separately). By construction:

- [histic_horizon](#): PASSES on Oa.
- Mineral horizons below; mollic / umbric NA (no BS reported).

Usage`make_histosol_canonical()`**Value**

A [PedonRecord](#).

`make_kastanozem_canonical`*Build the canonical Kastanozem fixture*

Description

Synthetic continental-semiarid Kastanozem on loess-like substrate: mollic surface (chroma 3, value 3) – dark enough for mollic but not dark enough for Chernozem (chroma 3 > 2 in the upper 20 cm); secondary carbonates accumulating in the Bk. By construction:

- `mollic`: PASSES.
- `kastanozem`: PASSES.
- `chernozem`, `phaeozem`: FAIL.

Usage`make_kastanozem_canonical()`**Value**

A [PedonRecord](#).

`make_latossolo_canonical`*Perfil canonico de Latossolo (SiBCS 5a ed., Cap 10)*

Description

Reusa fixture WRB Ferralsol – B latossolico imediatamente abaixo de A, sem horizonte argilico acima.

Usage`make_latossolo_canonical()`**Value**

A [PedonRecord](#) populated with the canonical horizons and site metadata for this reference profile.

`make_leptosol_canonical`*Build the canonical Leptosol fixture*

Description

Synthetic mountain-slope Leptosol on metamorphic rock: a thin A (10 cm) directly over continuous rock. By construction:

- `leptic_features`: PASSES (R at 10 cm \leq 25).
- Other diagnostics fail on thickness, missing data, or absent diagnostic features.

Usage`make_leptosol_canonical()`**Value**

A `PedonRecord`.

`make_lixisol_canonical`*Build the canonical Lixisol fixture*

Description

Synthetic Mediterranean / sub-tropical Lixisol on weathered calcareous parent material: argic horizon at Bt1 with low-activity clay (CEC/clay ~ 20) but high base saturation (BS ~ 70%) thanks to carbonate-buffered weathering. By construction:

- `argic`: PASSES on Bt1.
- `lixisol`: PASSES (CEC low, BS high).
- `acrisol`, `alisol`, `luvisol`: FAIL.

Usage`make_lixisol_canonical()`**Value**

A `PedonRecord`.

`make_luvisol_canonical`*Build the canonical Luvisol fixture*

Description

Synthetic temperate-zone Luvisol on loess: clear textural differentiation, Bt with clay coatings, high base saturation, high- activity clay. By construction:

- **argic**: PASSES on horizon Bt1 (clay increase from E (18%) to Bt1 (35%) gives ratio 1.94 in the 15-40% band; thickness 25 cm; texture clay loam; no glossic features).
- **ferralic**: FAILS (CEC/clay ~ 45 cmol_c/kg clay in the Bt – well above the 16 cmol_c/kg threshold).
- **mollic**: FAILS (A horizon: moist value 4 > 3, thickness 10 cm < 20 cm).

Usage`make_luvisol_canonical()`**Value**

A [PedonRecord](#).

`make_luvissole_canonical`*Perfil canonico de Luvissole (SiBCS 5a ed., Cap 11)*

Description

Solo com B textural argila Ta + V alta. Tipico do semiarido com rocha basica.

Usage`make_luvissole_canonical()`**Value**

A [PedonRecord](#) populated with the canonical horizons and site metadata for this reference profile.

`make_neossolo_canonical`*Perfil canonico de Neossolo Litolico (SiBCS 5a ed., Cap 12)*

Description

Solo raso sobre rocha continua dura. Sem horizonte B diagnostico.

Usage`make_neossolo_canonical()`**Value**

A [PedonRecord](#) populated with the canonical horizons and site metadata for this reference profile.

`make_nitisol_canonical`*Build the canonical Nitisol fixture*

Description

Synthetic East-African Nitisol on weathered basalt: clay-rich ($\geq 50\%$), Fe-rich (DCB $\sim 6\%$), polyhedral structure with shiny ped surfaces. By construction [nitic_horizon](#) passes.

Usage`make_nitisol_canonical()`**Value**

A [PedonRecord](#).

make_nitossolo_canonical

Perfil canonico de Nitossolo Vermelho (SiBCS 5a ed., Cap 13)

Description

Solo argiloso ($\geq 35\%$ argila desde superficie) com B nitico (estrutura forte em blocos + cerosidade), gradiente textural baixo ($B/A \leq 1.5$).

Usage

make_nitossolo_canonical()

Value

A [PedonRecord](#) populated with the canonical horizons and site metadata for this reference profile.

make_organossolo_canonical

Perfil canonico de Organossolo (SiBCS 5a ed., Cap 14)

Description

Solo organico saturado, com horizonte H historico ≥ 60 cm e SOC alto. Tipico de varzea / brejo.

Usage

make_organossolo_canonical()

Value

A [PedonRecord](#) populated with the canonical horizons and site metadata for this reference profile.

`make_phaeozem_canonical`*Build the canonical Phaeozem fixture*

Description

Synthetic humid-temperate Phaeozem on non-calcareous loess: mollic (chroma 2, value 2-3) and high BS, but no secondary carbonates anywhere – typical of more leached / less-arid steppe-forest transition. By construction:

- `mollic`: PASSES.
- `phaeozem`: PASSES.
- `chernoze`m, `kastanoze`m: FAIL (no carbonates).

Usage`make_phaeozem_canonical()`**Value**

A `PedonRecord`.

`make_planosol_canonical`*Build the canonical Planosol fixture*

Description

Synthetic temperate Planosol with abrupt textural change: sandy E (clay 12%) overlies a clay-rich Bt (35%) at 25 cm with an abrupt boundary. By construction `planic_features` passes.

Usage`make_planosol_canonical()`**Value**

A `PedonRecord`.

make_planossolo_canonical

Perfil canonico de Planossolo (SiBCS 5a ed., Cap 15)

Description

Solo com horizonte E sobrejacente a B planico (mudanca textural abrupta + cores neutras + cromas baixos).

Usage

make_planossolo_canonical()

Value

A [PedonRecord](#) populated with the canonical horizons and site metadata for this reference profile.

make_plinthosol_canonical

Build the canonical Plinthosol fixture

Description

Synthetic seasonally-saturated tropical Plinthosol: A horizon with typical Cerrado SOC; Btv with diagnostic plinthite (25% by volume over 60 cm); persistent plinthite at depth. By construction:

- [plinthic](#): PASSES on Btv and Cv.
- [argic](#), [ferrallic](#), [mollic](#), [spodic](#), [calcic](#), [gypsic](#), [salic](#): FAIL.

Usage

make_plinthosol_canonical()

Value

A [PedonRecord](#).

`make_plintossolo_canonical`*Perfil canonico de Plintossolo (SiBCS 5a ed., Cap 16)*

Description

Reusa fixture WRB Plinthosol – horizonte plintico iniciando dentro de 40 cm.

Usage`make_plintossolo_canonical()`**Value**

A [PedonRecord](#) populated with the canonical horizons and site metadata for this reference profile.

`make_podzol_canonical` *Build the canonical Podzol fixture*

Description

Synthetic boreal / temperate-coniferous Podzol: bleached E (low clay, low CEC), illuvial Bs with diagnostic Al/Fe oxalate accumulation, weathered C. By construction:

- [spodic](#): PASSES on Bs ($Al_{ox} + 0.5 * Fe_{ox} = 0.6$, pH 4.5, 40 cm thick).
- [argic](#), [ferralic](#), [mollic](#), [cambic](#), [plinthic](#), [calcic](#), [gypsic](#), [salic](#): FAIL.

Usage`make_podzol_canonical()`**Details**

E horizon Munsell is set to chroma 3 (rather than canonical 1-2 of a true albic) to keep `gleyic_properties` clearly negative under the conservative v0.2 criterion.

Value

A [PedonRecord](#).

`make_retisol_canonical`*Build the canonical Retisol fixture*

Description

Synthetic temperate Retisol on loess over clay-rich substrate: bleached E with glossic tongues penetrating the underlying argic Bt. By construction `retic_properties` passes via the "glossic" designation pattern; `argic` also passes (this is correct – Retisols are argic + retic features, and the WRB key tests RT before AC/LX/AL/LV).

Usage`make_retisol_canonical()`**Value**

A `PedonRecord`.

`make_solonchak_canonical`*Build the canonical Solonchak fixture*

Description

Synthetic Solonchak from a coastal-arid setting: surface salt accumulation gives the diagnostic salic horizon (EC 25 dS/m over 25 cm); EC declines but stays elevated in the Bz; non-saline C below. By construction:

- `salic`: PASSES on Az.
- `gypsic`, `calcic`: FAIL.
- `argic`, `ferralic`, `mollic`: FAIL.

Usage`make_solonchak_canonical()`**Value**

A `PedonRecord`.

`make_solonetz_canonical`*Build the canonical Solonetz fixture*

Description

Synthetic Solonetz on saline-sodic substrate: argic Btn with columnar structure and high exchangeable Na (ESP ~ 28%). By construction [natric_horizon](#) passes.

Usage`make_solonetz_canonical()`**Value**

A [PedonRecord](#).

`make_stagnosol_canonical`*Build the canonical Stagnosol fixture*

Description

Synthetic Stagnosol: redoximorphic features in a perched layer (Bg, 15-50 cm; redox 25%) but the deeper subsoil is well-drained (BC redox 2%, C redox 0). The decay-with-depth contrast is what distinguishes stagnic from gleyic. By construction [stagnic_properties](#) passes and [gleyic_properties](#) also passes (the surface redox qualifies for both); the WRB key tests Stagnosols (#16) and Gleysols (#9), so a real Stagnosol-typed fixture lands at Gleysols if both pass – the criteria differ in depth pattern, which is enough for the diagnostic functions but not for key precedence in v0.3. This is documented in the test as known overlap; v0.4 will add a stronger discriminator.

Usage`make_stagnosol_canonical()`**Value**

A [PedonRecord](#).

```
make_synthetic_pedon_with_spectra
```

Build a synthetic PedonRecord with attached spectra (testing aid)

Description

Generates a small, deterministic [PedonRecord](#) with `n_horizons` horizons and a Vis-NIR spectral matrix (350:2500 nm). Useful for exercising [fill_from_spectra](#) in tests and vignettes.

Usage

```
make_synthetic_pedon_with_spectra(  
  n_horizons = 5L,  
  wavelengths = 350:2500,  
  seed = 1L  
)
```

Arguments

<code>n_horizons</code>	Integer number of horizons (default 5).
<code>wavelengths</code>	Integer vector of wavelengths (default 350:2500).
<code>seed</code>	Integer seed for the RNG used to generate the spectra.

Value

A [PedonRecord](#) with a `$spectra$vnir` matrix attached.

```
make_technosol_canonical
```

Build the canonical Technosol fixture

Description

Synthetic urban / industrial Technosol: surface horizon with 30% anthropogenic artefacts (brick, glass, slag, plastic). By construction [technic_features](#) passes.

Usage

```
make_technosol_canonical()
```

Value

A [PedonRecord](#).

`make_umbrisol_canonical`*Build the canonical Umbrisol fixture*

Description

Synthetic humid-temperate Umbrisol on weathered acidic schist: deep organic-rich dark surface with low base saturation – the acid analogue of a Phaeozem. By construction [umbric_horizon](#) passes; [mollic](#) fails on BS < 50.

Usage`make_umbrisol_canonical()`**Value**

A [PedonRecord](#).

`make_vertisol_canonical`*Build the canonical Vertisol fixture*

Description

Synthetic Vertisol from a smectite-rich plain: deep clay (50-55%) with strong slickensides in the Bss horizon. Surface chroma 4 (above the mollic cap) so that [vertic_properties](#) is the only v0.2 diagnostic that passes. By construction:

- [vertic_properties](#): PASSES on Bss and BC.
- [argic](#), [ferralic](#), [mollic](#), [cambic](#), [plinthic](#), [spodic](#), [calcic](#), [gypsic](#), [salic](#): FAIL.

Usage`make_vertisol_canonical()`**Value**

A [PedonRecord](#).

```
make_vertissolo_canonical
```

Perfil canonico de Vertissolo (SiBCS 5a ed., Cap 17)

Description

Solo argiloso ($\geq 30\%$ argila desde superficie) com horizonte vertico (slickensides + fendas + clay alto) iniciando dentro de 100 cm. Reusa structure / fixture do WRB Vertisol.

Usage

```
make_vertissolo_canonical()
```

Value

A [PedonRecord](#) populated with the canonical horizons and site metadata for this reference profile.

```
mineral_material
```

Mineral material (WRB 2022 Ch 3.3.11): $< 20\%$ SOC AND $< 35\%$ volume artefacts containing $\geq 20\%$ organic carbon. The complement of organic_material / organotechnic_material.

Description

Mineral material (WRB 2022 Ch 3.3.11): $< 20\%$ SOC AND $< 35\%$ volume artefacts containing $\geq 20\%$ organic carbon. The complement of organic_material / organotechnic_material.

Usage

```
mineral_material(pedon, max_oc = 20, max_organotechnic = 35)
```

Arguments

```
pedon          A PedonRecord.
max_oc         Numeric threshold or option (see Details).
max_organotechnic
               Numeric threshold or option (see Details).
```

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

mollic	<i>Mollic horizon (WRB 2022)</i>
--------	----------------------------------

Description

Tests whether any near-surface horizon meets the mollic horizon criteria. The mollic horizon is the diagnostic surface horizon of Chernozems, Phaeozems, Kastanozems, and several other RSGs; it indicates a thick, dark, base-rich, organic-matter-enriched topsoil formed under steppe or comparable vegetation.

Usage

```
mollic(
  pedon,
  min_thickness = 20,
  min_oc = 0.6,
  min_bs = 50,
  surface_top_cm = 5
)
```

Arguments

pedon	A PedonRecord .
min_thickness	Minimum thickness in cm (default 20).
min_oc	Minimum SOC % (default 0.6).
min_bs	Minimum base saturation % (default 50).
surface_top_cm	Maximum top depth (cm) for a horizon to be considered "surface-related" (default 5). v0.1 uses this as a proxy for the WRB rule that mollic must form continuously from the soil surface (after mixing of upper 20 cm if required).

Details

Sub-tests called:

- test_mollic_color – moist value ≤ 3 , moist chroma ≤ 3 , dry value ≤ 5 .
- test_mollic_organic_carbon – SOC $\geq 0.6\%$.
- test_mollic_base_saturation – BS (NH₄OAc, pH 7) $\geq 50\%$.
- test_mollic_thickness – horizon thickness ≥ 20 cm.
- test_mollic_structure – not simultaneously massive AND very hard when dry.

v0.1 limitations: cumulative thickness across contiguous mollic-qualifying horizons is not yet supported – this matters for profiles where mollic criteria are met by an A1+A2 sequence but no single horizon is ≥ 20 cm thick. Mixing of upper 20 cm before the test (per WRB) is also deferred to v0.2.

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022). *World Reference Base for Soil Resources*, 4th edition. International Union of Soil Sciences, Vienna. Chapter 3 – Mollic horizon.

mudanca_textural_abrupta

Mudanca textural abrupta (SiBCS Cap 1, p 30-31)

Description

Aumento consideravel de argila em pequena distancia vertical (≤ 7.5 cm) na transicao A/E -> B:

- argila A < 200 g/kg: argila B $\geq 2x$ A; OR
- argila A 200-400 g/kg: incremento absoluto ≥ 200 g/kg (i.e. de 300 -> 500); OR
- argila A ≥ 400 g/kg: incremento absoluto ≥ 220 g/kg (i.e. de 420 -> 640).

Reuso de [abrupt_textural_difference](#) (WRB Ch 3.2.1) que ja codifica criterios essencialmente equivalentes.

Usage

mudanca_textural_abrupta(pedon)

Arguments

pedon A [PedonRecord](#).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

mulmic_material	<i>Mulmic material (WRB 2022 Ch 3.3.12): mineral material developed from organic material; \geq 8% SOC, with low BD, structural / chroma criteria.</i>
-----------------	---

Description

Mulmic material (WRB 2022 Ch 3.3.12): mineral material developed from organic material; \geq 8% SOC, with low BD, structural / chroma criteria.

Usage

```
mulmic_material(pedon, min_oc = 8, max_chroma = 2)
```

Arguments

pedon	A PedonRecord .
min_oc	Numeric threshold or option (see Details).
max_chroma	Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

natric_horizon	<i>Natric horizon (WRB 2022)</i>
----------------	----------------------------------

Description

Tests for the natric horizon: an argic horizon with diagnostic sodium accumulation (ESP \geq 15%) within at least one argic layer. Diagnostic of Solonetz.

Usage

```
natric_horizon(pedon, min_esp = 15, min_pH_h2o = 7)
```

Arguments

pedon	A PedonRecord .
min_esp	Minimum ESP % (default 15).
min_pH_h2o	Minimum pH(H ₂ O) for the ESP-only path (default 7.0; alkaline gate to exclude false-positive acidic Bt horizons).

Value

A [DiagnosticResult](#).

v0.9.76 designation + ESP-only inference (opt-in)

Field-described Solonetz profiles in NCSS / KSSL data routinely reach the natric ESP threshold (computed from `na_cmol` / `cec_cmol`) without satisfying the strict `argic()` clay-increase test, because surveyors record Btk-suffix designations (carbonates dominate the horizon designation choice) rather than Btn/Bn or `clay_pct` is missing.

With `options(soilKey.natric_designation_inference = TRUE)` the function accepts a layer as natric when the canonical argic test returns NA or FALSE AND *either*:

1. the designation matches `[A-Z][a-z0-9]*n` (an n master-letter modifier in the horizon name – e.g. \ Btn, Btnz, Bn, the curator’s direct assertion that natric features are present), OR
2. `ESP >= min_esp` on a B-prefixed subsoil layer (`top_cm > 20`) AND the layer’s `pH(H2O) >= 7` (alkaline – typical of true natric, excludes acidic Bt horizons that happen to read high Na from sea-spray).

Default is FALSE (canonical behaviour preserved).

References

IUSS Working Group WRB (2022), Chapter 3, Natric horizon.

nitric_horizon

Natric horizon (WRB 2022)

Description

Tests for the nitric horizon: a clay-rich ($\geq 30\%$), Fe-rich (DCB Fe $\geq 4\%$) subsurface horizon at least 30 cm thick. Diagnostic of Nitisols. WRB 2022 additionally requires polyhedral / nutty structure with shiny ped surfaces and a gradual (non-abrupt) clay decrease with depth.

Usage

```
nitric_horizon(
  pedon,
  min_clay = 30,
  min_fe_dcb = 4,
  min_thickness = 30,
  max_clay_drop_pct = 8,
  max_decrease_depth = 50
)
```

Arguments

pedon	A PedonRecord .
min_clay	Minimum clay % (default 30).
min_fe_dcb	Minimum DCB-extractable Fe % (default 4).
min_thickness	Minimum thickness in cm (default 30).
max_clay_drop_pct	Maximum clay drop (percentage points) between adjacent layers within max_decrease_depth before failing the gradual-decrease test (default 8).
max_decrease_depth	Depth window (cm) for the gradual-decrease check (default 50).

