

Package: tallieR (via r-universe)

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Title Import and Score ScoreMe App Questionnaire Data

Version 0.2.0

Description A companion package for the ScoreMe app (<https://scoreme.circadia-lab.uk>). Provides tools to import participant JSON exports, re-score validated questionnaires, and assemble tidy wide and long study-level data frames ready for downstream analysis in R. Stable instruments: ESS, ISI, DBAS-16, MEQ, PSQI, RU-SATED, STOP-BANG, KSS, MCTQ. Beta instruments (scoring ported from ScoreMe, not yet independently validated in tallieR): PHQ-2, PHQ-9, PHQ-15, GAD-7, GAD-2, BDI-II, BAI, DASS-21, PANSS, STAI-S, STAI-T, WHOQOL-BREF, MacArthur SSS, IPAQ-S, GPAQ, GSQ, AQ-10.

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as_tibble.tallier_export

Coerce a tallier_export to a tibble

Description

Converts a `tallier_export` object to a tibble by calling `scores_wide()` and coercing the result. One row per participant, one column per questionnaire, with participant metadata prepended by default.

Usage

```
as_tibble.tallier_export(x, ...)
```

Arguments

<code>x</code>	A <code>tallier_export</code> object.
<code>...</code>	Additional arguments passed to <code>scores_wide()</code> (e.g. <code>include_meta = FALSE</code>).

Details

This method is registered for `tibble::as_tibble()` and is available automatically when the `tibble` package is loaded.

Value

A tibble; see `scores_wide()` for column details.

Examples

```
## Not run:
exp <- read_scoreme("export.json")
tibble::as_tibble(exp)
tibble::as_tibble(exp, include_meta = FALSE)

## End(Not run)
```

as_tibble.tallier_study

Coerce a tallier_study to a tibble

Description

Converts a `tallier_study` object to a tibble by calling `scores_wide()` and coercing the result. One row per participant, one column per questionnaire, with participant metadata prepended by default.

Usage

```
as_tibble.tallier_study(x, ...)
```

Arguments

<code>x</code>	A <code>tallier_study</code> object.
<code>...</code>	Additional arguments passed to <code>scores_wide()</code> (e.g. <code>include_meta = FALSE</code>).

Details

This method is registered for `tibble::as_tibble()` and is available automatically when the `tibble` package is loaded.

Value

A tibble; see `scores_wide()` for column details.

Examples

```
## Not run:
study <- read_scoreme_dir("exports/")
tibble::as_tibble(study)

## End(Not run)
```

available_instruments

List available instruments

Description

Returns a data frame listing all built-in questionnaires supported by tallieR, with their IDs, full titles, clinical domain, maximum score, and beta status.

Usage

```
available_instruments()
```

Details

Beta instruments (`beta = TRUE`) are included in ScoreMe but have not yet been through full validation review in tallieR. Scoring algorithms match the ScoreMe app exactly; use with appropriate caution in clinical contexts.

Value

A `data.frame` with columns `id`, `title`, `domain`, `max_score`, `beta`.

Examples

```
available_instruments()

# View only stable instruments
subset(available_instruments(), !beta)

# View only beta instruments
subset(available_instruments(), beta)
```

completion_summary *Completion summary*

Description

Returns a data frame showing which questionnaires each participant has completed. Useful for monitoring data collection progress in longitudinal or multi-site studies.

Usage

```
completion_summary(obj, wide = FALSE, include_date = TRUE, include_meta = TRUE)
```

Arguments

<code>obj</code>	A <code>tallier_export</code> or <code>tallier_study</code> object.
<code>wide</code>	Logical. If <code>FALSE</code> (default), returns a long data frame with one row per participant \times questionnaire and a <code>completed</code> logical column. If <code>TRUE</code> , returns a wide data frame with one row per participant and one logical column per questionnaire.
<code>include_date</code>	Logical. If <code>TRUE</code> (default), adds a <code>completed_at</code> column in long format showing the timestamp of the most recent administration. Ignored when <code>wide = TRUE</code> .
<code>include_meta</code>	Logical. If <code>TRUE</code> (default), participant metadata columns are prepended.

