

mGWAS-Explorer Tutorial

-- explore results



Computer and Browser Requirements

- A personal computer with an Internet connection
- An up-to-date web browser that supports HTML5 with JavaScript enabled, such as Google Chrome (v50+), Firefox (3.0+), and Internet Explorer (9.0+)
- We recommend a ≥ 2 GHz CPU, 4 GB physical RAM with at least 2 GB free and a minimum of a 15-inch screen with a screen resolution of 1,280 × 800 or higher
- A mouse with scrolling support is required for network visualization

Starting up

- Go to the mGWAS-Explorer homepage (<https://www.mgwas.ca/mGWAS/faces/home.xhtml>)
- Click on the “**Search**” button to Search a SNP or metabolite
- Or “**Browse**” an individual mGWAS study

mGWAS-Explorer -- linking SNPs, genes, metabolites and diseases for functional insights

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Click an icon below to start

- SNPs**
 - Connect SNPs to genes, metabolites or diseases
- Metabolites**
 - Connect metabolites to SNPs, genes or diseases
- Genes**
 - Connect genes to SNPs, metabolites or diseases
- Search**
 - Search significant SNP-metabolite associations within 65 mGWAS
- Browse**
 - Browse individual mGWAS in Manhattan plot or network

Comprehensive Library
Comprehensive collection and deep annotation of results from [65 mGWAS publications](#). Support for searching a single item, exploring individual studies, and uploading a list.
Integrating with protein-protein interaction, SNP to disease, and metabolite to gene associations based on well-established databases.

Interactive Visualization
Users can easily browse and analyze SNP-based, gene-based, and metabolite-based networks in a systems-biology context.
Cross-phenotype association analysis can be performed to dissect shared genetic architecture between metabolism and disease from the SNP module.

Functional Profiling
Users can perform various functional analysis including SNP set enrichment analysis, gene set enrichment analysis, and metabolite set enrichment analysis.
Other features including topology analysis, searching different paths connecting SNPs, genes, metabolites, and diseases for hypothesis generation.

News & Updates

- Added support for metabolite-disease and gene-disease network (05/23/2022); [NEW](#)
- Redesigning home page (05/20/2022); [NEW](#)
- Updated tutorials and FAQs (05/13/2022); [NEW](#)
- Fixed issues with table browsing and table statistics (05/10/2022); [NEW](#)

Search a SNP or metabolite


- Users can search by either rsID or metabolite name
- Enter the search item (auto-complete is supported)
- Click “Search” button
- The results will display in the table.

Search by Enter search term
e.g., rs601338

Metabolite ↑↓	SNP ID ↑↓	Chr ↑↓	Position ↑↓	A1 ↑↓	A2 ↑↓	Beta ↑↓	P-value ↑↓	Consequence ↑↓	Nearest Gene ↑↓	PMID ↑↓
<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>
ADSGEGDFXAEggGVR*_ADpSGEGDFXAEggGVR*	rs601338	19	49206674	A	G	-0.0553	1.65e-20	stop_gained	FUT2	24816252
DSGEGDFXAEggGVR*_ADpSGEGDFXAEggGVR*	rs601338	19	49206674	A	G	-0.0443	1.26e-12	stop_gained	FUT2	24816252
ADpSGEGDFXAEggGVR	rs601338	19	49206674	A	G	0.0413	2.52e-11	stop_gained	FUT2	24816252

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Browse individual mGWAS study



mGWAS-Explorer -- linking SNPs, genes, metabolites and diseases for functional insights


