

Generate Manhattan plot from GAPIT output

In order to better understand the output of GAPIT an application was created to visualize and integrate the results.

The application can be found at: <http://icci-2:9100/manhattan/>

You need to be connected to the TAU network, so if you work from home or with Wi-Fi you need to connect with VPN.

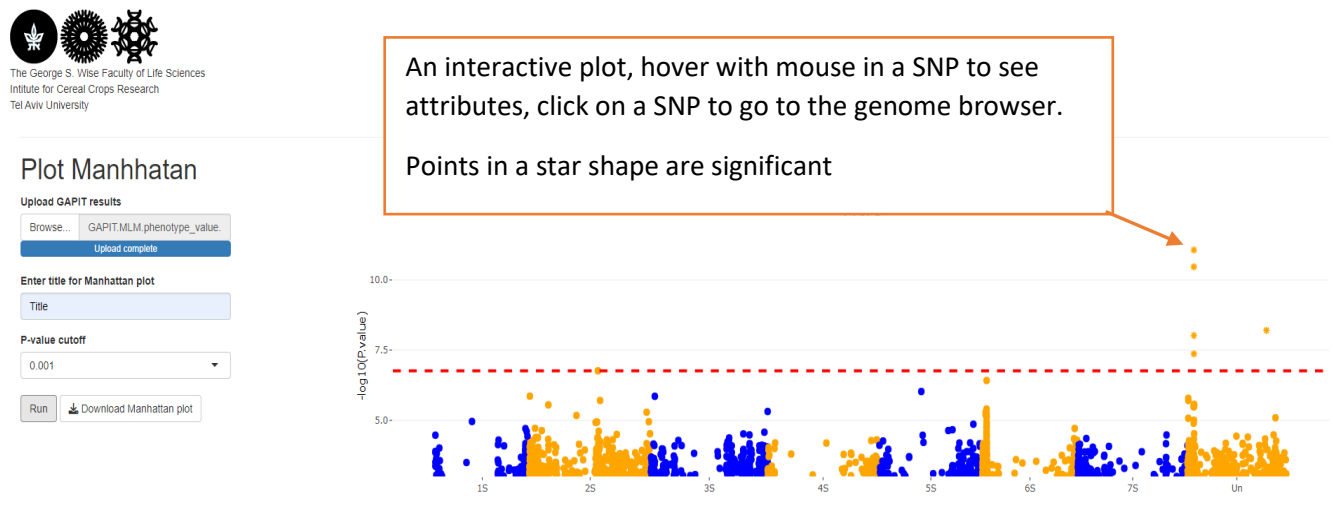
It is not recommended to upload files from home because it could take a long time.

How to use the application?

1. Create a Manhattan plot

The screenshot shows the 'Plot Manhattan' web application interface. At the top, there are three logos and the text 'The George S. Wise Faculty of Life Sciences, Institute for Cereal Crops Research, Tel Aviv University'. The main heading is 'Plot Manhhatan'. Below it, there is a section 'Upload GAPIT results' with a 'Browse...' button and a 'No file selected' status. To the left of this section, a callout box says 'Add title (optional)' with an arrow pointing to the 'Enter title for Manhattan plot' input field. To the right, a callout box says 'Select GAPIT results (wait for the 'Upload complete')' with an arrow pointing to the 'Browse...' button. Below the title field, there is a 'P-value cutoff' dropdown menu set to '0.001'. To the right of this, a callout box says 'Select P-value cutoff (Will present only data above this value)' with an arrow pointing to the dropdown. At the bottom, there are 'Run' and 'Download Manhattan plot' buttons. A callout box below these buttons says 'Execute (can take some time)' with an arrow pointing to the 'Run' button.