Details

When a participant has completed a questionnaire more than once, it is counted as complete and the most recent `completed_at` timestamp is reported (when `include_date = TRUE`).

Value

In long format: a `data.frame` with columns: participant metadata (optional), `questionnaire_id`, `completed` (logical), and optionally `completed_at` (character timestamp of most recent administration). In wide format: a `data.frame` with one row per participant and one logical column per questionnaire.

See Also

[scores_wide\(\)](#), [scores_long\(\)](#)

Examples

```
## Not run:
study <- read_scoreme_dir("exports/")

# Long format: one row per participant x questionnaire
completion_summary(study)
```

```
# Wide format: one row per participant
completion_summary(study, wide = TRUE)

# Without timestamps
completion_summary(study, include_date = FALSE)

## End(Not run)
```

cronbach_alpha	<i>Cronbach's alpha for one or more questionnaires</i>
----------------	--

Description

Computes Cronbach's alpha (a measure of internal consistency) for each questionnaire present in a `tallier_export` or `tallier_study` object. Item-level responses are extracted via `items_long()`, coerced to numeric, and a participant \times item matrix is constructed per questionnaire.

Usage

```
cronbach_alpha(obj, questionnaires = NULL, conf_level = 0.95, min_items = 2L)
```

Arguments

<code>obj</code>	A <code>tallier_export</code> or <code>tallier_study</code> object, or a data frame as returned by <code>items_long()</code> (must contain columns <code>participant_id</code> , <code>questionnaire_id</code> , <code>item_id</code> , <code>completed_at</code> , <code>response</code>).
<code>questionnaires</code>	Character vector of questionnaire IDs to include. Defaults to all questionnaires present in <code>obj</code> .
<code>conf_level</code>	Numeric. Confidence level for the CI (default 0.95). Uses the exact F-distribution method of Feldt et al. (1987).
<code>min_items</code>	Integer. Minimum number of numeric items required to attempt estimation (default 2).

Details

Non-numeric items (e.g. MCTQ clock times, STOP-BANG yes/no) are silently dropped before estimation. Questionnaires with fewer than 2 numeric items or fewer than 2 complete observations return NA with an explanatory note.

Value

A `data.frame` with one row per questionnaire and columns:

questionnaire_id Questionnaire identifier.
alpha Cronbach's alpha (standardised scale: $-\infty$ to 1).

ci_lower Lower bound of the `conf_level` CI.
ci_upper Upper bound of the `conf_level` CI.
n_items Number of numeric items used.
n_obs Number of complete observations (participants).
note NA on success, or a short message explaining why estimation failed.

References

Cronbach, L. J. (1951). Coefficient alpha and the internal structure of tests. *Psychometrika*, 16(3), 297–334. doi:10.1007/BF02310555

Feldt, L. S., Woodruff, D. J., & Salih, F. A. (1987). Statistical inference for coefficient alpha. *Applied Psychological Measurement*, 11(1), 93–103. doi:10.1177/014662168701100107

Examples

```
## Not run:
study <- read_scoreme_dir("exports/")

# All questionnaires
cronbach_alpha(study)

# Specific subset
cronbach_alpha(study, questionnaires = c("ess", "isi", "phq9"))

# From an items_long() data frame (e.g. already filtered)
items <- items_long(study)
cronbach_alpha(items)

## End(Not run)
```

interpret_all

Interpret all questionnaire scores in an export

Description

Returns a long data frame with one row per participant x questionnaire x administration, augmented with clinical interpretation columns (`label`, `color`, `description`). Mirrors the shape of `scores_long()` so the two can be joined by `participant_id + questionnaire_id + completed_at`.

