Perseus version:

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MED4:

https://rest.uniprot.org/uniprotkb/stream?compressed=true&fields=accession%2Cid%2Cprotein\_name%2Cgene\_names%2Corganism\_name%2Clength%2Cgene\_oln%2Ccc\_pathway%2Cxref\_refseq%2Cxref\_kegg%2Cgo\_p%2Cgo\_f%2Cgo\_c&format=tsv&query=%28%28taxonomy\_id%3A59919%29%29

check the distribution of missing values per row

* Log2
* Impute missing values
* Annotate rows (go/kegg)
* Histogram
* Select missing
* Normalization
* Subtract mode from columns
* Histogram – density plot
* Tests – multiple test – anova
* Fisher exact (fish)