**User Guide for Post-Analysis**

Here, we present the post-analysis for rescoring the identification of glycopeptides. For inquiries regarding post-analysis or other codes, please contact: [liang\_qiao@fudan.edu.cn](mailto:liang_qiao@fudan.edu.cn).

**Example data**

DeepGP results:

DeepGP\_result\_predictmonomz.csv

*The DeepGP\_result\_predictmonomz.csv file contains the DeepGP results for glycopeptides from the fission yeast dataset Yeast\_1. For instructions on file generation, please refer to the user guide.docx in the main folder.*

Sequence searching software results:

pGlycoDB-GP-FDR-Pro\_fissionyeast.txt

*This file contains the pGlyco3 results for glycopeptides from the fission yeast dataset Yeast\_1.*

The demo data for post-analysis is available at [Google Drive] (https://drive.google.com/drive/folders/1FGRUSyV-\_pBYnTG8tqaY2594TSKY8e-9).

**Perform the post-analysis using the command line**

This guide details how to perform post-analysis using command-line scripts. Advanced users can adapt these commands for other command-line interfaces.

1. Entry to the folder including DeepGP post-processing code files.

Users can navigate to the relevant folder using a command such as cd D:\DeepGP\_code. The path “D:\DeepGP\_code” signifies the directory containing the Python scripts for DeepGP post-processing code files.

1. This script calculates the combined metrics from DeepGP and pGlyco3 and generates an output file demonstrating the number of PSMs over a certain decoy ratio based on DeepGP+pGlyco3.

python reidentification\_post\_analysis.py --inputfile1 DeepGP\_result\_predictmonomz.csv --inputfile2 pGlycoDB-GP-FDR-Pro\_fissionyeast.txt --outputfile output.csv --Dataset Yeast

The description of the parameters of the command line:

--inputfile1: The first input file, expected to be a CSV file containing DeepGP output data. Default: DeepGP\_result\_predictmonomz.csv.

--inputfile2: The second input file, expected to be a tab-separated text file containing pGlyco3 output data. Default: pGlycoDB-GP-FDR-Pro\_fissionyeast.txt.

--outputfile: The name of the output file where the results will be saved. Default: output.csv.

Dataset: Specifies the dataset type, either Yeast or Mouse. Yeast refers to the re-identification experiments for the fission yeast datasets with high-mannose type glycans as targets. Mouse refers to the re-identification experiments for the mouse datasets with spectra without shuffling peaks as targets. Default: Yeast.

The output file contains the following columns:

Combined\_score: The combined score calculated from the input metrics. A combined score was formulated by adding the normalized score (sqrt-cosine similarity) from DeepGP and the normalized score (TotalScore) from pGlyco3.

#Decoy/#PSMs: The ratio of the number of decoy PSMs to the total PSMs at the given combined score threshold.

#PSMs: The number of PSMs at the given combined score threshold.