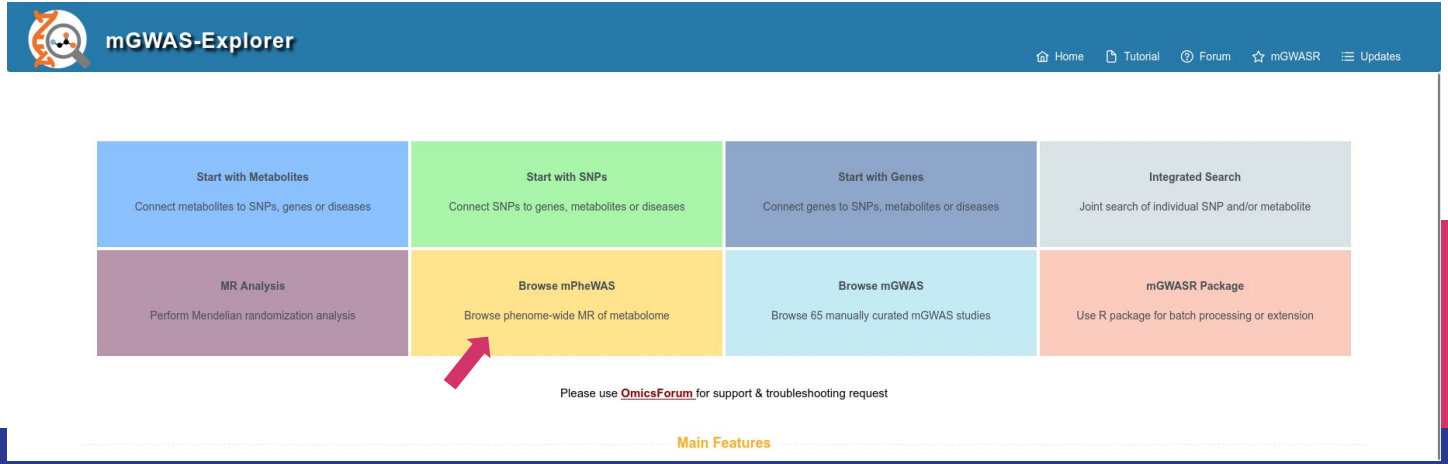
mGWAS-Explorer 2.0 Tutorial

–– Browse mPheWAS

Updated on 2023-06-07

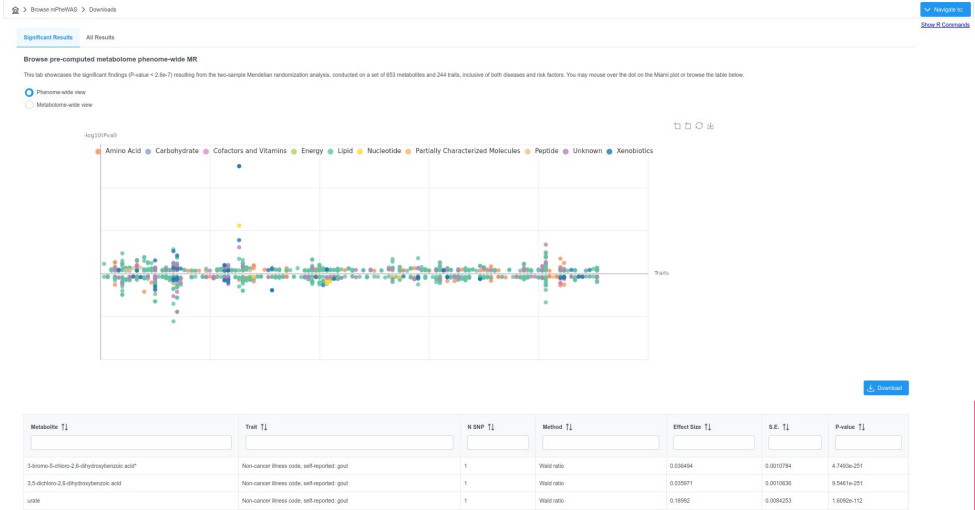
Introduction

- Welcome to the tutorial on the pre-computed Phenome-Wide MR Analysis module of mGWAS-Explorer 2.0.
- This feature allows for the systematic exploration of potential causal relationships between **825 metabolites** and **236 phenotypes**.
- This tutorial will guide you through how to use this module effectively.



