

# Package ‘smartid’

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**Title** Scoring and Marker Selection Method Based on Modified TF-IDF

**Version** 1.3.2

**Description** This package enables automated selection of group specific signature, especially for rare population. The package is developed for generating specific lists of signature genes based on Term Frequency-Inverse Document Frequency (TF-IDF) modified methods. It can also be used as a new gene-set scoring method or data transformation method. Multiple visualization functions are implemented in this package.

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'smartid-package.R' 'score-methods.R' 'select\_markers.R'  
'top\_markers.R' 'top\_markers-methods.R'

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cal_score	<i>calculate combined score</i>
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---

**Description**

compute TF (term/feature frequency), IDF (inverse document/cell frequency), IAE (inverse average expression of features) and combine the the final score

**Usage**

```
cal_score(  
  data,  
  tf = c("logtf", "tf"),  
  idf = "prob",  
  iae = "prob",  
  slot = "counts",  
  new.slot = "score",  
  par.idf = NULL,  
  par.iae = NULL  
)  
  
## S4 method for signature 'AnyMatrix'  
cal_score(  
  data,  
  tf = c("logtf", "tf"),  
  idf = "prob",  
  iae = "prob",  
  par.idf = NULL,  
  par.iae = NULL  
)  
  
## S4 method for signature 'SummarizedExperiment'  
cal_score(  
  data,  
  tf = c("logtf", "tf"),  
  idf = "prob",  
  iae = "prob",  
  slot = "counts",  
  new.slot = "score",  
  par.idf = NULL,  
  par.iae = NULL  
)
```

**Arguments**

data	an expression object, can be matrix or SummarizedExperiment
tf	a character, specify the TF method to use, can be "tf" or "logtf"

idf	a character, specify the IDF method to use. Available methods can be accessed using <code>idf_iae_methods()</code>
iae	a character, specify the IAE method to use. Available methods can be accessed using <code>idf_iae_methods()</code>
slot	a character, specify which slot to use when data is se object, optional, default 'counts'
new.slot	a character, specify the name of slot to save score in se object, optional, default 'score'
par.idf	other parameters for specified IDF methods
par.iae	other parameters for specified IAE methods

### Value

A list of matrices or se object containing combined score

### Examples

```
data <- matrix(rpois(100, 2), 10, dimnames = list(1:10))
cal_score(
  data,
  par.idf = list(label = sample(c("A", "B"), 10, replace = TRUE)),
  par.iae = list(label = sample(c("A", "B"), 10, replace = TRUE))
)
```

---

cal_score_init	<i>Calculate score for each feature in each cell</i>
----------------	--

---

### Description

Calculate score for each feature in each cell

### Usage

```
cal_score_init(
  expr,
  tf = c("logtf", "tf"),
  idf = "prob",
  iae = "prob",
  par.idf = NULL,
  par.iae = NULL
)
```

**Arguments**

expr	a count matrix, features in row and cells in column
tf	a character, specify the TF method to use, can be "tf" or "logtf"
idf	a character, specify the IDF method to use. Available methods can be accessed using <code>idf_iae_methods()</code>
iae	a character, specify the IAE method to use. Available methods can be accessed using <code>idf_iae_methods()</code>
par.idf	other parameters for specified IDF methods
par.iae	other parameters for specified IAE methods

**Value**

a list of combined score, tf, idf and iae

**Examples**

```
data <- matrix(rpois(100, 2), 10, dimnames = list(1:10))
label <- sample(c("A", "B"), 10, replace = TRUE)
smartid::cal_score_init(data,
  par.idf = list(label = label),
  par.iae = list(label = label)
)
```

---

gs_score	<i>compute overall score based on the given marker list</i>
----------	---

---

**Description**

compute overall score based on the given marker list

**Usage**

```
gs_score(data, features = NULL, slot = "score", suffix = "score")

## S4 method for signature 'AnyMatrix,ANY'
gs_score(data, features = NULL)

## S4 method for signature 'AnyMatrix,list'
gs_score(data, features = NULL, suffix = "score")

## S4 method for signature 'SummarizedExperiment,ANY'
gs_score(data, features = NULL, slot = "score", suffix = "score")
```

