

Package: stepdownfdp (via r-universe)

August 27, 2024

Title A Step-Down Procedure to Control the False Discovery Proportion

Version 1.0.0

Description Provides a step-down procedure for controlling the False Discovery Proportion (FDP) in a competition-based setup, implementing Dong et al. (2020) <[arXiv:2011.11939](https://arxiv.org/abs/2011.11939)>. Such setups include target-decoy competition (TDC) in computational mass spectrometry and the knockoff construction in linear regression.

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URL <https://github.com/uni-Arya/stepdownfdp>

Imports pracma, stats

Repository <https://uni-arya.r-universe.dev>

RemoteUrl <https://github.com/uni-arya/stepdownfdp>

RemoteRef HEAD

RemoteSha 0c5e7cd448d11fd0d03114e4238eabc16e6b35bb

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 fdp_sd

Convert winning scores and labels into discoveries

Description

fdp_sd takes the output of mirandom and additional statistical parameters to return the indices and winning scores of hypotheses that were rejected.

Usage

```
fdp_sd(
  scores_and_labels,
  alpha,
  conf,
  c = 0.5,
  lambda = 0.5,
  procedure = "standard"
)
```

Arguments

scores_and_labels	An $m \times 2$ matrix obtained via mirandom.
alpha	An FDP threshold.
conf	To control the FDP with $1 - \text{conf}$ confidence.
c	Determines the ranks of the target score that are considered winning. Defaults to $c = 0.5$ for single-decoy FDP-SD.
lambda	Determines the ranks of the target score that are considered losing. Defaults to $\lambda = 0.5$ for single-decoy FDP-SD.
procedure	Takes a value of "standard" (for non-randomised FDP-SD) or "coinflip" (for randomised FDP-SD).

Value

A list of 2 objects: the winning scores (discoveries) and indices (discoveries_ind) of rejected hypotheses.

Examples

```
set.seed(123)
target_scores <- rnorm(200, mean = 1.5)
decoy_scores <- matrix(rnorm(600, mean = 0), ncol = 3)
scores <- cbind(target_scores, decoy_scores)
scores_and_labels <- mirandom(scores)
fdp_sd(scores_and_labels, alpha = 0.1, conf = 0.1)
```

`mirandom`*Convert target/decoy scores into winning scores and labels*

Description

`mirandom` takes a collection of target and decoy scores for m hypotheses and returns a winning score and label attached to each. The argument scores must be organised in an $m \times (d + 1)$ matrix, where d is the number of decoy scores. The first column of scores must contain the target scores.

Usage

```
mirandom(scores, c = 0.5, lambda = 0.5)
```

Arguments

<code>scores</code>	An $m \times (d + 1)$ matrix where m is the number of hypothesis and d is the number of decoy scores for each hypothesis. The first column of scores are target scores and subsequent columns are decoy scores.
<code>c</code>	Determines the ranks of the target score that are considered winning. Defaults to $c = 0.5$ for single-decoy FDP-SD.
<code>lambda</code>	Determines the ranks of the target score that are considered losing. Defaults to $lambda = 0.5$ for single-decoy FDP-SD.

Value

A $m \times 2$ matrix where m is the number of hypotheses. The first column contains the winning scores and the second column contains the corresponding labels.

Examples

```
target_scores <- rnorm(200, mean = 1.5)
decoy_scores <- matrix(rnorm(600, mean = 0), ncol = 3)
scores <- cbind(target_scores, decoy_scores)
mirandom(scores)
```

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