The scope of pre-computed MR analysis

- Our Phenome-Wide MR analysis is based on five recent mGWAS, where we identified 1825 SNPs associated with 1016 metabolites.
- Post-selection criteria, we retain 1544 SNPs and 825 metabolites to perform a two-sample Mendelian Randomization (2SMR) analysis on 236 phenotypes.



Unpacking MR results

- In the user interface, you'll notice that the results are neatly organized under two separate tabs for easy navigation.
- The first tab is labeled "Significant Results," where you'll find only those associations that meet our significance threshold (table + plot).
- The second tab, labeled "All Results," provides a comprehensive view of all the associations analyzed, regardless of their significance level (table only).

Significant results

- The cutoff for a significant P value in our MR results is 2.57×10^{-7}.
- This stringent threshold is established by applying Bonferroni correction to adjust for multiple testing.

Enter your metabolite of interest into the search box.

Download

Click here to download the table.

Metabolite	Trait	N SNP	Method	Effect Size	S.E.	P-value
3-bromo-5-chloro-2,6-dihydroxybenzoic acid*	Non-cancer illness code, self-reported: gout	1	Wald ratio	0.036494	0.0010784	4.7493e-251
3,5-dichloro-2,6-dihydroxybenzoic acid	Non-cancer illness code, self-reported: gout	1	Wald ratio	0.035971	0.0010636	9.5461e-251
urate	Non-cancer illness code, self-reported: gout	1	Wald ratio	0.18992	0.0084253	1.6092e-112
nervonoylcarnitine (c24:1)*	Crohn's disease	3	Inverse variance weighted	-1.235	0.054936	6.3268e-112
x-11381	Inflammatory bowel disease	3	Inverse variance weighted	-0.82511	0.041097	1.1679e-89
nervonoylcarnitine (c24:1)*	Inflammatory bowel disease	3	Inverse variance weighted	-0.90932	0.045291	1.1679e-89
levulinoylcarnitine	Non-cancer illness code, self-reported: gout	5	Inverse variance weighted	0.017739	0.00094414	9.4124e-79
margaroylcarnitine (c17)*	Crohn's disease	2	Inverse variance weighted	-1.4977	0.084083	5.738e-71
x-11381	Non-cancer illness code, self-reported: asthma	3	Inverse variance weighted	0.047816	0.0027428	4.6252e-68
pc ae c36:3	Non-cancer illness code, self-reported: asthma	8	Inverse variance weighted	-0.021023	0.0012098	1.2411e-67
margaroylcarnitine (c17)*	Height	2	Inverse variance weighted	-0.34545	0.020239	2.5643e-65
linoleoylcarnitine (c18:2)*	Height	2	Inverse variance weighted	-0.28003	0.016406	2.5643e-65
x-24241	Non-cancer illness code, self-reported: gout	6	Inverse variance weighted	0.005736	0.00034507	4.7689e-62
pc ae c34:2	Crohn's disease	5	Inverse variance weighted	0.60583	0.038069	5.0584e-57
margaroylcarnitine (c17)*	Inflammatory bowel disease	2	Inverse variance weighted	-1.0991	0.06922	8.9079e-57

