Package: sewloreSpecimenTables (via r-universe)

October 17, 2026

Type Package

Title Explicitly Paired Fabric Specimen Measurement Tables

Version 0.1.0

Description Validates long-format paired specimen measurements, normalizes millimetres, centimetres and inches, and compares before and after values within an explicitly identified cohort, specimen, wash cycle and axis. Preserves original values and units and reports incomplete pairs without estimating missing observations. Provides descriptive cohort tables and spreadsheet-conscious CSV export. Example data are entirely synthetic and are not empirical research or fabric performance claims.

License MIT + file LICENSE

Encoding UTF-8

Depends R (>= 4.1.0)

Imports utils, stats

Suggests knitr

VignetteBuilder knitr

URL https://sewlore.com/pages/fabric-measurement-methods-guide, https://sewlore.com/

NeedsCompilation no

Repository https://gokimedia.r-universe.dev

Date/Publication 2026-10-17 20:19:02 UTC

RemoteUrl https://github.com/gokimedia/sewlore-sewing-tools

RemoteRef HEAD

RemoteSha aa58b3cff13fe3d2959c51ef0ca7277733190aca

RemoteSubdir packages/r/sewloreSpecimenTables

Contents

sewloreSpecimenTables-package 2
specimen-tables 2

Index **5**

`sewloreSpecimenTables-package`
Explicitly Paired Fabric Specimen Measurement Tables

Description

Local validation, physical-unit normalization, pairing and descriptive tabulation of before/after measurements. Original values and units remain visible. No telemetry or network calls occur in the analysis functions. All bundled example data are synthetic.

See Also

`pair_specimen_measurements`

`specimen-tables` *Explicitly Paired Specimen Measurement Tables*

Description

Validate long-format measurements, retain original units, and compare paired measurements within explicitly identified cohorts, specimens, wash cycles and axes. Included examples are entirely synthetic, not empirical observations.

Usage

```
read_specimen_csv(file)
validate_specimen_measurements(data)
pair_specimen_measurements(data, incomplete = c("error", "report"))
summarise_specimen_pairs(pairs)
write_specimen_pairs(pairs, file, spreadsheet_safe = TRUE)
synthetic_specimens()
```

Arguments

`file`	For import, an existing local UTF-8 CSV file. For export, a local output path; an existing file is overwritten.
`data`	Nonempty data frame with unique column names and required columns `specimen_id`, `wash_cycle`, `axis`, `stage`, `value`, `unit`; optional `cohort`. Stages are before and after; units are mm, cm and in. Cycle numbers are positive integers. Values are positive finite numbers.

`incomplete` Default `"error"` rejects a missing before or after observation. `"report"` retains incomplete pairs with a status and missing computed changes. No missing observation is estimated.

`pairs` The nonempty result of `pair_specimen_measurements`.

`spreadsheet_safe` If true, exported character cells beginning with a possible formula marker receive an apostrophe prefix. Numeric columns retain numeric signs. This changes affected exported labels, not the input object, and is a conservative precaution rather than a guarantee for every spreadsheet application.

Details

Comparison keys are cohort, specimen identifier, wash cycle and axis. A duplicate stage within a key is an error, including duplicate equal observations. Labels are trimmed; stage, unit and axis are lowercased. Cohort and specimen identifier remain case-sensitive. If cohort is omitted, the explicit output label is `unspecified`; callers must establish that observations are comparable before grouping them.

Every before/after pair must represent the intended baseline for that cycle. For cumulative change from an original baseline, supply that original measurement as each cycle's before value. The package never substitutes the first or previous cycle automatically.

One inch is 25.4 millimetres. Delta is after minus before in millimetres. Change percent is 100 times delta divided by before. Shrinkage percent is the negative of change percent: contraction is positive and expansion is negative. R uses floating-point arithmetic, so comparisons and rounding should account for numeric precision.

Summary means are unweighted means of per-specimen percentage changes. The standard deviation is descriptive spread across complete pairs, not measurement uncertainty or a confidence interval. It is missing for a single complete pair. No inference about fabric composition, care instructions or population performance is made.

Value

Import and validation return a normalized long data frame with `value_mm`, preserving additional input columns. Pairing returns a `sewlore_pairs` data frame with status, before/after input values and units, normalized values, delta, change and shrinkage percentages. Summary returns one row per cohort/cycle/axis including complete and missing counts and descriptive means, median and standard deviation. Export invisibly returns the normalized output path. `synthetic_specimens` returns the explicitly synthetic bundled example measurements.

See Also

https://sewlore.com/pages/fabric-measurement-methods-guide

Examples

```
data <- synthetic_specimens() # Synthetic demonstrations, not laboratory data.
pairs <- pair_specimen_measurements(data)
summarise_specimen_pairs(pairs)
path <- tempfile(fileext = ".csv")
```

```
write_specimen_pairs(pairs, path)
unlink(path)
```

Index

pair_specimen_measurements, *2*
pair_specimen_measurements
(specimen-tables), 2

read_specimen_csv (specimen-tables), 2

sewloreSpecimenTables
(sewloreSpecimenTables-package),
2
sewloreSpecimenTables-package, 2
specimen-tables, 2
summarise_specimen_pairs
(specimen-tables), 2
synthetic_specimens (specimen-tables), 2

validate_specimen_measurements
(specimen-tables), 2

write_specimen_pairs (specimen-tables),
2