



Spectra processing, statistical analysis and functional integration using MetaboAnalyst 5.0

Jianguo (Jeff) Xia, Associate Professor

jeff.xia@mcgill.ca | www.xialab.ca

McGill University, Montreal, QC Canada June 19, 2023



Acknowledgements





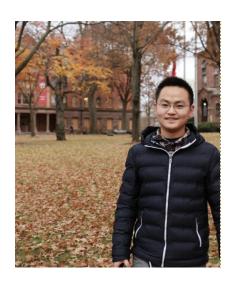








Your TAs







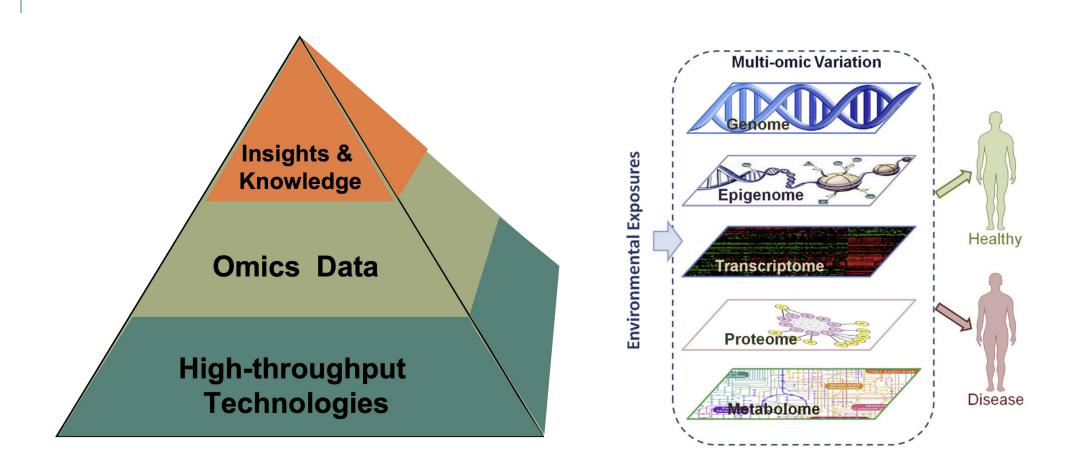
Qiang Jessica Yao

Schedule

```
Part I: 8:15 AM - 10:15 PM
  8:15 – 8:30: Opening lecture (Jeff)
   8:30 – 8:50: Section 1: LC-MS spectral processing (Qiang)
  8:50 – 9:15: Section 1: Hands on
   9:20 – 9:45: Section 2: Stats I – simple experimental design (Jessica)
   9:45 - 10:15: Section 2 Hands on
Part II: 10:30 AM – 12:30 PM
   10:30 - 10:50: Section 3: Functional analysis (Yao)
   10:50 - 11:10: Section 3: Hands on
   11:15 - 11:40: Section 4: Stats II - complex experimental design (Jessica)
   11:40 – 12:15: Section 4: Hands on
   12:15 – 12:30: Summary (Jeff)
```

A Gentle Introduction to Key Concepts in 'Omics Data Analysis

Omics & multi-omics era



Two distinct challenges

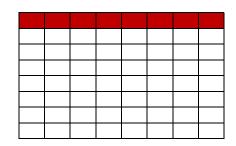
Size challenge (raw data)

- > Raw reads, spectra, images
- Large (GB ~TB)
- Large storage and computing resources

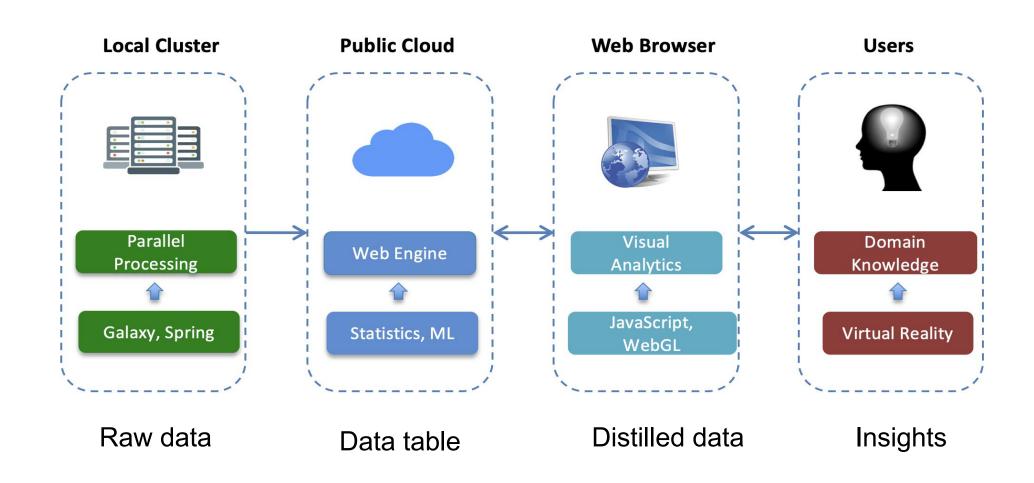
Complexity challenge (feature table)

