

dPvalAggregate

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Function to aggregate p values

Description

dPvalAggregate is supposed to aggregate a input matrix p-values into a vector of aggregated p-values. The aggregate operation is applied to each row of input matrix, each resulting in an aggregated p-value. The method implemented can be based on the order statistics of p-values or according to Fisher's method.

Usage

```
dPvalAggregate(pmatrix, method = c("orderStatistic", "fishers"),
order = ncol(pmatrix))
```

Arguments

pmatrix	a data frame or matrix of p-values
method	the method used. It can be either "orderStatistic" for the method based on the order statistics of p-values, or "fishers" for Fisher's method
order	an integer specifying the order used for the aggregation according to on the order statistics of p-values

Value

- ap: a vector with the length `nrow(pmatrix)`, containing aggregated p-values

Note

For each row of input matrix with the c columns, there are c p-values that are uniformly independently distributed over $[0,1]$ under the null hypothesis (uniform distribution). According to the order statistics, they follow the Beta distribution with the parameters $a = order$ and $b = c - order + 1$. According to the the Fisher's method, after transformation by $-2 * \sum^c \log(pvalue)$, they follow Chi-Squared distribution.

See Also

[dPvalAggregate](#)

Examples

```
# 1) generate an iid uniformly-distributed random matrix of 1000x3
pmatrix <- cbind(runif(1000), runif(1000), runif(1000))

# 2) aggregate according to the ordre statistics
ap <- dPvalAggregate(pmatrix, method="orderStatistic")

# 3) aggregate according to the Fisher's method
ap <- dPvalAggregate(pmatrix, method="fishers")
```