INTRODUCTION TO
GALAXY-P
Galaxy-P 101: Building up and using a proteomics workflow

In this very basic example we will introduce you to basics of Galaxy-P:

- Uploading database using Protein Database Downloader.
- Getting raw data from website.
- Peaklist processing including options and parameters.
- X! tandem search.
- PeptideProphet processing of X!tandem search.
- Converting PepXML to a table.
- Using ProteinProphet to process PeptideProphet results.
- FDR Analysis.
- Performing simple data manipulation
- Understanding Galaxy's History system
- Creating and editing workflows
- Applying workflows to your data.
Galaxy-P 101: Building up and using a proteomics workflow

• Just an introduction to the capabilities of Galaxy-P. 
The idea is to introduce you to basic components of Galaxy-P. We anticipate that the creative use of galaxy-P ‘workflows’ will improve as we spend more time on it.

• Galaxy-P 101 can be followed up by using instructions on the page. 
The aim is to cover the whole tutorial. However, we anticipate some delay due to discussion or some users to encounter problems as we proceed. The tutorial can also be followed up by using instructions on the page.

• First tutorial – and things might go wrong. 
Galaxy-P is running on disk that is not backed up, you should not assume data uploaded to or generated with Galaxy-P will be available in the future. Additionally, Galaxy-P is in very active development - things will break and things will change, so your patience is requested.
Workflow for Comparison of proteogenomic peptides (non-human identifications) between one-step and two-step process using peptide probabilities.

OUTPUT FROM LAST STEP IN THE WORKFLOW: Comparison of proteogenomic peptides (non-human identifications) between one-step and two-step process using peptide probabilities.

- The peptide probabilities of proteogenomic peptides, calculated after two-step method are on average higher (74.37%) as compared to one-step method (35.5%).
- When peptides with peptide probability greater than 95% were considered, 7 peptides were exclusively identified by two-step method, 5 were identified exclusively by one-step method and 7 were identified by both methods.
- These comparisons used only target database searches (No target-decoy databases and FDR analysis was used). We plan to perform these comparisons with FDR analysis on target-decoy database searches.
ProteinPilot Workflow within Galaxy-P.

https://galaxyp.msi.umn.edu/u/pratik/w/proteinpilot-workflow