

# Package ‘consortr’

May 8, 2026

**Title** Interactive Consort Flow Diagrams

**Version** 0.9.1

**Description** Shiny app for creating interactive consort flow diagrams and other types of flow diagrams, see Moher, Schulz and Altman (2001) <[doi:10.1016/S0140-6736\(00\)04337-3](https://doi.org/10.1016/S0140-6736(00)04337-3)>.

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**Encoding** UTF-8

**RoxygenNote** 7.1.1

**Imports** DiagrammeR, shiny, shinydashboard, tibble, dplyr, purrr, rlang, magrittr, data.table

**NeedsCompilation** no

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consortr	<i>Shiny app for generating consort flow diagrams and other types of flow diagrams</i>
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## Description

A consort diagram graphically depicts the passage of participants through a randomized clinical trial. This app can be used to easily create consort diagrams, and to visualize any other process where criteria are applied in succession to a dataset and it is of interest to know how many rows of the dataset remain after the application of each criterion.

**Usage**

```
consortr()
```

**Value**

none

**References**

Moher, Schulz and Altman (2001) The CONSORT statement: revised recommendations for improving the quality of reports of parallel-group randomised trials. *Lancet* **357**, 1191-94.

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consort\_from\_metadata *Function to generate consort diagrams*

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**Description**

Function to generate consort diagrams

**Usage**

```
consort_from_metadata(metadata, data)
```

**Arguments**

metadata	Metadata downloaded from shiny app
data	Data uploaded to the app for generating consort diagram

**Value**

graph created by DiagrammeR (graph object of class dgr\_graph)

**Examples**

```
data <- data.frame(a = c('m', 'm', 'n', 'n'),
                  b = c('p', 'p', 'q', 'q'))
metadata <- data.frame(label = c('All', "a=='m'"),
                      code = c(TRUE, "a=='m'"),
                      parent = c(0, 1),
                      color = c("black", "black"),
                      hidden = c(FALSE, FALSE),
                      split_var = c('a', NA))
consort_diagram <- consort_from_metadata(metadata, data)
```

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