**Arguments**

data	an expression object, can be matrix or SummarizedExperiment
features	vector or named list, feature names to compute score
slot	a character, specify which slot to use when data is se object, optional, default 'score'
suffix	a character, specify the name suffix to save score when features is a named list

**Value**

A vector of overall score for each sample

**Examples**

```
data <- matrix(rnorm(100), 10, dimnames = list(seq_len(10)))
gs_score(data, features = seq_len(3))
```

---

gs_score_init	<i>Calculate scores of each cell on given features</i>
---------------	--

---

**Description**

Calculate scores of each cell on given features

**Usage**

```
gs_score_init(score, features = NULL)
```

**Arguments**

score	matrix, features in row and samples in column
features	vector, feature names to compute score

**Value**

a vector of score

**Examples**

```
data <- matrix(rnorm(100), 10, dimnames = list(1:10))
gs_score_init(data, 1:5)
```

---

iae *standard inverse average expression*

---

### Description

standard inverse average expression

### Usage

```
iae(expr, features = NULL, thres = 0)
```

### Arguments

expr            a matrix, features in row and cells in column  
 features        vector, feature names or indexes to compute  
 thres           numeric, cell only counts when expr > threshold, default 0

### Details

$$\mathbf{IAE}_i = \log\left(1 + \frac{n}{N_{i,j} + 1}\right)$$

where  $n$  is the total number of cells,  $N_{i,j}$  is the counts of feature  $i$  in cell  $j$ .

### Value

a vector of inverse average expression score for each feature

### Examples

```
data <- matrix(rpois(100, 2), 10, dimnames = list(1:10))
smartid:::iae(data)
```

---

iae\_hdb *inverse average expression using hdbscan cluster as label*

---

### Description

inverse average expression using hdbscan cluster as label

### Usage

```
iae_hdb(expr, features = NULL, multi = TRUE, thres = 0, minPts = 2, ...)
```

**Arguments**

expr	a matrix, features in row and cells in column
features	vector, feature names or indexes to compute
multi	logical, if to compute based on binary (FALSE) or multi-class (TRUE)
thres	numeric, cell only counts when <code>expr &gt; threshold</code> , default 0
minPts	integer, minimum size of clusters, default 2. Details in <code>dbscan::hdbscan()</code> .
...	parameters for <code>dbscan::hdbscan()</code>

**Details**

Details as `iae_prob()`.

**Value**

a matrix of inverse average expression score

**Examples**

```
set.seed(123)
data <- matrix(rpois(100, 2), 10, dimnames = list(1:10))
smartid::iae_hdb(data)
```

---

iae_igm	<i>labeled inverse average expression: IGM</i>
---------	--

---

**Description**

labeled inverse average expression: IGM

**Usage**

```
iae_igm(expr, features = NULL, label, lambda = 7, thres = 0)
```

**Arguments**

expr	a matrix, features in row and cells in column
features	vector, feature names or indexes to compute
label	vector, group label of each cell
lambda	numeric, hyperparameter for IGM
thres	numeric, cell only counts when <code>expr &gt; threshold</code> , default 0



**Details**

$$\mathbf{IGM}_i = \log\left(1 + \lambda \frac{\max(\text{mean}(N_{i,j \in D})_k)}{\sum_k^K (\text{mean}(N_{i,j \in D})_k * r_k) + e^{-8}}\right)$$

where  $\lambda$  is the hyper parameter,  $N_{i,j \in D}$  is the counts of feature  $i$  in cell  $j$  within class  $D$ , and  $r_k$  is the rank of  $\text{mean}(N_{i,j \in D})_k$ .

**Value**

a vector of inverse gravity moment score for each feature

**Examples**

```
data <- matrix(rpois(100, 2), 10, dimnames = list(1:10))
smartid::iae_igm(data, label = sample(c("A", "B"), 10, replace = TRUE))
```

---

iae_m	<i>inverse average expression: max</i>
-------	--

---

**Description**

inverse average expression: max

**Usage**

```
iae_m(expr, features = NULL, thres = 0)
```

**Arguments**

expr	a matrix, features in row and cells in column
features	vector, feature names or indexes to compute
thres	numeric, cell only counts when expr > threshold, default 0

**Details**

$$\mathbf{IAE}_{i,j} = \log\left(1 + \frac{\max_{\{i' \in j\}}(n_{i'})}{\sum_{j=1}^n \max(0, N_{i,j} - \text{threshold}) + 1}\right)$$

where  $i$  is the feature  $i$  and  $i'$  is the feature except  $i$ ,  $N_{i,j}$  is the counts of feature  $i$  in cell  $j$ , and  $n_{i'}$  is  $\sum_{j=1}^n \text{sign}(N_{i,j} > \text{threshold})$ .