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Explore mGWAS Studies

ID	Biofluid	Study	Publication	Sample Size	Population	Genotyping Platform	Metabolomics Platform	Cutoff Threshold	Explore
65b	Blood	Viñuela_medRxiv_2021_targeted	Genetic analysis of blood molecular phenotypes reveals regulatory networks affecting complex traits: a DIRECT study	3029	European	Illumina HumanCore array (HCE24 v1.0)	BIOCRATES (AbsoluteIDQ™ p150 kit)	5e-08	View
65a	Blood	Viñuela_medRxiv_2021_untargeted	Genetic analysis of blood molecular phenotypes reveals regulatory networks affecting complex traits: a DIRECT study	3029	European	Illumina HumanCore array (HCE24 v1.0)	Metabolon (LC-MS/MS)	5e-08	View
64	Blood	Qin_medRxiv_2020	Genome-wide association and Mendelian randomization analysis prioritizes bioactive metabolites with putative causal effects on common diseases	8738	European	Illumina genome-wide SNP arrays (HumanCoreExome BeadChip, Human610-Quad BeadChip and HumanOmniExpress)	Thermo Q Exactive Orbitrap	4.5e-12	View
63	Blood	Borges_UKBB_2020	Metabolic biomarkers in the UK Biobank measured by Nightingale Health 2020	500000	European	Affymetrix genome-wide genotyping array	Nightingale NMR	5e-08	View
62	Blood	Montasser_bioRxiv_2021	Leveraging a founder population to identify novel rare-population genetic determinants of lipidome	650	Old Order Amish founder population	Affymetrix 500K array	Agilent (6550 Q-TOF LC/MS)	5e-08	View
61	Mitochondria	Aboulmaouahib_HMG_2021	First mitochondrial genome wide association study with metabolomics	2718	European	Illumina MiSeq	BIOCRATES (AbsoluteIDQ™ p150 kit)	1e-05	View
60	Blood	Harshfield_BM_2021	Genome-wide analysis of blood lipid metabolites in over 5000 South Asians reveals biological insights at cardiometabolic disease loci	13814+5662	European+South Asian	Illumina 660-Quad, Illumina HumanOmniExpress, Affymetrix	Thermo Q Exactive Orbitrap	8.9e-10	View
59	Blood	Luo_KJL_2021	Genome-wide association study of serum metabolites in the African American Study of Kidney Disease and Hypertension	619	African American	Illumina Infinium Multi-Ethnic Global BeadChip array	Metabolon HD4	1e-10	View









Or click the “Resources” tab from the menu bar to enter into this module.

Overview

 **mGWAS-Explorer** -- linking SNPs, genes, metabolites and diseases for functional insights

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Explore mGWAS Studies

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Click the link to view the original publication.

Click View button to enter the 3D Manhattan plot visualization page.

3D Manhattan plot

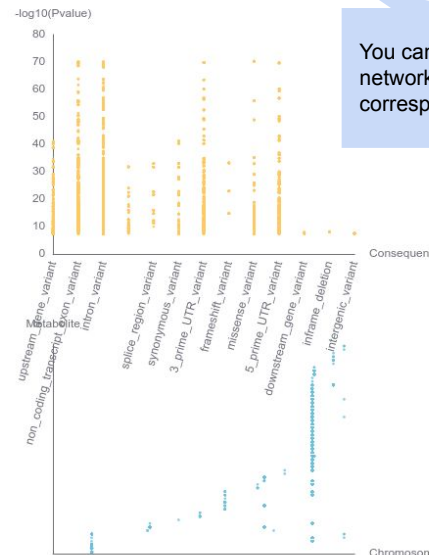
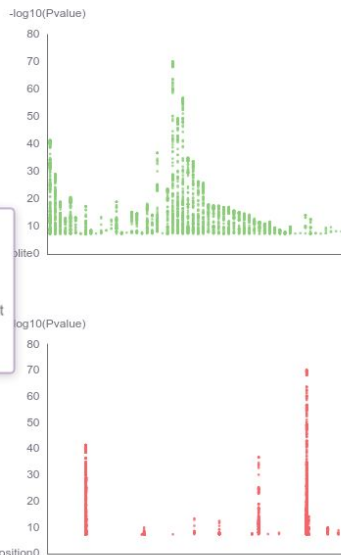
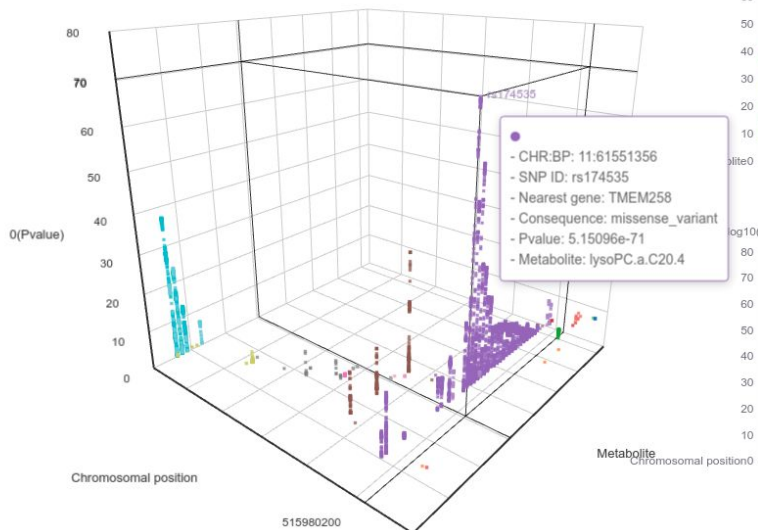
- Zoom in/out or rotate the 3D plot on the left to have a more focused view
- Mouseover on the dots to see detailed information

