1 INIT

2 build_data_sets

2.1 read protein data

LFQ: rel. quantification – for same protein across different samples

iBAQ: orthogonal comparison – for different proteins in the same sample

Intensity: supposed to be both

```
C:\ProgramData\Anaconda3\lib\site-packages\ipykernel_launcher.py:2: DtypeWarning: Columns (5,6,2764,2765,2773,2774,2775,2776) have mixed types. Specify dtype option on import or se
t low_memory=False.
```

2.2 read mrna data

we start with mapping the cells annotations from the MassSpec to mRNA :

2.3 multiply by mRNA to proteins ratio

We took the learned ratios between mRNA to MassSpec from:
"Wilhelm, M., Schlegl, J., Hahne, H. et al. Mass-spectrometry-based draft of the human proteome. Nature 509, 582–587 (2014)"

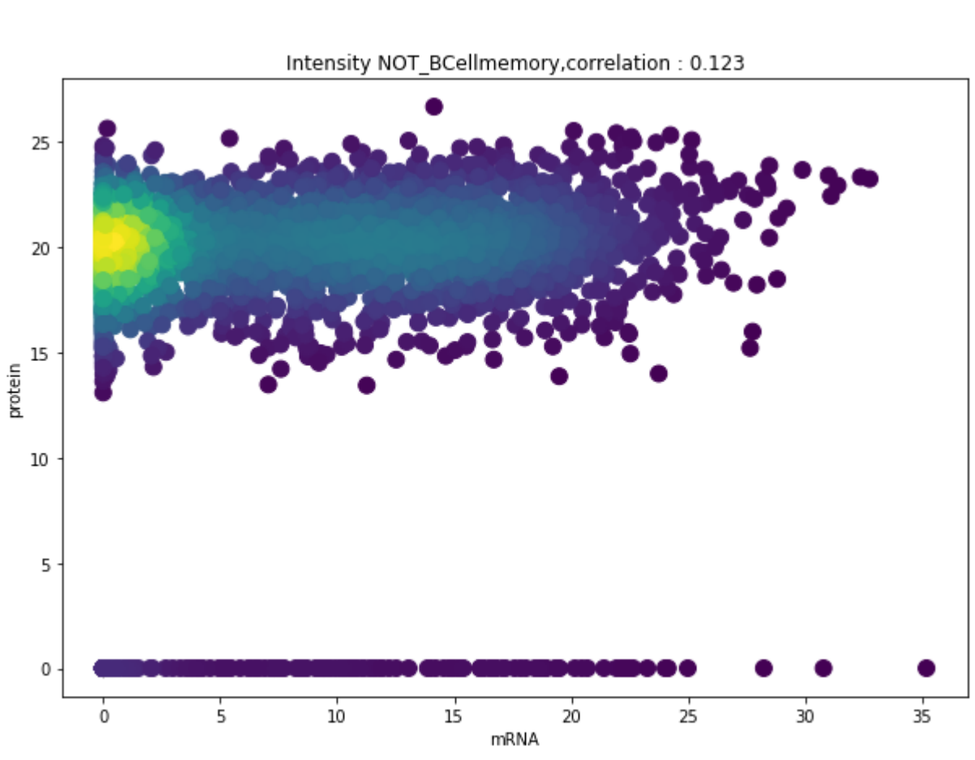
The ratio is a log ratio so we convert as needed

