

Part I: Normalization & Summarization

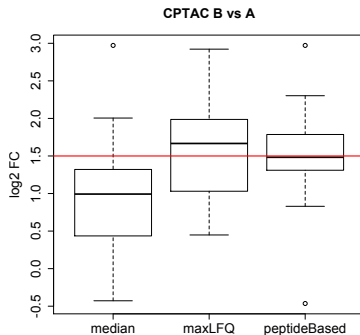
Lieven Clement

Proteomics Data Analysis

Comparison of FC estimates upon summarization

Problems

- strong peptide-effects
- \neq peptides/sample
- \neq # peptides/sample
- non-random missingness



Median Summarization vs Peptide Based Approach

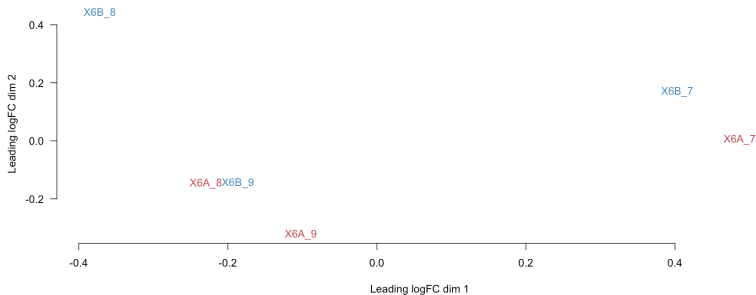
Median Summarization

Color variable ^[?]

treatment

MDS plot after full preprocessing ^[?]

- ☐ Plot MDS points
- ☒ Plot MDS labels



Median Summarization vs Peptide Based Approach

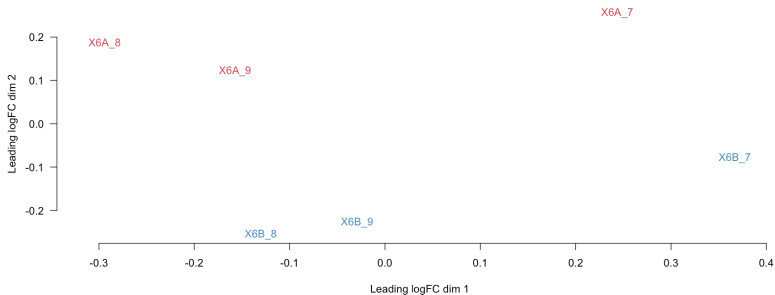
Peptide Based Approach

Color variable [\[?\]](#)

treatment

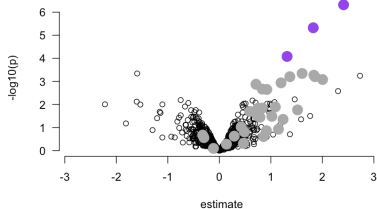
MDS plot after full preprocessing [\[?\]](#)

- ☐ Plot MDS points
- ☒ Plot MDS labels



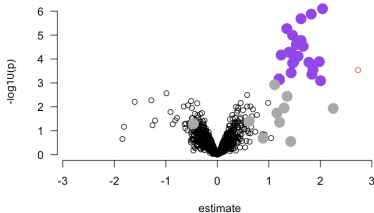
Median Summarization vs Peptide Based Approach

Median



2 UPS and 0 yeast

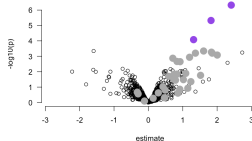
Peptide-based



12 UPS and 0 yeast

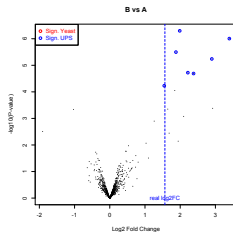
Median Summarization vs Peptide Based Approach

Median



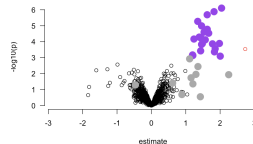
2 UPS and 0 yeast

MaxLFQ



7 UPS and 0 yeast

Peptide-based



12 UPS and 0 yeast