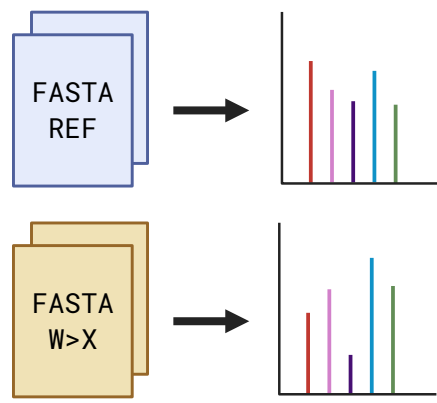
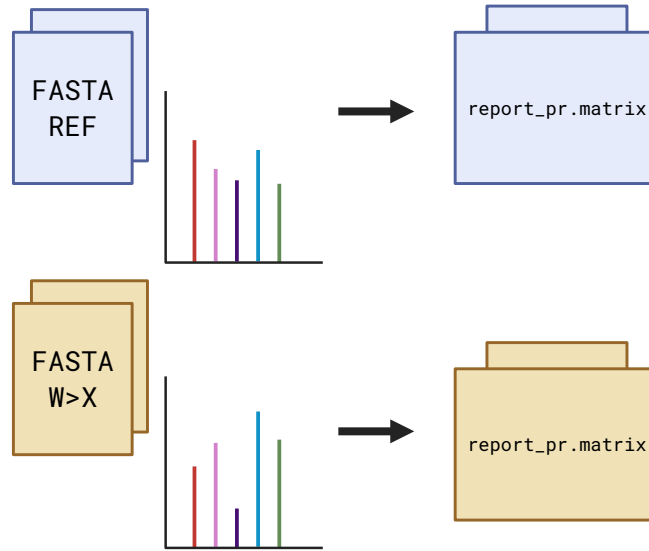


