

Package ‘FeatSeekR’

January 19, 2026

Type Package

Title FeatSeekR an R package for unsupervised feature selection

Version 1.10.0

Description FeatSeekR performs unsupervised feature selection using replicated measurements. It iteratively selects features with the highest reproducibility across replicates, after projecting out those dimensions from the data that are spanned by the previously selected features. The selected a set of features has a high replicate reproducibility and a high degree of uniqueness.

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Encoding UTF-8

Imports pheatmap, MASS, pracma, stats, SummarizedExperiment, methods

RxygenNote 7.2.3

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

VignetteBuilder knitr

BugReports <https://github.com/tcapraz/FeatSeekR/issues>

URL <https://github.com/tcapraz/FeatSeekR>

biocViews Software, StatisticalMethod, FeatureExtraction,
MassSpectrometry

Config/testthat/edition 3

git_url <https://git.bioconductor.org/packages/FeatSeekR>

git_branch RELEASE_3_22

git_last_commit 7b2ed7b

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2026-01-19

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calcFstat	<i>calcFstat</i>
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Description

calcFstat

Usage

```
calcFstat(data, fac)
```

Arguments

data	2 dimensional array with samples x features, where samples belongs different conditions. The function was adapted from the genefilter package.
fac	factor of length samples, indicating which sample belongs to which condition

Value

F-statistic for all features

check_input	<i>check_input</i>
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Description

Checks input data. Input data should be a 2 dimensional array with features x samples or SummarizedExperiment carrying one assay named data and colData indicating which sample belongs to which condition

Usage

```
check_input(data, max_features, conditions = NULL)
```

Arguments

data	input data provided to FeatSeek either SummarizedExperiment or 2 dimensional array with features x samples
conditions	if data is a 2 dimensional array with features x samples a factor indicating which sample corresponds to which condition must be provided

Value

SummarizedExperiment where condition information is stored in colData

FeatSeek

FeatSeek

Description

This function ranks features of a 2 dimensional array according to their reproducibility between conditions.

Usage

```
FeatSeek(
  data,
  conditions = NULL,
  max_features = NULL,
  init = NULL,
  verbose = TRUE
)
```

Arguments

data	SummarizedExperiment with assay named data, where samples belongs to different conditions. Which sample belongs to which condition should be indicated in colData slot conditions. Or matrix with features x samples. Each conditions have multiple samples from replicated measurements.
conditions	factor of length samples, indicating which sample belongs to which condition. Only required if data is provided as matrix.
max_features	integer number of features to rank
init	character vector with names of initial features. If NULL the feature with highest F-statistic will be used
verbose	logical indicating whether messages should be printed

Value

SummarizedExperiment containing one assay with the selected features. rowData stores for each selected feature the F-statistic under metric, the cumulative explained variance under explained_variance and the feature names under selected

Examples

```
# run FeatSeek to select the top 20 features
data <- array(rnorm(100*30), dim=c(30, 100),
dimnames <- list(paste("feature", seq_len(30)), NULL))
conds <- rep(seq_len(50), 2)
res <- FeatSeek(data, conds, max_features=20)

# res stores the 20 selected features ranked by their replicate
# reproducibility
```

FeatSeekR

FeatSeekR an R package for unsupervised feature selection

Description

FeatSeekR performs unsupervised feature selection using replicated measurements. It iteratively selects features with the highest reproducibility across conditions, after projecting out those dimensions from the data that are spanned by the previously selected features. The selected a set of features has a high replicate reproducibility and a high degree of uniqueness.

Details

For information on how to use this package please type `vignette("FeatSeekR-vignette")`.

Please post questions regarding the package to the Bioconductor Support Site:

<https://support.bioconductor.org>

Author(s)

Tümay Capraz

fit_lm

fit_lm

Description

Fit linear model for each feature as a function of the previously selected features S. The dimensions spanned by the selected features are projected out of the data by setting each feature to its residuals from the linear model fit.

