R packages for handling and analyzing data from protein correlation profiling

"Investigating temporal changes in the interactome"

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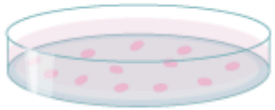
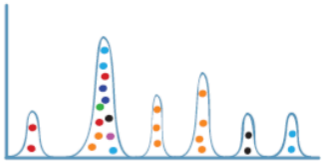
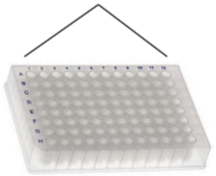
Current workflow



MCF10A

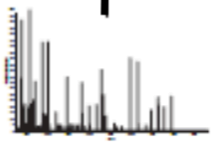




30 fractions

fractions based on size

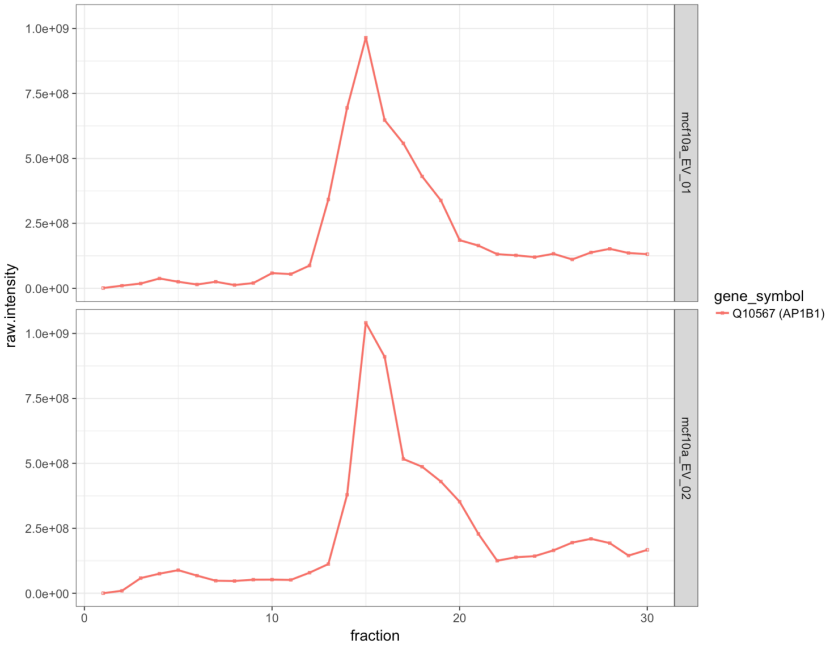
Digestion and peptide clean-up



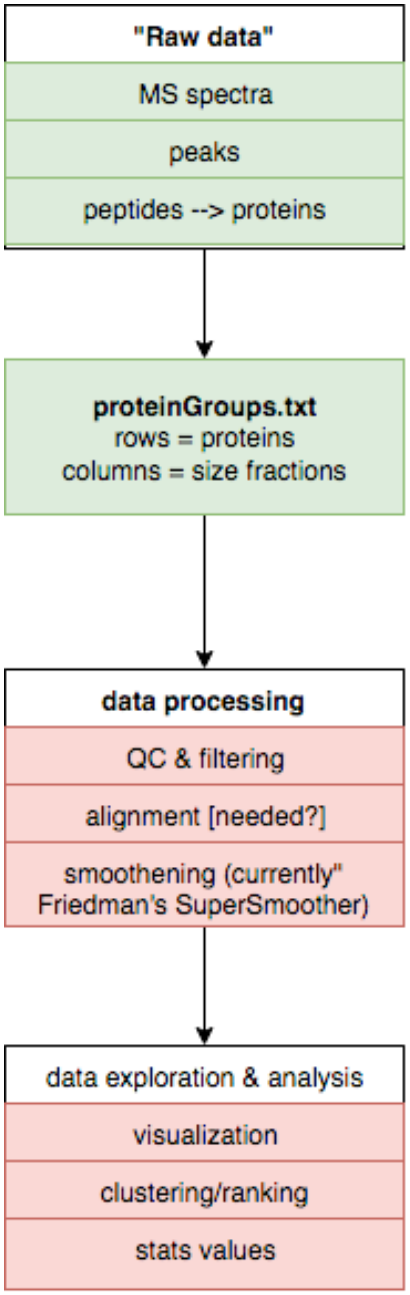
LC-MS/MS analysis

returns a very unwieldy txt file

rows = proteins (ca. 2-5K)
columns = 30x7 variables



example plot for 1 protein and 1 variable



Data package

- real-life dataset with 2 replicates from a total of 3 conditions
- raw data
- R-friendly format

Analysis package

- Identify proteins that change
- Identify proteins with similar profiles (=complexes)

Visualization/Exploration **Shiny**

- interactive plots
- data upload intro/retrieval from data base