



GenoTypeMapper

v.1.1

- A very small introduction -

-





Dear users,

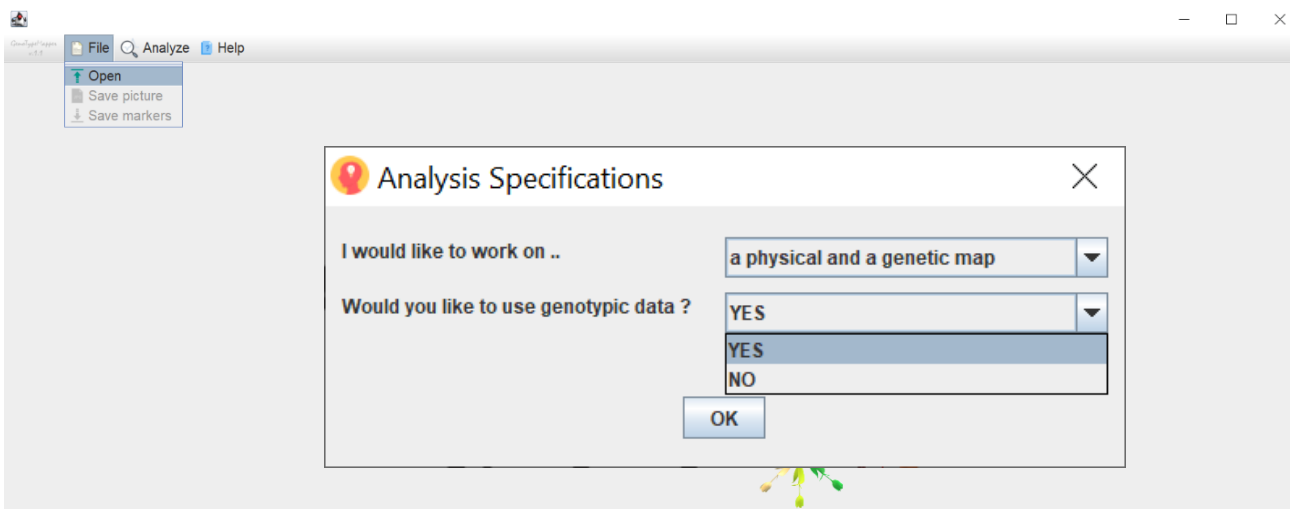
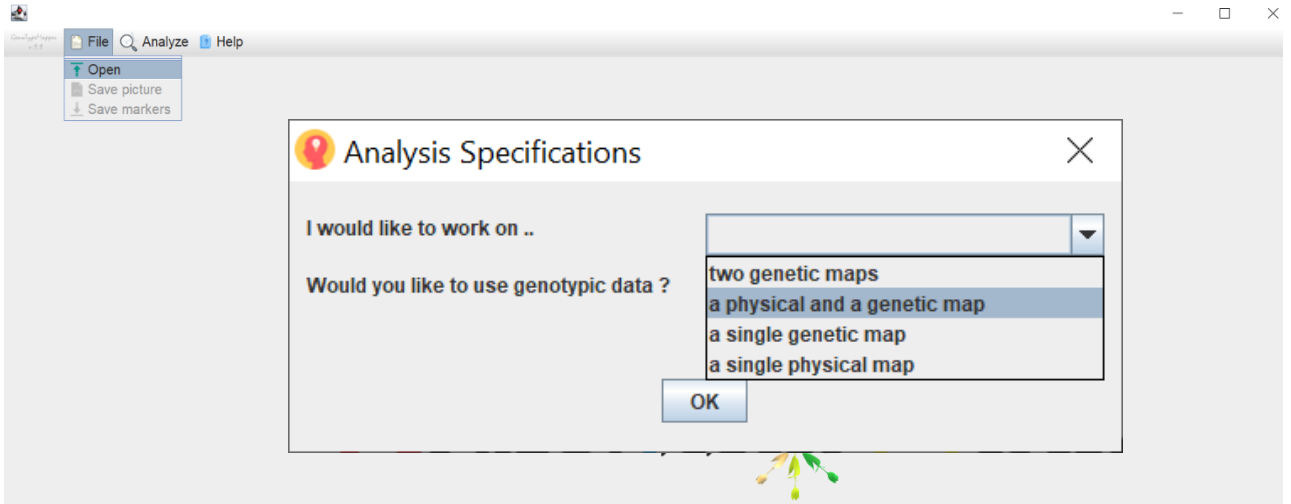
this little tutorial is intended to show how to use genotype mapper in an appropriate mapper. Testdata and example files are provided online and more detailed information about the use and purpose of this software can be obtained in our publication. Please do not hesitate to contact us personally if you have any questions.