Usage

```
interpret_all(obj, include_meta = TRUE, instruments = NULL)
```

Arguments

<code>obj</code>	A <code>tallier_export</code> or <code>tallier_study</code> object.
<code>include_meta</code>	Logical. If TRUE (default), participant metadata columns are prepended (same columns as <code>scores_long()</code>).
<code>instruments</code>	An optional named list of additional registry entries from <code>load_instrument()</code> or <code>load_instrument_dir()</code> .

Details

Scores that cannot be interpreted (unknown instrument, NA score, or composite score with no matching band) return NA in all three interpretation columns rather than an error, so the rest of the study data is unaffected.

Value

A `data.frame` with columns: participant metadata (optional), `questionnaire_id`, `completed_at`, `score`, `label`, `color`, `description`.

See Also

[interpret_score\(\)](#), [scores_long\(\)](#)

Examples

```
## Not run:
study <- read_scoreme_dir("exports/")
interps <- interpret_all(study)

# Join with scores_long() if you need both
scores <- scores_long(study)
full <- merge(scores, interps[
  c("participant_id", "questionnaire_id", "completed_at",
    "label", "color", "description")
], by = c("participant_id", "questionnaire_id", "completed_at"),
  all.x = TRUE)

## End(Not run)
```

`interpret_score`

Interpret a questionnaire score

Description

Returns a clinical interpretation for a given score on a given questionnaire, matching the score bands used in the ScoreMe app.

Usage

```
interpret_score(id, score, instruments = NULL)
```

Arguments

id Character. Questionnaire identifier.

score Numeric score (or named list for composite instruments).

instruments An optional named list of additional registry entries from `load_instrument()` or `load_instrument_dir()`.

Value

A list with elements `label`, `color` (hex), and `description`.

Examples

```
interpret_score("ess", 12)
interpret_score("meq", 65)
```

items_long

Item-level long table

Description

Returns a data frame with one row per participant \times questionnaire administration \times item. Useful for factor analysis, IRT, or item-level reliability checks.

Usage

```
items_long(obj, include_meta = TRUE, scored_items = FALSE, instruments = NULL)
```

Arguments

obj A `tallier_export` or `tallier_study` object.

include_meta Logical. If `TRUE` (default), participant metadata columns are included.

scored_items Logical. If `TRUE`, adds a `response_scored` column with reverse-scored values applied for instruments that define `reverse_items` (currently STAI-S and STAI-T). For all other items and instruments, `response_scored` equals `response`. Non-numeric responses (e.g. clock-time lists, yes/no) are left as-is. Defaults to `FALSE` to preserve existing behaviour.

instruments An optional named list of additional registry entries from `load_instrument()` or `load_instrument_dir()`, used when `scored_items = TRUE` to resolve reverse-scoring metadata for custom instruments.

Value

A `data.frame` with columns: participant metadata (optional), `questionnaire_id`, `completed_at`, `item_id`, `response`, and optionally `response_scored`.

<code>load_instrument</code>	<i>Load a custom instrument from a ScoreMe JSON spec</i>
------------------------------	--

Description

Reads a `.json` file produced for (or exported from) the ScoreMe app and compiles it into a tallieR registry entry. The result can be passed to `score_questionnaire()` via its `instruments` argument, combined with other custom entries using `c()`, or stored in a project-level list for reuse.

Usage

```
load_instrument(path)
```

Arguments

`path` Path to a `.json` file containing a ScoreMe instrument spec. See `vignette("custom-instruments")` or `system.file("extdata", "example_instrument.json", package = "tallieR")` for the expected schema.

Details

Supported scoring types: `"sum"`, `"weighted_sum"`, `"mean"`. For instruments with `"composite"` scoring (e.g. PSQI-style multi-component algorithms) the returned entry will score as NA and a warning is emitted each time scoring is attempted. You can override the compiled `score` function by assigning a custom one after loading (see examples).

Value

A named list (a single tallieR registry), where the name is the instrument `id` from the spec. Invisibly also carries the original spec in `spec`.

