

# Part I: Normalization & Summarization

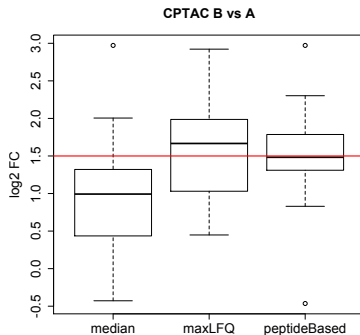
Lieven Clement

Proteomics Data Analysis 2018, Gulbenkian Institute, May 28 -June 1  
2018.

# 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

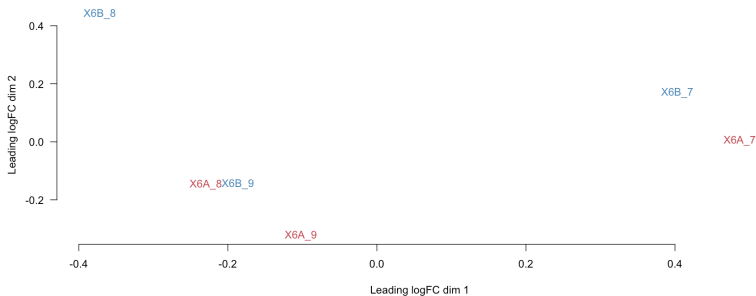
## Median Summarization

Color variable <sup>[?]</sup>

treatment

MDS plot after full preprocessing <sup>[?]</sup>

- ☐ Plot MDS points
- ☒ Plot MDS labels



# Median Summarization vs Peptide Based Approach

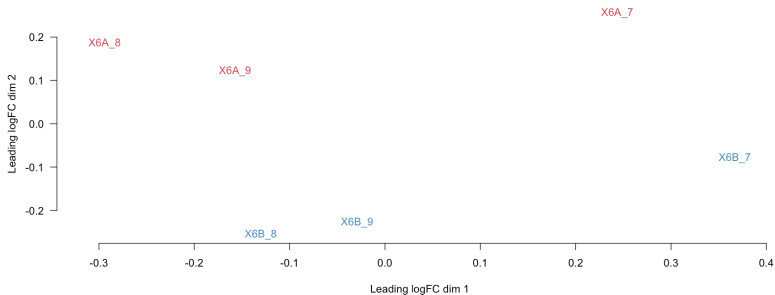
## Peptide Based Approach

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

treatment

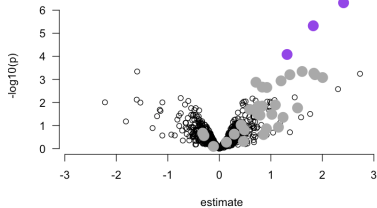
MDS plot after full preprocessing [\[?\]](#)

- ☐ Plot MDS points
- ☒ Plot MDS labels



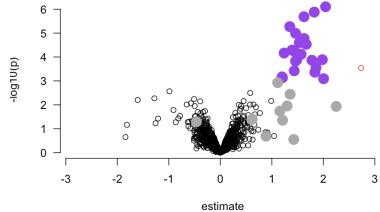
# Median Summarization vs Peptide Based Approach

Median



2 UPS and 0 yeast

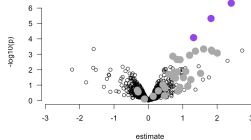
Peptide-based



12 UPS and 0 yeast

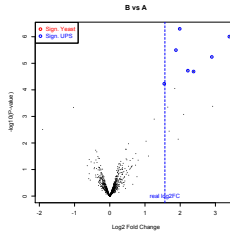
# Median Summarization vs Peptide Based Approach

Median



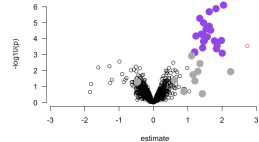
2 UPS and 0 yeast

MaxLFQ



7 UPS and 0 yeast

Peptide-based



12 UPS and 0 yeast