Results:



Plot Manhattan

Upload GAPIT results

Browse... GAPIT.MLM.phenotype_value
Upload complete

Enter title for Manhattan plot

Title

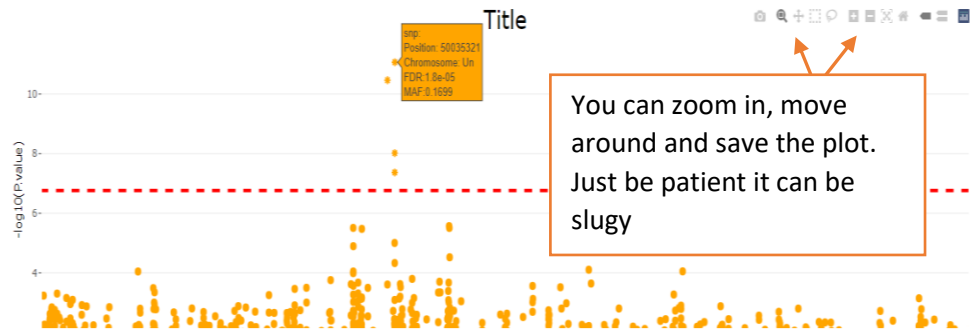
P-value cutoff

0.01

Run

Download Manhattan plot

Save as HTML which will keep the interactive features



You can zoom in, move around and save the plot. Just be patient it can be slugy

2. Plot phenotype data

In this section we will create a table of SNPs and plot the distribution of the phenotype data for each genotype. Use the same phenotypic table you used for the GWAS analysis.

Plot Phenotype

Upload phenotype table

Browse... No file selected

Upload phenotypes table

Genomic data:

☒ LD pruned

☐ All SNPs

Choose the genomic data you used in the GWAS analysis

Choose chromosome

All

If you focused on one Chromosome

Choose start position

0

Choose end position

1000000

You can choose to focus on a specific range (use this when loading large number of SNPs, i.e., when working with full data)

Choose geno-pheno plot type

☒ Violin

☐ Boxplot

Type of plot (interactive, can be switched after the plot was created)

Enter Y axis label (phenotypic measurement)

Enter title for geno-pheno plot

Enter plot title and/or y-axis label (optional)

Run

Download plot

Download geno-pheno table

Execute (can take some time)

Error: An error has occurred. Check your logs or contact the app author for clarification.

The result is a table with each SNP in the range selected and its GWAS results, you can sort the table by a column by clicking on the column name.
Usually you want to sort by the 'FDR_Adjusted_P.values' column to see the most significant SNPs

Show 10 entries

Search:

	pos	alleles	chrom	strand	SNP	P.value	maf	nobs	Rsquare.of.Model.without.SNP	Rsquare.of.Model.with.SNP	FDR_Adjusted_P.values	effect
1	1773	T/C	3S	+	S3S_1773	0.73269559738865	0.298543689320388	206	0.0489006371264074	0.0494486654349885	0.999085351007696	0.13864470419421
2	1789	T/A	3S	+	S3S_1789	0.156715592694318	0.0776699029126213	206	0.0489006371264074	0.0583577645492934	0.997996859883821	0.816086963643247
3	3663	A/G	UN	+	SUN_3663	0.453791739641032	0.0752427184466019	206	0.0489006371264074	0.051539999616421	0.997996859883821	-0.342269117654759
4	3674	G/A	UN	+	SUN_3674	0.10814892674416	0.138349514563107	206	0.0489006371264074	0.29254	0.997996859883821	0.568685578508412
5	3880	G/A	UN	+	SUN_3880	0.486363563540556	0.393203883495146	206	0.0489006371264074	0.83199	0.997996859883821	0.296814681582469
6	4210	G/C	UN	+	SUN_4210	0.128594834382299	0.0752427184466019	206	0.0489006371264074	0.55673	0.997996859883821	0.730683256726352
7	4282	T/A	UN	+	SUN_4282	0.936068417215576	0.169902912621359	206	0.0489006371264074	0.0489308570648156	0.999917753091038	0.0297736987318021
8	6256	G/A	UN	+	SUN_6256	0.238972418224612	0.0970873786407767	206	0.0489006371264074	0.0554359265584409	0.997996859883821	0.635398447321196
9	7099	C/T	6S	+	S6S_7099	0.957792641258053	0.133495145631068	206	0.0489006371264074	0.0489137826906644	0.999917753091038	-0.0225442410013266
10	7456	A/G	6S	+	S6S_7456	0.603145596240493	0.0703883495145631	206	0.0489006371264074	0.0501709365891894	0.998454777980995	-0.322317759388877

Showing 1 to 10 of 9.573 entries

Previous

1

2

3

4

5

...