See Also

[load_instrument_dir\(\)](#), [score_questionnaire\(\)](#), [available_instruments\(\)](#)

Examples

```
## Not run:
my_instr <- load_instrument("path/to/fss.json")

# Score a single result
score_questionnaire("fss", answers, instruments = my_instr)

# Combine with another custom instrument
```

```
registry <- c(load_instrument("fss.json"), load_instrument("vas_pain.json"))

# Override scoring for a composite instrument
my_psqi <- load_instrument("psqi_custom.json")
my_psqi$psqi_custom$score <- function(answers) { ... }

## End(Not run)
```

load_instrument_dir *Load all custom instruments from a directory*

Description

Reads every `.json` file in `dir`, compiles each as a tallieR registry entry, and returns a combined named list suitable for passing to `score_questionnaire()`.

Usage

```
load_instrument_dir(dir, pattern = "\\\\.json$")
```

Arguments

<code>dir</code>	Path to a directory containing ScoreMe instrument JSON files.
<code>pattern</code>	Regular expression used to filter filenames. Defaults to <code>"\\.\\.json\$"</code> .

Value

A named list of registry entries (one per successfully loaded file).

See Also

`load_instrument()`, `score_questionnaire()`

Examples

```
## Not run:
custom <- load_instrument_dir("instruments/")
score_questionnaire("fss", answers, instruments = custom)

## End(Not run)
```

omega_reliability *McDonald's omega for one or more questionnaires*

Description

Computes McDonald's omega (ω_t , total omega) as a measure of internal consistency for each questionnaire present in a `tallier_export` or `tallier_study` object. Omega is generally preferred over Cronbach's alpha for non-tau-equivalent items (i.e. items with unequal factor loadings), which is the norm in most psychological questionnaires.

Usage

```
omega_reliability(obj, questionnaires = NULL, min_items = 2L)
```

Arguments

obj A `tallier_export` or `tallier_study` object, or a data frame as returned by `items_long()` (must contain columns `participant_id`, `questionnaire_id`, `item_id`, `completed_at`, `response`).

questionnaires Character vector of questionnaire IDs to include. Defaults to all questionnaires present in `obj`.

min_items Integer. Minimum number of numeric items required to attempt estimation (default 2).

Details

Estimation uses a single-factor EFA via `stats::factanal()`. The formula applied is:

$$\omega_t = \frac{(\sum \lambda_i)^2}{(\sum \lambda_i)^2 + \sum (1 - \lambda_i^2)}$$

where λ_i are the standardised factor loadings.

Non-numeric items (e.g. MCTQ clock times, STOP-BANG yes/no) are silently dropped before estimation. Questionnaires with fewer items than observations, fewer than 2 numeric items, or non-convergent factor solutions return `NA` with an explanatory note.

Value

A `data.frame` with one row per questionnaire and columns:

questionnaire_id Questionnaire identifier.

omega McDonald's omega_t. Range: 0 to 1.

n_items Number of numeric items used.

n_obs Number of complete observations (participants).

note `NA` on success, or a short message explaining why estimation failed.

References

- McDonald, R. P. (1999). *Test theory: A unified treatment*. Lawrence Erlbaum Associates.
- Revelle, W., & Zinbarg, R. E. (2009). Coefficients alpha, beta, omega, and the glb: Comments on Sijtsma. *Psychometrika*, 74(1), 145–154. doi:10.1007/s113360089102z

See Also

[cronbach_alpha\(\)](#)

Examples

```
## Not run:
study <- read_scoreme_dir("exports/")

# All questionnaires
omega_reliability(study)

# Compare alpha and omega side by side
alpha <- cronbach_alpha(study, questionnaires = c("ess", "isi"))
omega <- omega_reliability(study, questionnaires = c("ess", "isi"))
merge(alpha[, c("questionnaire_id", "alpha", "n_obs")],
      omega[, c("questionnaire_id", "omega")],
      by = "questionnaire_id")

## End(Not run)
```

read_scoreme	<i>Read a ScoreMe JSON export</i>
--------------	-----------------------------------

Description

Reads a single JSON file exported from the ScoreMe app and returns a `tallier_export` object containing participant metadata and all questionnaire results.

