These scripts need **Python** and **R** installed. Will also need the ‘**scipy**’ and ‘**numpy**’ python libraries installed.

The input file needs to be copied into the same folder as the python script ‘score\_nodependencies.py’.

**Input file** is a 2D matrix of either spectral counts (MS2) or intensities (MS1) with samples in columns and identified proteins in rows. E.g.

Hs\_hekN\_1108.prot\_count\_uniqpeps2\_FDR0010 -------- Spectral count (MS2)

Hs\_hekN\_1108\_pqmsb\_filtmsb.tab -------------- Intensities (MS1)

**Output files** are also 2D matrices of scores only. They do not contain any labels. At the moment the labels (ie. The protein names) can be copied and pasted into the outputfile from the input file as first column and first row.

**Command to use**

* python score\_nodependencies.py [filename] [method can be one of euclidean|apex|poisson] [number of iterations 'only for poisson']

This python script will generate the 3 correlation scores.

* wcc.sh [filename] [weight]

This shell script transposes the input matrix passes it to the the R script ‘wcc.R’ to generate the weighted cross correlations.

**To generate apex score**

python score\_nodependencies.py Hs\_hekN\_1108.prot\_count\_uniqpeps2\_FDR0010 apex

**To generate euclidean correlation coefficient**

python score\_nodependencies.py Hs\_hekN\_1108\_pqmsb\_filtmsb.tab euclidean

**To generate poisson correlation coefficient**

python score\_nodependencies.py Hs\_hekN\_1108.prot\_count\_uniqpeps2\_FDR0010 poisson 1000

**To generate the weighted cross correlation**

./scripts/wcc.sh Hs\_hekN\_1108.prot\_count\_uniqpeps2\_FDR0010 1