- Feature table (abundance, intensities)
- Small (100s KB ~ MB)
- High-dimensional, missing values
- Data analysis starts here

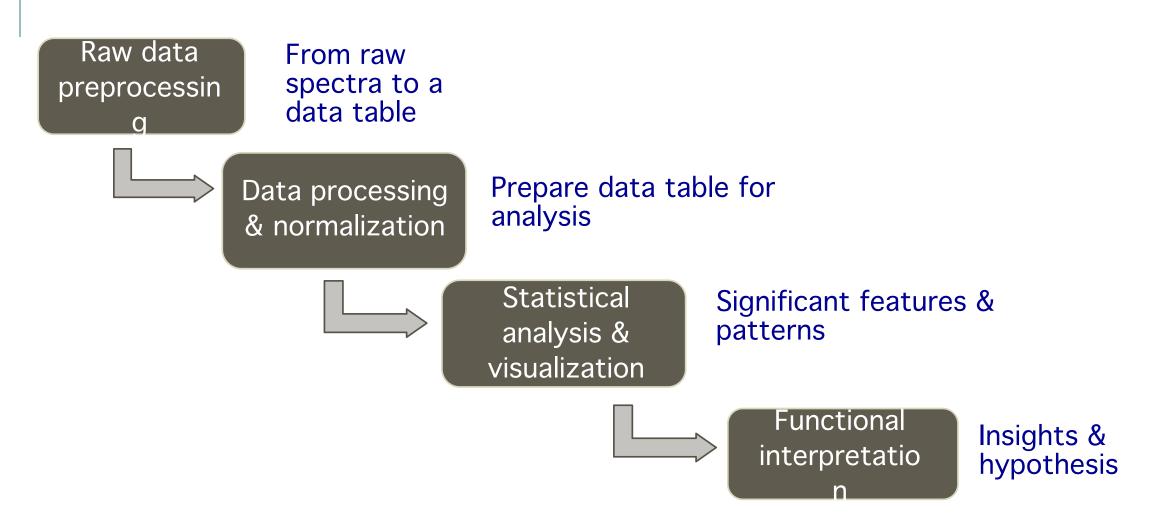




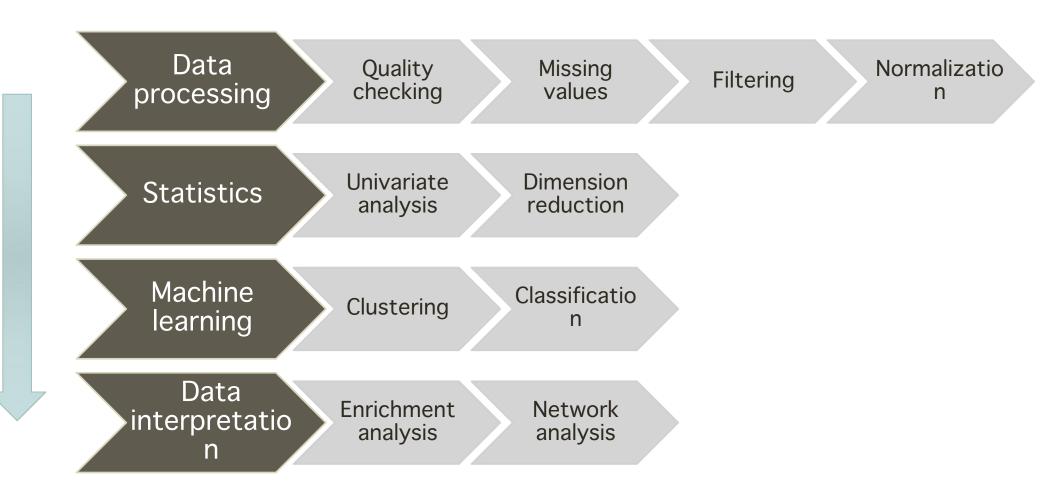
Omics data analytics framework



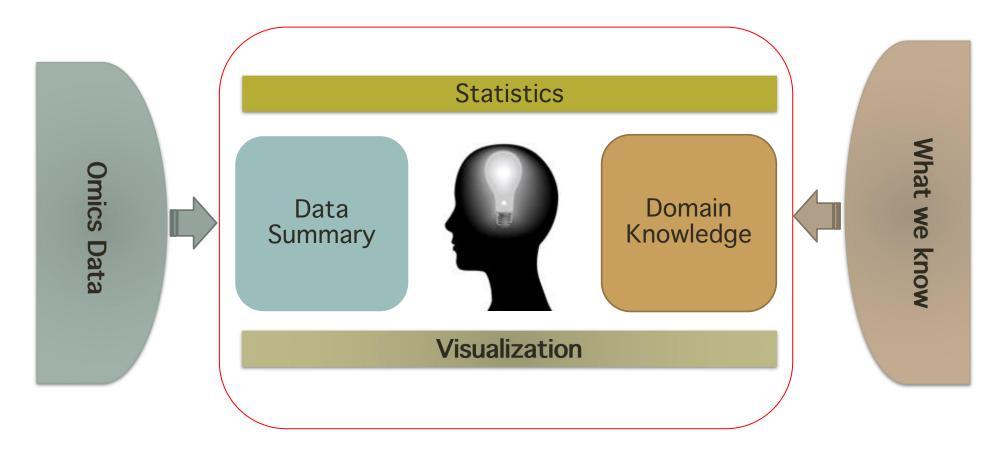
Omics Data Analysis (in a nutshell)



