SimianTools: A software suite for the interpretation of high throughput glycomics mass spectrometry data

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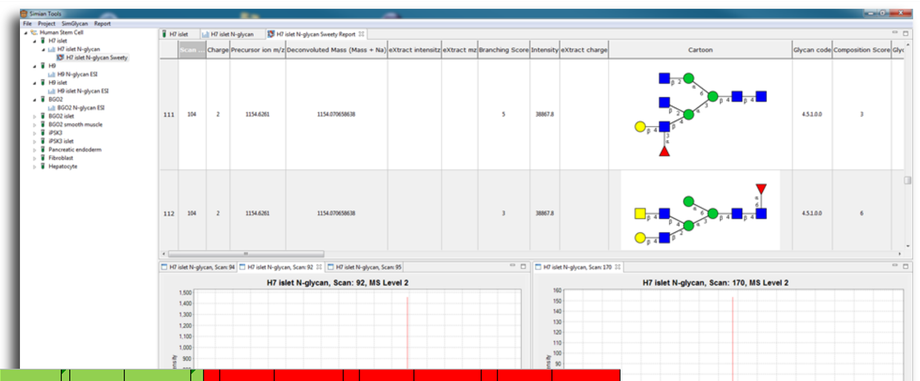
Introduction

Over the last decades the approaches for analyzing and identifying glycan structures using mass spectrometry have evolved from the study of single purified glycans towards the analysis of complex mixtures. However, most interpretation of the resulting datasets is still done manually. But comprehensive analysis of complex biological samples, producing several thousand mass spectra, consumes significant amount of time which consequently reduces the number of samples that can be analyzed. Therefore, development of high-throughput glycomics analysis software is crucial to efficiently tackle the large amount of data produced.

Samples

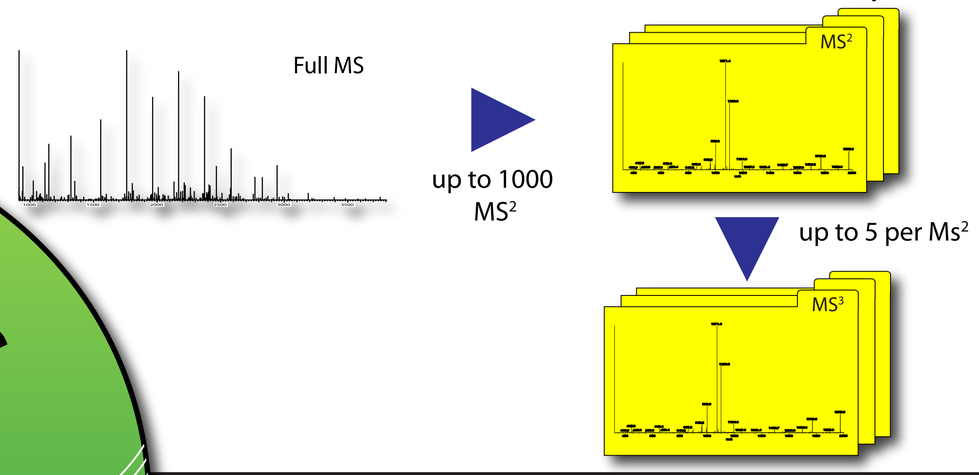
Glycans are released from their protein backbone, either enzymatically or chemically, and permethylated for enhanced sensitivity and structural determination. The mixture of free glycans is dissolved in 1 mM NaOH / 50 % methanol and infused directly into a linear ion trap mass spectrometer (Thermo LTQ Orbitrap Discovery) using a nanoelectrospray source. Glycan intact parent masses are determined by high resolution Full MS in the Orbitrap. Structural determinations are made by fragmentation of peaks 3 fold over baseline using collision induced dissociation (CID) in the ion trap.

