Analysing MaxQuant Output with R

FGC Zurich

30 September 2015

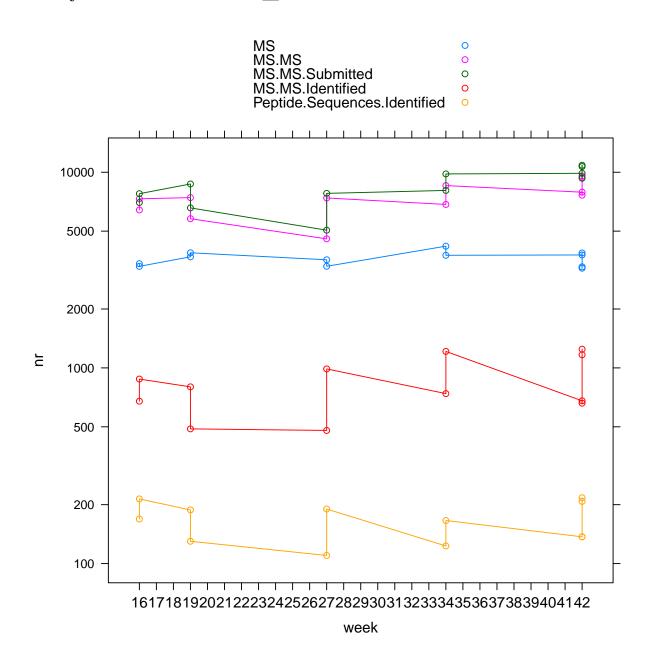
Contents

Prepare mrm table	1
Analysed Dataset is MPI_VE	2
Looking at measurement error	3
Looking at MSQC 1 peptide counts	4
Look at Intensities (by species)	5
Looking at intensities msqc1	6
Looking at retention time	8
Log fold change	10

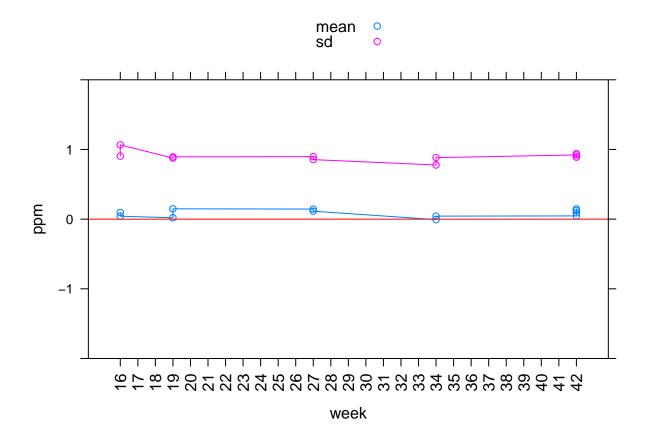
Prepare mrm table

- nr of assigned spectra (MS2) / versus total spectra
- How many H/L target peptides are identified
- Ratio among H/L of the target peptides
- Intensity of heavy or light over the runs