Common steps in omics workflow

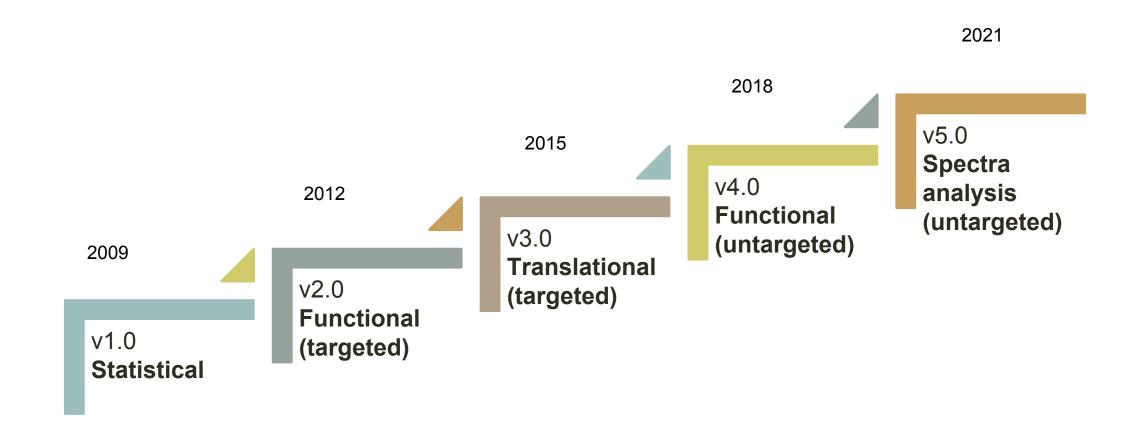


Don't forget biology & context

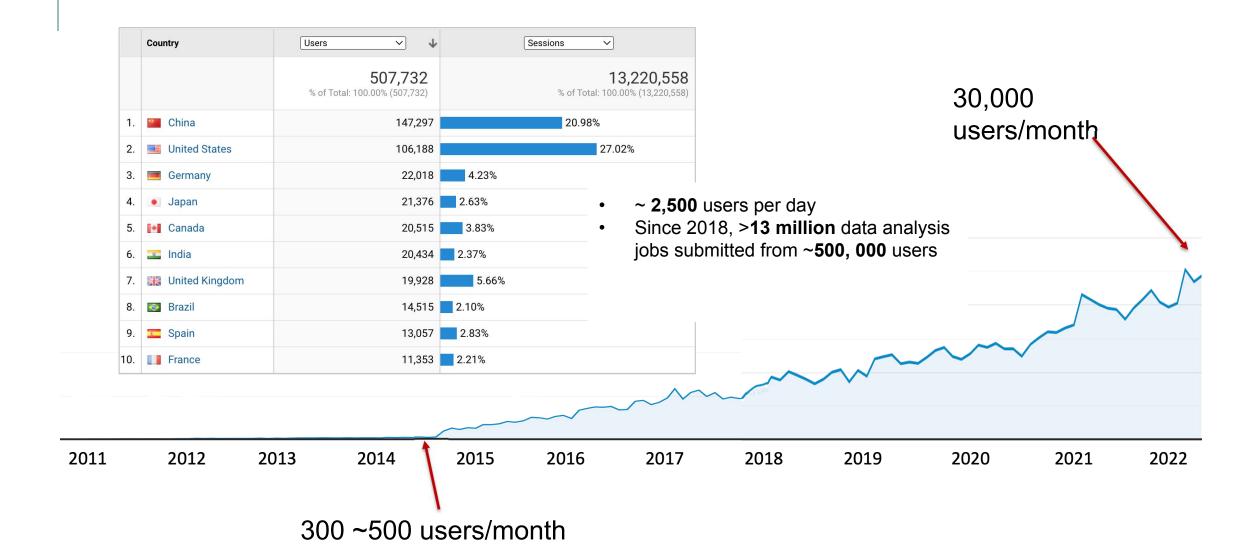


Put everything together and write your manuscript

Journey of MetaboAnalyst

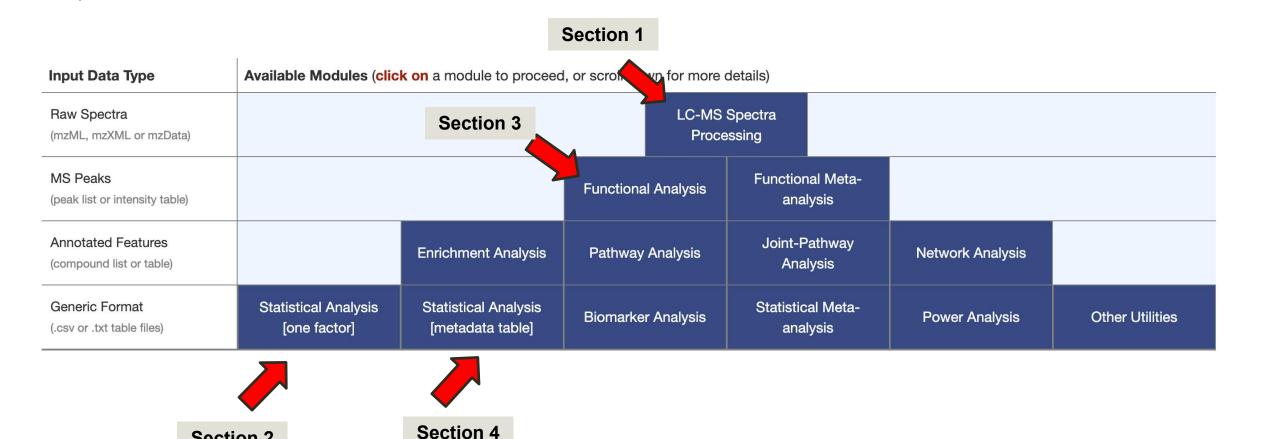


User Traffic (Google Analytics)

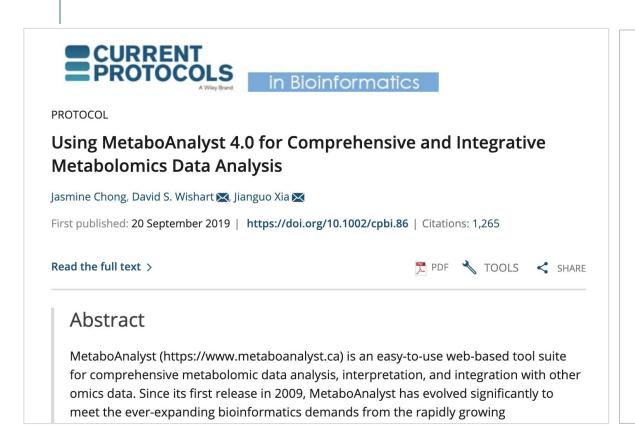


MetaboAnalyst 5.0 Modules

Section 2



Detailed protocols





Using MetaboAnalyst 5.0 for LC-HRMS spectra processing, multi-omics integration and covariate adjustment of global metabolomics data