**Value**

a matrix of inverse average expression score for each feature

**Examples**

```
data <- matrix(rpois(100, 2), 10, dimnames = list(1:10))
smartid:::iae_m(data)
```

iae\_prob

*labeled inverse average expression: probability based***Description**

labeled inverse average expression: probability based

**Usage**

```
iae_prob(expr, features = NULL, label, multi = TRUE, thres = 0)
```

**Arguments**

expr	a matrix, features in row and cells in column
features	vector, feature names or indexes to compute
label	vector, group label of each cell
multi	logical, if to compute based on binary (FALSE) or multi-class (TRUE)
thres	numeric, cell only counts when expr > threshold, default 0

**Details**

$$\mathbf{IAE}_{i,j} = \log\left(1 + \frac{\text{mean}(N_{i,j \in D})}{\max(\text{mean}(N_{i,j \in \hat{D}})) + e^{-8}} * \text{mean}(N_{i,j \in D})\right)$$

where  $N_{i,j \in D}$  is the counts of feature  $i$  in cell  $j$  within class  $D$ , and  $\hat{D}$  is the class except  $D$ .

**Value**

a matrix of inverse average expression score

**Examples**

```
data <- matrix(rpois(100, 2), 10, dimnames = list(1:10))
smartid:::iae_prob(data, label = sample(c("A", "B"), 10, replace = TRUE))
```

---

iae_rf	<i>labeled inverse average expression: relative frequency</i>
--------	---

---

### Description

labeled inverse average expression: relative frequency

### Usage

```
iae_rf(expr, features = NULL, label, multi = TRUE, thres = 0)
```

### Arguments

expr	a matrix, features in row and cells in column
features	vector, feature names or indexes to compute
label	vector, group label of each cell
multi	logical, if to compute based on binary (FALSE) or multi-class (TRUE)
thres	numeric, cell only counts when expr > threshold, default 0

### Details

$$\mathbf{IAE} = \log\left(1 + \frac{\text{mean}(N_{i,j \in D})}{\text{max}(\text{mean}(N_{i,j \in \hat{D}})) + e^{-8}}\right)$$

where  $N_{i,j \in D}$  is the counts of feature  $i$  in cell  $j$  within class  $D$ , and  $\hat{D}$  is the class except  $D$ .

### Value

a matrix of inverse average expression score

### Examples

```
data <- matrix(rpois(100, 2), 10, dimnames = list(1:10))
smartid:::iae_rf(data, label = sample(c("A", "B"), 10, replace = TRUE))
```

---

iae_sd	<i>inverse average expression using standard deviation (SD)</i>
--------	---

---

### Description

inverse average expression using standard deviation (SD)

### Usage

```
iae_sd(expr, features = NULL, log = FALSE, thres = 0)
```

### Arguments

expr	a matrix, features in row and cells in column
features	vector, feature names or indexes to compute
log	logical, if to do log-transformation
thres	numeric, cell only counts when expr > threshold, default 0

### Details

$$\mathbf{IAE} = \log\left(1 + sd(tf_i) * \frac{n}{\sum_{j=1}^n \max(0, N_{i,j}) + 1}\right)$$

where  $tf_i$  is the term frequency of feature  $i$ , see details in `tf()`,  $n$  is the total number of cells and  $N_{i,j}$  is the counts of feature  $i$  in cell  $j$ .

### Value

a vector of inverse average expression score for each feature

### Examples

```
data <- matrix(rpois(100, 2), 10, dimnames = list(1:10))
smartid:::iae_sd(data)
```

---

idf	<i>standard inverse cell frequency</i>
-----	--

---

**Description**

standard inverse cell frequency

**Usage**

```
idf(expr, features = NULL, thres = 0)
```

**Arguments**

expr	a matrix, features in row and cells in column
features	vector, feature names or indexes to compute
thres	numeric, cell only counts when expr > threshold, default 0

**Details**

$$\mathbf{IDF}_i = \log\left(1 + \frac{n}{n_i + 1}\right)$$

where  $n$  is the total number of cells,  $n_i$  is the number of cells containing feature  $i$ .