Details

Required (AND-combined) sub-tests:

- Profile does not have a ferralic horizon (Ferralsol path is canonical for the clay-rich + low-CEC corner).
- clay % \geq min_clay.
- fe_dcb_pct \geq min_fe_dcb.
- thickness \geq min_thickness.

Supplementary (soft-AND) sub-tests – evaluated when evidence is present in the pedon, evaluate to NA (not a fail) when missing:

- structure_type matches polyhedral / nutty / (sub)angular blocky.
- slickensides / shiny ped surfaces present (proxy for WRB's "shiny ped surfaces").
- clay does not decrease abruptly between adjacent layers within 50 cm of the surface (gradual-decrease pattern; drop > 8 percentage points fails).

Supplementary tests fail (return passed = FALSE) only when evidence actively contradicts the criterion; missing evidence is permissive.

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022), Chapter 3, Nitic horizon.

normalise_febr_sibcs *Canonicalise FEBR SiBCS names to match soilKey rule outputs.*

Description

FEBR ships SiBCS labels in mixed legacy/modern form ("Podzolicos" for old name of Argissoles, singular vs plural, Portuguese accents). This helper folds them to the form produced by `run_sibcs_key()` so that benchmark accuracies can be computed without false negatives.

Usage

```
normalise_febr_sibcs(x, level = c("order", "subordem"))
```

Arguments

`x` Character vector of FEBR SiBCS names.
`level` One of "order" (default) or "subordem".

Value

Character vector of normalised SiBCS names; NA for labels that are out-of-scope for the comparison (e.g.\ legacy "Solos" category).

See Also

[normalise_febr_wrb](#), [normalise_febr_usda](#)

normalise_febr_usda *Normalise FEBR USDA taxon strings to USDA Soil Taxonomy Order*

Description

FEBR ships USDA Soil Taxonomy labels at the subgroup or great-group granularity (e.g. "TYPIC HAPLUDULT", "ACRUSTOX"). The suffix of the final word encodes the Order: `...OX` -> Oxisols, `...ULT` -> Ultisols, `...EPT` -> Inceptisols, etc. This helper extracts the Order from the suffix so the benchmark can compare against `classify_usda()`\$`rsg_or_order` at `level = "order"`.

Usage

```
normalise_febr_usda(x)
```

Arguments

`x` Character vector of FEBR USDA names.

Value

Character vector of normalised Order names ("Oxisols", "Ultisols", "Inceptisols", ...).

normalise_febr_wrb *Normalise FEBR WRB taxon strings to RSG-only*

Description

FEBR ships WRB names with full qualifier strings, e.g. "HUMIC FERRALSOL", "HAPLIC ACRISOL (ALUMIC, HYPERDYSTRIC, ...)". The trailing word (before any qualifier parens) is the RSG. This helper extracts and normalises it to soilKey's plural Title Case form ("Ferralsols", "Acrisols"), matching `ClassificationResult$rsg_order`.

Usage

```
normalise_febr_wrb(x)
```

Arguments

x Character vector of FEBR WRB names.

Value

Character vector of normalised RSG names.

normalise_kssl_subgroup
 Normalise KSSL USDA subgroup labels for benchmark comparison

Description

KSSL stores 'samp_taxsubgrp' in lower-case, space-separated form ("typic hapludalfs", "aquic argiudolls"). soilKey's 'classify_usda()' returns Title Case names ("Typic Hapludalfs"). The benchmark runner at 'level = "subgroup"' lowercases both sides and trims whitespace, but this helper makes the normalisation explicit when users want to compare KSSL labels against arbitrary classifier output. Idempotent.

Usage

```
normalise_kssl_subgroup(x)
```

Arguments

x Character vector of KSSL subgroup names.

Value

Lowercase, single-space-separated vector.

ollama_is_running	<i>Is the local Ollama HTTP API reachable?</i>
-------------------	--

Description

Probes `http://127.0.0.1:11434/api/tags` (the standard Ollama endpoint) with a short HTTP HEAD-style GET. Returns TRUE only if the request returns HTTP 200 in under `timeout_s` seconds. Used by `vlm_pick_provider` for the provider = "auto" fallback chain. Override the URL via `options(soilKey.ollama_url = "http://host:port")`.

Usage

```
ollama_is_running(url = NULL, timeout_s = 1.5)
```

Arguments

<code>url</code>	Override URL to probe (default reads <code>getOption("soilKey.ollama_url", default = "http://127.0.0.1:11434/api/tags")</code>).
<code>timeout_s</code>	Request timeout in seconds (default 1.5).

Value

Logical scalar.

organic_material	<i>Organic material (WRB 2022 Ch 3.3.13): $\geq 20\%$ SOC + recognisability criteria. v0.3.3: SOC threshold only.</i>
------------------	--

Description

Organic material (WRB 2022 Ch 3.3.13): $\geq 20\%$ SOC + recognisability criteria. v0.3.3: SOC threshold only.

Usage

```
organic_material(pedon, min_oc = 20)
```

Arguments

<code>pedon</code>	A PedonRecord .
<code>min_oc</code>	Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

organotechnic_material

Organotechnic material (WRB 2022 Ch 3.3.14): $\geq 35\%$ volume of artefacts that themselves contain $\geq 20\%$ organic C. Soil itself has $< 20\%$ SOC.

Description

Organotechnic material (WRB 2022 Ch 3.3.14): $\geq 35\%$ volume of artefacts that themselves contain $\geq 20\%$ organic C. Soil itself has $< 20\%$ SOC.

Usage

`organotechnic_material(pedon, min_artefacts = 35, max_oc = 20)`

Arguments

pedon A [PedonRecord](#).
 min_artefacts Numeric threshold or option (see Details).
 max_oc Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

ornithogenic_material *Ornithogenic material (WRB 2022 Ch 3.3.15): bird-influenced topsoil. Mehlich-3 P ≥ 750 mg/kg + designation pattern Aornit|Bornit.*

Description

Ornithogenic material (WRB 2022 Ch 3.3.15): bird-influenced topsoil. Mehlich-3 P ≥ 750 mg/kg + designation pattern Aornit|Bornit.

Usage

`ornithogenic_material(pedon, min_p_mehlich3 = 750)`

Arguments

pedon A [PedonRecord](#).
 min_p_mehlich3 Numeric threshold or option (see Details).

Value

A `DiagnosticResult` recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

 ossl_demo_sa

Synthetic OSSL South America demo subset

Description

A small, deterministic, OSSL-shaped artefact for use in vignettes, examples and tests when the real Open Soil Spectral Library data is not available (no network, sensitive deployment, CI). The object has the canonical `list(Xr, Yr, metadata)` shape consumed by `predict_ossl_mbl / fill_from_spectra`, so the in-package demo path is identical to the real-data path.

Usage

```
ossl_demo_sa
```

Format

A list with three elements:

`Xr` Numeric matrix, 80 rows (synthetic profiles) x 2151 columns (wavelengths 350-2500 nm). Reflectance values in [0.05, 0.85].

`Yr` Data frame, 80 rows x 9 columns (`clay_pct`, `sand_pct`, `silt_pct`, `cec_cmol`, `bs_pct`, `ph_h2o`, `oc_pct`, `fe_dcb_pct`, `caco3_pct`). Property ranges follow the OSSL global summary statistics.

`metadata` Named list with provenance information (`region`, `n_profiles`, `snapshot`, `seed`, `note`, ...).

Details

This is a **synthetic** placeholder: the spectra are generated from a tropical-soil baseline plus property-correlated absorption bands (1400 nm OH-water, 1900 nm clay-OH, 2200 nm Al-OH, 900 nm Fe-oxide) with deterministic noise. It is *not* a substitute for real OSSL measurements. For paper-grade work, populate a real OSSL artefact via:

```
ossl_lib <- download_ossl_subset(region = "south_america")
```

Re-build the demo with `source("data-raw/build_ossl_demo.R")`.

Source

Synthetic; built by `data-raw/build_ossl_demo.R` with seed 20260430. The OSSL property ranges that drove the simulation come from Sanderman, J. *et al.* (2024), *Open Soil Spectral Library*, <https://soilspectroscopy.org/>.

Examples

```

data(ossl_demo_sa)
dim(ossl_demo_sa$Xr)
#> [1] 80 2151
head(ossl_demo_sa$Yr)

## Not run:
# Use it as the ossl_library argument to predict_ossl_mbl():
pedon <- make_synthetic_pedon_with_spectra()
fill_from_spectra(pedon,
                  library = "ossl",
                  method = "mbl",
                  ossl_library = ossl_demo_sa)

## End(Not run)

```

ossl_library_template *Canonical schema for an 'ossl_library' object*

Description

`predict_ossl_mbl` and `predict_ossl_plsr_local` take an `ossl_library` argument that must be a list with two named elements:

Usage

```

ossl_library_template(
  wavelengths = 350:2500,
  properties = c("clay_pct", "sand_pct", "silt_pct", "cec_cmol", "bs_pct", "ph_h2o",
                "oc_pct", "fe_dcb_pct", "caco3_pct")
)

```

Arguments

<code>wavelengths</code>	Integer vector of wavelengths (default 350:2500 nm for Vis-NIR/SWIR).
<code>properties</code>	Character vector of property column names to seed the empty Yr data.frame with.

Details

- Xr: numeric matrix, rows = OSSL training spectra, columns = wavelengths. Must align (after preprocessing) with the column space used by the spectra you predict on.
- Yr: data.frame keyed by property name (e.g. clay_pct, cec_cmol), one row per training spectrum.

This function returns an empty template you can populate from a real OSSL extract (e.g. via the `ossl-import` Python package or the public S3 mirror at <https://storage.googleapis.com/soilspec4gg-public/>). `soilKey` does **not** bundle OSSL data; until you populate this template with real values, all `'predict_ossl_*'` calls fall back to the deterministic synthetic predictor (which prints a warning).

Value

A list with Xr (a 0-row matrix of the right column dimension) and Yr (an empty data.frame with the requested columns).

oxic_usda	<i>Oxic horizon (USDA Soil Taxonomy)</i>
-----------	--

Description

The USDA oxic horizon is the diagnostic of Oxisols. Its central criteria match the WRB 2022 ferralic horizon closely enough that v0.2 simply delegates: every fixture that classifies as Oxisol via USDA also classifies as Ferralsol via WRB and vice-versa. The fine-grained differences (USDA's water-dispersible-clay test, the sand-fraction weatherable-mineral cut-offs) are tracked in the diagnostics.yaml for v0.8 refinement.

Usage

```
oxic_usda(pedon, ...)
```

Arguments

pedon	A PedonRecord .
...	Passed to ferralic .

Value

A [DiagnosticResult](#) (with name = "oxic_usda").

References

Soil Survey Staff (2014). *Keys to Soil Taxonomy*, 12th edition. USDA-NRCS, Washington DC. Chapter 3 – Diagnostic Horizons; oxic.

panpaic	<i>Panpaic horizon (WRB 2022 Ch 3.1)</i>
---------	--

Description

From Quechua *p'anpay* = "to bury". A buried diagnostic horizon (any horizon whose original surface was subsequently overlain by younger material). Used by the Panpaic qualifier and by the Cambisols / Anthrosols branches.

Usage

```
panpaic(pedon)
```

Arguments

pedon A [PedonRecord](#).

Details

v0.3.5 detection: designation pattern starting with a digit other than 1 (e.g. 2A, 2Bw, 3C) – the WRB / FAO convention for buried horizons – OR a b suffix in the designation (e.g. Ahb, Bwb).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

PedonRecord

PedonRecord: structured representation of a single pedon

Description

PedonRecord: structured representation of a single pedon

PedonRecord: structured representation of a single pedon

Details

The central data carrier in `soilKey`. A `PedonRecord` bundles everything we know about one soil profile: site metadata, the horizons table (with a fixed canonical schema — see [horizon_column_spec](#)), optional Vis-NIR/MIR spectra, profile photographs, source documents, and a provenance log that records, per (horizon, attribute) pair, where each value came from (measured, extracted_vlm, predicted_spectra, inferred_prior, user_assumed).

All diagnostic functions ([argic](#), [ferralic](#), [mollic](#), ...) consume a `PedonRecord` directly. The provenance log is what allows the final [ClassificationResult](#) to assign a meaningful evidence grade.

Value

An R6 object of class `PedonRecord`.

Public fields

`site` List. Site-level metadata: `lat`, `lon`, `crs` (default 4326), `date`, `country`, `elevation_m`, `slope_pct`, `aspect_deg`, `landform`, `parent_material`, `land_use`, `vegetation`, `drainage_class`, plus an arbitrary `id`.

`horizons` `data.table` with the canonical horizon schema.

`spectra` List with optional `vnir` matrix (rows = horizons, cols = wavelengths in nm), `mir` matrix, and metadata list.

`images` List of named lists describing profile photographs.

`documents` List of named lists describing source documents.

`provenance` `data.table` with columns `horizon_idx`, `attribute`, `source`, `confidence`, `notes`.

Methods**Public methods:**

- `PedonRecord$new()`
- `PedonRecord$validate()`
- `PedonRecord$to_aqp()`
- `PedonRecord$from_aqp()`
- `PedonRecord$add_measurement()`
- `PedonRecord$summary()`
- `PedonRecord$print()`
- `PedonRecord$clone()`

Method `new()`: Construct a `PedonRecord`.

Usage:

```
PedonRecord$new(
  site = NULL,
  horizons = NULL,
  spectra = NULL,
  images = NULL,
  documents = NULL,
  provenance = NULL
)
```

Arguments:

`site` List of site-level metadata.

`horizons` `data.frame`/`data.table` of horizons.

`spectra` Optional list with `vnir`, `mir`, metadata.

`images` Optional list of image descriptors.

`documents` Optional list of document descriptors.

`provenance` Optional `provenance data.table`; if `NULL`, an empty one is created.

Method `validate()`: Validate the record against soil-physical sanity rules.

Checks: top < bottom for every horizon; no overlapping depths; clay+silt+sand sum to 100 ± 2 where all three are reported; pH values plausible (1..12); CEC \geq sum of exchangeable bases (Ca, Mg, K, Na); Munsell value/chroma in plausible ranges; coarse fragments percent in [0, 100]; OC geographic ranges. Returns a list with `valid`, `errors`, `warnings`, `n_horizons`.

Usage:

```
PedonRecord$validate(strict = FALSE, verbose = TRUE)
```

Arguments:

`strict` If `TRUE`, throws on errors instead of returning.

`verbose` If `TRUE`, prints messages via cli.

Returns: Invisibly, a list summarising the validation outcome.

Method `to_aqp()`: Coerce to an `aqp SoilProfileCollection`.

Usage:

PedonRecord\$to_aqp()

Returns: A SoilProfileCollection. Requires the aqp package.

Method from_aqp(): Populate this record from an aqp SoilProfileCollection.

Usage:

```
PedonRecord$from_aqp(spc, top_col = "top_cm", bottom_col = "bottom_cm")
```

Arguments:

spc A SoilProfileCollection.

top_col Name of the top-depth column in spc (mapped to top_cm).

bottom_col Name of the bottom-depth column (mapped to bottom_cm).

Returns: Invisibly self (mutated in place).

Method add_measurement(): Add a measurement (or extracted/predicted value) and record its provenance.

Usage:

```
PedonRecord$add_measurement(
  horizon_idx,
  attribute,
  value,
  source = "measured",
  confidence = 1,
  notes = NA_character_,
  overwrite = FALSE
)
```

Arguments:

horizon_idx Integer horizon index (1-based).

attribute Name of the horizon column to set.

value New value for that cell.

source One of "measured", "extracted_vlm", "predicted_spectra", "inferred_prior", "user_assumed".

confidence Numeric in [0, 1].

notes Optional free-text note.

overwrite If FALSE (default) and the cell already has a value from a more authoritative source, leave it alone. If TRUE, overwrite.

Returns: Invisibly self.

Method summary(): Compact summary list (for serialization or testing).

Usage:

```
PedonRecord$summary(...)
```

Arguments:

... Ignored (S3 summary signature compatibility).

Method print(): Pretty-print the record.

Usage:

```
PedonRecord$print(...)
```

Arguments:

... Ignored (S3 print signature compatibility).

Method `clone()`: The objects of this class are cloneable with this method.

Usage:

```
PedonRecord$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
# The canonical fixtures return ready-built PedonRecords:
pedon <- make_ferralsol_canonical()
pedon$site$id
nrow(pedon$horizons)
```

```
pedons_from_spectral_table
```

Build PedonRecords with attached Vis-NIR/MIR spectra from a table

Description

Groups a reflectance + metadata table by profile and returns one [PedonRecord](#) per profile, with each profile's sample rows stacked into `$spectra$vnir` (rows = horizons, cols = wavelengths) and the lab attributes / depths written to the horizons. Taxonomic labels are stored in `$site` (`reference_wrb` / `reference_sibcs` / `reference_st`). These pedons are the query objects for `classify_*` (`gapfill = list(method = "spectra", ossl_library = <lib>)`).

Usage

```
pedons_from_spectral_table(
  reflectance,
  metadata,
  id_col = "id",
  profile_col = NULL,
  wavelengths = NULL,
  resample_to = NULL,
  property_map = NULL,
  label_map = NULL,
  normalize = c("auto", "none", "percent"),
  keep_properties = FALSE,
  verbose = TRUE
)
```

Arguments

reflectance	Reflectance data: a matrix / data.frame with rows = samples and columns named by wavelength (nm); OR a long data.frame with id_col, wavelength_nm, reflectance; OR a path to a CSV in either form.
metadata	A data.frame with one row per sample carrying id_col plus lab attributes and optional taxonomic labels and lat/ lon. Rows are aligned to reflectance by id_col.
id_col	Sample identifier column shared by both tables (default "id").
profile_col	Column grouping samples into profiles (default id_col: one profile per sample, e.g. a topsoil library).
wavelengths	Optional explicit wavelength vector (nm) when the reflectance columns are not wavelength-named.
resample_to	Optional target wavelength grid (nm) to linearly resample every spectrum onto (e.g. 350:2500); default keeps the native grid.
property_map, label_map	Optional named lists overriding the alias auto-detection, e.g. property_map = list(clay_pct = "ARGILA").
normalize	One of "auto" (divide by 100 when values look like percent), "percent", or "none".
keep_properties	If TRUE, also write the mapped lab attributes to the horizons (default FALSE – a field pedon usually has only the scan, which is the scenario the spectral fill targets).
verbose	Print a one-line summary (default TRUE).

Value

A list of [PedonRecord](#) objects.

See Also

[read_spectral_library](#), [benchmark_spectral_fill](#)

pedon_json_schema *JSON Schema for a soilKey PedonRecord*

Description

Returns a Draft-2020-12 JSON Schema describing the canonical PedonRecord structure: a site object with site-level metadata plus a horizons array where each element matches the canonical horizon schema documented by [horizon_column_spec](#).

Usage

```
pedon_json_schema(as = c("list", "json"), pretty = TRUE)
```

Arguments

`as` One of "list" (default; returns a structured R list ready to serialise) or "json" (returns a JSON string; requires the `jsonlite` package).

`pretty` Logical, only used for `as = "json"`.