Usage

`fit_lm(data, S, k)`

Arguments

data	data (2 dimensional array samples x features)
S	set of selected features
k	current iteration

Value

data with previously selected features projected out

init_selected*init_selected***Description**

Checks if preselected init features are in input data. If init is NULL, it is set to feature with highest condition correlation.

Usage

```
init_selected(init, se)
```

Arguments

init	preselected starting set of features
data	input data as SummarizedExperiment

Value

names of initial set of feature

plotSelectedFeatures*plotSelectedFeatures***Description**

plot correlation matrix of selected feature sets

Usage

```
plotSelectedFeatures(res, n_features = NULL, assay = "selected")
```

Arguments

res	result SummarizedExperiment from FeatSeek function
n_features	top n_features to plot. if NULL then the maximum number of features in res will be plotted
assay	assay slot to plot from result SummarizedExperiment object, default is the selected features slot

Value

returns heatmap of selected features

Examples

```
# run FeatSeek to select the top 20 features
data <- array(rnorm(100*30), dim=c(30,100),
              dimnames = list(paste("feature", seq_len(30)), NULL))
conds <- rep(seq_len(50), 2)
res <- FeatSeek(data, conds, max_features=20)

# res stores the 20 selected features ranked by their replicate
# reproducibility
# plot the top 5 features
plotSelectedFeatures(res, n_features=5)
```

plotVarianceExplained *plotVarianceExplained*

Description

plot variance explained from 1 to max_features in res

Usage

```
plotVarianceExplained(res)
```

Arguments

res	result SummarizedExperiment from FeatSeek function
-----	--

Value

returns plot of variance explained vs number of features

Examples

```
# run FeatSeek to select the top 20 features
data <- array(rnorm(100*30), dim=c(30,100),
              dimnames = list(paste("feature", seq_len(30)), NULL))
conds <- rep(seq_len(50), 2)
res <- FeatSeek(data, conds, max_features=20)

# res stores the 20 selected features ranked by their replicate
# reproducibility
plotVarianceExplained(res)
```

`simData`*simData*

Description

simulate Data with orthogonal feature clusters and replicated samples. Each feature cluster corresponds to a different latent factor and contains 10 redundant features. E.g. choosing samples = 100, n_latent_factors = 5 and replicates = 2 will simulate a 50 x 200 data matrix, where the first 100 samples belong to replicate 1 and sample 101-200 belong to replicate 2.

Usage

```
simData(conditions, n_latent_factors, replicates)
```

Arguments

conditions	number of conditions to generate samples from
n_latent_factors	number of latent factors to generate
replicates	number of replicates to generate

Details

simData constructs n_latent_factors by generating a random matrix \mathbf{Q} whose row vectors $\mathbf{Q}_{i \cdot} \sim \mathcal{N}(0, 1)$ with n samples and $i \in \{1, \dots, n_{\text{latent_factors}}\}$ are orthonormal, each corresponding to a different latent factor. To simulate a set of redundant feature groups, it generates 10 features $X_{j \cdot}$ for each latent factor $\mathbf{Q}_{i \cdot}$ by scaling each latent factor by a random factor $\delta_j \sim \mathcal{N}(0, 1)$ and adding replicate specific noise $\epsilon_c \sim \mathcal{N}(0, 0.1)$ with $c \in \{1, \dots, \text{replicates}\}$ preserving orthogonality.

Value

SummarizedExperiment object carrying simulated data, with colData indicating which sample belongs to which replicate

Examples

```
# simulate data 100 samples from 100 conditions, 20 features generated by 2
# latent factors and 2 replicates
simData(conditions=100, n_latent_factors=2, replicates=2)
```

`variance_explained` *variance_explained*

Description

`variance_explained`

Usage

`variance_explained(data, selected)`

Arguments

<code>data</code>	2 dimensional array samples x features
<code>selected</code>	character vector of selected features

Value

average variance explained by selected features

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