**Value**

a vector of inverse cell frequency score for each feature

**Examples**

```
data <- matrix(rpois(100, 2), 10, dimnames = list(1:10))
smartid::idf(data)
```

---

idf_hdb	<i>inverse document frequency using hdbscan cluster as label</i>
---------	--

---

**Description**

inverse document frequency using hdbscan cluster as label

**Usage**

```
idf_hdb(expr, features = NULL, multi = TRUE, thres = 0, minPts = 2, ...)
```

**Arguments**

<code>expr</code>	a matrix, features in row and cells in column
<code>features</code>	vector, feature names or indexes to compute
<code>multi</code>	logical, if to compute based on binary (FALSE) or multi-class (TRUE)
<code>thres</code>	numeric, cell only counts when <code>expr &gt; threshold</code> , default 0
<code>minPts</code>	integer, minimum size of clusters, default 2. Details in <code>dbscan::hdbscan()</code> .
<code>...</code>	parameters for <code>dbscan::hdbscan()</code>

**Details**

Details as `idf_prob()`.

**Value**

a matrix of inverse cell frequency score

**Examples**

```
set.seed(123)
data <- matrix(rpois(100, 2), 10, dimnames = list(1:10))
smartid::idf_hdb(data)
```

---

idf\_iae\_methods

*Get names of available IDF and IAE methods*

---

**Description**

Returns a named vector of IDF/IAE methods

**Usage**

```
idf_iae_methods()
```

**Value**

names of methods implemented

**Examples**

```
idf_iae_methods()
```

---

idf_igm	<i>labeled inverse cell frequency: IGM</i>
---------	--

---

**Description**

labeled inverse cell frequency: IGM

**Usage**

```
idf_igm(expr, features = NULL, label, lambda = 7, thres = 0)
```

**Arguments**

expr	a matrix, features in row and cells in column
features	vector, feature names or indexes to compute
label	vector, group label of each cell
lambda	numeric, hyperparameter for IGM
thres	numeric, cell only counts when expr > threshold, default 0

**Details**

$$\mathbf{IGM}_i = \log\left(1 + \lambda \frac{\max(n_{i,j \in D})_k}{\sum_k ((n_{i,j \in D})_k * r_k) + e^{-8}}\right)$$

where  $\lambda$  is the hyper parameter,  $n_{i,j \in D}$  is the number of cells containing feature  $i$  in class  $D$ ,  $r_k$  is the rank of  $n_{i,j \in D}$ .

**Value**

a vector of inverse gravity moment score for each feature

**Examples**

```
data <- matrix(rpois(100, 2), 10, dimnames = list(1:10))
smartid::idf_igm(data, label = sample(c("A", "B"), 10, replace = TRUE))
```

---

idf_m	<i>inverse cell frequency: max</i>
-------	------------------------------------

---

**Description**

inverse cell frequency: max

**Usage**

```
idf_m(expr, features = NULL, thres = 0)
```

**Arguments**

expr	a matrix, features in row and cells in column
features	vector, feature names or indexes to compute
thres	numeric, cell only counts when expr > threshold, default 0

**Details**

$$\mathbf{IDF}_{i,j} = \log\left(\frac{\max_{\{i' \in j\}}(n_{i'})}{n_i + 1}\right)$$

where  $i$  is the feature  $i$  and  $i'$  is the feature except  $i$ ,  $n_i$  is the number of cells containing feature  $i$ , and  $n_{i'}$  is the number of cells containing feature  $i'$ .