Value

A list (default) or a JSON string.

Examples

```
## Not run:
schema <- pedon_json_schema()
names(schema)
#> [1] "$schema"      "$id"           "title"         "type"          "required"      "properties"

# Validate a JSON profile against the schema:
if (requireNamespace("jsonvalidate", quietly = TRUE)) {
  schema_json <- pedon_json_schema(as = "json")
  jsonvalidate::json_validate('{"site":{...},"horizons":[...]}' ,
                              schema_json, engine = "ajv")
}

## End(Not run)
```

pedon_to_spc

Convert a soilKey PedonRecord to an aqp SoilProfileCollection

Description

The mapping respects aqp's expected column conventions and sets the metadata required by `getArgillicBounds()`, `getCambicBounds()`, and `mollicEpipedon()`:

Usage

```
pedon_to_spc(pedon)
```

Arguments

`pedon` A [PedonRecord](#).

Details

- `id` from `pedon$site$id`
- `top` / `bottom` from `top_cm` / `bottom_cm`
- `name` (designation) from `designation`
- `texcl` (texture class) derived via [texture_class_from_pct](#)

- clay, silt, sand from clay_pct / silt_pct / sand_pct
- m_hue, m_value, m_chroma, d_value, d_chroma from munsell_*_moist and munsell_*_dry

Internal use; the soilKey diagnostics call this on the fly when engine = "aqp". Direct use is supported for users who want to plug additional aqp algorithms (slab, slice, glom) into a soilKey workflow.

Value

A `aqp::SoilProfileCollection` with one site (the pedon) and one row per horizon.

petrocalcic	<i>Petrocalcic horizon (WRB 2022)</i>
-------------	---------------------------------------

Description

A continuously cemented variant of the calcic horizon. Same chemistry ($\text{CaCO}_3 \geq 15\%$) plus moderate-or-greater cementation in at least 50% of the layer.

Usage

```
petrocalcic(pedon, min_thickness = 10, min_caco3_pct = 15)
```

Arguments

pedon	A PedonRecord .
min_thickness	Numeric threshold or option (see Details).
min_caco3_pct	Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

petroduric	<i>Petroduric horizon (WRB 2022): cemented duric.</i>
------------	---

Description

Petroduric horizon (WRB 2022): cemented duric.

Usage

```
petroduric(pedon, min_thickness = 10, min_duripan_pct = 10)
```

Arguments

pedon A [PedonRecord](#).

min_thickness Numeric threshold or option (see Details).

min_duripan_pct Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

petrogypsic	<i>Petrogypsic horizon (WRB 2022): cemented gypsic.</i>
-------------	---

Description

Petrogypsic horizon (WRB 2022): cemented gypsic.

Usage

```
petrogypsic(pedon, min_thickness = 10, min_gypsum_pct = 5)
```

Arguments

pedon A [PedonRecord](#).

min_thickness Numeric threshold or option (see Details).

min_gypsum_pct Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

petroplinthic	<i>Petroplinthic horizon (WRB 2022): cemented plinthic.</i>
---------------	---

Description

Petroplinthic horizon (WRB 2022): cemented plinthic.

Usage

```
petroplinthic(pedon, min_thickness = 10, min_plinthite_pct = 15)
```

Arguments

pedon	A PedonRecord .
min_thickness	Numeric threshold or option (see Details).
min_plinthite_pct	Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

phaeozem	<i>Phaeozem RSG diagnostic (WRB 2022)</i>
----------	---

Description

Tests whether a profile satisfies the Phaeozem RSG criteria: a mollic horizon AND no secondary carbonate accumulation anywhere in the profile.

Usage

```
phaeozem(pedon)
```

Arguments

pedon	A PedonRecord .
-------	---------------------------------

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022), Chapter 5, Phaeozems.

pick_engine	<i>Choose the best diagnostic engine for a single pedon</i>
-------------	---

Description

Per-pedon heuristic: returns "aqp" if the pedon's horizon table has the morphological richness that makes aqp's canonical NRCS dispatch reliable, otherwise returns "soilkey" (the more permissive hand-coded path).

Usage

```
pick_engine(pedon, min_score = 3L)
```

Arguments

pedon	A PedonRecord .
min_score	Integer (1-5). Minimum completeness score for "aqp" engine to fire (default 3).

Value

Character: "aqp" or "soilkey".

Heuristic

We score each pedon on a 0-5 morphology-completeness scale; aqp fires when score \geq min_score (default 3). The five axes:

1. **Designation present** (any layer has a non-blank designation, e.g. "A1", "Bt2", "Bw").
2. **Texture quantitative** (any layer has both clay_pct and sand_pct populated).
3. **Munsell complete** (any layer has all three of munsell_hue_moist, munsell_value_moist, munsell_chroma_moist populated).
4. **Structure recorded** (any layer has a non-blank structure_grade).
5. **Clay films / argic evidence** (any layer has a non-blank clay_films_amount or designation pattern matching Bt).

Why this matters

On BDsolos RJ (data-rich), the heuristic recommends aqp for ~99 canonical thresholds). On LUCAS topsoil-only (data-sparse), it recommends aqp for ~0 clay-films / designation axes are unfilled. Calling `classify_*(pedon)` routed through the heuristic gives the correct engine per pedon, recovering both the BDsolos RJ lift AND the LUCAS robustness.

See Also

[argic](#), [cambic](#).

pick_engine_batch	<i>Per-pedon batch engine recommendation</i>
-------------------	--

Description

Vectorised version of [pick_engine](#) returning the recommended engine for each pedon in a list.

Usage

```
pick_engine_batch(pedons, min_score = 3L)
```

Arguments

pedons	A list of PedonRecord objects.
min_score	Integer; forwarded to pick_engine .

Value

Character vector of length(pedons) with values "aqp" or "soilkey".

pisoplinthic	<i>Pisoplinthic horizon (WRB 2022): pisolitic plinthic. v0.3.3 detects via designation pattern Bsp1 / Bvp1 or via plinthite $\geq 15\%$ AND structure_type containing 'pisol'.</i>
--------------	---

Description

Pisoplinthic horizon (WRB 2022): pisolitic plinthic. v0.3.3 detects via designation pattern Bsp1 / Bvp1 or via plinthite $\geq 15\%$ AND structure_type containing 'pisol'.

Usage

```
pisoplinthic(pedon, min_thickness = 15, min_plinthite_pct = 15)
```

Arguments

pedon	A PedonRecord .
min_thickness	Numeric threshold or option (see Details).
min_plinthite_pct	Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

pi_to_confidence	<i>Map a 95% prediction interval to a [0, 1] confidence score</i>
------------------	---

Description

Tightens confidence as the prediction interval narrows relative to the predicted value: confidence = $1 - (\text{PI95_width} / |\text{value}|) / 4$, floored at 0 and capped at 1. When value is near zero we fall back to an absolute-width heuristic so we never blow up.

Usage

```
pi_to_confidence(pi95_low, pi95_high, value = NULL)
```

Arguments

pi95_low	Lower 2.5% quantile of the prediction.
pi95_high	Upper 97.5% quantile of the prediction.
value	Optional point prediction. When supplied, normalisation is by $ \text{value} $; otherwise by $ \text{midpoint} $.

Details

Properties of the mapping:

- Zero-width interval -> confidence = 1.
- Interval whose width equals $|\text{value}| * 4$ -> confidence = 0.
- NA value or NA bounds -> confidence = 0.5 (neutral).

Value

Numeric in $[0, 1]$.

plaggic	<i>Plaggic horizon (WRB 2022): sod-derived topsoil ≥ 20 cm with low BD AND independent evidence of human input.</i>
---------	---

Description

v0.9.2.C tightening: the v0.3.3 implementation accepted ANY thick, low-BD, OC-rich A horizon, which over-fired across natural mollic / umbric / chernic surfaces. The diagnostic now requires, in addition to the OC + BD + thickness baseline, at least one independent anthropogenic-input marker:

- p_mehlich3_mg_kg ≥ 50 (sustained sod / manure additions concentrate Mehlich-3 P in the topsoil), OR

- `artefacts_pct > 0` (any human artefact volume fraction is sufficient as a presence signal), OR
- designation pattern `Ap1 / Ap1g / Apk / explicit "plagg"`.

Without one of those markers the diagnostic returns FALSE even when OC + BD + thickness pass. This mirrors the v0.9.1 `qual_plaggic` gate but enforces the rule at the diagnostic level so any caller (SiBCS, USDA, future modules) inherits the protection.

Usage

```
plaggic(
  pedon,
  min_thickness = 20,
  max_bd = 1.5,
  min_oc = 0.6,
  min_p_mehlich3 = 100
)
```

Arguments

<code>pedon</code>	A PedonRecord .
<code>min_thickness</code>	Numeric threshold or option (see Details).
<code>max_bd</code>	Numeric threshold or option (see Details).
<code>min_oc</code>	Numeric threshold or option (see Details).
<code>min_p_mehlich3</code>	Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

<code>planic_features</code>	<i>Planic features (WRB 2022)</i>
------------------------------	-----------------------------------

Description

Tests whether the profile shows an abrupt textural change between adjacent horizons (clay-doubling within 7.5 cm vertical distance, typically at the E/Bt boundary). Diagnostic of Planosols.

Usage

```
planic_features(pedon, min_ratio = 2, require_abrupt_boundary = TRUE)
```

Arguments

pedon	A PedonRecord .
min_ratio	Minimum clay ratio (default 2.0).
require_abrupt_boundary	If TRUE (default), the upper horizon must have boundary_distinctness matching "abrupt".

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022), Chapter 5, Planosols.

planosol	<i>Planosol RSG gate (WRB 2022 Ch 4, p 107)</i>
----------	---

Description

WRB-canonical: abrupt textural difference ≤ 75 cm AND, in 5 cm directly above or below the abrupt textural difference, stagnic properties ($\geq 50\%$ redoximorphic features) AND reducing conditions.

Usage

```
planosol(pedon, strict = NULL)
```

Arguments

pedon	A PedonRecord .
strict	Logical or NULL. When NULL (default) it resolves via <code>getOption("soilKey.rsg_strict", FALSE)</code> . TRUE disables the planic-features fallback.

Details

v0.3.4 enforces all three components. The 5-cm-window restriction is relaxed to "the layer immediately above or below the abrupt textural difference satisfies stagnic + reducing".

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

Tier-3 strict mode (v0.9.98)

With `strict = TRUE` the `planic_features` fallback path is disabled. Strict mode requires the canonical evidence – an abrupt textural difference *plus* measured stagnic and reducing conditions in the bracketing layer – and will not accept the simpler clay-doubling proxy on its own.

plinthic	<i>Plinthic horizon (WRB 2022)</i>
----------	------------------------------------

Description

Tests whether any horizon meets the plinthic horizon criteria. Plinthite is Fe-rich material that hardens irreversibly on repeated wetting and drying; the plinthic horizon is the diagnostic of Plinthosols.

Usage

```
plinthic(pedon, min_thickness = 15, min_plinthite_pct = 15)
```

Arguments

pedon	A PedonRecord .
min_thickness	Minimum thickness in cm (default 15).
min_plinthite_pct	Minimum volume % plinthite (default 15).

Details

Sub-tests:

- `test_plinthite_concentration` – plinthite volume % \geq 15
- `test_minimum_thickness` – thickness \geq 15 cm

v0.2 limitations: WRB 2022 also accepts profiles with \geq 40% red Fe-rich mottles as alternative criterion – not yet wired. The "irreversibly hardens" criterion is conceptual and requires field observation; v0.2 takes `plinthite_pct` as already representing true plinthite (as opposed to soft mottles).

Value

A [DiagnosticResult](#).

v0.9.72 designation morphological inference (opt-in)

Field-described Brazilian Plintossolos profiles (e.g.\ the Embrapa Redape curated dataset) routinely encode plinthite via the designation suffix *f* in the master letter sequence (e.g.\ Bt*f*, 2Bt*f*, C*f*) – the curator’s direct assertion that plinthite is present – without recording `plinthite_pct` as a numeric volume percent.

With `options(soilKey.plinthic_designation_inference = TRUE)` the function accepts a layer as plinthic when:

1. the canonical `plinthite_pct` test is NA for that layer, AND
2. the designation matches `[A-Z]+[A-Za-z]*f[0-9]?` (a *f* master-letter modifier in any sub-position).

Default is FALSE (canonical behaviour preserved).

References

IUSS Working Group WRB (2022), Chapter 3, Plinthic horizon.

`posterior_classify` *Bayesian posterior classifier (optional)*

Description

Combines a deterministic `ClassificationResult` with a spatial prior. The deterministic key remains authoritative – this function reports only an alternative probabilistic view useful for downstream uncertainty quantification.

Usage

```
posterior_classify(result, prior, epsilon = 0.001)
```

Arguments

<code>result</code>	A <code>ClassificationResult</code> from <code>classify_wrb2022</code> .
<code>prior</code>	A spatial-prior <code>data.table</code> (as returned by <code>spatial_prior</code>).
<code>epsilon</code>	Small smoothing constant added to all prior entries before normalising, so RSGs unseen by the prior do not receive zero posterior.

Details

Posterior is computed under the simple model:

$$P(\text{rsg}|\text{site}, \text{evidence}) \propto L(\text{rsg}|\text{evidence}) \times P(\text{rsg}|\text{site})$$

where the likelihood *L* is concentrated on the deterministic assignment (delta-1 at that code) by default, optionally smoothed if `key_passed_others` is supplied.

Value

A `data.table` with columns `rsg_code`, `prior`, `likelihood`, `posterior`.

```
predict.soilKey_pls_model
    Predict from a soilKey_pls_model
```

Description

S3 method that applies a trained PLSR model from [train_pls_from_oss1](#) to a (pre-processed) numeric matrix and returns predictions plus a 95 built from the cross-validated training RMSE.

Usage

```
## S3 method for class 'soilKey_pls_model'
predict(object, X, ...)
```

Arguments

object	A soilKey_pls_model object.
X	A pre-processed numeric matrix (rows = samples, columns = wavelengths). Must have the same column count used at training time.
...	Reserved.

Value

A data.frame with columns value, pi95_low, pi95_high, one row per sample.

```
predict_from_spectra    Predict soil properties from spectra
```

Description

Ergonomic, named entry point for the OSS1-backed predictive pipeline. Accepts either a [PedonRecord](#) or a numeric spectra matrix, applies the same preprocessing used at training time (recorded on each model), and returns predictions in the canonical long-form schema.

Usage

```
predict_from_spectra(
  pedon_or_spectra,
  models = NULL,
  properties = NULL,
  overwrite = FALSE,
  verbose = TRUE,
  ...
)
```

Arguments

pedon_or_spectra	A PedonRecord (predictions merged into the pedon) OR a numeric matrix / vector of raw Vis-NIR spectra (rows = horizons, columns = wavelengths).
models	A named list of soilKey_pls_model objects (output of train_pls_from_oss1). Required.
properties	Character vector of property names to predict. Defaults to all properties in models.
overwrite	Passed to fill_from_spectra when pedon_or_spectra is a PedonRecord.
verbose	Verbosity passed downstream.
...	Ignored (reserved for future backends).

Details

When pedon_or_spectra is a PedonRecord, this function delegates to [fill_from_spectra](#) with method = "pretrained" and the predictions are written back to the pedon (with source = "predicted_spectra" provenance). When pedon_or_spectra is a numeric matrix or vector, this function returns the prediction data.table directly without touching any pedon.

Value

Either the mutated PedonRecord (invisibly) or a data.table with columns horizon_idx, property, value, pi95_low, pi95_high, n_neighbors.

Examples

```
## Not run:
lib <- download_oss1_subset(region = "south_america")
models <- train_pls_from_oss1(lib,
                             properties = c("clay_pct", "ph_h2o"))
predict_from_spectra(my_pedon, models = models)

## End(Not run)
```

predict_lab_from_spectra

Predict CIE Lab from Vis-NIR reflectance spectra

Description

Convenience wrapper: [predict_xyz_from_spectra](#) followed by the standard CIE Lab transform under D65 / 2-degree observer.

Usage

```
predict_lab_from_spectra(spectra, wavelengths)
```

Arguments

spectra	Reflectance values, in 0..1 or 0..100. A numeric vector (one sample), a numeric matrix (rows = samples, cols = wavelengths) or a data.frame.
wavelengths	Numeric vector of the wavelengths (in nm) corresponding to the columns of spectra. Must cover at least 400-700 nm; values outside 380-780 are ignored.

Value

A data.frame with columns L, a, b.

predict_munsell_from_spectra

Predict Munsell hue / value / chroma from Vis-NIR reflectance spectra

Description

Combines [predict_xyz_from_spectra](#) with the Munsell renotation interpolation in **munsellinterpol** (CRAN, GPL). Returns hue (e.g. "7.5YR"), value (0..10) and chroma (0..20) per sample, plus the soilKey fields

Usage

```
predict_munsell_from_spectra(spectra, wavelengths, round_chip = TRUE)
```

Arguments

spectra	Reflectance values, in 0..1 or 0..100. A numeric vector (one sample), a numeric matrix (rows = samples, cols = wavelengths) or a data.frame.
wavelengths	Numeric vector of the wavelengths (in nm) corresponding to the columns of spectra. Must cover at least 400-700 nm; values outside 380-780 are ignored.
round_chip	If TRUE (default), snaps the predicted HVC to the nearest standard Munsell chip grid via <code>munsellinterpol::roundHVC()</code> . FALSE returns continuous HVC (useful for further numeric work).

Details

The Munsell renotation is defined under *Illuminant C*, while the colorimetry here is computed under D65, so the conversion goes XYZ -> CIELAB (D65) -> `munsellinterpol::LabToMunsell()`, which chromatically adapts D65 -> C internally. Feeding D65 chromaticities straight to `xyYtoMunsell()` would bias every colour toward green-yellow (a perfect neutral would return Chroma ~ 0.65 rather than 0); this routine avoids that. `munsell_hue_moist`, `munsell_value_moist`, `munsell_chroma_moist` ready to write into a [PedonRecord](#) via the pedon's `add_measurement` method (see also [fill_munsell_from_spectra](#)).

This is the v0.9.47 unblock for the v0.9.35 Argissolo Vermelho / Amarelo / Vermelho-Amarelo color-confusion case: when a user has Vis-NIR spectra (which Embrapa's BDsolos / FEBR do not include but the OSSL does), the Munsell hue can be recovered physically without waiting for the surveyor's morphological description.

Value

A data.frame with columns `munsell_hue_moist`, `munsell_value_moist`, `munsell_chroma_moist`, `munsell_string` (e.g. "7.5YR 4/6"), X, Y, Z, one row per sample.

Examples

```
## Not run:
# White reflector across the visible: should map to a near-neutral
# high-value Munsell color.
wl <- seq(380, 780, by = 5)
R <- rep(0.9, length(wl))
predict_munsell_from_spectra(R, wavelengths = wl)

## End(Not run)
```

predict_ossl_mbl

Memory-based learning prediction against the OSSL library

Description

Predicts a set of soil properties from pre-processed Vis-NIR or MIR spectra using *memory-based learning* (MBL) – the recommended OSSL workflow for heterogeneous libraries. Defaults follow the literature (Ramirez-Lopez et al., 2013): $k = 100$ neighbours, PLS-score dissimilarity, local PLS regression with 5 components, internal leave-one-out validation.

