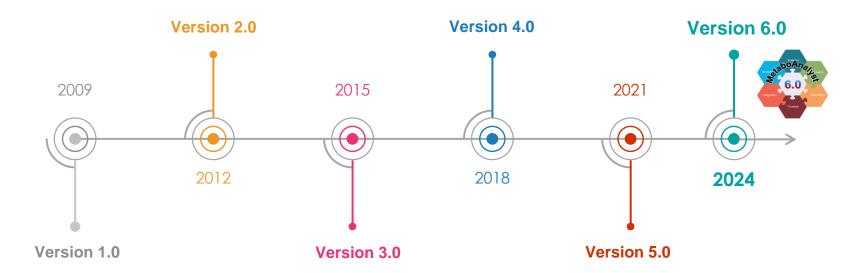


MetaboAnalyst 6.0

-- a unified platform for metabolomics data processing, analysis and interpretation

Overview of New Features

Our Roadmap



User Stats

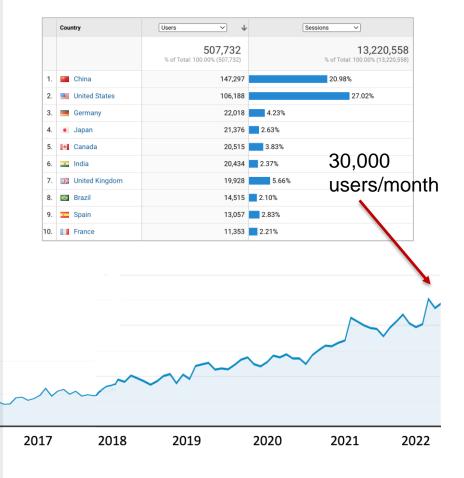
2011

2012

• ~ **3,000** users per day

2013

 Since 2018, >13 million data analysis jobs submitted from ~500, 000 users



300 ~500 users/month

2015

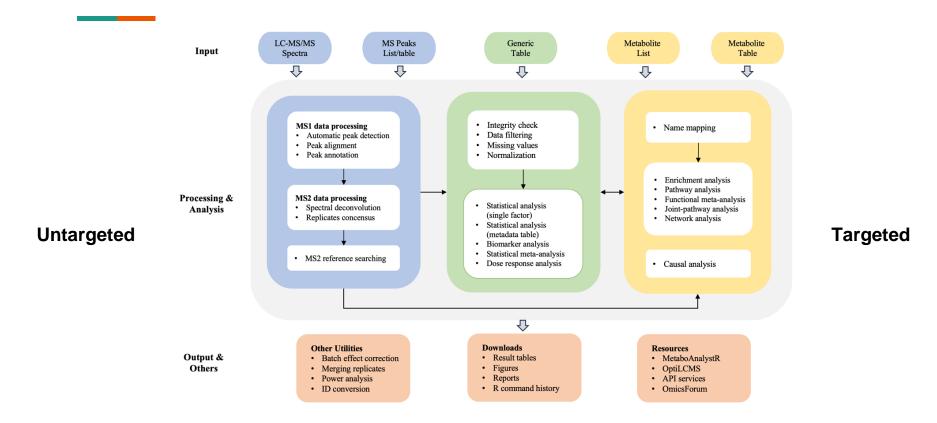
2016

2014

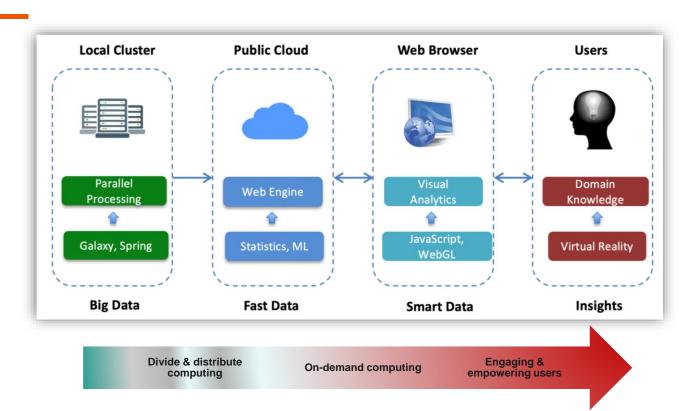
Main updates of all versions

Versions	Key Features	Details
1.0	Statistical analysis for targeted metabolomics	Focused on data processing, normalization and statistical analysis of metabolomics data;
2.0	Functional analysis for targeted metabolomics	Added metabolite set enrichment analysis (MSEA) and metabolic pathway analysis, as well as two-factor and time-series analyses.
3.0	Translational applications	Added biomarker analysis, power analysis, and joint-pathway analysis. Completely updated the web interface
4.0	Global metabolomics and reproducible analysis	Completely revamped web framework for scalable performance, with three new modules (MS peaks to pathways, biomarker meta-analysis, and network explorer), together with a companion R package (MetaboAnalystR)
5.0	Big data analytics - from raw spectra to functional insights	Leveraging local server - public cloud - user browsers to deliver end-to-end metabolomics data analysis, with support for spectral processing, comprehensive functional analysis and meta-analysis.
6.0	Unified workflow for raw spectra processing, statistical analysis and functional interpretation	Including raw spectra LC-MS/MS analysis (Asari algorithm and support for LC-MS2), covariate adjustment based on metadata table, enhanced functional analysis, dose response analysis and causal analysis, etc

Toward a unified workflow for metabolomics



Design Concept (under the hood)



Help Us Help You

Before you contact us or post on the forum,

- Have you read the Data Format and Tutorials?
 These resources provides detailed explanations for common questions received from users. Please first go through these resources as listed on the left bar.
- Have you tried our example data to see if the issue still exists?
 Most of the time, the issue is related to improper data format. Although we try to give informative error messages during data uploading, there are always exceptions. If our example works, download and examine our example datasets to get better idea
- Have you searched OmicsForum to see if similar questions asked before?
 OmicsForum (<u>www.omicsforum.ca</u>) is a newly launched platform for users to communicate and share experience when they are doing omics analysis with any tools from our team. FAQs of MetaboAnalyst are provided there and updated more frequently.
- Did you provide enough details so that the issue can be reproduced?
 Remote troubleshooting requires more information in order to figure out the exact cause of the issue. Please
 - Indicate which example data you used, or provide a copy of your data;
 - Document all steps leading to the issue. Sometimes screenshots may be necessary

Acknowledgements













New Tutorials for MetaboAnalyst 6.0

- Spectral Processing [LC-MS1 w/wo MS2]
- Peak Annotation [MS2-DDA/DIA]
- 3. Dose Response Analysis
- 4. Causal Analysis
- 5. Functional Analysis [LC-MS1 + MS2]