**Value**

a matrix of inverse cell frequency score for each feature

**Examples**

```
data <- matrix(rpois(100, 2), 10, dimnames = list(1:10))
smartid::idf_m(data)
```

---

idf_prob	<i>labeled inverse cell frequency: probability based</i>
----------	--

---

**Description**

labeled inverse cell frequency: probability based

**Usage**

```
idf_prob(expr, features = NULL, label, multi = TRUE, thres = 0)
```



**Arguments**

expr	a matrix, features in row and cells in column
features	vector, feature names or indexes to compute
label	vector, group label of each cell
multi	logical, if to compute based on binary (FALSE) or multi-class (TRUE)
thres	numeric, cell only counts when expr > threshold, default 0

**Details**

$$\mathbf{IDF}_{i,j} = \log\left(1 + \frac{\frac{n_{i,j \in D}}{n_{j \in D}}}{\max\left(\frac{n_{i,j \in \hat{D}}}{n_{j \in \hat{D}}}\right) + e^{-8}} \frac{n_{i,j \in D}}{n_{j \in D}}\right)$$

where  $n_{i,j \in D}$  is the number of cells containing feature  $i$  in class  $D$ ,  $n_{j \in D}$  is the total number of cells in class  $D$ ,  $\hat{D}$  is the class except  $D$ .

**Value**

a matrix of inverse cell frequency score

**Examples**

```
data <- matrix(rpois(100, 2), 10, dimnames = list(1:10))
smartid::idf_prob(data, label = sample(c("A", "B"), 10, replace = TRUE))
```

---

idf_rf	<i>labeled inverse cell frequency: relative frequency</i>
--------	---

---

**Description**

labeled inverse cell frequency: relative frequency

**Usage**

```
idf_rf(expr, features = NULL, label, multi = TRUE, thres = 0)
```

**Arguments**

expr	a matrix, features in row and cells in column
features	vector, feature names or indexes to compute
label	vector, group label of each cell
multi	logical, if to compute based on binary (FALSE) or multi-class (TRUE)
thres	numeric, cell only counts when expr > threshold, default 0

**Details**

$$\mathbf{IDF}_{i,j} = \log\left(1 + \frac{\frac{n_{i,j \in D}}{n_{j \in D}}}{\max\left(\frac{n_{i,j \in \hat{D}}}{n_{j \in \hat{D}}}\right) + e^{-8}}\right)$$

where  $n_{i,j \in D}$  is the number of cells containing feature  $i$  in class  $D$ ,  $n_{j \in D}$  is the total number of cells in class  $D$ ,  $\hat{D}$  is the class except  $D$ .

**Value**

a matrix of inverse cell frequency score

**Examples**

```
data <- matrix(rpois(100, 2), 10, dimnames = list(1:10))
smartid::idf_rf(data, label = sample(c("A", "B"), 10, replace = TRUE))
```

---

idf_sd	<i>inverse cell frequency using standard deviation (SD)</i>
--------	---

---

**Description**

inverse cell frequency using standard deviation (SD)

**Usage**

```
idf_sd(expr, features = NULL, log = FALSE, thres = 0)
```

**Arguments**

expr	a matrix, features in row and cells in column
features	vector, feature names or indexes to compute
log	logical, if to do log-transformation
thres	numeric, cell only counts when expr > threshold, default 0

**Details**

$$\mathbf{IDF}_i = \log\left(1 + sd(tf_i) * \frac{n}{n_i + 1}\right)$$

where  $tf_i$  is the term frequency of feature  $i$ , see details in `tf()`,  $n$  is the total number of cells and  $n_i$  is the number of cells containing feature  $i$ .

**Value**

a vector of inverse cell frequency score for each feature

**Examples**

```
data <- matrix(rpois(100, 2), 10, dimnames = list(1:10))
smartid::idf_sd(data)
```

---

markers_hdbscan	<i>select markers using HDBSCAN method</i>
-----------------	--

---

**Description**

select markers using HDBSCAN method

**Usage**

```
markers_hdbscan(
  top_markers,
  column = ".dot",
  s_thres = NULL,
  method = c("max.one", "remove.min"),
  minPts = 5,
  plot = FALSE,
  ...
)
```

**Arguments**

top_markers	output of <a href="#">top_markers()</a>
column	character, specify which column used as group label
s_thres	NULL or numeric, only features with score > threshold will be returned, if NULL will use 2 * average probability as threshold
method	can be "max.one" or "remove.min", if to only keep features in 1st component or return features not in the last component
minPts	integer, minimum size of clusters for <a href="#">dbscan::hdbscan()</a>
plot	logical, if to plot mixture density and hist
...	other params for <a href="#">dbscan::hdbscan()</a>