Usage

```
predict_ossl_mbl(
  X,
  properties,
  region = "global",
  k = 100L,
  ossl_library = NULL,
  ...
)
```

Arguments

X	A pre-processed numeric matrix (rows = horizons, columns = wavelengths).
properties	Character vector of OSSL-supported property names.
region	One of "global", "south_america", "north_america", "europe", "africa".
k	Integer number of neighbours.
ossl_library	Optional list with the OSSL training spectra (X_r) and reference values (Y_r , a data.frame keyed by properties). When NULL, the synthetic path is used.
...	Additional arguments forwarded to <code>resemble::mbl</code> .

Details

If `resemble::mbl` is installed and an `ossl_library` artefact is supplied (a list with elements `Xr`, `Yr`) the function delegates to `resemble::mbl()`; otherwise it returns a deterministic synthetic prediction conditioned on the input spectra so that downstream code, tests and vignettes run without external dependencies. The fallback is annotated via the `notes` attribute on the returned `data.table`.

Value

A `data.table` with columns `horizon_idx`, `property`, `value`, `pi95_low`, `pi95_high`, `n_neighbors`. The "backend" attribute records which path was taken ("resemble" or "synthetic").

References

Ramirez-Lopez, L., Behrens, T., Schmidt, K., Stevens, A., Demattê, J. A. M., & Scholten, T. (2013). The spectrum-based learner: A new local approach for modeling soil Vis-NIR spectra of complex datasets. *Geoderma*, 195–196, 268–279.

predict_ossl_plsr_local

Local PLSR prediction against the OSSL library

Description

Selects the `k` nearest neighbours to each test spectrum in the OSSL training set and fits a local PLS regression. Like `predict_ossl_mbl`, this function dispatches to `resemble::mbl` (with a `local_algorithm = "pls"` setting) when the dependency is available; otherwise it falls back to the synthetic predictor.

Usage

```
predict_ossl_plsr_local(
  X,
  properties,
  region = "global",
  k = 100L,
  ossl_library = NULL,
  ...
)
```

Arguments

<code>X</code>	A pre-processed numeric matrix (rows = horizons, columns = wavelengths).
<code>properties</code>	Character vector of OSSL-supported property names.
<code>region</code>	One of "global", "south_america", "north_america", "europe", "africa".
<code>k</code>	Integer number of neighbours.
<code>ossl_library</code>	Optional list with the OSSL training spectra (<code>Xr</code>) and reference values (<code>Yr</code> , a <code>data.frame</code> keyed by <code>properties</code>). When <code>NULL</code> , the synthetic path is used.
<code>...</code>	Additional arguments forwarded to <code>resemble::mbl</code> .

Value

A data.table with the same schema as [predict_oss1_mbl](#).

predict_oss1_pretrained
Pre-trained OSSL prediction

Description

Applies the OSSL-distributed pre-trained PLSR / Cubist models for a set of soil properties to pre-processed spectra. Pre-trained models are loaded from `oss1_models`, a named list of property models that each must implement a `predict(model, X)` interface returning a data.frame with columns `value`, `pi95_low`, `pi95_high`. When `oss1_models` is NULL, the synthetic predictor is used.

Usage

```
predict_oss1_pretrained(
  X,
  properties,
  region = "global",
  oss1_models = NULL,
  ...
)
```

Arguments

<code>X</code>	A pre-processed numeric matrix (rows = horizons, columns = wavelengths).
<code>properties</code>	Character vector of OSSL-supported property names.
<code>region</code>	One of "global", "south_america", "north_america", "europe", "africa".
<code>oss1_models</code>	Optional named list of pre-trained models, keyed by property name.
<code>...</code>	Reserved.

Value

A data.table with columns `horizon_idx`, `property`, `value`, `pi95_low`, `pi95_high`, `n_neighbors`. `n_neighbors` is `NA_integer_` for pre-trained models. The "backend" attribute records which path was taken.

`predict_xyz_from_spectra`*Predict CIE XYZ tristimulus values from Vis-NIR reflectance spectra*

Description

Numerically integrates user reflectance against the CIE 1931 2-degree Standard Observer color-matching functions, weighted by the D65 illuminant. Returns the tristimulus values X , Y , Z on the standard scale where $Y = 100$ for a perfect diffuse white.

Usage

```
predict_xyz_from_spectra(spectra, wavelengths)
```

Arguments

<code>spectra</code>	Reflectance values, in 0..1 or 0..100. A numeric vector (one sample), a numeric matrix (rows = samples, cols = wavelengths) or a <code>data.frame</code> .
<code>wavelengths</code>	Numeric vector of the wavelengths (in nm) corresponding to the columns of <code>spectra</code> . Must cover at least 400-700 nm; values outside 380-780 are ignored.

Value

A `data.frame` with columns X , Y , Z , one row per sample.

See Also

[predict_lab_from_spectra](#), [predict_munsell_from_spectra](#).

`preprocess_spectra`*Pre-process Vis-NIR or MIR spectra*

Description

Applies a chosen pre-processing pipeline to a numeric matrix of soil spectra. Rows are samples (typically horizons) and columns are wavelengths. Returns a numeric matrix; SG-based methods shorten the spectrum by $w - 1$ columns at the edges (default $w = 5$ so two columns are dropped from each side).

Usage

```
preprocess_spectra(X, method = c("snv+sg1", "snv", "sg1"), w = 5L, p = 2L)
```

Arguments

X	Numeric matrix or data.frame of spectra (rows = samples, columns = wavelengths). Wavelengths should be evenly spaced.
method	One of "snv", "sg1", "snv+sg1". Default "snv+sg1".
w	Window size for the SG filter. Must be odd; default 5.
p	Polynomial order for the SG filter. Default 2.

Details

Supported method values:

"snv" Standard Normal Variate. Each row is centered on its own mean and divided by its own standard deviation.

"sg1" Savitzky-Golay 1st derivative with a window of five wavelengths and a quadratic polynomial.

"snv+sg1" SNV followed by SG1 (default; the standard pipeline used by OSSL pretrained models for Vis-NIR).

If `prospectr` is available, we use `prospectr::standardNormalVariate` and `prospectr::savitzkyGolay` (Rcpp implementation, faster and supports arbitrary window/polynomial). The native fallback uses the classical 5-point first-derivative coefficients $(-2, -1, 0, 1, 2) / 10$, which is the closed-form Savitzky-Golay solution for window 5 / polynomial 2 / derivative 1.

Value

A numeric matrix. Column names (wavelengths) are preserved where possible; SG trimming drops $(w - 1) / 2$ columns from each edge.

References

Savitzky, A., & Golay, M. J. E. (1964). Smoothing and differentiation of data by simplified least squares procedures. *Analytical Chemistry*, 36(8), 1627–1639.

Barnes, R. J., Dhanoa, M. S., & Lister, S. J. (1989). Standard Normal Variate transformation and de-trending of near-infrared diffuse reflectance spectra. *Applied Spectroscopy*, 43(5), 772–777.

Stevens, A., & Ramirez-Lopez, L. (2024). *prospectr*: Misc. functions for processing and sample selection of spectroscopic data. R package version 0.2.7.

Examples

```
set.seed(1)
X <- matrix(runif(5 * 2151, 0, 1), nrow = 5)
colnames(X) <- 350:2500
Xp <- preprocess_spectra(X, method = "snv+sg1")
dim(Xp) # 5 x 2147 (4 columns dropped by SG window 5)
```

pretic	<i>Pretic horizon (WRB 2022): "Amazonian Dark Earth" (terra preta de indio) horizon – thick anthropogenic surface with high P, SOC, and incorporated charcoal / pottery.</i>
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Description

Pretic horizon (WRB 2022): "Amazonian Dark Earth" (terra preta de indio) horizon – thick anthropogenic surface with high P, SOC, and incorporated charcoal / pottery.

Usage

```
pretic(pedon, min_thickness = 20, min_oc = 1.5, min_p_mehlich3 = 30)
```

Arguments

pedon	A PedonRecord .
min_thickness	Numeric threshold or option (see Details).
min_oc	Numeric threshold or option (see Details).
min_p_mehlich3	Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

```
print.soilKey_pls_model
```

Print method for soilKey_pls_model

Description

Print method for soilKey_pls_model

Usage

```
## S3 method for class 'soilKey_pls_model'
print(x, ...)
```

Arguments

x	A soilKey_pls_model object.
...	Reserved.

Value

The object, invisibly.

prior_consistency_check

Check consistency between a deterministic RSG assignment and a spatial prior

Description

Returns a list describing whether the assigned RSG is plausible under the given prior. The deterministic classification is never overridden – this is purely a sanity-check signal.

Usage

```
prior_consistency_check(rsg_code, prior, threshold = 0.01)
```

Arguments

rsg_code	Two-letter RSG code (e.g. "FR"). Either the rsg_or_order from a ClassificationResult (in which case it must be the RSG name; we try to translate via the trace) or the bare code from a key trace entry.
prior	A spatial-prior data.table from spatial_prior .
threshold	Probability below which an assignment is flagged inconsistent (default 0.01).

Value

A list with elements:

- consistent: TRUE / FALSE / NA.
- p: probability of the assigned RSG in the prior (or NA_real_ if not found).
- threshold: the threshold used.
- status: a short status string – "consistent", "inconsistent", or "no_data".
- note: human-readable explanation.
- top_prior: data.table with the top three classes from the prior (for messages).

protocalcic_properties

Protocalcic properties (WRB 2022 Ch 3.2.8)

Description

Visible secondary carbonate accumulations, less than the calcic gate. Detects via caco3_pct between 0.5 and the calcic threshold (15) AND designation effervescence pattern (k).

Usage

```
protocalcic_properties(pedon, min_caco3_pct = 0.5, max_caco3_pct = 15)
```

Arguments

pedon A [PedonRecord](#).
min_caco3_pct Numeric threshold or option (see Details).
max_caco3_pct Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

protogypsic_properties

Protogypsic properties (WRB 2022 Ch 3.2.9): visible secondary gypsum \geq 1% but below the gypsic gate.

Description

Protogypsic properties (WRB 2022 Ch 3.2.9): visible secondary gypsum \geq 1% but below the gypsic gate.

Usage

```
protogypsic_properties(pedon, min_caso4_pct = 1, max_caso4_pct = 5)
```

Arguments

pedon A [PedonRecord](#).
min_caso4_pct Numeric threshold or option (see Details).
max_caso4_pct Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

protovertic	<i>Protovertic horizon (WRB 2022 Ch 3.1)</i>
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Description

A weakly developed vertic horizon – the swelling/shrinking machinery is present but does not reach the full vertic intensity (cracks too narrow, or slickensides only "few", or thickness too small). Used by the Protovertic qualifier; relevant for soils that would be Vertisols if the cracks/slickensides were a notch stronger.

Usage

```
protovertic(pedon, min_clay = 30, min_thickness = 15)
```

Arguments

pedon	A PedonRecord .
min_clay	Numeric threshold or option (see Details).
min_thickness	Numeric threshold or option (see Details).

Details

v0.3.5 detection: clay \geq 30% AND any positive vertic evidence (slickensides at \geq "few" OR cracks_width_cm \geq 0.2 OR a wedge/lenticular structure_type) AND thickness \geq 15 cm. The positive cases that pass the strict [vertic_horizon](#) test are explicitly excluded so the two diagnostics partition the vertic-spectrum cleanly.

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

read_febr_pedons	<i>Load FEBR datasets as a list of PedonRecord objects</i>
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Description

Wraps febr::readFEBR() (CRAN package, FEBR v1.9.9+ recommended) and adapts the returned camada (layer) + observacao tables to the soilKey schema. Auto-detects Munsell columns across the ~6 distinct conventions found in the 200 FEBR datasets that carry color data, parses PT-BR Munsell strings ("2, 5YR 3/6") and converts FEBR's standard units to soilKey conventions.

Usage

```
read_febr_pedons(
  dataset_codes = c("ctb0039"),
  febr_repo = NULL,
  min_munsell_coverage = 0,
  verbose = TRUE
)
```

Arguments

`dataset_codes` Character vector of FEBR dataset IDs (e.g. `c("ctb0032", "ctb0562")`). Pass "all" to download every Munsell-bearing dataset; this is heavy (network calls per dataset). Default: a small curated sample for development.

`febr_repo` Optional override for the FEBR repository location, forwarded to `febr::readFEBR`.

`min_munsell_coverage` Drop pedons whose horizons are *all* missing Munsell. Default 0 (keep all); set to 0.5 to keep only pedons with at least 50 horizons having a Munsell hue.

`verbose` If TRUE (default), prints per-dataset join statistics.

Details

Per the May 2026 scan, ~80 [febr_index_munsell](#) to get the curated list of Munsell-bearing dataset IDs.

Value

A list of [PedonRecord](#) objects with `site$id = FEBR observacao_id`, `site$reference_sibcs =` the surveyor's classification when available, and one horizon per FEBR camada row.

See Also

[febr_index_munsell](#), [load_bdsolos_csv](#).

Examples

```
## Not run:
# Single dataset (35 perfis, 100% Munsell coverage)
pedons <- read_febr_pedons("ctb0039")

# Multiple datasets
pedons <- read_febr_pedons(c("ctb0032", "ctb0562", "ctb0568"))

# All Munsell-bearing datasets (slow; 200 datasets, ~36k horizons)
all_pedons <- read_febr_pedons("all")

## End(Not run)
```

read_spectral_library *Read a Vis-NIR / MIR reflectance + lab table into an OSSL-shaped library*

Description

Turns an arbitrary spectral dataset (e.g. a Brazilian Vis-NIR/MIR library) into the canonical list (Xr, Yr, metadata) object consumed by `fill_from_spectra` and `classify_by_spectral_neighbours`. Column names are mapped to the package's canonical attributes (clay_pct, sand_pct, ..., and the taxonomic label columns wrb_rsg / sibcs_ordem / usda_order) via a built-in alias table (including Portuguese headers such as *argila / silte / carbono*) or an explicit `property_map / label_map`.

Usage

```
read_spectral_library(
  reflectance,
  metadata,
  id_col = "id",
  wavelengths = NULL,
  resample_to = NULL,
  property_map = NULL,
  label_map = NULL,
  normalize = c("auto", "none", "percent"),
  verbose = TRUE
)
```

Arguments

reflectance	Reflectance data: a matrix / data.frame with rows = samples and columns named by wavelength (nm); OR a long data.frame with id_col, wavelength_nm, reflectance; OR a path to a CSV in either form.
metadata	A data.frame with one row per sample carrying id_col plus lab attributes and optional taxonomic labels and lat/ lon. Rows are aligned to reflectance by id_col.
id_col	Sample identifier column shared by both tables (default "id").
wavelengths	Optional explicit wavelength vector (nm) when the reflectance columns are not wavelength-named.
resample_to	Optional target wavelength grid (nm) to linearly resample every spectrum onto (e.g. 350:2500); default keeps the native grid.
property_map, label_map	Optional named lists overriding the alias auto-detection, e.g. <code>property_map = list(clay_pct = "ARGILA")</code> .
normalize	One of "auto" (divide by 100 when values look like percent), "percent", or "none".
verbose	Print a one-line summary (default TRUE).

Value

A list with `Xr` (numeric reflectance matrix), `Yr` (data frame of mapped properties + labels + lat/lon), and metadata (provenance). Ready to pass as `ossl_library=`.

See Also

[pedons_from_spectral_table](#), [benchmark_spectral_fill](#), [fill_from_spectra](#)

reducing_conditions	<i>Reducing conditions (WRB 2022 Ch 3.2.10) – per-pedon test wrapping test_reducing_conditions.</i>
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Description

Reducing conditions (WRB 2022 Ch 3.2.10) – per-pedon test wrapping `test_reducing_conditions`.

Usage

```
reducing_conditions(pedon, min_redox_pct = 5)
```

Arguments

`pedon` A [PedonRecord](#).
`min_redox_pct` Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

report	<i>Render a soilKey classification report</i>
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Description

Produces a pedologist-facing report from one or more [ClassificationResult](#) objects, optionally including the source [PedonRecord](#). The HTML output is fully self-contained (single file, inline CSS); the PDF output goes through `rmarkdown::render()` and therefore requires a working LaTeX install (or one of the alternative engines accepted by `rmarkdown`).

Usage

```
report(
  x,
  file,
  format = c("auto", "html", "pdf"),
  pedon = NULL,
  title = NULL,
  include_family = FALSE,
  specifiers = FALSE,
  lang = c("en", "pt"),
  ...
)
```

Arguments

<code>x</code>	A <code>ClassificationResult</code> , a list of <code>ClassificationResults</code> , or a <code>PedonRecord</code> (in which case all three keys are run automatically).
<code>file</code>	Output path. The format is inferred from the extension (<code>.html</code> or <code>.pdf</code>) unless format is given explicitly.
<code>format</code>	One of <code>"auto"</code> , <code>"html"</code> , <code>"pdf"</code> .
<code>pedon</code>	Optional <code>PedonRecord</code> ; when provided, its horizons table and provenance log are included.
<code>title</code>	Optional report title.
<code>include_family</code>	When <code>x</code> is a <code>PedonRecord</code> (so the three keys are run here), passes through to <code>classify_usda</code> to append the USDA family (5th category) to the subgroup. Default <code>FALSE</code> keeps the output byte-identical to earlier versions.
<code>specifiers</code>	When <code>x</code> is a <code>PedonRecord</code> , passes through to <code>classify_wrb2022</code> to attach WRB depth specifiers (Epi-/Endo-/...) to depth-anchored qualifiers. Default <code>FALSE</code> . Both flags are ignored when <code>x</code> is already a (list of) <code>ClassificationResult</code> .
<code>lang</code>	Report language; <code>"en"</code> (default) or <code>"pt"</code> (Brazilian Portuguese).
<code>...</code>	Passed to method-specific renderers.

Details

This is an S3 generic with methods for `ClassificationResult`, `list`, and `PedonRecord`. Most users call `report()` directly with a list of three results (`list(classify_wrb2022(p), classify_sibcs(p), classify_usda(p))`) to get a cross-system one-pager.

Value

The output path, invisibly.

Examples

```
pedon <- make_ferralsol_canonical()
out <- file.path(tempdir(), "soilkey_report.html")
report(pedon, file = out, pedon = pedon)
file.exists(out)
```

report_html	<i>Render a soilKey classification report as self-contained HTML</i>
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Description

See [report](#) for the generic. This function writes a single-file HTML report with inline CSS (no external network requests, no 'htmltools' dependency) so it can be emailed or archived as-is.

Usage

```
report_html(  
  x,  
  file,  
  pedon = NULL,  
  title = NULL,  
  include_family = FALSE,  
  specifiers = FALSE,  
  lang = c("en", "pt"),  
  ...  
)
```

Arguments

x	A ClassificationResult, list of results, or PedonRecord.
file	Output .html path.
pedon	Optional PedonRecord.
title	Report title.
include_family, specifiers	Passed through to the keys when x is a PedonRecord; see report .
lang	Report language; "en" (default) or "pt" (Brazilian Portuguese).
...	Currently unused.

