**Instruction**

**Clustering\_Prot\_Phos.m**

1] Aim: Normalize expression levels of proteins/phosphopeptides & Identify clusters

2] Required functions: aoNMF\_subtyping, aonmf, auto

3] Input file:

Raw abundances of proteins/phosphopeptides per TMT channels for each MS2 scan

4] Input variable:

allo\_raw (# protein/phosphopeptides × # samples): raw abundance values of all proteins/phosphopeptides

5] Output variables

[1] FC\_q (# expressed proteins/phosphopeptides × # samples): Normalized fold-changes of expressed proteins/phosphopeptides (detected in every sample)

[2] CG\_mad30\_c2 : Clustergram of samples in two clusters from MAD30 clustering