Package: aggregation (via r-universe)

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Type Package

Title p-Value Aggregation Methods

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Description Contains functionality for performing the following methods of p-value aggregation: Fisher's method [Fisher, RA (1932, ISBN: 9780028447308)], the Lancaster method (weighted Fisher's method) [Lancaster, HO (1961, <doi:10.1111/j.1467-842X.1961.tb00058.x>)], and Sidak correction [Sidak, Z (1967, <doi:10.1080/01621459.1967.10482935>)]. Please cite Yi et al., the manuscript corresponding to this package [Yi, L et al., (2017), <doi:10.1101/190199>].

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Imports stats

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Contents

`fisher` *Fisher's Method*

Description

Aggregate p-values with equal weights. Equivalent to the Lancaster method with all p-values weighted at 2.

Usage

```
fisher(pvalues)
```

Arguments

`pvalues`	A vector of p-values (i.e. between 0 and 1) to be aggregated with Fisher's method. NAs will be filtered out.

Examples

```
fisher(c(.1, .2, .3))
```

`lancaster` *Lancaster method*

Description

Weighted p-value aggregation.

Usage

```
lancaster(pvalues, weights)
```

Arguments

`pvalues`	A vector of p-values (i.e. between 0 and 1). NAs will be filtered out.
`weights`	A vector of weights, each associated with its respective p-value. Weights must be nonegative. NAs and negative weights will be filtered out with corresponding p-values.

Examples

```
lancaster(c(.1, .5), c(2, 4))
```

`sidak` *Perform the Sidak method.*

Description

The Sidak method uses the minimum p-value but corrects it for the number of p-values that are aggregated.

Usage

```
sidak(pvalues)
```

Arguments

`pvalues`	A vector of p-values to be aggregated. NAs will be filtered.

Examples

```
sidak(c(.1, .2, .3))
```

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