Value

The output path, invisibly.

`report_pdf`*Render a soilKey classification report as PDF*

Description

See [report](#) for the generic dispatcher. This function assembles a temporary ‘.Rmd’ file with the same content as [report_html](#) (site, cross-system summary, classification cards, horizons, provenance) and renders it via `rmarkdown::render()`.

Usage

```
report_pdf(  
  x,  
  file,  
  pedon = NULL,  
  title = NULL,  
  include_family = FALSE,  
  specifiers = FALSE,  
  lang = c("en", "pt"),  
  ...  
)
```

Arguments

<code>x</code>	A <code>ClassificationResult</code> , list of results, or <code>PedonRecord</code> .
<code>file</code>	Output <code>.pdf</code> path.
<code>pedon</code>	Optional <code>PedonRecord</code> .
<code>title</code>	Report title.
<code>include_family, specifiers</code>	Passed through to the keys when <code>x</code> is a <code>PedonRecord</code> ; see report .
<code>lang</code>	Report language, "en" (default) or "pt" (Brazilian Portuguese).
<code>...</code>	Passed to <code>rmarkdown::render()</code> .

Value

The output path, invisibly.

report_to_qgis	<i>Export a classification result + pedon to a QGIS GeoPackage</i>
----------------	--

Description

Writes a single GeoPackage (.gpkg) that QGIS reads natively, containing one POINT layer (the profile location with all classification metadata as attributes) plus two attribute-only tables (the horizons schema and the provenance log). Lets a pedologist overlay the soilKey result on a soil-survey base map or join it with field-campaign vector data without writing R or SQL.

Usage

```
report_to_qgis(
  pedon,
  classifications,
  file,
  report_html = NULL,
  overwrite = TRUE
)
```

Arguments

pedon	A PedonRecord .
classifications	A list of one to three ClassificationResult objects, named wrb / sibcs / usda. Pass the output of classify_from_documents verbatim, or build the list manually.
file	Output path (.gpkg). Created with parents.
report_html	Optional path to a sibling HTML report (rendered via report_html) – stored in the report_html attribute of pedon_point so QGIS users can launch the report from the feature pop-up.
overwrite	If TRUE (default), an existing file is replaced; otherwise an error is thrown.

Value

The output file path, invisibly. Side-effect: writes a multi-layer GeoPackage.

Geometry handling

The point geometry uses the pedon's site CRS (pedon\$site\$crs, default EPSG:4326). When the site has no coordinates, the function still writes the two attribute tables but skips the point layer and emits a warning.

Layer schema

pedon_point site_id, country, year, lat, lon, crs, wrb_name, wrb_rsg, wrb_grade, wrb_principal, wrb_supplementary, sibcs_name, sibcs_ordem, sibcs_grade, usda_name, usda_order, usda_grade, n_horizons, report_html (relative path), generated_at.

horizons_table site_id, horizon_idx, top_cm, bottom_cm, designation, plus the canonical horizon_column_spec() attributes when present.

provenance_log site_id, horizon_idx, attribute, source, confidence, notes.

See Also

[report](#) for HTML / PDF reports; [classify_from_documents](#) for the high-level one-liner that produces compatible classifications.

Examples

```
## Not run:
pedon <- make_ferralsol_canonical()
results <- list(
  wrb = classify_wrb2022(pedon, on_missing = "silent"),
  sibcs = classify_sibcs(pedon, include_familia = TRUE),
  usda = classify_usda(pedon)
)
report_to_qgis(pedon, results,
  file = "perfil_042.gpkg",
  report_html = "perfil_042.html")
# In QGIS: Layer -> Add Layer -> Add Vector Layer -> perfil_042.gpkg

## End(Not run)
```

resolve_wrb_qualifiers

Resolve WRB 2022 qualifiers for a Reference Soil Group

Description

Walks the YAML qualifier list for a given RSG code and tests every principal / supplementary qualifier against the pedon. Returns the resolved canonical name pieces (principal + supplementary) plus a per-qualifier trace.

Usage

```
resolve_wrb_qualifiers(pedon, rsg_code, rules = NULL, specifiers = FALSE)
```

Arguments

pedon	A PedonRecord .
rsg_code	Two-letter RSG code (e.g. "FR" for Ferralsols).
rules	Optional pre-loaded rules list (saves I/O when many RSGs are tested).
specifiers	If TRUE, auto-attach WRB Ch 5 depth specifiers (Epi-/Endo-/Bathy-/Amphi-/Panto-/Kato-) to depth-anchored qualifiers based on the feature's actual depth. Default FALSE leaves names byte-identical to earlier versions.

Value

A list with principal (character vector), supplementary (character vector), trace, and trace_supplementary.

retic_properties	<i>Retic properties (WRB 2022)</i>
------------------	------------------------------------

Description

Tests whether any horizon designation indicates retic features (glossic tongues of bleached material penetrating into a clay- enriched horizon). v0.3 detects these via designation pattern matching "glossic|retic|albeluvic" (case-insensitive). Diagnostic of Retisols.

Usage

```
retic_properties(pedon, pattern = "glossic|retic|albeluvic")
```

Arguments

pedon	A PedonRecord .
pattern	Regex (default "glossic retic albeluvic").

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022), Chapter 5, Retisols.

run_all_benchmarks *Run the full soilKey benchmark suite and (optionally) write a report*

Description

Auto-detects which reference datasets are available locally, runs each via [benchmark_unified](#), adds the offline canonical sanity row and the AfSP sample when present, and returns a tidy accuracy summary. When `report_path` is given, a consolidated Markdown report is written.

Usage

```
run_all_benchmarks(
  datasets = "auto",
  paths = NULL,
  max_n = 300L,
  level = "order",
  report_path = NULL,
  verbose = TRUE
)
```

Arguments

<code>datasets</code>	"auto" (default) detects available datasets; otherwise any subset of <code>c("bdsolos", "febr", "kssl", "lucas_esdb", "redape")</code> , the literal "canonical" (only the fixture sanity row), or "all" (every dataset regardless of availability – absent ones are skipped).
<code>paths</code>	Named list of dataset paths (see benchmark_unified). NULL uses the package defaults (override the root via <code>options(soilKey.benchmark_root = "...")</code>).
<code>max_n</code>	Cap on pedons per dataset (keeps the run fast). Default 300.
<code>level</code>	Comparison level forwarded where supported (currently the suite reports at "order" / top level).
<code>report_path</code>	File to write the Markdown report to, TRUE to auto-name one under <code>inst/benchmarks/reports/</code> , or NULL (default) for no file.
<code>verbose</code>	Print progress.

Value

Invisibly, a list with summary (data.frame: dataset, system, n_compared, accuracy), `per_system` (pooled), raw (full `benchmark_unified` output), weak (zero-recall classes) and `config`.

See Also

[benchmark_unified](#), [benchmark_redape](#).

Examples

```
## Not run:
res <- run_all_benchmarks(max_n = 250,
                          report_path = TRUE)

res$summary

## End(Not run)
```

run_classify_app *Launch the soilKey interactive classification Shiny app*

Description

Opens a local Shiny app ("Pro") that drives the soilKey pipeline from a browser – no R code required: build a pedon from a canonical fixture, a CSV upload, or an interactive horizon editor; classify under WRB 2022 / SiBCS 5 / USDA ST 13 with the full key trace; run VLM photo extraction, OSSL spectral gap-fill, the SoilGrids spatial prior, an interactive **leaflet** map that queries the class prior at a clicked point, and a Monte-Carlo robustness analysis; and download a cross-system HTML or PDF report. The interface is bilingual (English / Portuguese; see lang).

Usage

```
run_classify_app(
  ui = c("pro", "classic"),
  lang = c("en", "pt"),
  port = NULL,
  launch.browser = TRUE,
  ...
)
```

Arguments

ui	Kept for back-compatibility. "pro" (default) launches the professional multi-tab app. "classic" – the original single-page uploader – was retired in v0.9.117 ; passing it now emits a deprecation warning and launches the Pro app instead.
lang	Initial interface language: "en" (default) or "pt" (Brazilian Portuguese). Can also be switched live from the app's navbar.
port	Port for the local server. Default lets Shiny choose.
launch.browser	Whether to open the app in the default browser (default TRUE).
...	Additional arguments passed to runApp .

Details

Needs the optional packages **bslib**, **shinyWidgets**, **plotly** and **leaflet** (all in Suggests); the function raises a clear, copy-pasteable error if any are missing.

Value

Invisibly the value returned by `shiny::runApp()`.

Examples

```
## Not run:
run_classify_app()      # professional multi-tab app (English)
run_classify_app(lang = "pt") # interface em portugues

## End(Not run)
```

`run_demo`*Launch the soilKey Shiny demo (one-screen GUI)*

Description

Opens a Shiny app that lets a non-coder pick one of the 31 canonical profiles or upload a small horizons CSV, click **Classify**, and read the WRB / SiBCS / USDA names plus the deterministic key trace and the evidence grade. Useful for live demos, classroom teaching, and for pedologists who want to verify the package on a profile they already know without writing R code.

Usage

```
run_demo(...)
```

Arguments

```
...          Forwarded to shiny::runApp() (e.g. port = 4321, launch.browser = FALSE,
             host = "0.0.0.0").
```

Details

Requires the shiny package. The taxonomic key is still deterministic: no VLM is invoked from the GUI.

Value

Invisibly, the value returned by `shiny::runApp()`.

Examples

```
## Not run:
  soilKey::run_demo()

## End(Not run)
```

run_sibcs_grande_grupo

Resolve o grande grupo (3o nivel) de um pedon classificado em uma subordem SiBCS

Description

v0.7.3: itera os Grandes Grupos da subordem em ordem canonica via o engine generico [run_taxa_list](#); a primeira test-block que passa captura o perfil. Os Grandes Grupos sao carregados de `inst/rules/sibcs5/grandes-grupos` (split por ordem) e mergeados pelo [load_rules](#).

Usage

```
run_sibcs_grande_grupo(pedon, subordem_code, rules = NULL)
```

Arguments

pedon	A PedonRecord .
subordem_code	Codigo da subordem (e.g. "OJ" para Organossolos Tiomorficos).
rules	Lista de regras carregada via load_rules .

Details

Quando a subordem nao tem bloco de Grandes Grupos definido (ainda nao virado para todas as ordens), retorna `list(assigned = NULL, trace = list())` – comportamento nao-fatal que permite [classify_sibcs](#) parar no 2o nivel sem erro.

Value

Lista com `assigned` (entrada YAML do Grande Grupo ou NULL) e `trace`.

run_sibcs_key

Roda a chave SiBCS 5a edicao sobre um pedon

Description

Roda a chave SiBCS 5a edicao sobre um pedon

Usage

```
run_sibcs_key(pedon, rules = NULL)
```

Arguments

pedon	A PedonRecord .
rules	Conjunto de regras pre-carregado; se NULL, le <code>inst/rules/sibcs5/key.yaml</code> .

Value

Lista com assigned (entrada YAML da ordem atribuida) e trace.

run_sibcs_subgrupo	<i>Resolve o subgrupo (4o nivel) de um pedon classificado em um Grande Grupo SiBCS</i>
--------------------	--

Description

v0.7.3.B: itera os Subgrupos do Grande Grupo em ordem canonica via o engine generico [run_taxa_list](#); a primeira test-block que passa captura o perfil. Os Subgrupos sao carregados de `inst/rules/sibcs5/subgrupos/<ordem>`. (split por ordem) e mergeados pelo [load_rules](#).

Usage

```
run_sibcs_subgrupo(pedon, gg_code, rules = NULL)
```

Arguments

pedon	A PedonRecord .
gg_code	Codigo do Grande Grupo (e.g. "OJF" para Organossolos Tiomorficos Fibricos).
rules	Lista de regras carregada via load_rules .

Details

Em contraste com o 3o nivel (Grandes Grupos de Organossolos), Subgrupos de Cap 14 SEMPRE tem catch-all tests:{default:true} como ultima entrada de cada lista (subgrupo "tipico"), entao a classificacao sempre desce ao 4o nivel quando o GG foi resolvido.

Value

Lista com assigned (entrada YAML do Subgrupo ou NULL) e trace.

run_sibcs_subordem	<i>Resolve a subordem de um pedon ja classificado em uma ordem SiBCS</i>
--------------------	--

Description

Itera as subordens da ordem em ordem canonica via o engine generico [run_taxa_list](#); a primeira cuja test-block passa captura o perfil. Se nenhuma passar, retorna a ultima subordem (catch-all tests:{default:true}).

Usage

```
run_sibcs_subordem(pedon, ordem_code, rules = NULL)
```

Arguments

pedon	A PedonRecord .
ordem_code	Codigo de uma letra da ordem (e.g. "L" para Latossolos).
rules	Lista de regras carregada via load_rules .

Value

Lista com assigned (entrada YAML da subordem ou NULL se a ordem nao tiver bloco) e trace.

run_taxa_list	<i>Iterate a flat taxa list and evaluate tests in canonical order</i>
---------------	---

Description

Internal iterator extracted from [run_taxonomic_key](#) so nested categorical levels (subordens, grandes grupos, subgrupos, familias) can be iterated directly, without going through the `rules[[level_key]]` indirection that only makes sense at the top level.

Usage

```
run_taxa_list(pedon, taxa)
```

Arguments

pedon	A PedonRecord .
taxa	A list of taxon entries; each entry must have code, name, and tests fields, where tests is a block parseable by evaluate_rsg_tests .

Details

Behavioural note: when taxa is empty or NULL, returns `list(assigned = NULL, trace = list())` – a sub-level lookup with no canonical entries is non-fatal. The top-level [run_taxonomic_key](#) keeps the stricter "missing list is an error" semantics by guarding before calling this helper.

Value

A list with assigned (the entry of the assigned taxon, or NULL when taxa was empty) and trace.

run_taxonomic_key *Run a taxonomic key (system-agnostic engine)*

Description

Iterates over the taxa list at rules[[level_key]] in canonical order; the first taxon whose tests pass is assigned. evaluate_rsg_tests is reused as the per-taxon evaluator regardless of system – the test combinator semantics (all_of / any_of / default / not_implemented_v01) are the same in all three systems.

Usage

```
run_taxonomic_key(pedon, rules, level_key)
```

Arguments

pedon	A PedonRecord .
rules	A parsed rule set (output of load_rules).
level_key	Name of the taxa list inside rules: typically "rsgs" (WRB), "orders" (USDA), or "ordens" (SiBCS).

Details

Used at the TOP level (RSG / Order / Ordem). For nested categorical levels (subordens, grandes grupos, subgrupos, familias) iterate the flat taxa list directly via [run_taxa_list](#).

Value

A list with assigned (the YAML entry of the assigned taxon) and trace (one entry per taxon tested).

run_usda_great_group *Run the USDA Great Group key for a given Suborder*

Description

Run the USDA Great Group key for a given Suborder

Usage

```
run_usda_great_group(pedon, suborder_code, rules = NULL)
```

Arguments

pedon	A PedonRecord .
suborder_code	The Suborder code (e.g. "AA" for Histels).
rules	Optional pre-loaded rule set.

Value

A list with assigned and trace; assigned is NULL if the Suborder has no great-groups YAML.

run_usda_key	<i>Run the USDA Soil Taxonomy Order key over a pedon</i>
--------------	--

Description

Run the USDA Soil Taxonomy Order key over a pedon

Usage

```
run_usda_key(pedon, rules = NULL)
```

Arguments

pedon	A PedonRecord .
rules	Optional pre-loaded rule set; if NULL, reads inst/rules/usda/key.yaml.

Value

A list with assigned (the YAML entry of the assigned Order) and trace.

run_usda_subgroup	<i>Run the USDA Subgroup key for a given Great Group</i>
-------------------	--

Description

Run the USDA Subgroup key for a given Great Group

Usage

```
run_usda_subgroup(pedon, great_group_code, rules = NULL)
```

Arguments

pedon	A PedonRecord .
great_group_code	The Great Group code (e.g. "AAA" for Folistels).
rules	Optional pre-loaded rule set.

Value

A list with assigned and trace; assigned is NULL if the Great Group has no subgroups YAML.

run_usda_suborder	<i>Run the USDA Suborder key for a given Order</i>
-------------------	--

Description

Run the USDA Suborder key for a given Order

Usage

```
run_usda_suborder(pedon, order_code, rules = NULL)
```

Arguments

pedon	A PedonRecord .
order_code	The Order code (e.g. "GE" for Gelisols).
rules	Optional pre-loaded rule set.

Value

A list with assigned and trace; assigned is NULL if the Order has no suborders YAML.

run_wrb_key	<i>Run the WRB 2022 key over a pedon</i>
-------------	--

Description

Iterates over the RSGs in canonical key order; the first RSG whose tests pass is assigned. RSGs whose tests return NA (stubbed diagnostics or insufficient data) are skipped and recorded in the trace.

Usage

```
run_wrb_key(pedon, rules = NULL)
```

Arguments

pedon	A PedonRecord .
rules	Optional pre-loaded rule set; if NULL, reads inst/rules/wrb2022/key.yaml.

Value

A list with assigned (the YAML entry for the assigned RSG) and trace (one entry per RSG tested, in order).

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022). *World Reference Base for Soil Resources*, 4th edition. International Union of Soil Sciences, Vienna. Chapter 3.1.20 – Salic horizon (p. 49).

saprico	<i>Material organico saprico (SiBCS Cap 14)</i>
---------	---

Description

Material organico altamente decomposto: < 17% de fibras esfregadas OU indice de von Post H7-H10. Discrimina Organossolos Sapricos no 3o nivel categorico.

Usage

saprico(pedon)

Arguments

pedon A [PedonRecord](#).

Value

[DiagnosticResult](#).

References

Embrapa (2018), SiBCS 5a ed., Cap 14 (Organossolos), pp 224-226.

save_oss1_models	<i>Save / load trained OSSL-backed PLSR models</i>
------------------	--

Description

Thin wrappers around saveRDS / readRDS that also verify the deserialised object's shape. The on-disk file carries the soilKey version, training time and preprocess label as attributes; [load_oss1_models](#) preserves them.

Usage

save_oss1_models(models, path)

load_oss1_models(path)

Arguments

models	Output of train_pls_from_oss1 .
path	File path. Use .rds or .RData as the suffix (saveRDS is used regardless).

Value

save_oss1_models() returns path invisibly. load_oss1_models() returns the model list.

shrink_swell_cracks	<i>Shrink-swell cracks (WRB 2022 Ch 3.2.12) – per-pedon test wrapping test_shrink_swell_cracks.</i>
---------------------	---

Description

Shrink-swell cracks (WRB 2022 Ch 3.2.12) – per-pedon test wrapping test_shrink_swell_cracks.

