

# mfrmr quick reference

mfrmr package

## Data to fitted results

A compact reference for the data review / fit / summary / plot / 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. Check data roles, score support, and missing codes

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

data_review <- describe_mfrm_data(
  toy, person = "Person", facets = c("Rater", "Criterion"),
  score = "Score", rating_min = 1, rating_max = 4
)
summary(data_review)

# Declare only codes that mean missing in the study.
dirty_review <- describe_mfrm_data(
  dirty_data, "Person", c("Rater", "Criterion"), "Score",
  missing_codes = c(99, 999, -1, "N/A", "")
)
```

Confirm retained and zero-count categories and inspect the score map. Use the same `rating_min`, `rating_max`, `keep_original`, and `missing_codes` decisions in `fit_mfrm()`.

## 2. Fit

```
fit <- fit_mfrm(  
  toy,  
  person = "Person",  
  facets = c("Rater", "Criterion"),  
  score = "Score",  
  method = "MML",           # recommended starting method  
  model = "RSM",            # use PCM/GPCM only with a model rationale  
  rating_min = 1,  
  rating_max = 4  
)
```

For PCM, set the step facet explicitly when its role is not unambiguous. Treat bounded GPCM as a slope-aware sensitivity extension and read `gpcm_capability_matrix()` before using downstream helpers.

## 3. Read summaries, then draw the required Wright map

```
fit_summary <- summary(fit, profile = "fit", detail = "brief")  
  
# Comprehensive FACETS-organized review; mfrmr remains the estimator.  
review <- summary(fit, profile = "facets", detail = "brief")  
res <- review$results  
diag <- res$diagnostics  
  
# Primary final-scale display: all locations plus available facet uncertainty.  
plot(res, type = "wright", renderer = "native",  
      show_ci = TRUE, top_n = Inf, preset = "publication")
```

Read optimizer status and terminal-gradient guidance before interpreting estimates. The native map is the primary result because it keeps facet uncertainty and fitted step locations visible.

## 4. Add only the diagnostics needed for the question

```
# Reuse review diagnostics; rerun only for explicit custom settings.  
diag_pca <- diagnose_mfrm(fit, residual_pca = "both")  
  
# Optional follow-up: x = Infit, y = measure. Persons are opt-in.  
plot(fit, type = "fit_pathway", diagnostics = diag,  
      fit_stat = "Infit", include_person = FALSE)
```

## 5. 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
```

## 6. 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)

# Requires a study data frame containing the named grouping column.
dff <- analyze_dff(fit, diagnostics = diag,
                  facet = "Rater", group = "Group", data = your_data)
plot_dif_summary(dff)

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

## 7. Hierarchical structure and small-N review

```
review <- facet_small_sample_review(fit)
summary(review)

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"
)
```

## 8. 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)
```

## 9. Plot surface (selected)

| Function                                                             | Purpose                                               |
|----------------------------------------------------------------------|-------------------------------------------------------|
| plot(fit)                                                            | Wright map (default)                                  |
| plot_wright_unified(fit, renderer="facets")                          | Optional FACETS-style * ruler; visual convention only |
| plot(fit, type="fit_pathway", diagnostics=diag, include_person=TRUE) | Infit-vs-measure pathway; person rows opt-in          |
| 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; CIs for Rasch-family fits              |
| plot_anchor_drift(drift, type="forest")                              | Wave-level anchor CI forest                           |
| plot(chain, type="graph")                                            | Bipartite wave/anchor graph                           |

## 10. Reproducibility and export

```
# The default warning reminds you that this does not deidentify the files.
export_mfrm_bundle(fit, diagnostics = diag,
                  output_dir = "mfrmr_bundle/")
export_mfrm_results(res, output_dir = "mfrmr-results",
                  preset = "starter", overwrite = TRUE)
# Add acknowledge_sensitive = TRUE only after reviewing every intended file
# and confirming that the destination follows the study's handling policy.
manifest <- build_mfrm_manifest(fit, diagnostics = diag)
# manifest$environment, $dependencies, $input_hash, $session_info,
# $hierarchical_review, $missing_recoding, $shrinkage_review
replay_script <- build_mfrm_replay_script(fit, path = "replay_mfrmr.R")
```

## 11. FACETS and ConQuest users

- Keep the native Wright map with available facet uncertainty as the primary mfrmr display. Use `renderer = "facets"` when readers benefit from FACETS-style asterisks and ruler layout; this does not reproduce FACETS estimation.

```
rubric_labels <- setNames(  
  your_rubric_labels,  
  fit$prep$score_map$OriginalScore  
)  
plot_wright_unified(  
  fit, renderer = "facets", show_ci = FALSE,  
  category_labels = rubric_labels  
)
```

- Use `facets_feature_coverage()` for feature-by-feature alternatives.
- Use `build_conquest_overlap_bundle(fit_lr)` only after fitting the documented unidimensional MML comparison. Run the generated `.cqc` file in ConQuest, then pass its four CSV exports to `normalize_conquest_overlap_exports()` and `review_conquest_overlap()`.
- mfrmr does not execute FACETS or ConQuest and does not claim general numerical equivalence with either program.

### Package links

- Source and documentation: <https://github.com/Ryuya-dot-com/mfrmr>
- Citation: `citation("mfrmr")`

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