**Value**

a list of markers for each group

**Examples**

```
data <- matrix(rnorm(100), 10, dimnames = list(1:10))
top_n <- top_markers(data, label = rep(c("A", "B"), 5))
markers_hdbscan(top_n, minPts = 2)
```

---

markers\_mclust      *select markers using mclust EM method*

---

### Description

select markers using mclust EM method

### Usage

```
markers_mclust(  
  top_markers,  
  column = ".dot",  
  prob = 0.99,  
  s_thres = NULL,  
  method = c("max.one", "remove.min"),  
  plot = FALSE,  
  ...  
)
```

### Arguments

top_markers	output of <a href="#">top_markers()</a>
column	character, specify which column used as group label
prob	numeric, probability cutoff for 1st component classification
s_thres	NULL or numeric, only features with score > threshold will be returned, if NULL will use 2 * average probability as threshold
method	can be "max.one" or "remove.min", if to only keep features in 1st component or return features not in the last component
plot	logical, if to plot mixture density and hist
...	other params for <a href="#">mclust::densityMclust()</a>

### Value

a list of markers for each group

### Examples

```
data <- matrix(rnorm(100), 10, dimnames = list(1:10))  
top_n <- top_markers(data, label = rep(c("A", "B"), 5))  
markers_mclust(top_n)
```

---

markers_mixmdl	<i>select markers using mixtools EM method</i>
----------------	--

---

**Description**

select markers using mixtools EM method

**Usage**

```
markers_mixmdl(
  top_markers,
  column = ".dot",
  prob = 0.99,
  k = 3,
  ratio = 2,
  dist = c("norm", "gamma"),
  maxit = 1e+05,
  plot = FALSE,
  ...
)
```

**Arguments**

top_markers	output of <a href="#">top_markers()</a>
column	character, specify which column used as group label
prob	numeric, probability cutoff for 1st component classification
k	integer, number of components of mixtures
ratio	numeric, ratio cutoff of 1st component mu to 2nd component mu, only when ratio > cutoff will return markers for the group
dist	can be one of "norm" and "gamma", specify if to use <a href="#">mixtools::normalmixEM()</a> or <a href="#">mixtools::gammamixEM()</a>
maxit	integer, maximum number of iterations for EM
plot	logical, if to plot mixture density and hist
...	other params for <a href="#">mixtools::normalmixEM()</a> or <a href="#">mixtools::gammamixEM()</a>

**Value**

a list of markers for each group

**Examples**

```
set.seed(1000)
data <- matrix(rnorm(100), 10, dimnames = list(1:10))
top_n <- top_markers(data, label = rep(c("A", "B"), 5))
markers_mixmdl(top_n, k = 3)
```

---

ova_score_boxplot	<i>boxplot of features overall score</i>
-------------------	--

---

**Description**

boxplot of features overall score

**Usage**

```
ova_score_boxplot(data, features, ref.group, label, method = "t.test")
```

**Arguments**

data	matrix, features in row and samples in column
features	vector, feature names to plot
ref.group	character, reference group name
label	vector, group labels
method	character, statistical test to use, details in <a href="#">ggpubr::stat_compare_means()</a>

**Value**

ggplot object

**Examples**

```
data <- matrix(rnorm(100), 10, dimnames = list(1:10))
ova_score_boxplot(data, 1:5, ref.group = "A", label = rep(c("A", "B"), 5))
```

---

scale_mgm	<i>scale by mean of group mean for imbalanced data</i>
-----------	--

---

**Description**

scale by mean of group mean for imbalanced data

**Usage**

```
scale_mgm(expr, label, pooled.sd = FALSE)
```

**Arguments**

expr	matrix
label	a vector of group label
pooled.sd	logical, if to use pooled SD for scaling

**Details**

$$z = \frac{x - \frac{\sum_k^{n_D} (\mu_k)}{n_D}}{s}$$

where  $\mu_k$  is the mean of  $x$  in  $k^{th}$  class, and  $n_D$  is the number of classes,  $s$  is the standard deviation of  $x$ , when pooled. `.sd` is set to be `TRUE`,  $s$  will be replaced with  $s_{pooled}$ ,  $s_{pooled} = \sqrt{\frac{\sum_k^{n_D} (n_k - 1) s_k^2}{\sum_k^{n_D} n_k - k}}$