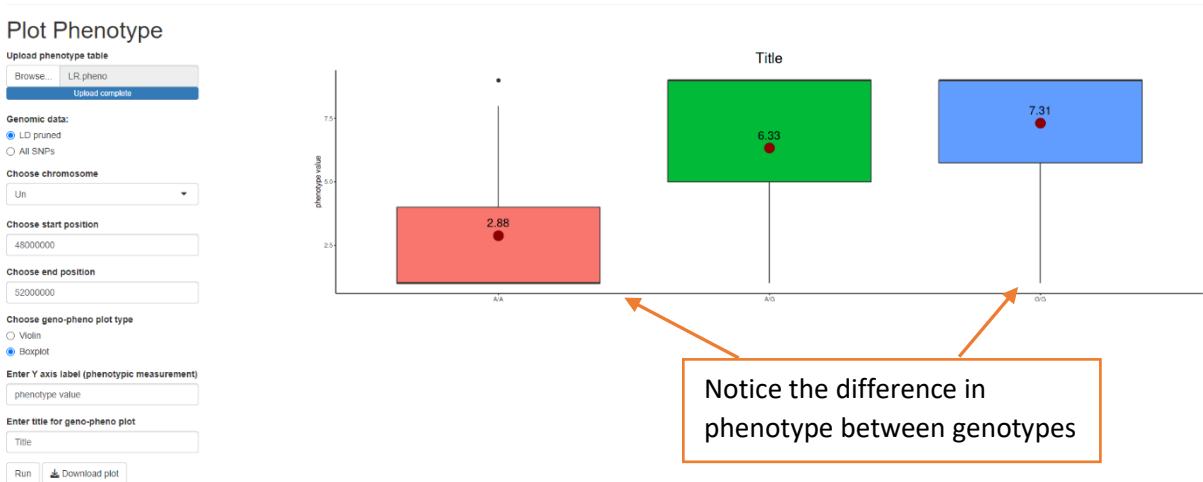
958

Next

Sort by significant

Then select the row of the SNP you want and a plot will show on top, with the phenotype values for each genotype, you can select different row and the plot will change accordingly.

Also, you can change the type of plot between 'violin' and 'boxplot' and download the table and plot.



3. Plot geographical location

When selecting a SNP, another table is created that shows the SNP, accession, genotype, phenotype and location for each accession and for the chosen SNP:

Show entries Search:

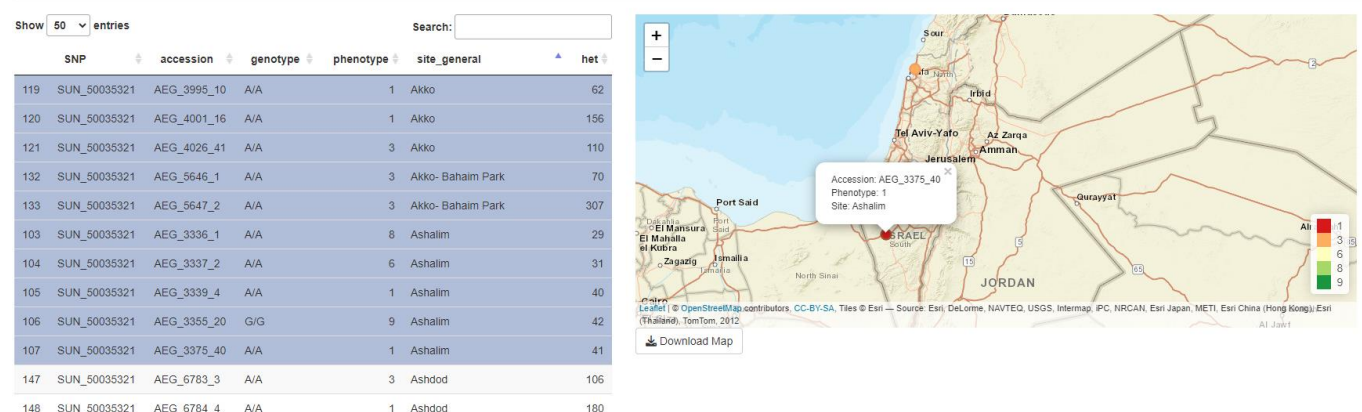
	SNP	accession	genotype	phenotype	site_general	het
12	SUN_50035321	AEG_1187_8	G/G	9	Mash'abbe Sade	459
14	SUN_50035321	AEG_1207_3	G/G	9	Tel Mond	405
17	SUN_50035321	AEG_1264_10	G/G	9	Qiryat Ono	100
31	SUN_50035321	AEG_1358_4	A/A	9	Giv'at Brenner	67
33	SUN_50035321	AEG_1409_4	G/G	9	Re'im	54
43	SUN_50035321	AEG_1515_7	G/G	9	Kefar Yona	205
68	SUN_50035321	AEG_2247_4	A/A	9	Nahal Liman	275
72	SUN_50035321	AEG_2265_22	G/G	9	Nahal Liman	533
76	SUN_50035321	AEG_2341_4	A/A	9	Shomerat	64
82	SUN_50035321	AEG_25_14	G/G	9		
87	SUN_50035321	AEG_284_44	G/G	9	Shedema	41

