

# Package: corrmeta (via r-universe)

September 6, 2024

**Title** Correlated Meta-Analysis (corrmeta)

**Version** 1.0.0

**Author** Woo Seok Jung <jungw@wustl.edu>, Michael Province  
<mprovince@wustl.edu>

**Maintainer** Woo Seok Jung <jungw@wustl.edu>

**Description** Performs Correlated Meta-Analysis (corrmeta) across multiple OMIC scans, accounting for hidden non-independencies between elements of the scans due to overlapping samples, related samples, or other information.

**biocViews** Genetics, GenomeWideAssociation, SNP, StatisticalMethod, Software

**License** MIT + file LICENSE

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.1

**VignetteBuilder** knitr

**LazyData** true

**Suggests** testthat (>= 3.0.0), BiocStyle, knitr, rmarkdown, qpdf

**Config/testthat/edition** 3

**Imports** dplyr, polycor, stats, tidyr, magrittr

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

**RemoteUrl** <https://github.com/wsjung/corrmeta>

**RemoteRef** HEAD

**RemoteSha** 86f0d71573ced7bdb43e9272cb56405f40800656

## Contents

|                                    |   |
|------------------------------------|---|
| fishp . . . . .                    | 2 |
| generate_random_p_values . . . . . | 3 |

|                               |   |
|-------------------------------|---|
| polycorr . . . . .            | 3 |
| pvalues_to_zscores . . . . .  | 4 |
| snp_example . . . . .         | 5 |
| snp_example_missing . . . . . | 5 |
| tetracorr . . . . .           | 5 |

|              |          |
|--------------|----------|
| <b>Index</b> | <b>7</b> |
|--------------|----------|

---

|       |   |
|-------|---|
| fishp | <i>Calculate Fisher's method p-value and meta-analysis statistics</i> |
|-------|---|

---

## Description

Calculate Fisher's method p-value and meta-analysis statistics

## Usage

```
fishp(df, vars, df_sigma, sum_sigma)
```

## Arguments

|           |  |
|-----------|--|
| df        | data frame with "markname" and study names as column names.      |
| vars      | character vector of study names to include in the meta-analysis. |
| df_sigma  | data frame of tetrachoric correlations.                          |
| sum_sigma | sum of tetrachoric correlations.                                 |

## Value

A data frame with columns 'markname', 'sum\_chisq', 'sum\_z', 'sum\_sigma\_var', 'pvalue', 'meta\_z', 'meta\_p', 'meta\_nlog10p'

## Examples

```
data(snp_example)
head(snp_example)
varlist <- c("trt1", "trt2", "trt3")
tc <- tetracorr(snp_example, varlist)
fishp(snp_example, varlist, tc$sigma, tc$sum_sigma)
```

---

`generate_random_p_values`*Generates a list of random p-values with mixed significant and non-significant values*

---

**Description**

Generates a list of random p-values with mixed significant and nonsignificant values

**Usage**

```
generate_random_p_values(n, ratio_significant)
```

**Arguments**

|                                |  |
|--------------------------------|--|
| <code>n</code>                 | number of samples                      |
| <code>ratio_significant</code> | fraction of p-values to be significant |

---

`polycorr`*Calculate Polychoric Correlations*

---

**Description**

This function calculates the polychoric correlations between pairs of variables in a given data frame. It returns a data frame with the row and column names of the variables, the polychoric correlation coefficient, and its standard error.

**Usage**

```
polycorr(data, varlist)
```

**Arguments**

|                      |  |
|----------------------|--|
| <code>data</code>    | data frame with "markname" and study names as column names.      |
| <code>varlist</code> | character vector of study names to include in the meta-analysis. |

**Value**

data frame with polychoric correlation coefficients and standard errors

**Author(s)**

Woo Jung

**See Also**[polychor](#)**Examples**

```
data(snp_example)
varlist <- c("trt1", "trt2", "trt3")
polycorr(snp_example, varlist)
```

---

pvalues\_to\_zscores      *Convert P-values to Z-scores*

---

**Description**

This function takes a data frame of p-values and converts them to Z-scores using the quantile function for the standard normal distribution.

**Usage**

```
pvalues_to_zscores(df_pvalues)
```

**Arguments**

df\_pvalues      data frame containing p-values

**Value**

data frame containing Z-scores

**Author(s)**

Woo Jung

**See Also**[qnorm](#)**Examples**

```
data(snp_example)
head(snp_example)
pvalues_to_zscores(snp_example)
```

---

|             |                                    |
|-------------|------------------------------------|
| snp_example | <i>Example SNP summary dataset</i> |
|-------------|------------------------------------|

---

**Description**

This data set provides 3 simulated 19-sample SNP-trait association p-values

**Usage**

```
snp_example
```

**Format**

A dataframe containing 19 observations across 3 SNP scans

---

|                     |  |
|---------------------|--|
| snp_example_missing | <i>Example SNP summary dataset with missing values</i> |
|---------------------|--|

---

**Description**

This data set provides 3 simulated 19-sample SNP-trait association p-values where some samples are removed to reflect missing values.

**Usage**

```
snp_example_missing
```

**Format**

A dataframe containing 19 observations across 3 SNP scans

---

|           |   |
|-----------|---|
| tetracorr | <i>Calculate Tetrachoric Correlations</i> |
|-----------|---|

---

**Description**

This function calculates the tetrachoric correlations between pairs of variables in a given data frame. It returns a list containing a data frame with the tetrachoric correlation coefficients, and the sum of the tetrachoric correlations if the input variable was in p-value form.

**Usage**

```
tetracorr(data, varlist)
```

**Arguments**

`data` data frame with "markname" and study names as column names.  
`varlist` character vector of study names to include in the meta-analysis.

**Value**

list containing a data frame with tetrachoric correlation coefficients, and the sum of the tetrachoric correlations if the input variable was in p-value form.

**Author(s)**

Woo Jung

**See Also**

[polychor](#)

**Examples**

```
data(snp_example)
head(snp_example)
varlist <- c("trt1", "trt2", "trt3")
tetracorr(snp_example, varlist)
```

# Index

- \* **Z-scores**
  - pvalues\_to\_zscores, 4
- \* **correlation,**
  - polycorr, 3
  - tetracorr, 5
- \* **datasets**
  - snp\_example, 5
  - snp\_example\_missing, 5
- \* **p-values,**
  - pvalues\_to\_zscores, 4
- \* **polychoric**
  - polycorr, 3
- \* **tetrachoric**
  - tetracorr, 5

fishp, 2

generate\_random\_p\_values, 3

polychor, 4, 6

polycorr, 3

pvalues\_to\_zscores, 4

qnorm, 4

snp\_example, 5

snp\_example\_missing, 5

tetracorr, 5