

# Package: syncR (via r-universe)

July 1, 2026

**Title** Integrate and Coordinate Data Across the Circadia Lab Package Ecosystem

**Version** 0.1.0

**Description** syncR is the integrator and coordinator of the Circadia Lab R ecosystem. It pulls sociodemographic and questionnaire data from tallieR, sleep diary data from slumbR, and actigraphy-derived circadian metrics from zeitR into a single unified, participant-indexed database. syncR::sync() — pulling everything into alignment, just like the SCN does.

**License** MIT + file LICENSE

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.2

**URL** <https://github.com/circadia-bio/syncR>

**BugReports** <https://github.com/circadia-bio/syncR/issues>

**Imports** dplyr, rlang, cli

**Suggests** zeitR, slumbR, tallieR, testthat (>= 3.0.0), knitr, rmarkdown

**Remotes** circadia-bio/zeitR, circadia-bio/slumbR, circadia-bio/tallieR

**Config/testthat/edition** 3

**VignetteBuilder** knitr

**Repository** <https://circadia-bio.r-universe.dev>

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 sync

*Synchronise data across the Circadia Lab package ecosystem*


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## Description

`sync()` is the primary entry point for `syncR`. It pulls sociodemographic and questionnaire data from **tallieR**, sleep diary data from **slumbR**, and actigraphy-derived circadian metrics from **zeitR** into a single unified, participant-indexed database.

*`syncR::sync()` — pulling everything into alignment, just like the SCN does.*

## Usage

```
sync(
  tallie = NULL,
  slumb = NULL,
  zeit = NULL,
  id_col = "participant_id",
  join = c("left", "inner", "full")
)
```

## Arguments

<code>tallie</code>	A data frame of sociodemographic / questionnaire data, typically the output of <code>tallieR::export()</code> . Pass <code>NULL</code> to omit.
<code>slumb</code>	A data frame of sleep diary data, typically the output of <code>slumbR::export()</code> . Pass <code>NULL</code> to omit.
<code>zeit</code>	A data frame of actigraphy / circadian metrics, typically the output of <code>zeitR::export()</code> . Pass <code>NULL</code> to omit.
<code>id_col</code>	Character. Name of the participant ID column shared across all input data frames. Defaults to <code>"participant_id"</code> .
<code>join</code>	Character. Type of join to perform when combining sources. One of <code>"left"</code> (default), <code>"inner"</code> , or <code>"full"</code> .

## Value

A tibble with one row per participant per night (where applicable), containing columns from all supplied sources, indexed by `id_col`.

## Examples

```
## Not run:
db <- sync(
  tallie = tallieR::export(),
  slumb = slumbR::export(),
  zeit = zeitR::export()
)
```

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## End(Not run)

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