You can search, sort and choose how many rows to display and also download the table.

By selecting rows from the table, a map will be shown and the location of the selected accessions will be visible and will be colored by the value of the phenotype, you can hover or click on a point for more information.

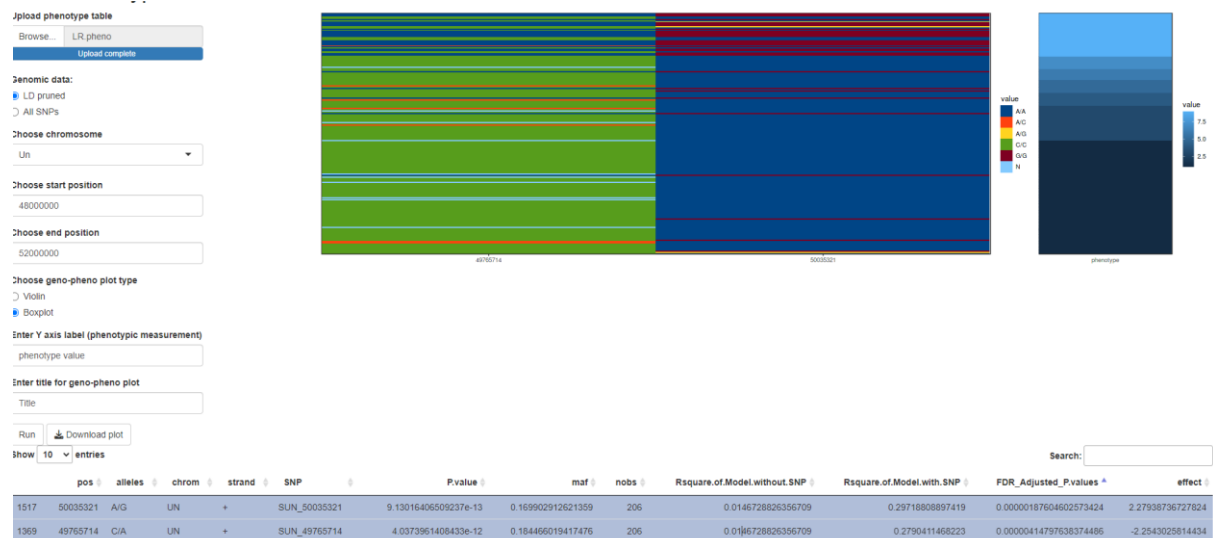
You can also download the map to PDF.

In this example I have selected all accession collected from Akko and Ashalim:



4. Compare SNPs

If you select 2 or more rows the plot will change to a comparison of genotypes and phenotypic value between the selected SNPs:



Notice the connection between genotype A/A for the SNP on the left (second in the table) with genotype G/G for the SNP on the right (first in table), this could point to the LD between the SNPs. Not really sure what this plot is good for, but it sure is nice.

The table that was used for the map is now showing the genotypes of the selected SNPs:

	accession	49765714	50035321
204	AE_337	A/A	G/G
203	AE_335	A/A	G/G
202	AE_125	A/A	G/G
201	AE_124	C/C	A/A
200	AE_121	C/C	A/A
199	AEG_9750_1	A/A	G/G
198	AEG_9748_13	C/C	A/A
197	AEG_9744_9	A/A	A/G
196	AEG_9742_7	A/A	G/G
195	AEG_9583_0	A/A	G/G
194	AEG_9577_1	A/A	G/G
193	AEG_8771_1	C/C	A/G
192	AEG_8719_24	C/C	A/A