Analysed Dataset is MPI_VE



Looking at measurement error



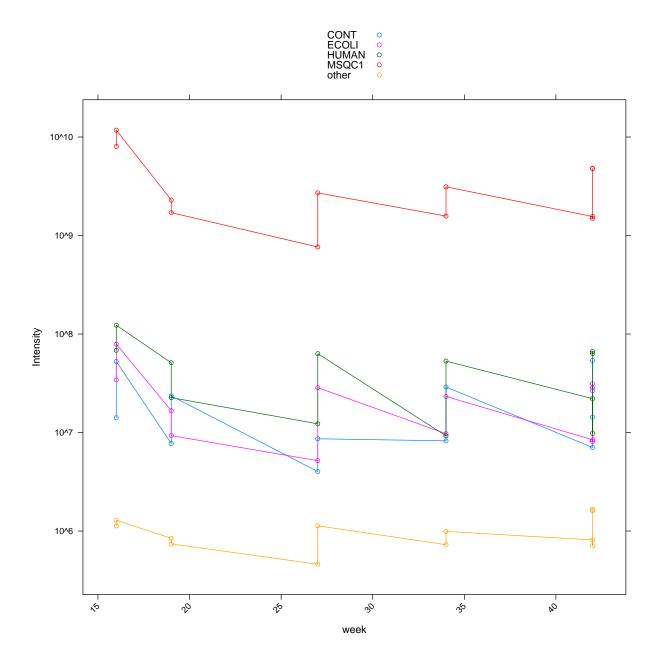
Looking at MSQC 1 peptide counts

all peptide count . H+L H L **VLDALQAIK** SADFTNFDPR NLSVEDAAR **GYSIFSYATK GAGAFGYFEVTHDITK GGPFSDSYR** pepcount - 20 **FEDENFILK FSTVAGESGSADTVR** EGHLSPDIVAEQK ESDTSYVSLK AVQQPDGLAVLGIFLK ALIVLAHSER

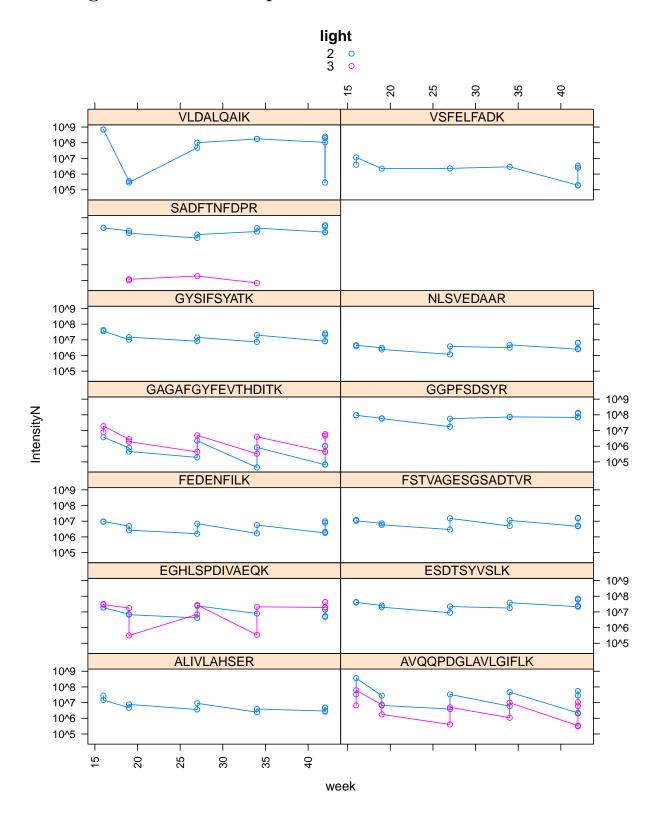
week

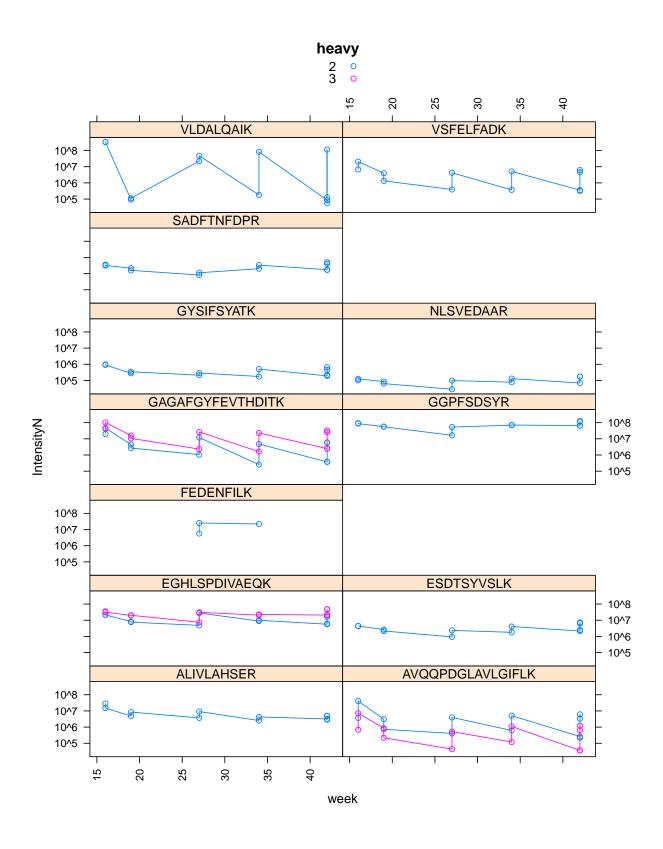
 $^{+++}$

Look at Intensities (by species)