Home > Resources > 3D Manhattan Plot

Current Study: [Genetic analysis of blood molecular phenotypes reveals regulatory networks affecting complex traits: a DIRECT study](#)

[View Table](#)

[View Network](#)



You can view the table or network by clicking the corresponding button.

Table View

Home > Resources > 3D Manhattan Plot > Table

Metabolite ↑↓	SNP ID ↑↓	Chr ↑↓	Position ↑↓	A1 ↑↓	A2 ↑↓	Beta ↑↓	P-value ↑↓	Consequence ↑↓	Nearest Gene ↑↓
<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>	<input type="text"/>
lysoPC.a.C20.4	rs174535	11	61551356	C	T	-0.315567	5.15096e-71	missense_variant	TMEM258
lysoPC.a.C20.4	rs174530	11	61546592	G	A	-0.315155	7.98443e-71	non_coding_transcript_exon_variant	MYRF
lysoPC.a.C20.4	rs174536	11	61551927	C	A	-0.315062	8.80937e-71	non_coding_transcript_exon_variant	TMEM258
lysoPC.a.C20.4	rs174528	11	61543499	C	T	-0.314979	9.62401e-71	intron_variant	MYRF
lysoPC.a.C20.4	rs174529	11	61543961	C	T	-0.314917	1.02748e-70	intron_variant	MYRF
lysoPC.a.C20.4	rs174546	11	61569830	T	C	-0.314548	1.52057e-70	3_prime_UTR_variant	FADS1
lysoPC.a.C20.4	rs174554	11	61579463	G	A	-0.314472	1.64797e-70	intron_variant	FADS1
lysoPC.a.C20.4	rs35473591	11	61586328	CT	C	-0.314435	1.71315e-70	intron_variant	FADS1
lysoPC.a.C20.4	rs174568	11	61593816	T	C	-0.314391	1.79423e-70	3_prime_UTR_variant	FADS2
lysoPC.a.C20.4	rs3834458	11	61594920	C	CT	-0.314355	1.86558e-70	intron_variant	FADS2
lysoPC.a.C20.4	rs174545	11	61569306	G	C	-0.314333	1.90892e-70	3_prime_UTR_variant	FADS1
lysoPC.a.C20.4	rs174553	11	61575158	G	A	-0.314291	1.99488e-70	intron_variant	FADS1
lysoPC.a.C20.4	rs174551	11	61573684	C	T	-0.314235	2.11753e-70	5_prime_UTR_variant	FADS1
lysoPC.a.C20.4	rs174547	11	61570783	C	T	-0.31417	2.26777e-70	intron_variant	FADS1
lysoPC.a.C20.4	rs174550	11	61571478	C	T	-0.31417	2.26777e-70	5_prime_UTR_variant	FADS1