Usage

```
read_scoreme(path, rescore = TRUE, instruments = NULL)
```

Arguments

<code>path</code>	Path to a <code>.json</code> file exported from ScoreMe.
<code>rescore</code>	Logical. If <code>TRUE</code> (default), scores are recomputed from item-level answers using the built-in tallieR scoring functions. If <code>FALSE</code> , the scores stored in the export file are used as-is.
<code>instruments</code>	An optional named list of custom instrument registry entries created by <code>load_instrument()</code> or <code>load_instrument_dir()</code> . When <code>rescore = TRUE</code> , these are merged with the built-in registry so that custom questionnaires in the export can be scored. Entries in <code>instruments</code> take precedence over built-ins with the same id.

Value

A `tallier_export` object: a list with elements:

`exported_at` Timestamp of the export (character).

`export_version` Schema version string.

`participants` A list of parsed participant records.

`n_participants` Number of participants.

See Also

[load_instrument\(\)](#), [load_instrument_dir\(\)](#)

Examples

```
## Not run:
exp <- read_scoreme("my_study_export.json")
print(exp)
wide <- scores_wide(exp)

# With custom instruments
custom <- load_instrument("fss.json")
exp <- read_scoreme("export.json", instruments = custom)
wide <- scores_wide(exp)

## End(Not run)
```

<code>read_scoreme_dir</code>	<i>Read a directory of ScoreMe JSON exports</i>
-------------------------------	---

Description

Reads all `.json` files in a directory and combines them into a single `tallier_study` object. Useful when each participant's data was exported as a separate file, or when multiple batch exports need to be merged.

Usage

```
read_scoreme_dir(
  dir,
  rescore = TRUE,
  pattern = "\\\\.json$",
  instruments = NULL
)
```

Arguments

<code>dir</code>	Path to a directory containing <code>.json</code> export files.
<code>rescore</code>	Logical. Passed to <code>read_scoreme()</code> .
<code>pattern</code>	Regular expression used to filter filenames. Defaults to "*.json\$" (all JSON files).
<code>instruments</code>	An optional named list of custom instrument registry entries, passed through to <code>read_scoreme()</code> . See <code>load_instrument()</code> .

Value

A `tallier_study` object: a list with elements:

- `files` Character vector of files read.
- `participants` Combined list of all participant records.
- `n_participants` Total number of participants.

Examples

```
## Not run:
study <- read_scoreme_dir("exports/")
wide <- scores_wide(study)

## End(Not run)
```

<code>score_all</code>	<i>Score all questionnaires in an export</i>
------------------------	--

Description

Convenience wrapper that rescores every result entry in a `tallier_export` or `tallier_study` object. This is called automatically when `rescore = TRUE` in `read_scoreme()`.

Usage

```
score_all(obj, instruments = NULL)
```

Arguments

<code>obj</code>	A <code>tallier_export</code> or <code>tallier_study</code> object.
<code>instruments</code>	An optional named list of additional registry entries from <code>load_instrument()</code> or <code>load_instrument_dir()</code> , merged with the built-in registry before scoring. Entries in <code>instruments</code> take precedence over built-ins with the same id.

Value

The same object with scores updated in-place.

`score_questionnaire` *Score a questionnaire from item-level answers*

Description

Computes the score for a single questionnaire using the official scoring algorithm embedded in `tallieR`, or a custom scoring function compiled from a ScoreMe JSON spec via `load_instrument()`.

Usage

```
score_questionnaire(id, answers, instruments = NULL)
```

Arguments

<code>id</code>	Character. Questionnaire identifier (e.g. "ess", "psqi"). See <code>available_instruments()</code> for valid IDs. For custom instruments, this must match the <code>id</code> field in the spec passed to <code>instruments</code> .
<code>answers</code>	A named list of item responses, as exported by ScoreMe. Keys are item IDs (e.g. "ess1", "psqi2"); values are the raw responses (numeric, character "yes"/"no", or clock-time list).
<code>instruments</code>	An optional named list of additional instrument registry entries, as returned by <code>load_instrument()</code> or <code>load_instrument_dir()</code> . These are searched first, before the built-in registry, so a custom entry can override a built-in if needed.

