mspms

MSPMSINR
P4 P3 P2 P1 P1' P2' P3' P4'

Data Preparation

Preparing data exported from proteomics software
- prepare_peaks()
- prepare_pd()
- prepare_fragpipe()

Calculating all possible cleavages of peptide library
- calculate_all_cleavages()

Data Processing

Data transformation, normalization, and imputation
- process_qf()

Convert to tidy format
- mspms_tidy()

Statistics

Calculate log2 fold change and perform T-tests
- log2fc_t_test()

Calculate log2 fold change and statistics using limma.
- limma_stats()

Visualization

Quality control
- plot_nd_peptides()
- plot_qc_check()

PCA
-plot_volcano()

Heatmap
- plot_heatmap()

Volcano plot
-plot_volcano()

Time course
- plot_time_course()

Cleavage position plot
- plot_cleavage_pos()

iceLogo
-plot_icelogo()
-plot_all_icelogos()

Report
-generate_report()

Only a subset of functions are exported to the user in an effort to make the package API intuitive.
Helper functions can be found in the helper_functions.R file name corresponding to the type of functions it assists with.