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Network Building

The screenshot shows a web interface for building networks. At the top, there is a breadcrumb trail: Resources > 3D Manhattan Plot > Table > Network Builder. Below this, there is a section titled "Tables" with a paragraph explaining that pair-wise tables and supporting information are listed, and users can click table names to download complete tables or browse (max. 1000 entries). A "Proceed" button is mentioned at the bottom. Below the text is a table with one row: "snp2met_study [SNP:1352, Metabolite: 59]" with a "Browse" button to its right. Below this is a section titled "Networks" with a paragraph explaining that the default network shows top SNP-metabolite associations based on p-value rankings. It also mentions that multiple isolated networks will be generated, with a big 'continent' and several small 'islands'. Below this text is a table with 4 columns: Networks, Nodes, Edges, and Topology. The table contains 7 rows of network data. At the bottom of the interface, there are two buttons: "Previous" and "Proceed". On the right side, there is a sidebar titled "Network Tools:" with a dropdown arrow. It contains several blue buttons: "Degree Filter", "Betweenness Filter", "Shortest Path Filter", "Manual Batch Filter", "Minimum Network", "Steiner Forest Network", and "Reset Network".

Tables

The pair-wise tables together with the supporting information are listed below. You can click the table name to download the complete table, or browse the tables (max. 1000 entries). Click the **Proceed** button at the bottom to directly explore the results in a network context.

snp2met_study [SNP:1352, Metabolite: 59]	Browse
--	------------------------

Networks

For better visualization, the default network only shows the top SNP-metabolite associations (edges) based on their p-value rankings (top 10,000 edges when the total number of edges are greater than 10,000). You may use the Network Tools to further reduce the size.

In some cases, multiple isolated networks will be generated, with a big 'continent' containing most of queries, and several small 'islands' containing one or a few queries. These networks will be available for visual analysis in the next step.

Networks	Nodes	Edges	Topology
mgwas1	635	1473	View
mgwas2	395	2689	View
mgwas3	281	397	View
mgwas4	41	42	View
mgwas5	18	17	View
mgwas6	13	13	View
mgwas7	5	4	View

[Previous](#) [Proceed](#)

Network Tools:

- Degree Filter
- Betweenness Filter
- Shortest Path Filter
- Manual Batch Filter
- Minimum Network
- Steiner Forest Network
- Reset Network

- The table results and network summaries will display on the page.
- The networks will be available for visual analytics in the next step.

Network viewer

The screenshot displays a network viewer interface with a central network graph and several side panels. The graph shows a complex network of nodes and edges, with three prominent hub nodes: L-Acetylcarnitine (bottom), Propionylcarnitine (top), and L-Carnitine (right). The nodes are represented by blue squares, and the edges are thin grey lines. The interface includes a top menu bar with various options like Network, Background, View, Layout, Node, Edge, Scope, and Download. On the left, there is a Node Explorer panel with a search bar and a table of nodes. On the right, there is a Function Explorer panel with a query input and a table of results. At the bottom right, there is a Module Explorer panel with an algorithm dropdown and a table of modules. The interface also features a toolbar with various icons for navigation and manipulation.

Top menu bar

Node explorer

Function explorer

Module explorer

Name	Degree	Betweenness	Input
<input type="checkbox"/> L-Acetylcarnitine	199	31496.33	
<input type="checkbox"/> L-Carnitine	116	13997.05	
<input type="checkbox"/> Propionylcarnitine	76	5921.12	
<input type="checkbox"/> 2-Octenoylcarni	6	835.5	
<input type="checkbox"/> rs1171617	3	298.5378	
<input type="checkbox"/> rs1171616	3	298.5378	
<input type="checkbox"/> rs1171614	3	298.5378	
<input type="checkbox"/> rs1171615	3	298.5378	
<input type="checkbox"/> rs72815843	3	298.5378	
<input type="checkbox"/> rs1171619	3	298.5378	
<input type="checkbox"/> rs1171620	3	298.5378	
<input type="checkbox"/> rs72334103	3	298.5378	
<input type="checkbox"/> rs146108230	3	298.5378	
<input type="checkbox"/> rs34931109	3	298.5378	
<input type="checkbox"/> rs34567437	3	298.5378	
<input type="checkbox"/> rs11006681	3	298.5378	
<input type="checkbox"/> rs1171618	3	298.5378	
<input type="checkbox"/> rs12356193	3	298.5378	
<input type="checkbox"/> rs11516732	3	298.5378	

Name	Hits	Pval	Color
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Module	Size	Pval	Color
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==The End==