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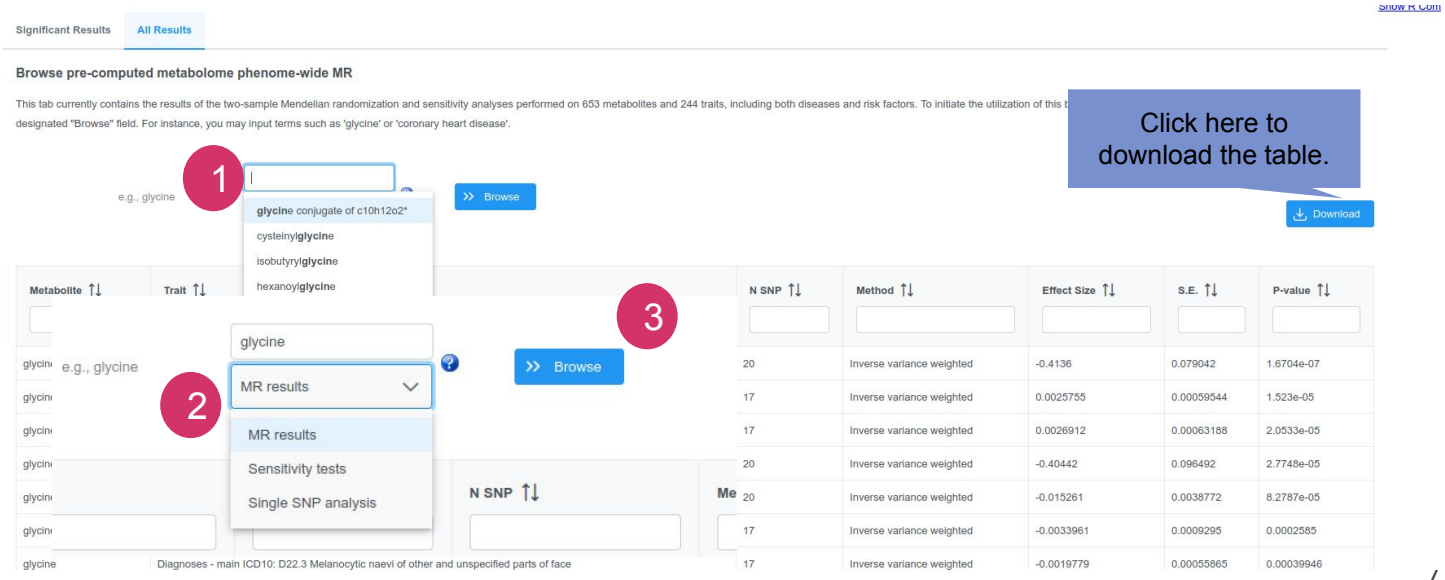
Interpreting the Miami plot

Switch between phenome-wide or metabolome-wide view.

- The Miami plot provides a clear visual summary of the phenome-wide Mendelian randomization results.
- Traits are sorted according to biologically meaningful categories on the x-axis.
- The y-axis represents the -$\log_{10}$ P value of the MR results.
- Positive and negative effect MR results are depicted on the top and bottom half of the plot respectively.
- The color coding indicates different metabolite super pathways.
- Hover your mouse over any point to display more detailed information.

Browse all results

- To start exploring all the results, simply click on the tab labeled "All Results." Once there, you will see a search box. This is where you can enter the name of a metabolite or trait that you're interested in. For example, you could type in 'glycine' or 'coronary heart disease.'
- Below the search box, you'll see options to select between "MR results," "Sensitivity tests," or "Single SNP analysis." Choose the one that is most relevant to your research needs. Once you've made your selection, click on the "Browse" button to start viewing the data.



Conclusion - utilizing pre-computed phenome-wide MR

- Phenome-Wide MR analysis is a powerful tool that allows for the systematic investigation of potential causal relationships between metabolites and phenotypes.
- We invite you to use mGWAS-Explorer 2.0 to explore these pre-computed results and apply these insights to your research.
- Your feedback and questions are invaluable to us. If you encounter any issues, have suggestions for improvements, or simply want to share your success stories with mGWAS-Explorer 2.0, please do not hesitate to post on our OmicsForum: https://omicsforum.ca/c/mgwas-explorer/12