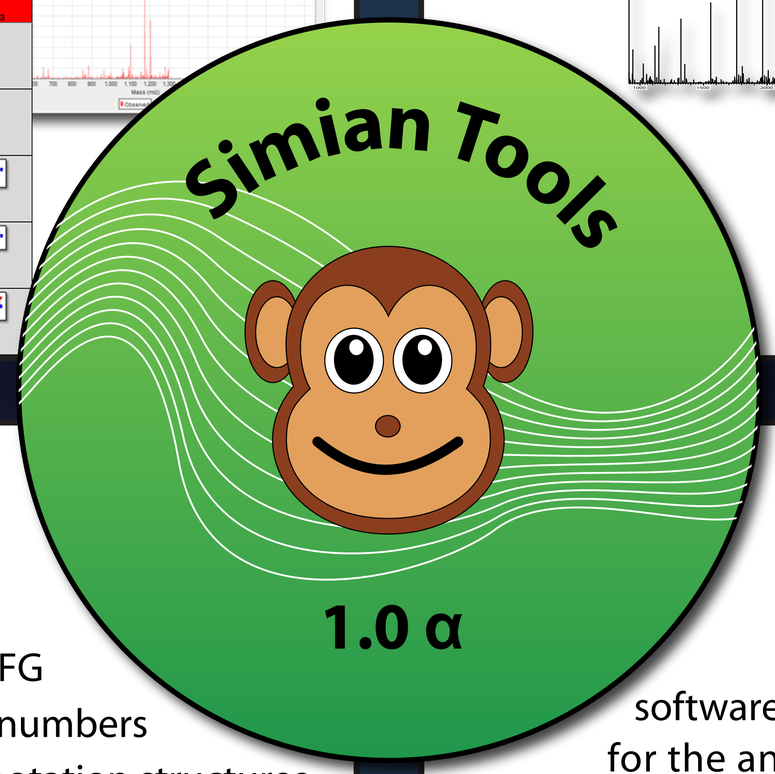
Simian Tools II



Mass spectrometry data

A typical sample can generate up to several thousand MS^n spectra that must be interpreted and annotated. Doing this manual can take up to several months. (Semi-)automatic methods are required.

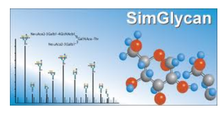




SimianTools I

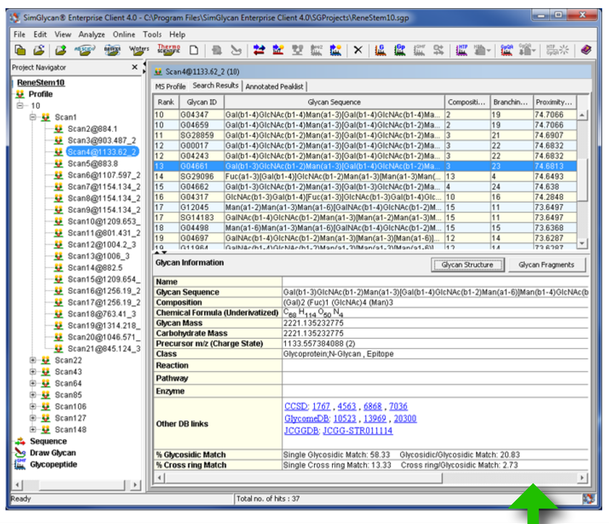
- Stand-alone JAVA program
- Import of SimGlycan™ data
- Enrichment of SimGlycan™ Annotation with CFG cartoons and structure/spectrum derived key numbers
- User defined selection and de-selection of annotation structures
- Spectrum viewer for MS^2 spectra
- Graphical user interface to organize the experiment, meta information and data
- Export to Excel
- Side by side comparison of several experiment from different MS or samples

SimGlycan™



http://www.premierbiosoft.com/glycan/

Commercial software application for the annotation of glycomics MS data. Similar to Sequest or Mascot, spectra are annotated with structures from a database. The program allows spectral features to be explored one by one and the annotations can be exported to a CSV file.

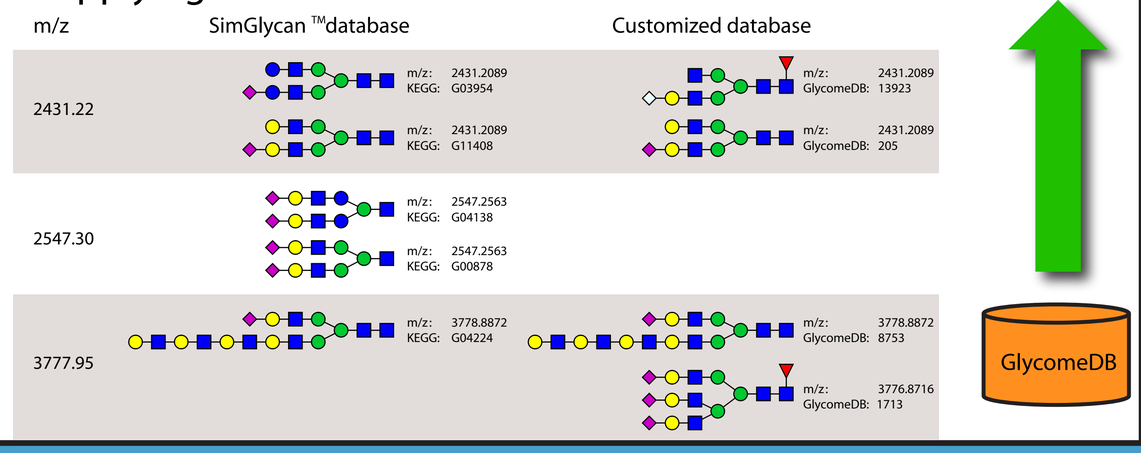


Next Steps

- Import and display of fragmentation information
- Full MS spectrum viewer with structure annotations
- MS^n spectrum viewer with fragment annotations
- Integration of conversion methodes from raw files to mzXML files
- On the fly generation of glycan cartoons and fragment cartoons
- Capture more meta information to make the data set MIRAGE (**M**inimum **I**nformation **R**equired for **A** **G**lycomics **E**xperiment) compliant
- Edit option for annotation data
- Improve Excel export to consider user settings in SimianTools
- Release version 1.0

SimGlycanDatabaseBot

The database Bot is a JAVA application that allows users to create customized SimGlycan™ databases by downloading structures from GlycomeDB (http://www.glycome-db.org) and applying user defined filters.



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