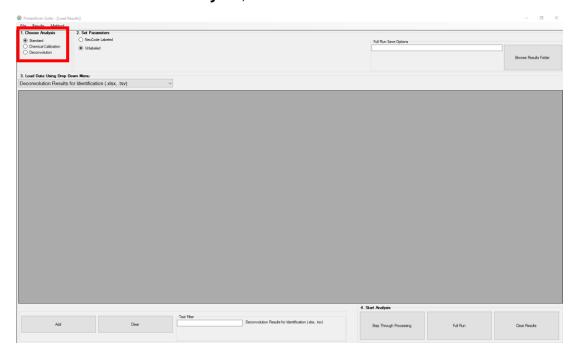
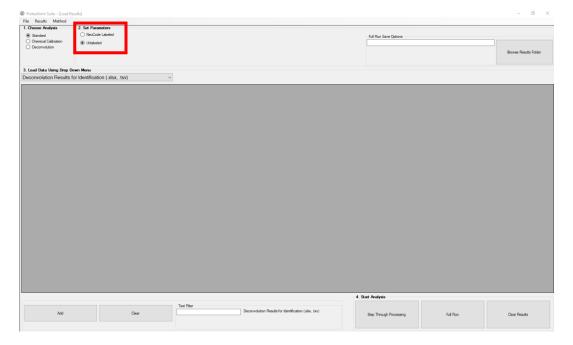
## **Analyzing Data in Proteoform Suite**

This tutorial document is for constructing proteoform families from intact-mass data in version 0.3.5 of Proteoform Suite.

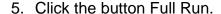
1. Under Choose Analysis, select Standard.

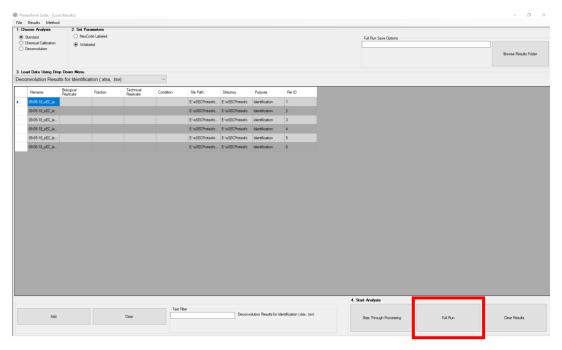


2. Under Set Parameters, select Unlabeled.



- 3. Click the Add button under the grid view under the Load Data Using Drop Down Menu for "Deconvolution Results for Identification (.xlsx, .tsv)". Select all .tsv files in the folder "less\_than\_50\_kDa" in the Vignettes folder in release 0.3.5 of Proteoform Suite. These are the results from deconvolution of MS1 spectra from raw files publicly available on the MassIVE platform (MSV000080365, <a href="mailto:ftp://mSV000080365@massive.ucsd.edu.">ftp://mSV000080365@massive.ucsd.edu.</a>).
- 4. Change the drop-down menu under the **Load Data Using Drop Down Menu** to "Protein Databases and PTM lists (.xml, .xml.gz, .fasta, .txt)". Click the Add button under the right grid view, and add all files in the folder "Database" in the Vignettes folder in release 0.3.5 of Proteoform Suite.





- 6. A message box will ask "Use presets for this Full Run?". Select Yes, then select the .xml method file in the folder "less\_than\_50\_kDa" in the Vignettes folder in release 0.3.5 of Proteoform Suite.
- 7. A message box will ask "Add files at the listed path if they still exist?" Select No.
- 8. A message box will ask "Choose a results folder for this Full Run?" If you select Yes, you can choose a folder on your computer to automatically save results.
- 9. The program will now automatically run. A message box will show when complete.
- 10. You can use the Results tab to navigate through the different results pages.