**Value**

scaled matrix

**Examples**

```
scale_mgm(matrix(rnorm(100), 10), label = rep(letters[1:2], 5))
```

---

score_barplot	<i>barplot of processed score</i>
---------------	-----------------------------------

---

**Description**

barplot of processed score

**Usage**

```
score_barplot(top_markers, column = ".dot", f_list, n = 30)
```

**Arguments**

top_markers	output of <code>top_markers()</code>
column	character, specify which column used as group label
f_list	a named list of markers
n	numeric, number of returned top genes for each group

**Value**

ggplot object

**Examples**

```
data <- matrix(rnorm(100), 10, dimnames = list(1:10))
top_n <- top_markers(data, label = rep(c("A", "B"), 5))
score_barplot(top_n)
```

---

sim_sce_test	<i>scRNA-seq test data of 4 groups simulated by splatter.</i>
--------------	---

---

**Description**

A SingleCellExperiment object containing 4 groups with each group up-regulated DEGs saved in metadata.

**Usage**

```
data(sim_sce_test)
```

**Format**

A SingleCellExperiment object of 100genes \* 400 cells.

**Value**

SingleCellExperiment

**Source**

[splatter::splatSimulate\(\)](#)

---

sin_score_boxplot	<i>boxplot of split single feature score</i>
-------------------	--

---

**Description**

boxplot of split single feature score

**Usage**

```
sin_score_boxplot(data, features = NULL, ref.group, label, method = "t.test")
```

**Arguments**

data	matrix, features in row and samples in column
features	vector, feature names to plot
ref.group	character, reference group name
label	vector, group labels
method	character, statistical test to use, details in <a href="#">ggpubr::stat_compare_means()</a>

**Value**

faceted ggplot object



## Examples

```
data <- matrix(rnorm(100), 10, dimnames = list(1:10))
sin_score_boxplot(data, 1:2, ref.group = "A", label = rep(c("A", "B"), 5))
```

---

smartid\_Package

*Scoring and Marker Selection method based on modified TF-IDF*

---

## Description

smartid This package enables automated selection of group specific signature, especially for rare population. The package is developed for generating specific lists of signature genes based on TF-IDF modified methods. It can also be used as a new gene-set scoring method or data transformation method. Multiple visualization functions are implemented in this package.

## Value

Marker list and scores

## Author(s)

Jinjin Chen <chen.j@wehi.edu.au>

## See Also

Useful links:

- <https://davislaboratory.github.io/smartid>
- Report bugs at <https://github.com/DavisLaboratory/smartid/issues>

---

tf

*compute term/feature frequency within each cell*

---

## Description

compute term/feature frequency within each cell

## Usage

```
tf(expr, log = FALSE)
```

## Arguments

expr            a count matrix, features in row and cells in column  
log             logical, if to do log-transformation

**Details**

$$\mathbf{TF}_{i,j} = \frac{N_{i,j}}{\sum_j N_{i,j}}$$

where  $N_{i,j}$  is the counts of feature  $i$  in cell  $j$ .

**Value**

a matrix of term/gene frequency

**Examples**

```
data <- matrix(rpois(100, 2), 10, dimnames = list(1:10))
smartid:::tf(data)
```

---

top_markers	<i>scale score and return top markers</i>
-------------	---

---

**Description**

scale and transform score and output top markers for groups

**Usage**

```
top_markers(
  data,
  label,
  n = 10,
  use.glm = TRUE,
  batch = NULL,
  scale = TRUE,
  use.mgm = TRUE,
  softmax = TRUE,
  slot = "score",
  ...
)

## S4 method for signature 'AnyMatrix'
top_markers(
  data,
  label,
  n = 10,
  use.glm = TRUE,
  batch = NULL,
  scale = TRUE,
  use.mgm = TRUE,
  softmax = TRUE,
```

```

    slot = "score",
    ...
  )

## S4 method for signature 'SummarizedExperiment'
top_markers(
  data,
  label,
  n = 10,
  use.glm = TRUE,
  batch = NULL,
  scale = TRUE,
  use.mgm = TRUE,
  softmax = TRUE,
  slot = "score",
  ...
)