Details

Instruments marked `beta = TRUE` in `available_instruments()` are newer additions whose scoring has been ported from ScoreMe but has not yet been independently validated in `tallieR`. A warning is emitted for these instruments; suppress with `suppressWarnings()` if needed.

Value

For most instruments: a single numeric score. For composite instruments (PSQI, MCTQ, DASS-21, PANSS, WHOQOL-BREF): a named list of subscale and total scores.

See Also

`load_instrument()`, `load_instrument_dir()`

Examples

```
score_questionnaire("ess", list(ess1 = 2, ess2 = 1, ess3 = 0,
                                ess4 = 3, ess5 = 1, ess6 = 0,
                                ess7 = 2, ess8 = 1))
```

```
## Not run:
# Score using a custom instrument loaded from a JSON spec
my_instr <- load_instrument("path/to/fss.json")
score_questionnaire("fss", answers, instruments = my_instr)

## End(Not run)
```

scores_long	<i>Long score table</i>
-------------	-------------------------

Description

Returns a data frame with one row per participant \times questionnaire \times administration (i.e. all history is retained).

Usage

```
scores_long(obj, include_meta = TRUE)
```

Arguments

obj A `tallier_export` or `tallier_study` object.
include_meta Logical. If `TRUE` (default), participant metadata columns are included.

Value

A `data.frame` with columns: participant metadata (optional), `questionnaire_id`, `completed_at`, `score`.

scores_wide	<i>Wide score table</i>
-------------	-------------------------

Description

Returns a data frame with one row per participant and one column per questionnaire. When a participant completed a questionnaire more than once, only the most recent administration is included (use `scores_long()` to retain all administrations).

Usage

```
scores_wide(obj, include_meta = TRUE)
```

Arguments

obj A `tallier_export` or `tallier_study` object.
include_meta Logical. If `TRUE` (default), participant metadata columns (code, name, age, sex, etc.) are prepended.

Value

A `data.frame` with columns: participant metadata (if requested) followed by one numeric score column per questionnaire.

Examples

```
## Not run:
study <- read_scoreme_dir("exports/")
wide <- scores_wide(study)
head(wide)

## End(Not run)
```

```
summary.tallier_export
```

Summarise a tallier_export object

Description

Prints a structured overview of a `tallier_export`, including participant count, instruments present, per-instrument completion rates, and the date range of administrations. The summary statistics are also returned invisibly as a list for programmatic use.

Usage

```
## S3 method for class 'tallier_export'
summary(object, ...)
```

Arguments

<code>object</code>	A <code>tallier_export</code> object.
<code>...</code>	Ignored.

Value

Invisibly, a list with elements `n_participants`, `instruments`, `completion` (a data frame), and `date_range`.

Examples

```
## Not run:
exp <- read_scoreme("export.json")
summary(exp)

# Access stats programmatically
s <- summary(exp)
s$completion
```

```
## End(Not run)
```

```
summary.tallier_study  
  Summarise a tallier_study object
```

Description

Prints a structured overview of a `tallier_study`, including participant count, number of source files, instruments present, per-instrument completion rates, and the date range of administrations. The summary statistics are also returned invisibly as a list for programmatic use.

Usage

```
## S3 method for class 'tallier_study'  
summary(object, ...)
```

Arguments

<code>object</code>	A <code>tallier_study</code> object.
<code>...</code>	Ignored.

Value

Invisibly, a list with elements `n_participants`, `n_files`, `instruments`, `completion` (a data frame), and `date_range`.

Examples

```
## Not run:  
study <- read_scoreme_dir("exports/")  
summary(study)  
  
# Access stats programmatically  
s <- summary(study)  
s$completion  
  
## End(Not run)
```

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