## STEP 1

**DIA-NN**  
Predicted spectral library generation

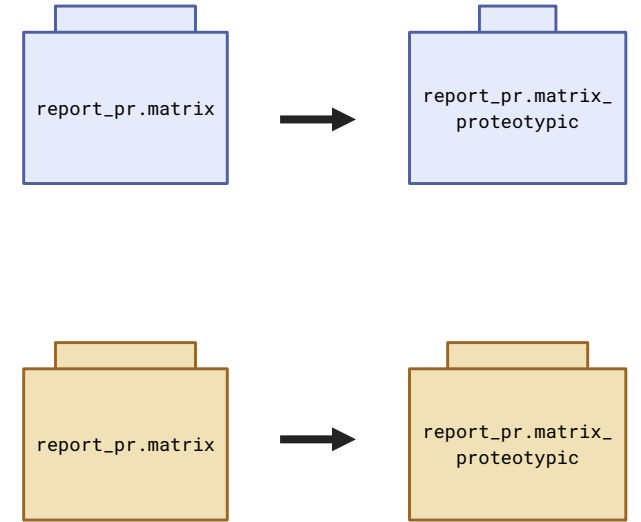


**DIA-NN**  
Relative protein quantification



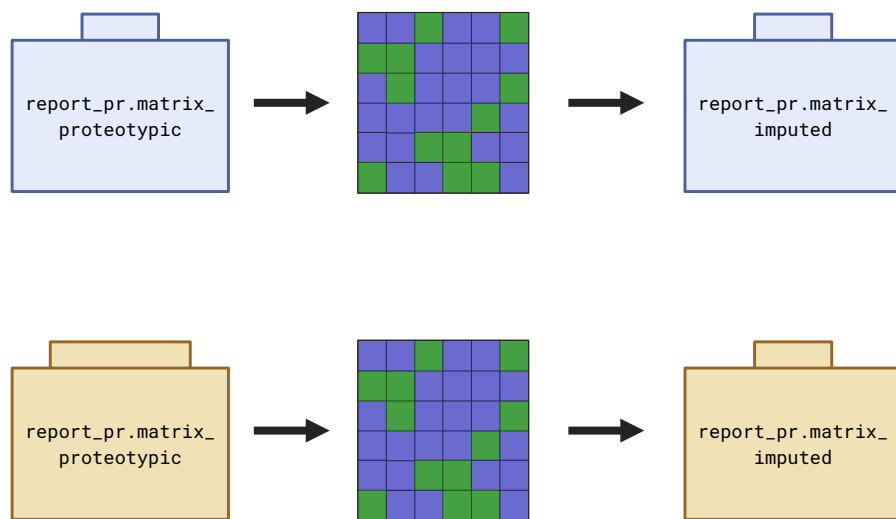
## STEP 2

**Perseus**  
Filter proteotypic values



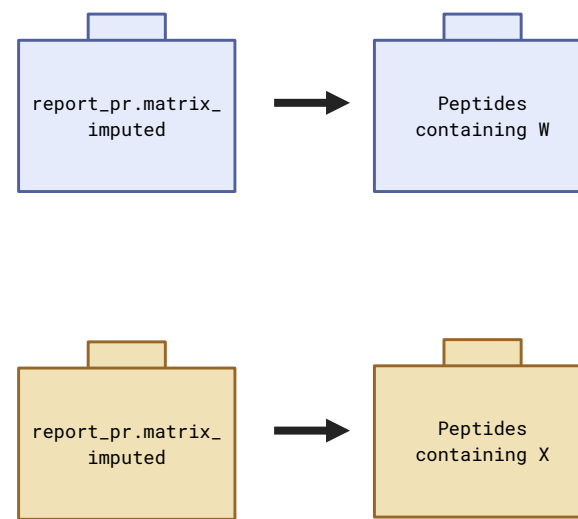
## STEP 3

**imputeLCMD - R**  
Impute missing values (impute.MinDet)

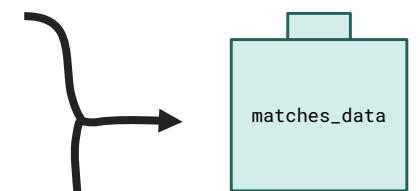


## STEP 4

**Perseus**  
Join datasets

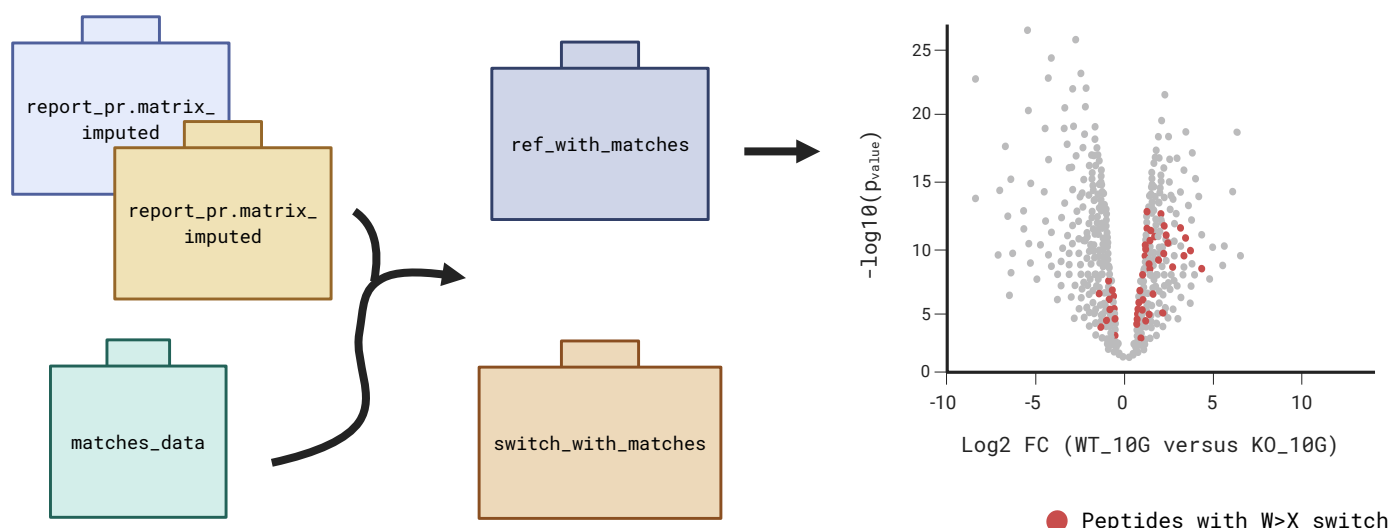


**Excel**  
Search for presence of  
XXX(W/X)XXX peptides



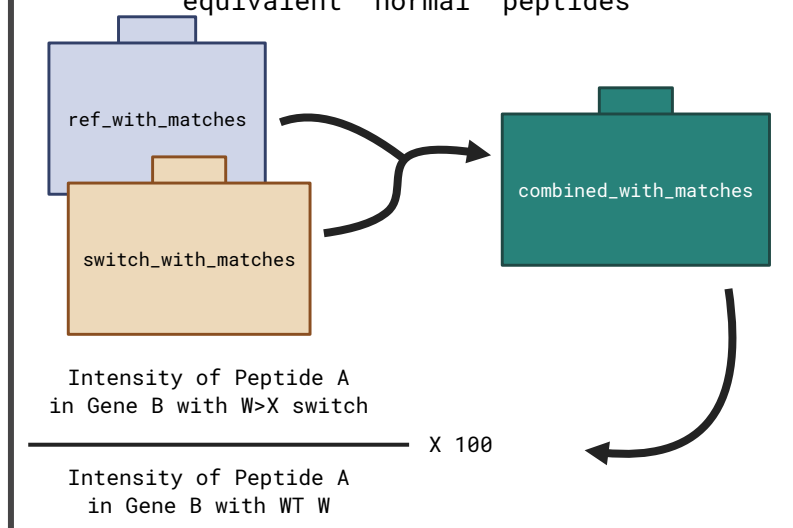
## STEP 5

**Perseus**  
Find (up/downregulated) proteins with a switched peptide



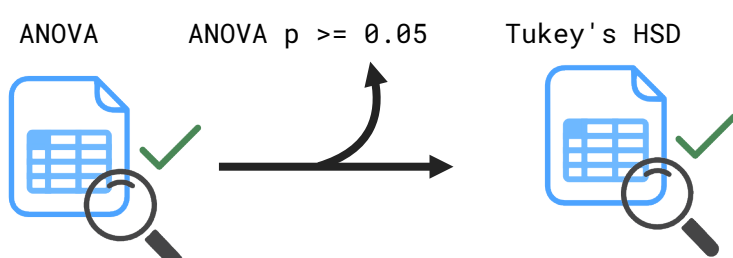
## STEP 6

**R**  
Normalise abundance of switched peptides against  
equivalent "normal" peptides



## STEP 7

**R**  
For each peptide, determine if there are significant  
differences in peptide abundance (as % of reference) between  
conditions of interest



Tukey's HSD p.adj >= 0.05