```

### Arguments

data	an expression object, can be matrix or SummarizedExperiment
label	a vector of group label
n	integer, number of returned top genes for each group
use.glm	logical, if to use <code>stats::glm()</code> to compute group mean score, if TRUE, also compute mean score difference as output
batch	a vector of batch labels, default NULL
scale	logical, if to scale data by row
use.mgm	logical, if to scale data using <code>scale_mgm()</code>
softmax	logical, if to apply softmax transformation on output
slot	a character, specify which slot to use when data is se object, optional, default 'score'
...	params for <code>top_markers_abs()</code> or <code>top_markers_glm()</code>

### Value

A tibble with top n feature names, group labels and ordered scores

### Examples

```

data <- matrix(rgamma(100, 2), 10, dimnames = list(1:10))
top_markers(data, label = rep(c("A", "B"), 5))

```

---

top_markers_abs	<i>calculate group median, MAD or mean score and order genes based on scores</i>
-----------------	--

---

### Description

calculate group median, MAD or mean score and order genes based on scores

### Usage

```
top_markers_abs(
  data,
  label,
  n = 10,
  pooled.sd = FALSE,
  method = c("median", "mad", "mean"),
  scale = TRUE,
  use.mgm = TRUE,
  softmax = TRUE,
  tau = 1
)
```

### Arguments

data	matrix, features in row and samples in column
label	a vector of group label
n	integer, number of returned top genes for each group
pooled.sd	logical, if to use pooled SD for scaling
method	character, specify metric to compute, can be one of "median", "mad", "mean"
scale	logical, if to scale data by row
use.mgm	logical, if to scale data using <a href="#">scale_mgm()</a>
softmax	logical, if to apply softmax transformation on output
tau	numeric, hyper parameter for softmax

### Value

a tibble with feature names, group labels and ordered processed scores

### Examples

```
data <- matrix(rgamma(100, 2), 10, dimnames = list(1:10))
top_markers_abs(data, label = rep(c("A", "B"), 5))
```

---

top_markers_glm	<i>calculate group mean score using glm and order genes based on scores difference</i>
-----------------	--

---

### Description

calculate group mean score using glm and order genes based on scores difference

### Usage

```
top_markers_glm(  
  data,  
  label,  
  n = 10,  
  family = gaussian(),  
  batch = NULL,  
  scale = TRUE,  
  use.mgm = TRUE,  
  pooled.sd = FALSE,  
  softmax = TRUE,  
  tau = 1  
)
```

### Arguments

data	matrix, features in row and samples in column
label	a vector of group label
n	integer, number of returned top genes for each group
family	family for glm, details in <a href="#">stats::glm()</a>
batch	a vector of batch labels, default NULL
scale	logical, if to scale data by row
use.mgm	logical, if to scale data using <a href="#">scale_mgm()</a>
pooled.sd	logical, if to use pooled SD for scaling
softmax	logical, if to apply softmax transformation on output
tau	numeric, hyper parameter for softmax

### Value

a tibble with feature names, group labels and ordered processed scores

### Examples

```
data <- matrix(rgamma(100, 2), 10, dimnames = list(1:10))  
top_markers_glm(data, label = rep(c("A", "B"), 5))
```

---

top_markers_init	<i>compute group summarized score and order genes based on processed scores</i>
------------------	---

---

### Description

compute group summarized score and order genes based on processed scores

### Usage

```
top_markers_init(
  data,
  label,
  n = 10,
  use.glm = TRUE,
  batch = NULL,
  scale = TRUE,
  use.mgm = TRUE,
  softmax = TRUE,
  ...
)
```

### Arguments

data	matrix, features in row and samples in column
label	a vector of group label
n	integer, number of returned top genes for each group
use.glm	logical, if to use <code>stats::glm()</code> to compute group mean score, if TRUE, also compute mean score difference as output
batch	a vector of batch labels, default NULL
scale	logical, if to scale data by row
use.mgm	logical, if to scale data using <code>scale_mgm()</code>
softmax	logical, if to apply softmax transformation on output
...	params for <code>top_markers_abs()</code> or <code>top_markers_glm()</code>

### Value

a tibble with feature names, group labels and ordered processed scores

### Examples

```
data <- matrix(rgamma(100, 2), 10, dimnames = list(1:10))
top_markers_init(data, label = rep(c("A", "B"), 5))
```

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