3 compare sets

3.1 compare all proteins to all genes

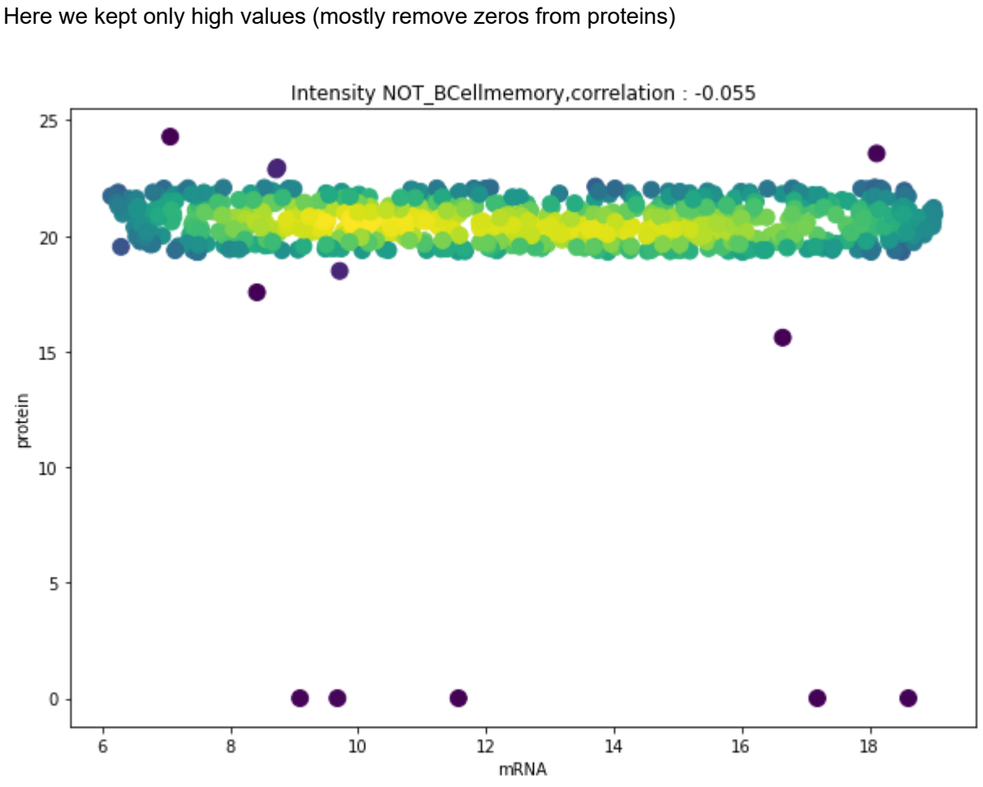
3.1.1 med value of genes

Here we took the median value of each protein (between Jan versions) and compare them to the adjusted mRNA values :

