

# Package ‘stepdownfdp’

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**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) <[doi:10.48550/arXiv.2011.11939](https://doi.org/10.48550/arXiv.2011.11939)>. Such setups include target-decoy competition (TDC) in computational mass spectrometry and the knockoff construction in linear regression.

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**Encoding** UTF-8

**RoxygenNote** 7.1.2

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

**Imports** pracma, stats

**NeedsCompilation** no

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**Repository** CRAN

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`fdp_sd`*Convert winning scores and labels into discoveries*

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### 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

<code>scores_and_labels</code>	An $m \times 2$ matrix obtained via <code>mirandom</code> .
<code>alpha</code>	An FDP threshold.
<code>conf</code>	To control the FDP with $1 - \text{conf}$ confidence.
<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.
<code>procedure</code>	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)
```

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

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**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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