

mfrmr cheatsheet (2 pages)

mfrmr authors

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Quick reference: mfrmr 0.1.6

A two-page reference for the fit / diagnose / report loop in mfrmr. Every snippet assumes `library(mfrmr)` and a long-format `data.frame` with `Person`, one or more facet columns, and `Score`.

1. Fit

```
toy <- load_mfrmr_data("example_core")

fit <- fit_mfrm(
  toy,
  person = "Person",
  facets = c("Rater", "Criterion"),
  score = "Score",
  method = "MML",           # default; "JML" for exploratory speed
  model = "RSM"             # "PCM", "GPCM" (bounded) also supported
  # quad_points = 31 (default, publication tier; 7/15 for iteration)
)
```

2. Diagnose

```
diag <- diagnose_mfrm(fit, residual_pca = "none")
# diagnostic_mode = "both" (default) runs residual + strict marginal.
summary(fit)
summary(diag)
```

3. Report / APA

```
chk <- reporting_checklist(fit, diagnostics = diag)
apa <- build_apa_outputs(fit, diag)
cat(apa$report_text)

tbl <- apa_table(fit, which = "facets", diagnostics = diag)
kab <- as_kable(tbl)      # Markdown / HTML via kableExtra
ft  <- as_flextable(tbl)  # Word / PowerPoint via flextable
```

4. Bias / DFF / Equivalence

```
bias <- estimate_bias(fit, diag, facet_a = "Rater", facet_b = "Criterion")
summary(bias)
plot_bias_interaction(bias, plot = "ranked", show_ci = TRUE)

dff <- analyze_dff(fit, diagnostics = diag,
                  facet = "Rater", group = "Group", data = toy)
plot_dif_summary(dff)

eq <- analyze_facet_equivalence(fit, facet = "Rater", ci_level = 0.95)
plot_facet_equivalence(eq, type = "forest")
```

5. Hierarchical structure and small-N audit

```
audit <- facet_small_sample_audit(fit)
summary(audit)

icc <- compute_facet_icc(
  toy, facets = c("Rater", "Criterion"),
  score = "Score", person = "Person",
  ci_method = "profile"      # "boot" for parametric bootstrap CI
)

h <- analyze_hierarchical_structure(
  toy, facets = c("Rater", "Criterion"),
  ci_method = "profile"
)
```

6. Empirical-Bayes shrinkage for small-N facets

```
# Integrated:
fit_eb <- fit_mfrm(toy, "Person", c("Rater", "Criterion"), "Score",
                  method = "MML", facet_shrinkage = "empirical_bayes")
shrinkage_report(fit_eb)

# Post-hoc:
fit_eb2 <- apply_empirical_bayes_shrinkage(fit)
```

7. Plot surface (selected)

Function	Purpose
plot(fit)	Wright map (default)
plot(fit, type = "bundle")	Wright + pathway + CCC
plot(fit, type = "ccc_overlay")	Model + observed theta-bin dots
plot(fit, type = "wright", group=..., group_data=...)	DIF density overlay
plot(fit, type = "shrinkage")	Shrinkage direction arrows
plot_threshold_ladder(fit)	Category threshold ordering
plot_person_fit(fit, diag)	Per-person Infit/Outfit bubble
plot_rater_severity_profile(fit, diag)	Rater ranking + CI bands
plot_bias_interaction(bias, plot="heatmap")	Bias cell heatmap
plot_displacement(fit, show_ci=TRUE)	Anchor displacement lollipop
plot_fair_average(fit, show_ci=TRUE)	Fair averages + delta-method CI
plot_anchor_drift(drift, type="forest")	Wave-level anchor CI forest
plot.mfrm_equating_chain(chain, type="graph")	Bipartite wave/anchor graph
plot_apa_figure_one(fit)	Publication 2x2 composite
plot_dif_summary(dff)	DIF effect-size summary

8. Reproducibility and export

```
export_mfrm_bundle(fit, diagnostics = diag, path = "mfrmr_bundle/")
manifest <- build_mfrm_manifest(fit, diagnostics = diag)
# manifest$environment, $dependencies, $input_hash, $session_info,
# $hierarchical_audit, $missing_recoding, $shrinkage_audit
replay_script <- build_mfrm_replay_script(fit, path = "replay_mfrmr.R")
```

9. Missing-code pre-processing

```
fit <- fit_mfrm(  
  dirty_data, "Person", c("Rater", "Criterion"), "Score",  
  missing_codes = TRUE      # 99 / 999 / -1 / "N/A" / "" -> NA  
)  
fit$prep$missing_recoding
```

Package links

- Documentation: https://ryuya-dot-com.github.io/R_package_mfrm/
- Source: https://github.com/Ryuya-dot-com/R_package_mfrm
- Citation: `citation("mfrm")`

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