

Preprocessing

1. Preprocessing proteomics data

- prepare_peaks()
- prepare_pd()

2. Preprocessing peptide library

- calculate_all_cleavages()

Quality Control

1. Checking the percentage of peptides in library detected

- qc_check()

2. Identifying the components of Peptide Library Not Detected.

- find_nd_peptides()

3. Visualizing QC Results

- plot_qc_check()
- plot_nd_peptides()
- plot_rt_qc()

Processing

1. Normalize data

- normalyse()

2. Remove outliers

- outliers()

3. Data Imputation

- impute()

4. Cleavage motif determination

- join_with_library()
- cterm_cleavage()
- nterm_cleavage()

add_cleavages()

mspms()

5. Consolidating data

- prepare_for_stats()
- polish()

Statistics / Visualization Preparation

1. Log2 fold change

- mspms_log2fc()

2. T- tests

- mspms_t_test()

3. Log2 fold change + t-tests

- log2fc_t_test()
- log2fct_time()
- log2fct_condition()

3. Anova

- mspms_anova()

4. Count of cleavages by position

- count_of_cleavages_per_pos()

5. iceLogo

- calc_AA_count_of_motif()
- calc_prop_of_motif()
- calc_AA_motif_zscore()
- calc_sig_zscores()
- calc_percent_difference()
- calc_AA_fold_change()
- prepare_sig_p_diff()
- prepare_pd()
- prepare_fc()
- extract_re()

prepare_icelogo_data()

Visualizations

1. Principle component analysis

- plot_pca()

2. Heatmap/unsupervised hierarchical clustering

- plot_heatmap()

3. Volcano plot

- plot_volcano()

4. Cleavage position plot

- plot_cleavage_pos()

5. Icelogo plots

- plot_icelogo()
- plot_all_icelogos()



Integrated in
Shiny App



Integrated in
generate_report()