

Package ‘gleeR’

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Title glee for differential protein expression

Version 0.1

Description What the package does (one paragraph)

Depends R (>= 3.2.0)

License GPL-2

LazyData true

Imports dplyr

NeedsCompilation no

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calcs	<i>calculate standard deviation</i>
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Description

using the log-values of xbar

Usage

calcs(model, x)

calc_stn_pval	<i>calculate signal-to-noise and p-values</i>
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Description

using resampled distribution

Usage

```
calc_stn_pval(A, B, m, num_iter)
```

data_ok	<i>check the spectral count data</i>
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Description

dimensions must match with specification, and all values must be positive

Usage

```
data_ok(D, nA, nB)
```

diff_exp_table	<i>calculate diff-exp statss</i>
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Description

and return the results as a data.frame

Usage

```
diff_exp_table(stn_pval, Prot, num_digits)
```

fit_model	<i>fit the specified model</i>
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Description

in each condition separately

Usage

```
fit_model(A, B, fit_type)
```

getPvals	<i>calculate p-values</i>
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Description

for each protein, using the generated STN distribution

Usage

```
getPvals(model_stn, iter, model_stn_dist)
```

getSTNdistrib	<i>estimate the STN distribution</i>
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Description

as a dplyr data_frame

Usage

```
getSTNdistrib(A, nA, nB, iter, xbar0_replace, best_model)
```

model_fit_plots	<i>plot model-fit</i>
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Description

mean-vs-stdev and signal-level

Usage

```
model_fit_plots(m, outfile)
```

stn_pval_plots	<i>plot stn against p-value</i>
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Description

and stn for each protein

Usage

```
stn_pval_plots(stn_pval, outfile)
```

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