

Supplemental Table 1. Open Source Data Analysis Tools

Supported Omics Data Types	Open Source Omics Analytic Tool	Web-Based	Computer-Based
Multi-omics	<ul style="list-style-type: none"> Galaxy usegalaxy.org <ul style="list-style-type: none"> In addition to genomics analyses, Galaxy is used for epigenomic, proteomic, transcriptomic, and metabolomic analyses Galaxy also supports the Galaxy ToolShed (toolshed.g2.bx.psu.edu) which is a repository of analytical tools and workflows developed by Galaxy community members 3Omics 3omics.cmdm.tw <ul style="list-style-type: none"> Visualization tool that assists with the integration of transcriptomic, proteomic and metabolomic data 	<p>X</p> <p>X</p>	
Genomic	<ul style="list-style-type: none"> shinyGASTool github.com/kordk/shinyGASTool <ul style="list-style-type: none"> Facilitates candidate gene association studies Accessible on Windows or requires R 		X
Epigenomic	<ul style="list-style-type: none"> EpiExplorer epiexplorer.mpi-inf.mpg.de <ul style="list-style-type: none"> Facilitates interactive exploration of large epigenomic datasets Facilitates filtering genomic regions for the identification and prioritization of candidate regions VisR visrsoftware.github.io <ul style="list-style-type: none"> Framework for analyzing sequencing data Accessible on Mac OS X, Linux and Windows Requires R 	X	X
Transcriptomic	<ul style="list-style-type: none"> Differential Expression Interactive Visual Analysis (DEIVA) github.com/Hypercubed/DEIVA <ul style="list-style-type: none"> Visual analytical tool Assists researchers to identify and locate genes ExpressionDB github.com/5c077/ExpressionDB/wiki <ul style="list-style-type: none"> Available for use online or in RStudio Facilitates exploring, visualizing and sharing GE data Accessible for RNA-seq or microarray data Shiny Transcriptome Analysis Resource Tool (START) App github.com/jminnier/STARTapp <ul style="list-style-type: none"> Facilitates RNA-seq upload, analysis and visualization Requires R VisR visrsoftware.github.io 	<p>X</p> <p>X</p>	<p>X</p> <p>X</p> <p>X</p>
Proteomic	<ul style="list-style-type: none"> MixProTool wsslearning.shinyapps.io/MixProTool <ul style="list-style-type: none"> Facilitates data analysis and visualization OpenMS openms.de <ul style="list-style-type: none"> Supported on Windows, Linux, and Mac OS systems Trans-Proteomic Pipeline tools.proteomecenter.org/software.php <ul style="list-style-type: none"> Available for use on Linux and Windows systems and can build on Mac OS X 	X	<p>X</p> <p>X</p>
Metabolomic	<ul style="list-style-type: none"> MetaboAnalyst 4.0 metaboanalyst.ca <ul style="list-style-type: none"> Free repository of tools for analyzing high-throughput metabolomics data Accepts data input from NMR, LC-MS, or GC-MS The companion R package, MetaboAnalystR, assists with reproducible data analysis OpenMS openms.de/metabolomics <ul style="list-style-type: none"> Facilitates metabolite quantification and identification XCMS Online xcmsonline.scripps.edu <ul style="list-style-type: none"> Facilitates statistical analysis of LC-MS and GC-MS data 	<p>X</p> <p>X</p>	<p>X</p> <p>X</p>
Microbiome	<ul style="list-style-type: none"> Integrated Microbiome Analysis Pipeline (iMAP) github.com/tmbuza/iMAP <ul style="list-style-type: none"> Facilitates data analysis, integration and visualization MicrobiomeAnalyst microbiomeanalyst.ca <ul style="list-style-type: none"> Facilitates data filtering, transformation, and analysis Facilitates interactive data visualization 	X	X

Abbreviations: NMR = nuclear magnetic resonance spectroscopy; LC-MS = liquid chromatography-mass spectrometry; GC-MS = gas chromatography-mass spectrometry