

# Package: MetSizeR (via r-universe)

October 11, 2024

**Title** A Shiny App for Sample Size Estimation in Metabolomic Experiments

**Version** 2.0.0

**Date** 2021-08-20

**Description** Provides a Shiny application to estimate the sample size required for a metabolomic experiment to achieve a desired statistical power. Estimation is possible with or without available data from a pilot study.

**License** GPL (>= 3)

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.1.1

**Imports** dplyr, ggplot2, MetabolAnalyze, Rfast, shiny, shinythemes, stats, tools, utils, vroom

**Suggests** rmarkdown, knitr

**VignetteBuilder** knitr

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

**RemoteUrl** <https://github.com/kfinucane/metsizer>

**RemoteRef** HEAD

**RemoteSha** 8b9d71c78cc70bdc34b02dd7cf9ce362351940e4

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metsize

*Metsize*


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### Description

Function to estimate sample size required to achieve a desired statistical power.

### Usage

```
metsize(
  pilot = pilot,
  n1 = 4,
  n2 = 4,
  p = 200,
  prop = 0.25,
  covars = covars,
  ncovar = 0,
  model = "PPCA",
  plot.prop = FALSE,
  target.fdr = 0.05,
  Targeted = FALSE
)
```

### Arguments

pilot	A matrix containing pilot data, if available.
n1	Sample group 1 minimum sample size to consider.
n2	Sample group 2 minimum sample size to consider.
p	Number of bins in the data.
prop	Expected proportion of significant bins.
covars	Matrix of covariates, if available. Categorical covariates should be included as X-1 dummy variables for a covariate with X levels.
ncovar	The number of covariates present. For Z numeric covariates and Y categorical covariates with X total levels, this should be Z + X - Y.
model	The chosen model.
plot.prop	TRUE/FALSE should sample size be calculated for varying proportions of significant bins?
target.fdr	The desired false discovery rate.
Targeted	TRUE/FALSE is the experiment intended as targeted analysis?

### Value

List containing the estimated sample size with the per-group sample size breakdown, results of FDR calculations for each sample size tested, results for varying the proportion of significant metabolites, the number of bins input, the number of covariates input, the model type used, the input minimum sample sizes for group 1 and group 2, and the desired FDR.

## References

G. Nyamundanda, I. C. Gormley, Y. Fan, W. M. Gallagher and L. Brennan, BMC Bioinformatics, 2013, 14, 338.

## Examples

```
metsize(pilot = NULL, n1 = 4, n2 = 4, p = 200, prop = 0.2, covars = NULL,  
        ncovar = 0, model = "PPCA", plot.prop = FALSE, target.fdr = 0.10,  
        Targeted = FALSE)  
metsize(pilot = NULL, n1 = 6, n2 = 4, p = 100, prop = 0.1, covars = NULL,  
        ncovar = 2, model = "PPCCA", plot.prop = FALSE, target.fdr = 0.05,  
        Targeted = TRUE)
```

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MetSizeR

*MetsizeR Launcher*

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## Description

Launches the Shiny application for the MetsizeR functionality. The interactive application allows estimation of the sample size required for a metabolomic experiment to achieve a desired statistical power.

## Usage

```
MetSizeR()
```

## References

G. Nyamundanda, I. C. Gormley, Y. Fan, W. M. Gallagher and L. Brennan, BMC Bioinformatics, 2013, 14, 338.

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