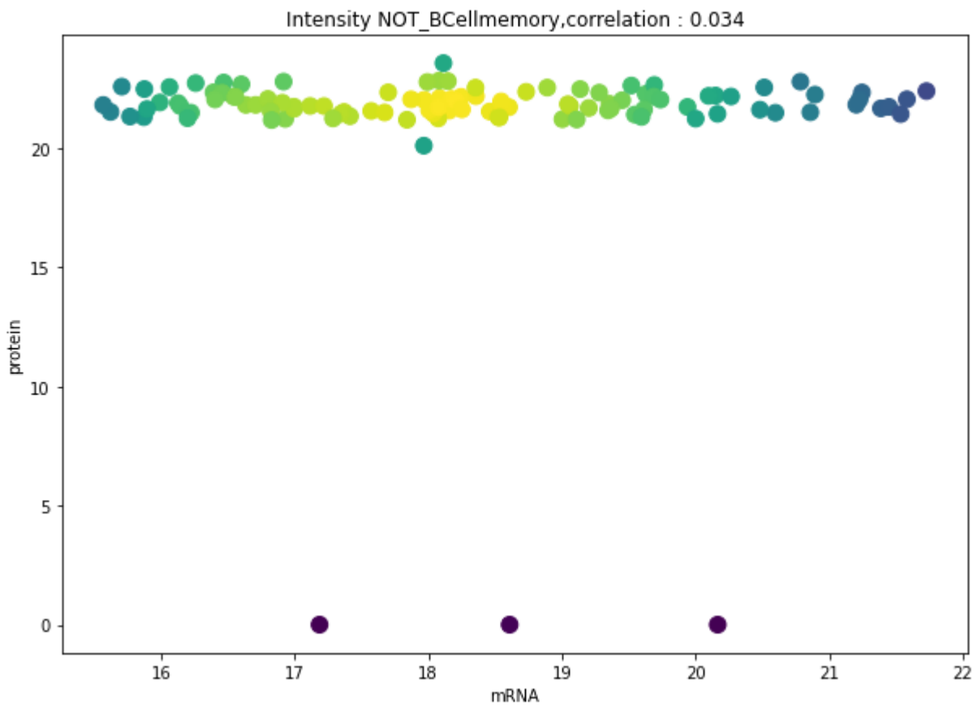


3.1.2 med values + taking only percantile 0.5 to 0.9

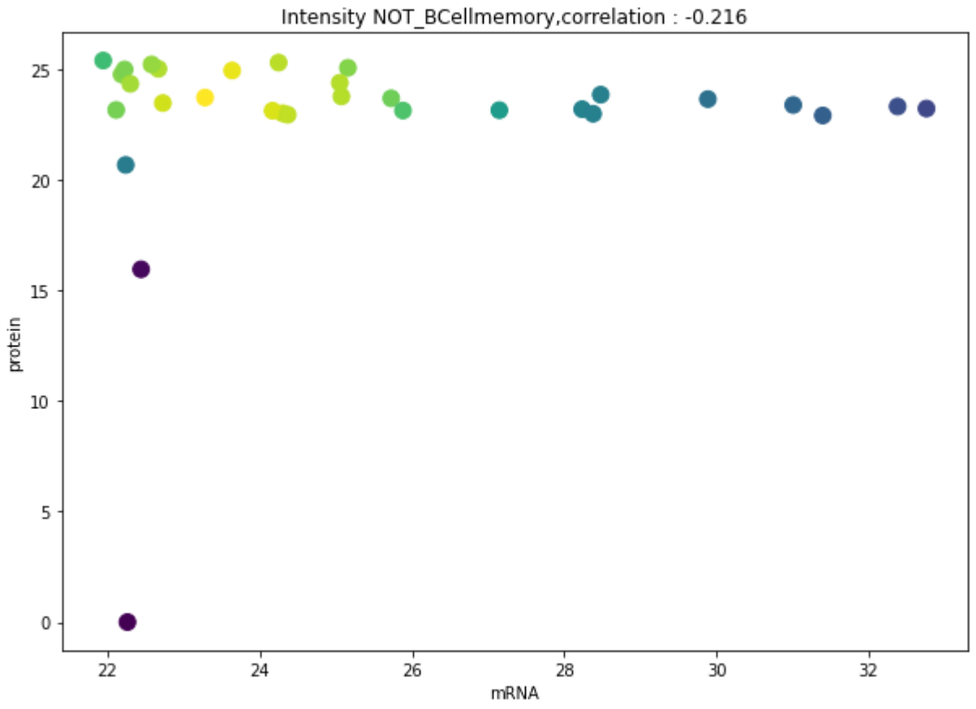
Here we kept only high values (mostly remove zeros from proteins)