Usage

```
shrink_swell_cracks(pedon, min_width_cm = 0.5)
```

Arguments

pedon	A PedonRecord .
min_width_cm	Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

sideralic_properties	<i>Sideralic properties (WRB 2022 Ch 3.2.13)</i>
----------------------	--

Description

Mineral material with a relatively low CEC. WRB 2022 (3.2.13) requires BOTH:

1. one or both of: clay $\geq 8\%$ AND CEC/clay < 24 cmol_c/kg clay; OR bulk CEC < 2 cmol_c/kg soil;
2. evidence of soil formation as defined in criterion 3 of the cambic horizon (test_cambic_soil_formation).

Both must be met by the SAME layer. Criterion 2 was added in v0.9.127 (previously only criterion 1 was enforced); where the soil-formation evidence cannot be assessed (no Munsell/clay/Fe/carbonate adjacency data) the result is NA rather than a false positive.

Usage

```
sideralic_properties(pedon, max_cec_per_clay = 24, max_bulk_cec = 2)
```

Arguments

```
pedon          A PedonRecord.
max_cec_per_clay
                Numeric threshold or option (see Details).
max_bulk_cec   Numeric threshold or option (see Details).
```

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

```
soilgrids_usda_lut   SoilGrids -> USDA Soil Order lookup table (placeholder)
```

Description

Reserved for the future SoilGrids USDA layer. Currently returns the 12 USDA Order codes mapped to integers 1..12.

Usage

```
soilgrids_usda_lut()
```

Value

Named character vector.

```
soilgrids_wrb_lut   SoilGrids -> WRB code lookup table
```

Description

Maps the integer raster values used by the SoilGrids 2.0 "MostProbable WRB" layer to soilKey's two-letter RSG codes (the codes used in `inst/rules/wrb2022/key.yaml`).

Usage

```
soilgrids_wrb_lut()
```

Details

The numeric values follow the order used by ISRIC; users with a different convention can override this via the `lut` argument to [spatial_prior_soilgrids](#).

Value

Named character vector: names are integer-as-character ("1", "2", ...), values are RSG codes.

soil_classes_at_location

Likely soil classes at a geographic location (spatial classification aid)

Description

Returns a ranked list of the soil Reference Soil Groups (or SiBCS orders, or USDA orders) most likely to occur at the given point, based on a global or regional dominant-soil raster (SoilGrids 2.0 by default). This is the ***before-you-have-a-pedon helper***: a pedologist arriving in the field can call it with the GPS coordinates of the planned profile pit and see which classes are expected, plus what attributes typically distinguish them.

Usage

```
soil_classes_at_location(
  lat,
  lon,
  system = c("wrb2022", "sibcs", "usda"),
  buffer_m = 1000,
  source_url = NULL,
  top_n = 5,
  verbose = TRUE
)
```

Arguments

lat, lon	Numeric WGS-84 coordinates.
system	Classification system. One of "wrb2022" (default), "sibcs", "usda".
buffer_m	Radius in metres around the point used to gather raster pixels (default 1000 m, i.e. roughly 4 SoilGrids pixels).
source_url	Path / URL of the dominant-soil raster.
top_n	Keep the top N classes by probability (default 5).
verbose	Emit a cli summary.

Details

This function does **not** classify a profile. The deterministic key in [classify_wrb2022](#) / [classify_sibcs](#) / [classify_usda](#) remains the only thing that assigns a class from horizon data. The output here is purely informational – a "shopping list" of what to confirm.

Value

A list as described under **Output**.

Data source

For real use, point `source_url` at a regional SoilGrids "MostProbable WRB" GeoTIFF / COG (one of the cuts at <https://files.isric.org/soilgrids/latest/data/wrb/>). For tests, `options(soilKey.test_raster = "/tmp/syn.tif")` is honoured. When no source is given, the function emits a `cli_alert_warning()` and returns an empty result – it does **not** pretend to know.

Output

A list with three elements:

`distribution` A `data.table` with columns `rsg_code`, `rsg_name`, `probability`, sorted by descending probability.

`typical_attributes` A `data.table` keyed by `rsg_code` with the canonical attribute ranges that distinguish each class (clay range, CEC range, BS range, etc.). The values come from the WRB 2022 / SiBCS 5 / KST 13ed canonical thresholds, NOT from the raster.

`site` The site list passed in, plus the buffer radius and the source URL.

See Also

[spatial_prior_soilgrids](#) for the post-classification consistency check.

Examples

```
## Not run:
# Mata Atlântica, Rio de Janeiro state.
res <- soil_classes_at_location(
  lat      = -22.7,
  lon      = -43.7,
  system   = "wrb2022",
  source_url = "https://files.isric.org/soilgrids/latest/data/wrb/MostProbable.vrt"
)
res$distribution      # ranked list of likely RSGs
res$typical_attributes # canonical thresholds per RSG to confirm

## End(Not run)
```

<code>soil_organic_carbon</code>	<i>Soil organic carbon (WRB 2022 Ch 3.3.16): organic C that does NOT belong to artefacts. v0.3.3: any layer with <code>oc_pct</code> \geq 0.1 and <code>artefacts_industrial_pct</code> $<$ 35.</i>
----------------------------------	--

Description

Soil organic carbon (WRB 2022 Ch 3.3.16): organic C that does NOT belong to artefacts. v0.3.3: any layer with `oc_pct` \geq 0.1 and `artefacts_industrial_pct` $<$ 35.

Usage

```
soil_organic_carbon(pedon, min_oc = 0.1, max_artefacts = 35)
```

Arguments

pedon A [PedonRecord](#).

min_oc Numeric threshold or option (see Details).

max_artefacts Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

solimovic_material	<i>Solimovic material (WRB 2022 Ch 3.3.17): hetero genous mass-movement material on slopes / footslopes (formerly "colluvic"). v0.3.3: detects via rock_origin == "colluvial" OR layer_origin == "solimovic".</i>
--------------------	---

Description

Solimovic material (WRB 2022 Ch 3.3.17): hetero genous mass-movement material on slopes / footslopes (formerly "colluvic"). v0.3.3: detects via rock_origin == "colluvial" OR layer_origin == "solimovic".

Usage

```
solimovic_material(pedon)
```

Arguments

pedon A [PedonRecord](#).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

somblic	<i>Somblic horizon (WRB 2022): subsurface accumulation of humus that qualified neither as spodic nor as a true mollic-like horizon (low-base-saturation cool tropical highlands). v0.3.3 detects via designation pattern + OC criteria (BS < 50, OC > 0.6, depth > 25 cm).</i>
---------	---

Description

Somblic horizon (WRB 2022): subsurface accumulation of humus that qualified neither as spodic nor as a true mollic-like horizon (low-base-saturation cool tropical highlands). v0.3.3 detects via designation pattern + OC criteria (BS < 50, OC > 0.6, depth > 25 cm).

Usage

```
somblic(
  pedon,
  min_thickness = 15,
  min_oc = 0.6,
  max_bs = 50,
  min_top_cm = 25,
  min_oc_increase = 0.1
)
```

Arguments

pedon	A PedonRecord .
min_thickness	Numeric threshold or option (see Details).
min_oc	Numeric threshold or option (see Details).
max_bs	Numeric threshold or option (see Details).
min_top_cm	Numeric threshold or option (see Details).
min_oc_increase	Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

spatial_prior	<i>Spatial prior over RSGs (or Orders) at a pedon's location</i>
---------------	--

Description

Top-level dispatcher. Reads a categorical raster of soil classes (SoilGrids globally, Embrapa for Brazil), buffers the pedon's coordinates, tallies pixel classes within the buffer, and returns the empirical class frequency as a probability distribution.

Usage

```
spatial_prior(
  pedon,
  source = c("soilgrids", "embrapa"),
  system = c("wrb2022", "usda"),
  ...
)
```

Arguments

pedon	A PedonRecord with non-NULL site\$lat / site\$lon.
source	Backend to query: "soilgrids" (default) or "embrapa".
system	Classification system: "wrb2022" (default) or "usda". Embrapa source forces "sibcs5" internally regardless of this argument.
...	Passed through to the backend (spatial_prior_soilgrids or spatial_prior_embrapa).

Details

The prior is intentionally separate from the deterministic key. Pass the returned data.table to [classify_wrb2022](#) via the prior argument; the result will then carry a prior_check entry (consistent / inconsistent / not_run).

Value

A data.table with columns rsg_code (character) and probability (numeric, summing to 1). Empty if the buffer extracts no valid pixels – callers should check nrow().

spatial_prior_embrapa *Embrapa national soil-class spatial prior (Brazil only)*

Description

v0.5 stub. Reads a user-provided categorical raster of SiBCS orders / suborders, buffers the pedon's site, tallies pixel classes, and returns a probability distribution over SiBCS codes (or, with a user-provided LUT, over WRB equivalents).

Usage

```
spatial_prior_embrapa(
  pedon,
  raster_path = NULL,
  buffer_m = 3750,
  lut = NULL,
  n_classes_top = 10,
  ...
)
```

Arguments

pedon	A PedonRecord .
raster_path	Required. Path to a local categorical raster (GeoTIFF) of Embrapa SiBCS classes. There is no built-in file in v0.5 – download the polygon map from https://www.embrapa.br/solos/sibcs and rasterise it.
buffer_m	Buffer radius in metres (default 3750, i.e. ~15-cell neighbourhood at 250 m resolution).
lut	Optional named character vector mapping raster integer values to soil-class codes. If NULL, raster categories are used as-is (terra::levels).
n_classes_top	Keep only the top N classes (default 10).
...	Reserved.

Details

Unlike SoilGrids, Embrapa does not publish per-pixel probabilities, so the empirical frequency over a neighbourhood window (default 15 x 15 cells = ~3.75 km radius at 250 m resolution) is used as an approximation.

Value

A data.table with columns rsg_code, probability.

```
spatial_prior_soilgrids
      SoilGrids spatial prior
```

Description

Reads a categorical raster of dominant Reference Soil Groups around the pedon's site, buffers the point in metric coordinates, extracts all pixel values within the buffer, and returns the empirical class frequency as a probability distribution over RSG codes.

Usage

```
spatial_prior_soilgrids(
  pedon,
  system = c("wrb2022", "usda"),
  buffer_m = 250,
  source_url = NULL,
  n_classes_top = 10,
  lut = NULL,
  ...
)
```

Arguments

pedon	A PedonRecord with non-NULL <code>site\$lat</code> and <code>site\$lon</code> .
system	Classification system; "wrb2022" (default) maps SoilGrids integer codes through the WRB lookup table. "usda" is reserved for a future SoilGrids-USDA layer.
buffer_m	Buffer radius in metres around the point (default 250 m, i.e. one SoilGrids pixel).
source_url	Optional. A path or URL accepted by <code>terra::rast</code> . If NULL, falls back to <code>getOption("soilKey.test_raster")</code> .
n_classes_top	Keep only the top N classes by frequency (default 10). Set to <code>Inf</code> to keep all.
lut	Optional named integer vector mapping raster values to RSG codes. Default is soilgrids_wrb_lut ; pass a custom one if your raster uses different codes.
...	Reserved for future use.

Value

A `data.table` with columns `rsg_code`, `probability`.

Data source

For real use, pass `source_url` pointing at a SoilGrids "MostProbable WRB" GeoTIFF / COG, e.g. one of the regional cuts published at <https://files.isric.org/soilgrids/latest/data/wrb/>. For tests, set `options(soilKey.test_raster = "/path/to/syn.tif")` to point at a local synthetic raster – this avoids network access in CI.

Coordinate handling

We use `sf::st_transform` when `sf` is available; otherwise we fall back to `terra::project` on a single-point `SpatVector`. The buffer is constructed in metric (UTM) coordinates so `buffer_m` is in metres regardless of the pedon CRS. The raster itself is queried in its native CRS via `terra`'s automatic reprojection.

See Also

[spatial_prior](#), [soilgrids_wrb_lut](#).

spodic	<i>Spodic horizon (WRB 2022)</i>
--------	----------------------------------

Description

Tests whether any horizon meets the spodic horizon criteria. The spodic horizon is an illuvial horizon with active Al + Fe oxalate- extractable material plus organic matter; diagnostic of Podzols.

Usage

```
spodic(
  pedon,
  min_thickness = 2.5,
  min_alfe = 0.5,
  max_ph = 5.9,
  min_oc_in_b = 0.5,
  engine = NULL
)
```

Arguments

<code>pedon</code>	A PedonRecord .
<code>min_thickness</code>	Minimum thickness in cm (default 2.5).
<code>min_alfe</code>	Minimum (Al _{ox} + 0.5 * Fe _{ox}) percent (default 0.5).
<code>max_ph</code>	Maximum ph _{h2o} (default 5.9).
<code>min_oc_in_b</code>	Minimum OC % in the candidate Bh / Bs layer for the v0.9.19 morphological inference path when Al / Fe oxalate are missing (default 0.5).
<code>engine</code>	One of "soilkey" (default; strict v0.9.19 morphological path requires Bh / Bs / Bhs designation + albic E above) or "aqp" (relaxed v0.9.84 path: any B* below E* with OC translocation peak). When NULL, reads <code>getOption("soilKey.diagnostic_engine")</code> .

Details

Sub-tests:

- test_spodic_aluminum_iron – $(Al_{ox} + 0.5 * Fe_{ox}) \geq 0.5\%$
- test_ph_below – $ph_{h2o} \leq 5.9$
- test_minimum_thickness – $thickness \geq 2.5 \text{ cm}$

v0.2 limitations: the WRB color criterion (hue 5YR or yellower with chroma ≤ 5 , or specific dark colors) is not enforced. The $(Al_{ox} + Fe_{ox})/clay \geq 0.05$ alternative ratio test is not yet wired. Both deferred to v0.3.

Value

A [DiagnosticResult](#).

v0.9.84 engine="aqp" relaxation

KSSL+NASIS Spodosols routinely use generic "B1" / "B2" / "Bw" designations rather than the specific Bh / Bs / Bhs that the v0.9.19 morphological-inference path requires. Of 14 KSSL+NASIS Podzol references, only 1 / 14 passes spodic via the v0.9.19 path; 7 / 14 have BOTH an E-designated albic-eligible horizon above AND an OC peak in a B horizon below (the canonical Podzol illuviation signature) but use generic B / Bw designations and so fail strict morph.

When engine = "aqp" (read from `getOption("soilKey.diagnostic_engine", "soilkey")`) when engine is NULL) AND Al / Fe oxalate is unmeasured AND the v0.9.19 strict path did not fire, accept any B* designation below an E*-designated horizon when:

- $ph_{h2o} \leq max_{ph}$ in the B horizon, AND
- $oc_{pct} \geq min_{oc_in_b}$ in the B horizon, AND
- OC in the B is greater than the maximum OC in any horizon above (the translocation signature).

Default engine is "soilkey" – canonical behaviour bit-for-bit preserved.

References

IUSS Working Group WRB (2022), Chapter 3, Spodic horizon.

stagnic_properties *Stagnic properties (WRB 2022)*

Description

Tests for redoximorphic features driven by perched water. Distinct from gleyic (groundwater): stagnic features appear in upper layers AND redox decreases substantially with depth (the perched layer sits above a slowly permeable subsoil that itself is not saturated).

Usage

```
stagnic_properties(
  pedon,
  max_top_cm = 100,
  min_redox_pct = 5,
  decay_factor = 3
)
```

Arguments

pedon	A PedonRecord .
max_top_cm	Maximum top depth (cm) of candidate shallow layers (default 100).
min_redox_pct	Minimum redox feature percent in the shallow layer (default 5).
decay_factor	Required factor of redox decrease with depth (default 3, i.e., deeper redox < shallow / 3).

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022), Chapter 3, Stagnic properties.

st_features_canonical *USDA Soil Taxonomy diagnostic features canonical table*

Description

Convenience wrapper for `canonical_reference("ST_features")`. Returns an 84-row data.frame with one row per diagnostic feature (epipedon / subsurface horizon / property / material) and columns: group, name, chapter, page, description, criteria. The criteria column is a list-column; each element holds the parsed criteria text per feature.

Usage

```
st_features_canonical(prefer_pkg = TRUE)
```

Arguments

prefer_pkg	If TRUE (default), prefer the installed SoilTaxonomy package over the vendored copy. Set to FALSE to force the vendored copy (e.g. for reproducibility of a specific soilKey release).
------------	--

Value

The canonical Soil Taxonomy diagnostic-features reference (a list / data.frame).

subgrupo_planossolo_espessos

Subgrupo "espessos" de Planossolos (B planico profundo, > 100 cm)

Description

Discrimina os Subgrupos espessos de Planossolos (Cap 15: SNs Espessos, SNo Espessos, SXs Espessos, SXal Espessos, SXd Espessos, SXe Espessos): B planico cujo topo ocorre entre `min_top_cm` (exclusivo) e `max_top_cm` (inclusivo).

Usage

```
subgrupo_planossolo_espessos(pedon, min_top_cm = 100, max_top_cm = 200)
```

Arguments

<code>pedon</code>	A PedonRecord .
<code>min_top_cm</code>	Profundidade minima exclusiva do topo do B planico (default 100; passa se top > 100).
<code>max_top_cm</code>	Profundidade maxima inclusiva (default 200).

Details

Implementacao: identifica B planico via [B_planico](#), captura o topo (mais raso) das camadas que passam, e testa se cai em (`min_top_cm`, `max_top_cm`].

Value

[DiagnosticResult](#).

References

Embrapa (2018), SiBCS 5a ed., Cap 15 (Planossolos), pp 251-260.

subgrupo_planossolo_mesicos

Subgrupo "mesicos" de Planossolos (B planico topo em [50, 100] cm)

Description

Discrimina os Subgrupos mesicos de Planossolos (Cap 15: SNs Mesicos, SNo Mesicos, SXs Mesicos, SXal Mesicos, SXd Mesicos, SXe Mesicos): B planico cujo topo ocorre entre `min_top_cm` (inclusivo) e `max_top_cm` (inclusivo).

Usage

```
subgrupo_planossolo_mesicos(pedon, min_top_cm = 50, max_top_cm = 100)
```

Arguments

pedon	A PedonRecord .
min_top_cm	Profundidade minima inclusiva (default 50).
max_top_cm	Profundidade maxima inclusiva (default 100).

Value

[DiagnosticResult](#).

References

Embrapa (2018), SiBCS 5a ed., Cap 15 (Planossolos).

subgrupo_plintossolo_endico_concrecionario

Subgrupo "endico" de Plintossolos Concrecionarios (topo de horizonte concrecionario \geq 40 cm)

Description

Discrimina o Subgrupo FFcoEn (Plintossolos Petricos Concrecionarios endicos): horizonte concrecionario cujo topo ocorre a \geq min_top_cm cm.

Usage

```
subgrupo_plintossolo_endico_concrecionario(pedon, min_top_cm = 40)
```

Arguments

pedon	A PedonRecord .
min_top_cm	Profundidade minima inclusiva (default 40).

Value

[DiagnosticResult](#).

References

Embrapa (2018), SiBCS 5a ed., Cap 16, p 264.

subgrupo_plintossolo_endico_litoplintico

Subgrupo "endico" de Plintossolos Litoplinticos (topo de horizonte litoplintico \geq 40 cm)

Description

Discrimina o Subgrupo FFlpEn (Plintossolos Petricos Litoplinticos endicos): horizonte litoplintico cujo topo ocorre a \geq min_top_cm cm.

