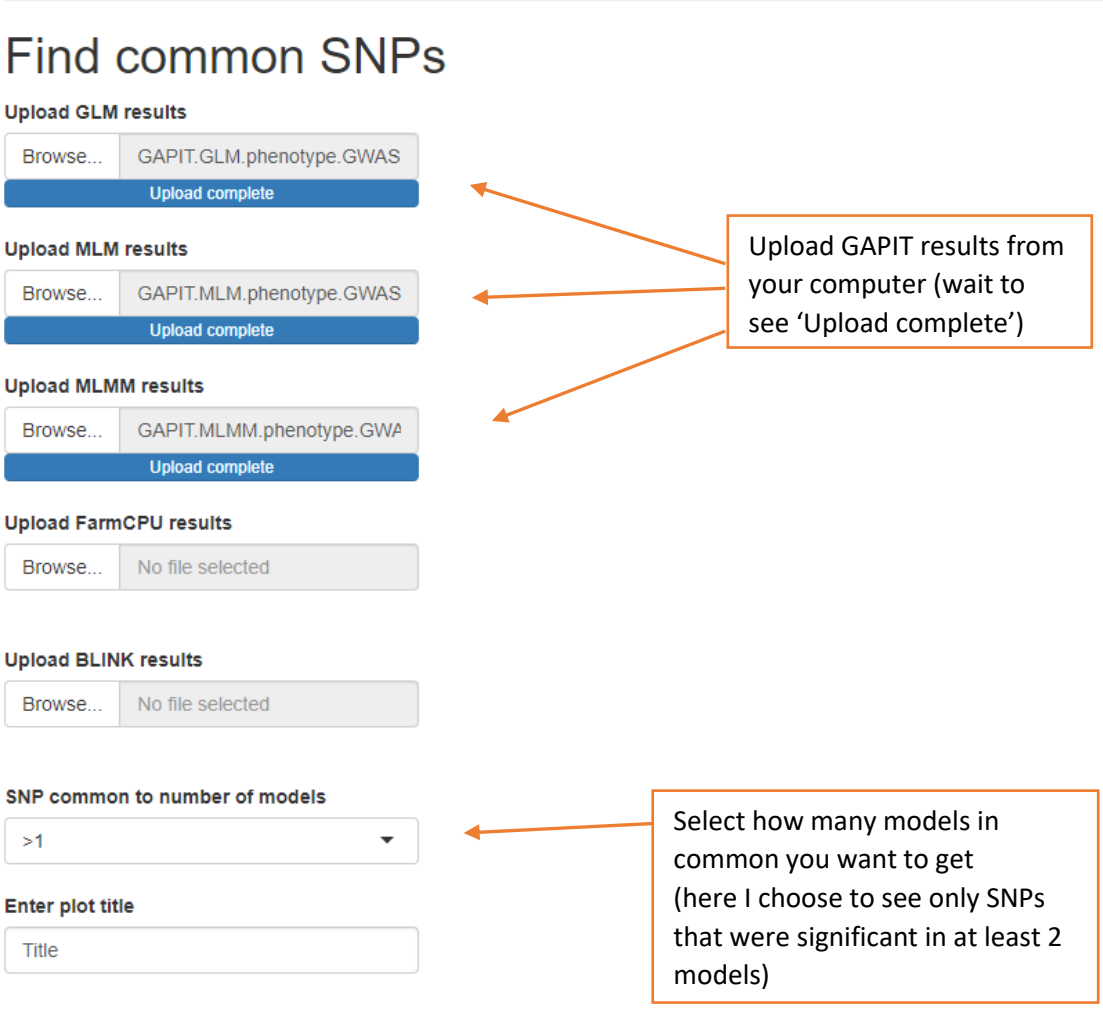
Compare significant SNP from different GAPIT models

Often, we run GAPIT with several models, so one question we want to know is if the same SNPs turn out significant in the different models.
An application that takes GAPIT results of different models (usually of the same run) and plot the common significant SNPs for n models can be found at: http://icci-2:9100/manhattan/

How to use the application?

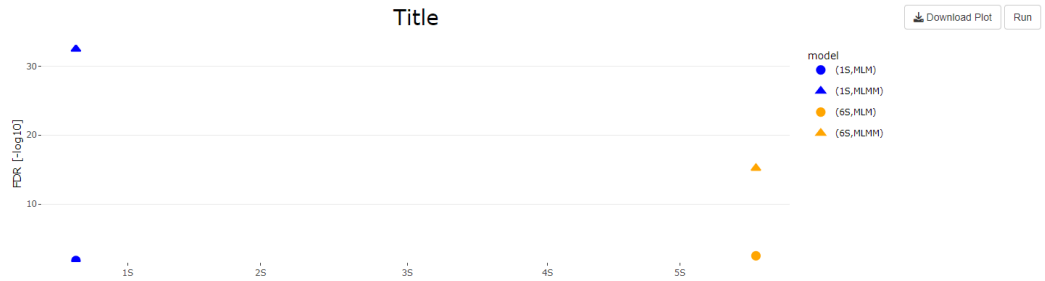
You need to be connected to the TAU network and have csv results files of GAPIT on your computer, in this example I used only 3 models out of the 5 possible.



Then select 'run' to get the plot.

The output is a kind of Manhattan plot that annotate each model with a different shape, in the output below you can see that there are two SNPs that are common to two models, one on chromosome one and another on chromosome six, in both cases the models are only MLM and MLMM.

The plot is interactive, you can click on a point and it will open the genome browser at the location of the SNP. You can also save the plot.



Show 10 entries

Search:

	Position	SNP	Chromosome	P.value	maf	nobs	Rsquare.of.Model.without.SNP	Rsquare.of.Model.with.SNP	FDR_Adjusted_P.values	effect	model	N_models
8	41441094	S1S_41441094	1S	7.55316855053631e-9	0.311224489795918	196	0.377530859312512	0.495469675566698	0.00865534341187384	1.5498264725923	MLM	2
9	41441094	S1S_41441094	1S	1.17324443489857e-39	0.311224489795918	196			2.410756853452e-33		MLMM	2
13	78807624	S6S_78807624	6S	1.07939747854242e-8	0.0663265306122449	196	0.377530859312512	0.49280279173239	0.00865534341187384	-2.21792210163606	MLM	2
14	78807624	S6S_78807624	6S	6.15820265555351e-22	0.0663265306122449	196			6.32686966808647e-16		MLMM	2