3.1.3 med values + taking only percantile 0.95 to 0.8



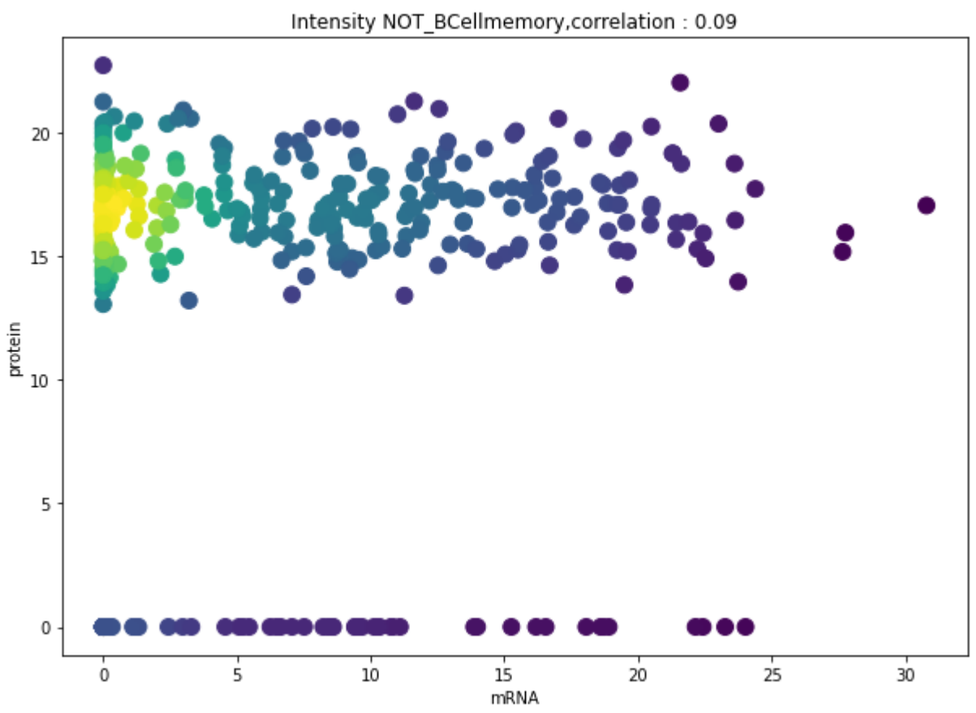
3.1.4 med values + taking only percantile 0.95 to 1



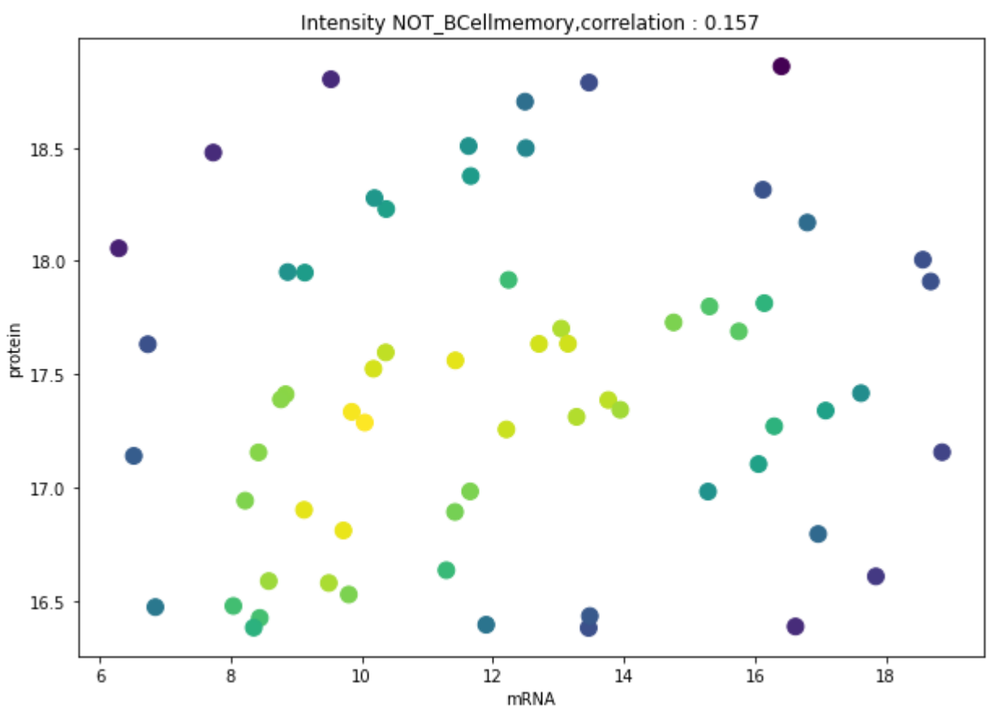
3.2 remove high STD proteins

Here we removed proteins we are "not sure about". aka - proteins where the std between versions is bigger then 0.8

3.2.1 med value of genes



3.2.2 med values + taking only percantile 0.5 to 0.9



3.2.3 med values + taking only percantile 0.99 to 0.7