Usage

```
subgrupo_plintossolo_endico_litoplintico(pedon, min_top_cm = 40)
```

Arguments

pedon	A PedonRecord .
min_top_cm	Profundidade minima inclusiva (default 40).

Value

[DiagnosticResult](#).

References

Embrapa (2018), SiBCS 5a ed., Cap 16, p 264.

subgrupo_plintossolo_espessos

Subgrupo "espessos" de Plintossolos (horizonte plintico topo $>$ 100 cm)

Description

Discrimina os Subgrupos espessos de Plintossolos Argiluvicos (FT*Es) e Haplicos (FXacEs, FXdEs, FXeEs): horizonte plintico cujo topo ocorre entre min_top_cm (exclusivo) e max_top_cm (inclusivo).

Usage

```
subgrupo_plintossolo_espessos(pedon, min_top_cm = 100, max_top_cm = 200)
```

Arguments

pedon	A PedonRecord .
min_top_cm	Profundidade minima exclusiva (default 100).
max_top_cm	Profundidade maxima inclusiva (default 200).

Value

[DiagnosticResult](#).

References

Embrapa (2018), SiBCS 5a ed., Cap 16 (Plintossolos), pp 261-272.

takyric_properties	<i>Takyric properties (WRB 2022 Ch 3.2.15) – per-pedon test wrapping test_takyric_surface.</i>
--------------------	--

Description

Takyric properties (WRB 2022 Ch 3.2.15) – per-pedon test wrapping test_takyric_surface.

Usage

takyric_properties(pedon)

Arguments

pedon A [PedonRecord](#).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

technic_features	<i>Technic features (WRB 2022)</i>
------------------	------------------------------------

Description

Tests for any of three WRB 2022 alternative qualifying conditions for Technosols:

1. Artefacts \geq artefacts_min_pct (default 20%) by volume within the upper max_top_cm (default 100 cm).
2. A continuous geomembrane (geomembrane_present == TRUE) within the upper 100 cm.
3. Technic hard material (concrete, asphalt, mine spoil) with technic_hardmaterial_pct \geq hardmaterial_min_pct (default 95%) at the surface (top_cm \leq hardmaterial_max_top_cm, default 5).

Either path qualifies.

Usage

```

technic_features(
  pedon,
  artefacts_min_pct = 20,
  max_top_cm = 100,
  hardmaterial_min_pct = 95,
  hardmaterial_max_top_cm = 5
)

```

Arguments

pedon A [PedonRecord](#).

artefacts_min_pct Minimum artefact percent (default 20).

max_top_cm Maximum top depth (cm) for the artefact and geomembrane paths (default 100).

hardmaterial_min_pct Minimum hard-material coverage (%) for the technic-hard-material path (default 95).

hardmaterial_max_top_cm Surface depth window (cm) for the technic-hard-material path (default 5).

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022), Chapter 5, Technosols.

technic_hard_material *Technic hard material (WRB 2022 Ch 3.3.18): consolidated human-made material (asphalt, concrete, worked stones).*

Description

Technic hard material (WRB 2022 Ch 3.3.18): consolidated human-made material (asphalt, concrete, worked stones).

Usage

```

technic_hard_material(pedon)

```

Arguments

pedon A [PedonRecord](#).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

tephric_material	<i>Tephric material (WRB 2022 Ch 3.3.19): \geq 30% volcanic glass in 0.02-2 mm fraction AND no andic / vitric properties.</i>
------------------	--

Description

Tephric material (WRB 2022 Ch 3.3.19): \geq 30% volcanic glass in 0.02-2 mm fraction AND no andic / vitric properties.

Usage

```
tephric_material(pedon, min_glass = 30)
```

Arguments

pedon	A PedonRecord .
min_glass	Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

terrific	<i>Terrific horizon (WRB 2022): topsoil thickened by long-term application of mineral material (sediment / sand additions). v0.3.3: thickness \geq 20 cm + designation Au / Apc.</i>
----------	---

Description

Terrific horizon (WRB 2022): topsoil thickened by long-term application of mineral material (sediment / sand additions). v0.3.3: thickness \geq 20 cm + designation Au / Apc.

Usage

```
terrific(pedon, min_thickness = 20)
```

Arguments

pedon	A PedonRecord .
min_thickness	Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

texture_class_from_pct

NRCS texture-class shorthand from clay / silt / sand percent

Description

aqp's `getArgillicBounds()` requires an NRCS texture class column (e.g. "SCL", "C", "CL", "FS"). `soilKey` horizons only carry the percent fractions; this helper derives the class from the standard USDA texture triangle.

Usage

```
texture_class_from_pct(clay, silt, sand)
```

Arguments

clay	Numeric vector of clay percent (0-100).
silt	Numeric vector of silt percent.
sand	Numeric vector of sand percent. (clay + silt + sand should sum to ~100; mild deviations are tolerated.)

Details

Returns the standard NRCS abbreviation:

COS	Coarse sand
S	Sand
FS	Fine sand
VFS	Very fine sand
LS	Loamy sand
LFS	Loamy fine sand
SL	Sandy loam
FSL	Fine sandy loam
L	Loam
SIL	Silt loam
SI	Silt
SCL	Sandy clay loam
CL	Clay loam
SICL	Silty clay loam
SC	Sandy clay
SIC	Silty clay
C	Clay

Implementation follows the canonical USDA texture triangle; vector-ised over the input. NA in / NA out.

Value

Character vector of NRCS texture class abbreviations.

thionic	<i>Thionic horizon (WRB 2022): post-oxidation acid sulfate horizon. Requires sulfidic_s_pct >= 0.01 AND pH(H2O) <= 4.</i>
---------	---

Description

Thionic horizon (WRB 2022): post-oxidation acid sulfate horizon. Requires sulfidic_s_pct >= 0.01 AND pH(H2O) <= 4.

Usage

```
thionic(pedon, min_thickness = 15, max_pH = 4, min_sulfidic_s = 0.01)
```

Arguments

pedon A [PedonRecord](#).

min_thickness Numeric threshold or option (see Details).

max_pH Numeric threshold or option (see Details).

min_sulfidic_s Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

train_pls_from_oss1	<i>Train pre-trained PLSR models from an OSS1 library</i>
---------------------	---

Description

Iterates over properties and fits one PLSR model per target against the OSS1 spectra in `oss1_library$Xr`, with internal cross-validation to pick the optimal number of components per property. The returned list is a drop-in replacement for the `oss1_models` argument of [predict_oss1_pretrained](#) and [fill_from_spectra](#).


```
result <- predict_from_spectra(my_pedon, models = models)
## End(Not run)
```

tsitelic

Tsitelic horizon (WRB 2022 Ch 3.1)

Description

From Georgian *tsiteli* = red. A red colour-defined horizon formed on weathered basalt or similar Fe-rich parent material in Caucasian / Mediterranean settings. Used by the Cambisols key (Ch 4 p 123, criterion 4) and by the Tsitelic qualifier.

Usage

```
tsitelic(pedon, min_thickness = 10)
```

Arguments

pedon A [PedonRecord](#).
min_thickness Numeric threshold or option (see Details).

Details

Diagnostic criteria (v0.3.5 simplification):

- Munsell hue $\leq 2.5\text{YR}$ (i.e. 2.5YR, 10R, 7.5R, 5R, 2.5R) AND value ≤ 4 (moist) AND chroma ≥ 4 (moist);
- evidence of soil formation (cambic-style criterion 3) proxied by clay $\geq 8\%$ AND structure_grade not "single grain" / "massive";
- thickness ≥ 10 cm.

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

umbric_horizon	<i>Umbric horizon (WRB 2022)</i>
----------------	----------------------------------

Description

Tests for the umbric horizon – a thick, dark, organic-rich surface horizon like mollic, but with low base saturation (< 50%). Diagnostic of Umbrisols.

Usage

```
umbric_horizon(  
  pedon,  
  min_thickness = 20,  
  min_oc = 0.6,  
  max_bs = 50,  
  surface_top_cm = 5  
)
```

Arguments

pedon	A PedonRecord .
min_thickness	Minimum thickness (cm; default 20).
min_oc	Minimum SOC % (default 0.6).
max_bs	Maximum base saturation % (default 50; profile must be BELOW this).
surface_top_cm	Maximum top_cm for surface-related layers (default 5).

Details

Implementation reuses every mollic sub-test except the BS test, which is inverted via `test_bs_below`.

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022), Chapter 3, Umbric horizon.

usda_to_wrb_rsg	<i>USDA Soil Taxonomy <-> WRB Reference Soil Group correlation table</i>
-----------------	--

Description

Returns the single most-common WRB RSG for a given USDA Order + optional Suborder. Based on IUSS WRB (2022) Annex 6.

Usage

```
usda_to_wrb_rsg(usda_order, usda_suborder = NULL)
```

Arguments

usda_order	Character vector of USDA Order names. Case-insensitive; trailing 's' stripped (e.g.\ both "Mollisols" and "Mollisol" accepted).
usda_suborder	Optional character vector of USDA Suborder names (case-insensitive) used to refine the mapping. Same length as usda_order or recycled.

Value

Character vector of WRB Reference Soil Group names (singular, no plural 's'). NA for unrecognised inputs.

Caveat

This is a "best-guess" cross-walk for benchmark validation only. Real-world correlation requires per-pedon evaluation of WRB diagnostic horizons. Use this function to derive a reasonable *expected* WRB classification from a USDA-classified pedon (e.g.\ from KSSL/NASIS) so that `classify_wrb2022()` can be validated against an external taxonomy on the same profiles.

References

IUSS Working Group WRB (2022). *World Reference Base for Soil Resources*, 4th edition, Annex 6. International Union of Soil Sciences, Vienna.

Examples

```
usda_to_wrb_rsg("Mollisols")
#> "Phaeozem"
usda_to_wrb_rsg("Aridisols", "Salids")
#> "Solonchak"
usda_to_wrb_rsg(c("Spodosols", "Oxisols", "Vertisols"))
#> c("Podzol", "Ferralsol", "Vertisol")
```

```
validate_horizon_geometry
      Validate horizon depth geometry
```

Description

A pure, side-effect-free check of a horizon table's depth geometry, independent of any [PedonRecord](#). The Pro app's Pedon builder calls it to give immediate feedback while horizons are edited, and it is a handy guard before constructing a profile from an untrusted CSV.

Usage

```
validate_horizon_geometry(horizons)
```

Arguments

`horizons` A data frame with at least numeric `top_cm` and `bottom_cm` columns (and optionally a `designation` column).

Details

It reports two severities:

errors (these make a sane classification impossible) a missing or non-numeric `top_cm`/`bottom_cm`; a negative depth; a horizon whose `top_cm` \geq `bottom_cm` (inverted or zero thickness); two horizons whose depths overlap.

warnings (allowed, but worth surfacing) the shallowest horizon not starting at the surface (0 cm); a gap between consecutive horizons; horizons entered out of increasing-depth order; a duplicated horizon designation.

This complements `PedonRecord$validate()`, which additionally checks chemistry (texture sums, pH, CEC vs bases, Munsell ranges); use that for a built record and this for a raw table.

Value

A list with `valid` (logical; TRUE when there are no errors), `errors` and `warnings` (character vectors of human-readable English messages), and `details` – a named list of the offending row indices (or values) per check, so a caller can compose its own (e.g. localised) messages.

Examples

```
h <- data.frame(top_cm = c(0, 20, 55), bottom_cm = c(20, 55, 90),
               designation = c("A", "AB", "Bt"))
validate_horizon_geometry(h)$valid      # TRUE
```

```
bad <- data.frame(top_cm = c(0, 40), bottom_cm = c(50, 30)) # overlap+inverted
validate_horizon_geometry(bad)$errors
```

validate_pedon_json	<i>Validate a PedonRecord against the JSON schema</i>
---------------------	---

Description

Convenience wrapper that converts a [PedonRecord](#) (or a compatible list) to JSON and validates it via `jsonvalidate::json_validate` against the canonical schema returned by [pedon_json_schema](#).

Usage

```
validate_pedon_json(x)
```

Arguments

`x` A [PedonRecord](#) or a list with the same shape.

Details

Use this BEFORE calling `classify_*` when ingesting data from external systems (web APIs, ETL pipelines, multimodal extraction) to catch schema violations early.

Value

A logical scalar (TRUE when valid). Validation errors appear as the `errors` attribute when FALSE.

Examples

```
## Not run:
p <- make_ferralsol_canonical()
validate_pedon_json(p)
#> [1] TRUE

## End(Not run)
```

vertic_horizon	<i>Vertic horizon (WRB 2022 Ch 3.1)</i>
----------------	---

Description

Stricter than the vertic `*properties*`: the vertic `*horizon*` requires $\geq 30\%$ clay throughout, slickensides at \geq "common" level, AND shrink-swell cracks ≥ 0.5 cm wide. Used by Vertisols. v0.9.19 adds an OR-alternative COLE-based linear-extensibility path: `summed(cole_value * thickness)` over the upper 100 cm ≥ 6 cm passes the diagnostic even when slickensides + cracks are not recorded (KST 13ed Ch 16 LE alternative, p 343).

Usage

```
vertic_horizon(
  pedon,
  min_clay = 30,
  min_thickness = 25,
  min_le_cm = 6,
  le_max_depth_cm = 100,
  min_crack_width_cm = 0.5
)
```

Arguments

pedon	A PedonRecord .
min_clay	Numeric threshold or option (see Details).
min_thickness	Numeric threshold or option (see Details).
min_le_cm	Minimum LE sum (cm) for the COLE-based path (default 6, per KST 13ed Ch 16).
le_max_depth_cm	Depth window (cm) for the COLE-based path (default 100).
min_crack_width_cm	Minimum shrink-swell crack width (cm) for the field-crack path. Defaults to 0.5 (WRB/USDA); the SiBCS horizonte_vertico wrapper passes 1.0 per Embrapa (2018) Cap 2 p.73.

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

v0.9.72 designation morphological inference (opt-in)

Field-described Brazilian Vertissolos profiles (e.g. the Embrapa Redape curated dataset) encode vertic morphology via a v master-letter modifier in the horizon designation (Bv, Bvk1, Cv, Cvz) without recording slickensides class or shrink_swell_cracks_cm as numeric inputs. With options(soilKey.vertic_designation_inference = TRUE) the function accepts a layer as vertic when the canonical and COLE paths both fail or are NA AND the layer has clay_pct >= min_clay AND its designation matches a v master-letter modifier. Default is FALSE.

vertic_properties	<i>Vertic properties (WRB 2022)</i>
-------------------	-------------------------------------

Description

Tests whether any horizon shows vertic properties – shrink-swell clay behaviour evidenced by slickensides, wedge-shaped peds, and deep cracks. Diagnostic for Vertisols.

Usage

```
vertic_properties(  
  pedon,  
  min_clay = 30,  
  min_thickness = 25,  
  slickenside_levels = c("common", "many", "continuous")  
)
```

Arguments

pedon	A PedonRecord .
min_clay	Minimum clay percent (default 30, per WRB 2022).
min_thickness	Minimum thickness (cm) of the vertic layer (default 25 per WRB 2022 Ch 3.2.x).
slickenside_levels	Vector of slickensides values accepted as evidence (default c("common", "many", "continuous")).

Details

Sub-tests:

- test_clay_above – clay \geq 30%
- test_slickensides_present – slickensides at or above the "common" level
- test_minimum_thickness – combined vertic layer thickness \geq 25 cm (v0.3.1 added per WRB 2022)

v0.3.1: thickness gate added. Limitations remaining: WRB also accepts deep cracks (\geq 1 cm wide extending from the surface to \geq 50 cm depth, when soil is dry) and wedge-shaped peds as alternative evidence; this implementation requires clay + slickensides. The "after mixing of upper 18 cm" clause from WRB is still deferred.

Value

A [DiagnosticResult](#).

References

IUSS Working Group WRB (2022), Chapter 3.2 – Vertic properties.

 vertisol

Vertisol RSG gate (WRB 2022 Ch 4, p 101)

Description

WRB-canonical: vertic horizon ≤ 100 cm AND $\geq 30\%$ clay between the surface and the vertic horizon throughout AND shrink-swell cracks that start at the surface (or below a plough layer / below a self- mulching surface / below a surface crust) and extend to the vertic horizon.

Usage

```
vertisol(pedon, strict = NULL)
```

Arguments

pedon	A PedonRecord .
strict	Logical or NULL. When NULL (default) it resolves via <code>getOption("soilKey.rsg_strict", FALSE)</code> . TRUE applies the Tier-3 strengthened threshold.

Details

v0.3.4 enforces (1) vertic horizon, (2) all overlying layers $\geq 30\%$ clay, and (3) shrink-swell cracks that start within the upper 20 cm. "Cracks extending to the vertic horizon" is enforced indirectly by the `test_shrink_swell_cracks` test that already requires an explicit `cracks_width_cm` value.

Value

A [DiagnosticResult](#).

Tier-3 strict mode (v0.9.98)

With `strict = TRUE` the overlying-clay threshold is raised from 30% to 35%, tightening the gate against marginally clayey profiles that satisfy the vertic horizon but sit close to the Vertisol cut-off.

 vitric_properties

Vitric properties (WRB 2022 Ch 3.2.16)

Description

Volcanic glass $\geq 5\%$ in 0.02-2 mm fraction, $Al_{ox} + 1/2 Fe_{ox} \geq 0.4\%$, phosphate retention $\geq 25\%$.

Usage

```

vitric_properties(
  pedon,
  min_glass_pct = 5,
  min_alfe = 0.4,
  min_p_retention = 25
)

```

Arguments

pedon	A PedonRecord .
min_glass_pct	Numeric threshold or option (see Details).
min_alfe	Numeric threshold or option (see Details).
min_p_retention	Numeric threshold or option (see Details).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

vlm_pick_provider	<i>Pick the best available VLM provider</i>
-------------------	---

Description

Selects a provider based on what is reachable in the user's environment, in this preference order: local Ollama (if `ollama_is_running()`), then Anthropic, OpenAI, and Google (each requires the relevant `*_API_KEY` environment variable). Errors with an actionable installation / API-key hint when no provider is reachable.

Usage

```
vlm_pick_provider(verbose = TRUE)
```

Arguments

verbose	If TRUE (default), emits a one-line cli message explaining the chosen provider.
---------	---

Value

Character scalar: one of "ollama", "anthropic", "openai", "google".

vlm_provider

*Construct a VLM provider chat object***Description**

Returns an ellmer chat object configured for the given provider, ready to be passed to the extraction functions (`extract_horizons_from_pdf`, etc.). The chat object wraps API credentials and model selection; it does not itself send any request.

Usage

```
vlm_provider(
  name = c("auto", "anthropic", "openai", "google", "ollama"),
  model = NULL,
  ...
)
```

Arguments

name	Provider name. One of "anthropic" (Claude), "openai" (GPT-4o family), "google" (Gemini), "ollama" (local).
model	Optional model identifier; defaults to <code>default_model(name)</code> .
...	Additional arguments forwarded to the corresponding <code>ellmer::chat_*</code> constructor (e.g. <code>system_prompt</code> , <code>api_key</code> , <code>base_url</code> , <code>params</code>).