Zhiqiang Pang¹, Guangyan Zhou¹, Jessica Ewald ©², Le Chang ©³, Orcun Hacariz¹, Niladri Basu² and Jianguo Xia © 1,3 ⋈

Liquid chromatography coupled with high-resolution mass spectrometry (LC-HRMS) has become a workhorse in global metabolomics studies with growing applications across biomedical and environmental sciences. However, outstanding bioinformatics challenges in terms of data processing, statistical analysis and functional interpretation remain critical barriers to the wider adoption of this technology. To help the user community overcome these barriers, we have made major updates to the well-established MetaboAnalyst platform (www.metaboanalyst.ca). This protocol extends the previous 2011 Nature Protocol by providing stepwise instructions on how to use MetaboAnalyst 5.0 to: optimize parameters for LC-HRMS spectra processing; obtain functional insights from peak list data; integrate metabolomics data with transcriptomics data or combine multiple metabolomics datasets; conduct exploratory statistical analysis with complex metadata. Parameter optimization may take ~2 h to complete depending on the server load, and the remaining three stages may be executed in ~60 min.

Logistics

MetaboAnalyst 5.0 Workshop Checklist

Wifi Account: Metabolomics 2023

Code: Falls2023

Instructions & Materials:

https://github.com/xia-lab/Metabolomics_2023

We have set up multiple servers:

- https://www.metaboanalyst.ca
- https://new.metaboanalyst.ca
- https://genap.metaboanalyst.ca

User Forum:

https://omicsforum.ca

Cautions & Recommendations

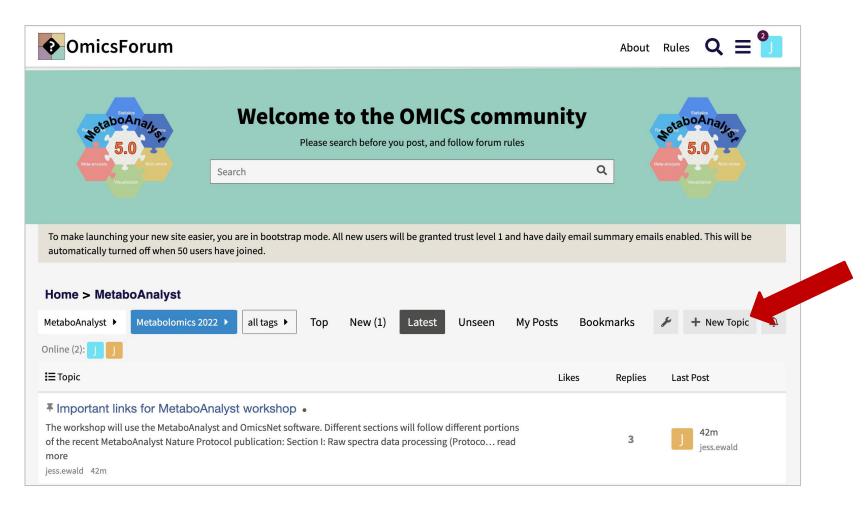
Page display may be slow due to bandwidth limitation in this room

- Be patient
- Do not open multiple tabs to MetaboAnalyst (results will overwrite each other!)
- Form a group and share computers (see next page)

Group forming

- > 2~3 people per group
 - Make new friends
 - Help each other & reduce stress
- Share laptops
 - One for displaying tutorial, and one for using MetaboAnalyst
 - Reduce bandwidth consumption

https://omicsforum.ca



- Current topics in MetaboAnalyst: ~700
- > Please search topics or open a new topic

Schedule

Part I: 8:15 AM - 10:15 PM

```
8:15 – 8:30: Opening lecture (Jeff)
  8:30 – 8:50: Section 1: LC-MS spectral processing (Qiang)
   8:50 - 9:15: Section 1: Hands on
   9:20 – 9:45: Section 2: Stats I – simple experimental design (Jessica)
   9:45 - 10:15: Section 2 Hands on
Part II: 10:30 AM – 12:30 PM
   10:30 – 10:50: Section 3: Functional analysis (Yao)
   10:50 - 11:10: Section 3: Hands on
   11:15 - 11:40: Section 4: Stats II - complex experimental design (Jessica)
   11:40 – 12:15: Section 4: Hands on
   12:15 – 12:30: Summary (Jeff)
```