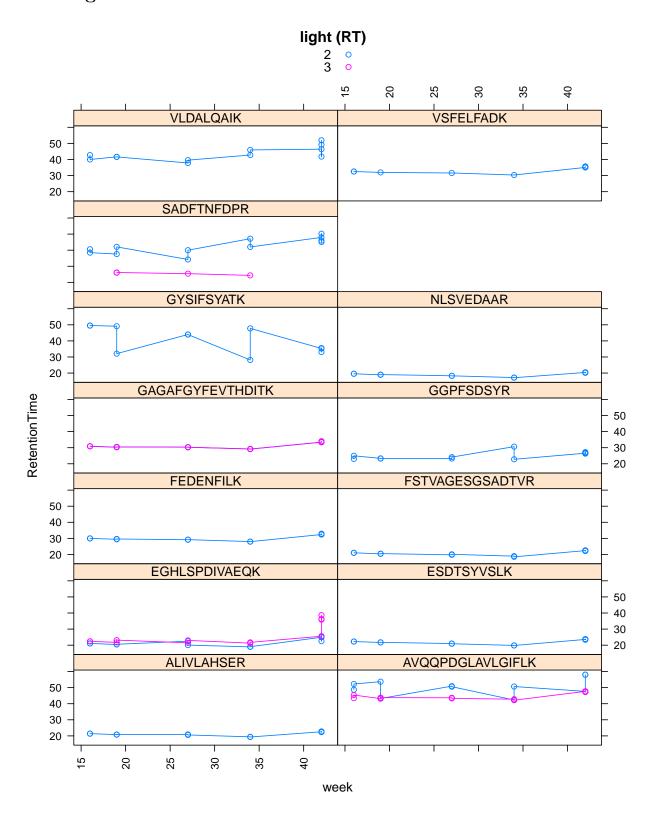


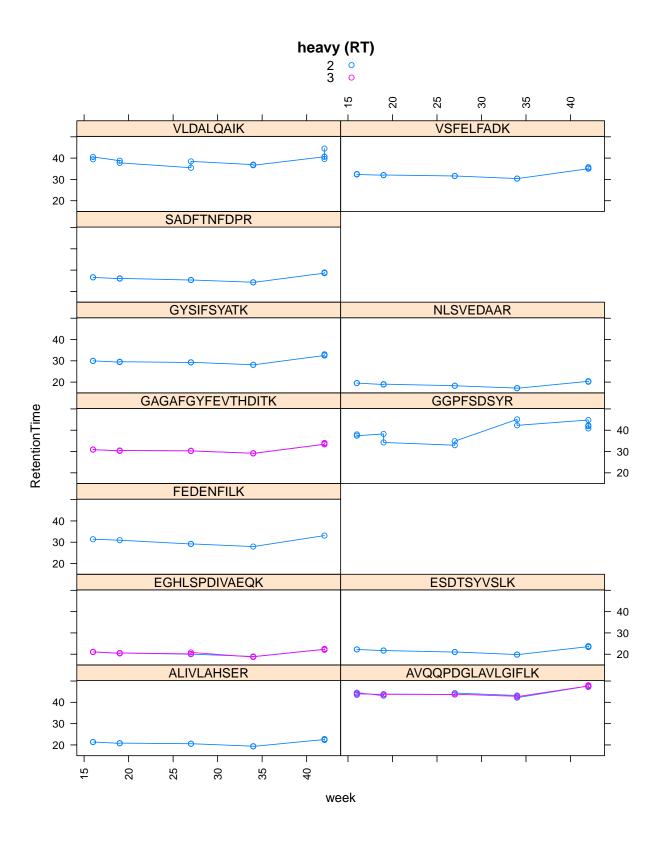
Looking at intensities msqc1





Looking at retention time





Log fold change

Warning in inner_join_impl(x, y, byx, byy): joining factors with ## different levels, coercing to character vector