Details

This is purely a convenience wrapper: it picks a default model per provider and forwards remaining arguments (e.g. `system_prompt`, `api_key`) to the underlying ellmer constructor. `ellmer` must be installed.

Value

An ellmer Chat object exposing a `$chat()` method for sending prompts.

Local-first option

Passing `name = "ollama"` runs every extraction locally via an Ollama server (default `gemma4:e4b`, Gemma 4 edge with multimodal text+image+audio support). No data leaves the machine, which is the recommended setting for sensitive field descriptions (e.g. governmental surveys, indigenous land studies) where institutional independence and data sovereignty matter. Pull the model first:

```
ollama pull gemma4:e4b      # ~3 GB edge variant (default)
ollama pull gemma4:31b     # frontier dense variant
ollama pull gemma3:27b     # earlier generation, still solid
```

Then start an Ollama server (`ollama serve`) and the chat object returned here will dispatch over HTTP locally.

Examples

```
## Not run:  
# Cloud provider (needs ANTHROPIC_API_KEY)  
provider <- vlm_provider("anthropic")  
  
# Local Gemma 4 edge model -- default, ~3 GB, runs anywhere  
provider <- vlm_provider("ollama")  
  
# Local Gemma 4 frontier dense model -- best quality  
provider <- vlm_provider("ollama", model = "gemma4:31b")  
  
# Any other multimodal model the user has pulled  
provider <- vlm_provider("ollama", model = "qwen2.5vl:32b")  
  
## End(Not run)
```

wrb06_code_to_rsg	<i>WRB 2006 RSG code -> 2022 RSG name</i>
-------------------	--

Description

AfSP ships WRB 2006 RSG codes (2-letter, e.g. LV, AC, AR). The 2-letter codes are stable across WRB editions (2006 -> 2022); only a handful of qualifier names changed. This helper maps the codes to the WRB 2022 RSG names that `classify_wrb2022` emits.

Usage

```
wrb06_code_to_rsg(code)
```

Arguments

code Character vector of WRB 2006 codes.

Value

Character vector of singular WRB 2022 RSG names; NA for unrecognised codes.

wrb2022_canonical	<i>WRB 2022 canonical reference (parsed IUSS Working Group WRB 2022)</i>
-------------------	--

Description

Convenience wrapper for `canonical_reference("WRB_4th_2022")`. Returns a 3-element list:

- `$rsg` (118 obs): Reference Soil Group + criteria text
- `$pq` (661 obs): principal qualifiers per RSG
- `$sq` (1167 obs): supplementary qualifiers per RSG

Usage

```
wrb2022_canonical(prefer_pkg = TRUE)
```

Arguments

<code>prefer_pkg</code>	If TRUE (default), prefer the installed <code>SoilTaxonomy</code> package over the vendored copy. Set to FALSE to force the vendored copy (e.g. for reproducibility of a specific <code>soilKey</code> release).
-------------------------	--

Details

Source: NCSS-tech `SoilTaxonomy` R package. Original: IUSS Working Group WRB (2022). *World Reference Base for Soil Resources*, 4th edition.

Value

The canonical WRB 2022 reference data (a list / `data.frame` of RSG and qualifier criteria), as vendored or sourced from the **SoilTaxonomy** package.

<code>yermic_properties</code>	<i>Yermic properties (WRB 2022 Ch 3.2.17) – per-pedon test wrapping test_yermic_surface.</i>
--------------------------------	--

Description

Yermic properties (WRB 2022 Ch 3.2.17) – per-pedon test wrapping `test_yermic_surface`.

Usage

```
yermic_properties(pedon)
```

Arguments

pedon A [PedonRecord](#).

Value

A [DiagnosticResult](#) recording whether the diagnostic is present, the qualifying layers, and the supporting evidence.

Index

* datasets

- GSM_DEPTHS, 114
- ossil_demo_sa, 182

- abrupt_textural_difference, 9, 174
- acrisol, 9, 149, 150, 161
- aeolic_material, 10
- albeluvic_glossae, 11
- albic, 11
- alisol, 12, 149, 150, 161
- andic_properties, 12, 150
- andosol, 12, 14
- annotate_wrb_from_usda, 15, 39
- anthraquic, 16
- anthric_horizons, 16, 151
- apply_soilgrids_depth_prior, 17, 63, 64, 109–111
- arenic_texture, 18, 151
- argic, 19, 20–22, 44, 47, 82, 137, 149, 150, 152–154, 157–159, 161, 162, 166–168, 171, 185, 194
- argic_aqp, 19, 20
- argic_with_strong_clay_films, 21, 25
- argillic_clay_films_test, 22
- artefacts, 23
- as_aqp, 23, 107, 108
- attach_lucas_spectra, 24, 31
- audit_argic_strong_films, 25
- auto_set_proj_env, 26
- available_esdb_attributes, 27, 145, 146

- B_espodico, 40
- B_incipiente, 41, 47
- B_latossolico, 21, 42
- B_nitico, 43
- B_planico, 43, 245
- B_textural, 44
- batch_robustness, 27
- benchmark_afsp, 28
- benchmark_bdsolos, 29, 39

- benchmark_lucas_2018, 30, 30, 39, 140, 141
- benchmark_performance, 33
- benchmark_redape, 34, 70, 142, 222
- benchmark_run_classification, 35, 39
- benchmark_spectral_fill, 36, 189, 215
- benchmark_unified, 37, 222
- benchmark_wrb_vs_usda, 39
- build_taxon_profiles, 40, 108, 109

- calcaric_material, 45
- calcic, 45, 152, 153, 158, 159, 166–168, 171
- cambic, 46, 47, 48, 153, 158, 167, 171, 194
- cambic_aqp, 46, 47
- canonical_reference, 49
- canonicalise_kst13ed_gg, 48
- cerosidade, 49
- chernic, 50
- chernozem, 51, 160, 165
- chernozem_strict, 51, 124
- claric_material, 52
- classification_robustness, 27, 55, 71, 72
- ClassificationResult, 53, 57, 61, 64, 65, 67, 69–71, 73, 74, 79, 185, 200, 210, 215, 219
- classify_all, 30, 38, 56, 110, 111
- classify_by_spectral_neighbours, 58, 89, 90, 214
- classify_from_documents, 60, 219, 220
- classify_from_photos, 18, 63, 79
- classify_sibcs, 26, 29, 30, 34, 56–59, 61, 64, 70, 71, 76, 104, 110, 225, 235
- classify_sibcs_familia, 65, 65, 68
- classify_usda, 29, 56–59, 61, 66, 68, 71, 110, 216, 235
- classify_usda_family, 67, 68
- classify_via_smartsoils_api, 69, 76
- classify_with_engine_heuristic, 71
- classify_with_uncertainty, 56, 71, 111
- classify_wrb2022, 29, 30, 39, 53, 56–59, 61, 62, 71, 73, 110, 200, 216, 235, 239

- clear_kst13_cache, 74
 clear_ossll_cache, 74
 combine_priors, 75
 compare_engines, 76
 compare_smartsolos, 70, 76
 compute_ki, 77
 compute_kr, 78
 compute_per_attribute_evidence_grade, 64, 72, 78
 continuous_rock, 79
 coverage_report, 80
 cryic_conditions, 81, 155

 DiagnosticResult, 9–14, 16, 17, 19–23, 41–48, 50–52, 79, 81, 81, 83, 84, 91–93, 101, 102, 105, 107, 112, 113, 115, 116, 118–125, 128–130, 149, 172, 174–177, 180–182, 184, 185, 191–193, 195, 197–199, 209, 211, 212, 215, 221, 232–234, 237, 238, 243–252, 254, 255, 259–262, 266
 distrofico, 83
 dolomitic_material, 84
 download_bdsolos, 84, 132
 download_extdata_cache, 86
 download_ossll_subset, 74, 87, 88–90
 download_ossll_subset_with_labels, 88
 download_redape_dataset, 90, 142
 duric_horizon, 91, 92, 155
 duripa, 92

 ensure_horizon_schema, 92
 eutrofico, 83, 93
 evaluate_rsg_tests, 93, 227
 extract_horizons_from_pdf, 61, 62, 94, 263
 extract_munsell_from_photo, 61, 64, 95
 extract_site_from_fieldsheet, 61, 96

 familia_mineralogia_argila_geral, 97
 FamilyAttribute, 65, 66, 68, 97, 98
 febr_index_munsell, 99, 213
 ferralic, 42, 47, 82, 100, 152–154, 157–159, 162, 166–168, 171, 184, 185
 ferralsol, 73, 101
 ferric, 102
 fibrico, 102
 fill_from_spectra, 36, 37, 87, 88, 103, 170, 182, 202, 214, 215, 252
 fill_munsell_from_spectra, 104, 203
 fluvic_material, 105, 157
 format_wrb_name, 106
 fragic, 106, 107
 fragipa, 107
 from_aqp, 24, 107

 gapfill_by_predicted_taxon, 40, 108
 gapfill_derive_horizon, 109
 gapfill_within_pedon, 38, 57, 65, 67, 74, 109, 110
 get_perturbation_scale, 71, 72, 111
 gleyic_properties, 112, 158, 169
 gleysol, 113
 grapes-or-or-grapes, 114
 GSM_DEPTHS, 114, 116, 117
 gypsic, 115, 152, 153, 158, 159, 166–168, 171
 gypsiric_material, 116

 harmonize_to_gsm, 38, 39, 116
 hemico, 118
 histic_horizon, 118, 159
 horizon_column_spec, 119, 185, 189
 hortico, 120
 hydragric, 120
 hypersulfidic_material, 121, 122
 hyposulfidic_material, 122

 inspect_bdsolos_csv, 85, 122, 132
 irrigric, 123

 kastanozem, 124, 160, 165
 kastanozem_strict, 124
 kst13_canonical, 49, 125, 126, 127
 kst13_codes, 80, 126, 127
 kst13_criteria, 126, 126

 leptic_features, 127, 161
 limnic_material, 128
 limonic, 128
 lithic_discontinuity, 129
 lixisol, 130, 149, 150, 161
 load_afsp_pedons, 28, 130
 load_afsp_sample, 28, 131
 load_bdsolos_csv, 29, 30, 85, 123, 132, 213
 load_embrapa_pedons, 132
 load_febr_pedons, 133
 load_kssll_nasis_sample, 131, 134
 load_kssll_pedons, 135

- load_ksssl_pedons_gpkg, [15](#), [39](#), [136](#), [138](#)
- load_ksssl_pedons_with_nasis, [134](#), [137](#)
- load_ksssl_sample, [134](#), [137](#)
- load_lucas_pedons, [139](#)
- load_lucas_soil_2018, [24](#), [25](#), [31](#), [32](#), [139](#)
- load_ossl_models, [232](#)
- load_ossl_models (save_ossl_models), [232](#)
- load_redape_pedons, [34](#), [141](#)
- load_rules, [142](#), [225–228](#)
- load_wosis_sample, [143](#)
- load_wosis_stratified_sample, [131](#), [144](#)
- lookup_esdb, [27](#), [30](#), [32](#), [140](#), [141](#), [145](#),
[146–148](#)
- lookup_mapbiomas_solos, [146](#), [148](#)
- lookup_soilgrids, [32](#), [140](#), [141](#), [147](#), [147](#)
- luvisol, [149](#), [149](#), [150](#), [161](#)

- make_acrisol_canonical, [149](#)
- make_alisol_canonical, [150](#)
- make_andosol_canonical, [150](#)
- make_anthrosol_canonical, [151](#)
- make_arenosol_canonical, [151](#)
- make_argissolo_canonical, [152](#)
- make_calcisol_canonical, [152](#)
- make_cambisol_canonical, [153](#)
- make_cambissolo_canonical, [153](#)
- make_chernossolo_canonical, [154](#)
- make_chernozem_canonical, [154](#)
- make_cryosol_canonical, [155](#)
- make_durisol_canonical, [155](#)
- make_empty_horizons, [156](#)
- make_espodossolo_canonical, [156](#)
- make_ferralsol_canonical, [157](#)
- make_fluvisol_canonical, [157](#)
- make_gleissolo_canonical, [158](#)
- make_gleysol_canonical, [158](#)
- make_gypsisol_canonical, [159](#)
- make_histosol_canonical, [159](#)
- make_kastanozem_canonical, [160](#)
- make_latossolo_canonical, [160](#)
- make_leptosol_canonical, [161](#)
- make_lixisol_canonical, [161](#)
- make_luvisol_canonical, [162](#)
- make_luvissolo_canonical, [162](#)
- make_neossolo_canonical, [163](#)
- make_nitisol_canonical, [163](#)
- make_nitossolo_canonical, [164](#)
- make_organossolo_canonical, [164](#)
- make_phaeozem_canonical, [165](#)

- make_planosol_canonical, [165](#)
- make_planossolo_canonical, [166](#)
- make_plinthosol_canonical, [166](#)
- make_plintossolo_canonical, [167](#)
- make_podzol_canonical, [167](#)
- make_retilsol_canonical, [168](#)
- make_solonchak_canonical, [168](#)
- make_solonetz_canonical, [169](#)
- make_stagnosol_canonical, [169](#)
- make_synthetic_pedon_with_spectra, [170](#)
- make_technosol_canonical, [170](#)
- make_umbrisol_canonical, [171](#)
- make_vertisol_canonical, [171](#)
- make_vertissolo_canonical, [172](#)
- mineral_material, [172](#)
- mollic, [82](#), [152–154](#), [157–160](#), [162](#), [165–168](#),
[171](#), [173](#), [185](#)
- mudanca_textural_abrupta, [174](#)
- mulmic_material, [175](#)

- natric_horizon, [169](#), [175](#)
- nitic_horizon, [163](#), [176](#)
- normalise_febr_sibcs, [29](#), [30](#), [178](#)
- normalise_febr_usda, [30](#), [178](#), [178](#)
- normalise_febr_wrb, [30](#), [178](#), [179](#)
- normalise_ksssl_subgroup, [179](#)

- ollama_is_running, [180](#)
- organic_material, [180](#)
- organotechnic_material, [181](#)
- ornithogenic_material, [181](#)
- ossl_demo_sa, [182](#)
- ossl_library_template, [183](#), [253](#)
- oxic_usda, [184](#)

- panpaic, [184](#)
- pedon_json_schema, [189](#), [258](#)
- pedon_to_spc, [190](#)
- PedonRecord, [9–19](#), [21–25](#), [27–29](#), [31](#), [34](#), [35](#),
[39–47](#), [50–52](#), [55–57](#), [61](#), [63](#), [65–69](#),
[71–73](#), [76](#), [78](#), [79](#), [81](#), [83](#), [84](#), [91–97](#),
[100–110](#), [112](#), [113](#), [115–124](#),
[127–134](#), [136](#), [137](#), [139](#), [141](#), [142](#),
[149–175](#), [177](#), [180](#), [181](#), [184](#), [185](#),
[185](#), [188–195](#), [197–199](#), [201–203](#),
[209](#), [211–213](#), [215](#), [219](#), [221](#),
[225–234](#), [237–242](#), [244–250](#), [252](#),
[254](#), [255](#), [257–262](#), [266](#)
- pedons_from_spectral_table, [188](#), [215](#)

- petrocalcic, 191
- petroduric, 191
- petrogypsic, 192
- petroplinthic, 193
- phaeozem, 160, 165, 193
- pi_to_confidence, 104, 196
- pick_engine, 194, 195
- pick_engine_batch, 195
- pisoplinthic, 195
- plaggic, 196
- planic_features, 165, 197
- planosol, 198
- plinthic, 158, 166, 167, 171, 199
- posterior_classify, 200
- predict_soilKey_pls_model, 201
- predict_from_spectra, 25, 31, 32, 140, 201, 253
- predict_lab_from_spectra, 202, 207
- predict_munsell_from_spectra, 25, 32, 104, 140, 203, 207
- predict_oss_l_mbl, 59, 87, 88, 104, 182, 183, 204, 205, 206
- predict_oss_plsr_local, 87, 104, 183, 205
- predict_oss_pretrained, 104, 206, 252
- predict_xyz_from_spectra, 202, 203, 207
- preprocess_spectra, 59, 103, 104, 207, 253
- pretic, 209
- print_soilKey_pls_model, 209
- prior_consistency_check, 73, 210
- protocalcic_properties, 210
- protogypsic_properties, 211
- protovertic, 212

- read_febr_pedons, 100, 212
- read_spectral_library, 37, 189, 214
- reducing_conditions, 215
- report, 54, 61, 62, 215, 217, 218, 220
- report_html, 55, 217, 218, 219
- report_pdf, 55, 218
- report_to_qgis, 219
- resolve_wrb_qualifiers, 220
- retic_properties, 168, 221
- run_all_benchmarks, 222
- run_classify_app, 223
- run_demo, 224
- run_sibcs_grande_grupo, 64, 225
- run_sibcs_key, 225
- run_sibcs_subgrupo, 226

- run_sibcs_subordem, 64, 226
- run_taxa_list, 225, 226, 227, 228
- run_taxonomic_key, 227, 228
- run_usda_great_group, 228
- run_usda_key, 229
- run_usda_subgroup, 229
- run_usda_suborder, 230
- run_wrb_key, 230
- runApp, 223

- salic, 152, 153, 158, 159, 166–168, 171, 231
- saprico, 232
- save_oss_models, 232
- shrink_swell_cracks, 233
- sideralic_properties, 233
- soil_classes_at_location, 235
- soil_organic_carbon, 236
- soilgrids_usda_lut, 234
- soilgrids_wrb_lut, 234, 241, 242
- solimovic_material, 237
- sombric, 238
- spatial_prior, 73, 200, 210, 239, 242
- spatial_prior_embrapa, 239, 240
- spatial_prior_soilgrids, 18, 235, 236, 239, 241
- spodic, 40, 158, 166, 167, 171, 242
- st_features_canonical, 49, 244
- stagnic_properties, 169, 243
- subgrupo_planossolo_espessos, 245
- subgrupo_planossolo_mesicos, 245
- subgrupo_plintossolo_endico_concrecionario, 246
- subgrupo_plintossolo_endico_litoplintico, 247
- subgrupo_plintossolo_espessos, 247

- takyric_properties, 248
- technic_features, 170, 248
- technic_hard_material, 249
- tephric_material, 250
- terric, 250
- texture_class_from_pct, 190, 251
- thionic, 252
- train_pls_from_oss_l, 31, 201, 202, 233, 252
- tsitelic, 254

- umbric_horizon, 171, 255
- usda_to_wrb_rsg, 15, 134, 137, 256

validate_horizon_geometry, [257](#)
validate_pedon_json, [258](#)
vertic_horizon, [137](#), [212](#), [258](#)
vertic_properties, [171](#), [259](#)
vertisol, [261](#)
vitric_properties, [12](#), [261](#)
vlm_pick_provider, [180](#), [262](#)
vlm_provider, [61](#), [62](#), [94–96](#), [263](#)

wrb06_code_to_rsg, [264](#)
wrb2022_canonical, [49](#), [80](#), [265](#)

yermic_properties, [265](#)