With best regards,

Mathieu and Co-authors



1. Select „File“ and „Open“. Then select the type of map(s) and if you would like to analyse genotypic data or not.



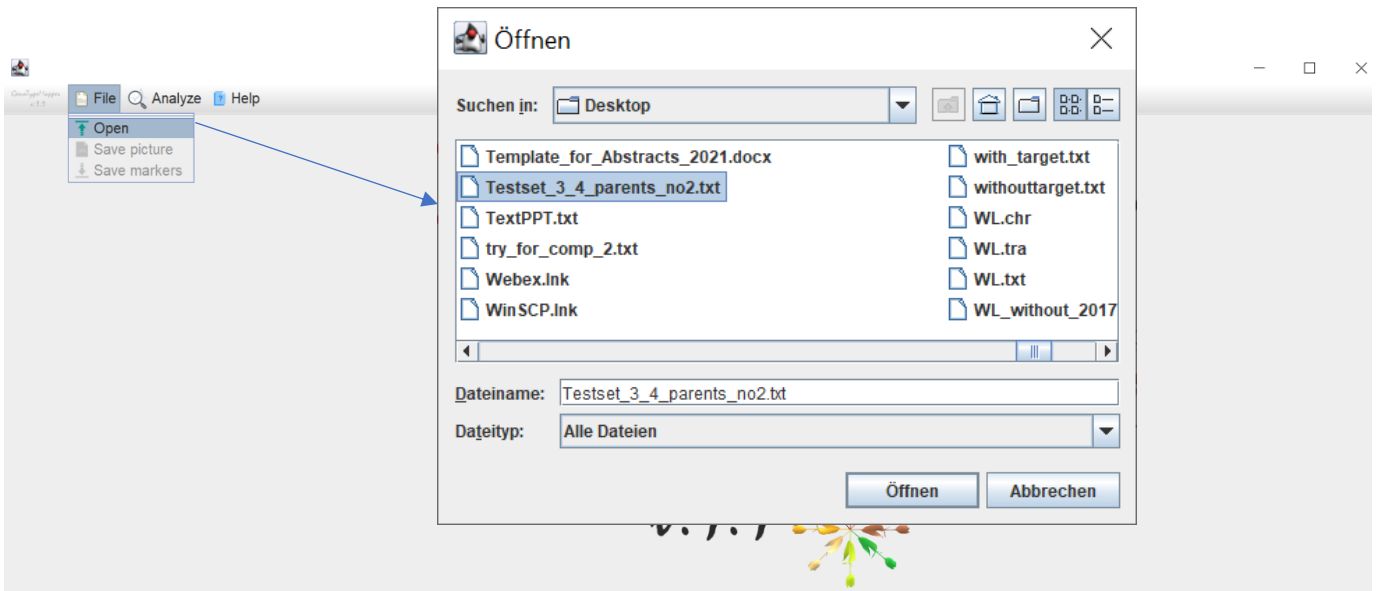
Structure of the input file

The input data format always requires nine columns. Mandatory information is written in bold, additional information in *italics*. Information that is not available should be indicated with "NA". Please note that the chromosome, the marker name, and a physical and/or genetic position must be provided to the program.

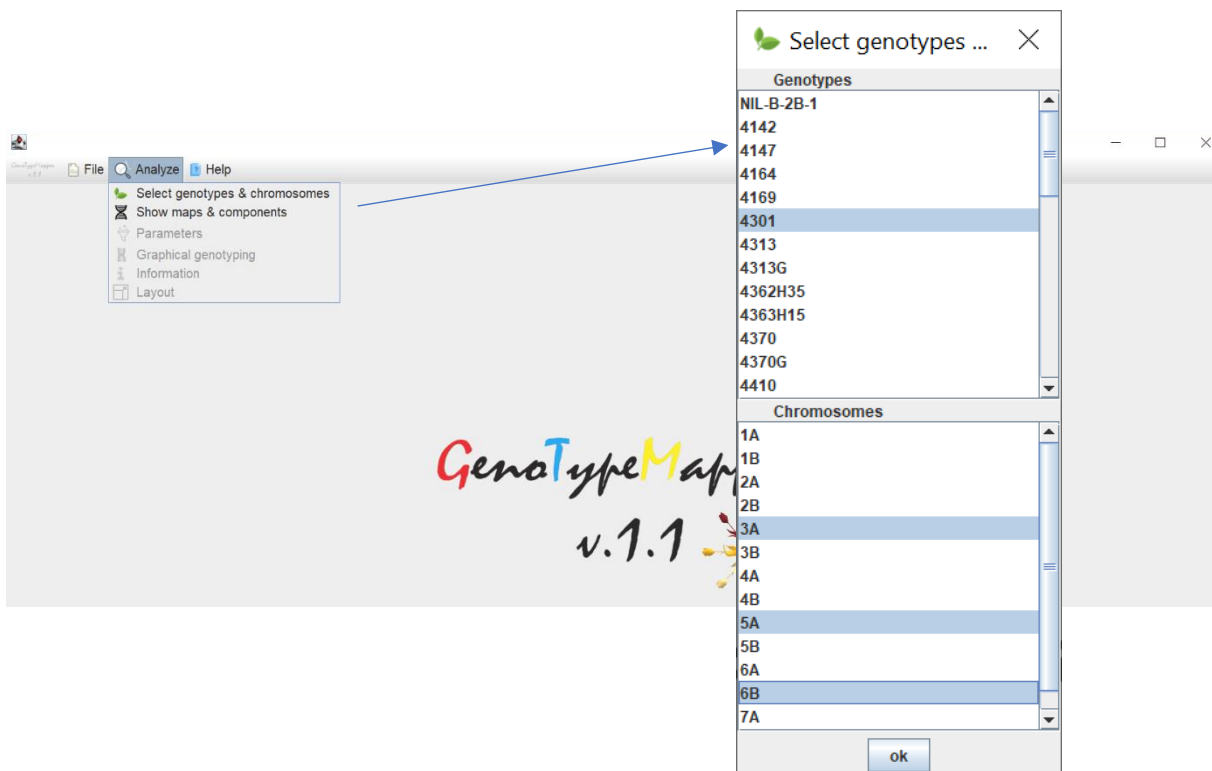
Chr	Marker	<i>Genetic position</i>	<i>Physical or genetic position</i>	<i>Lod-value</i>	<i>P1</i>	<i>P2</i>	<i>P3</i>	<i>P4</i>
1A	SNP_1	0.00	12,000	3.0	A	T	A	A



2. Then select the input file. (You might use our example files that are provided on our website.)

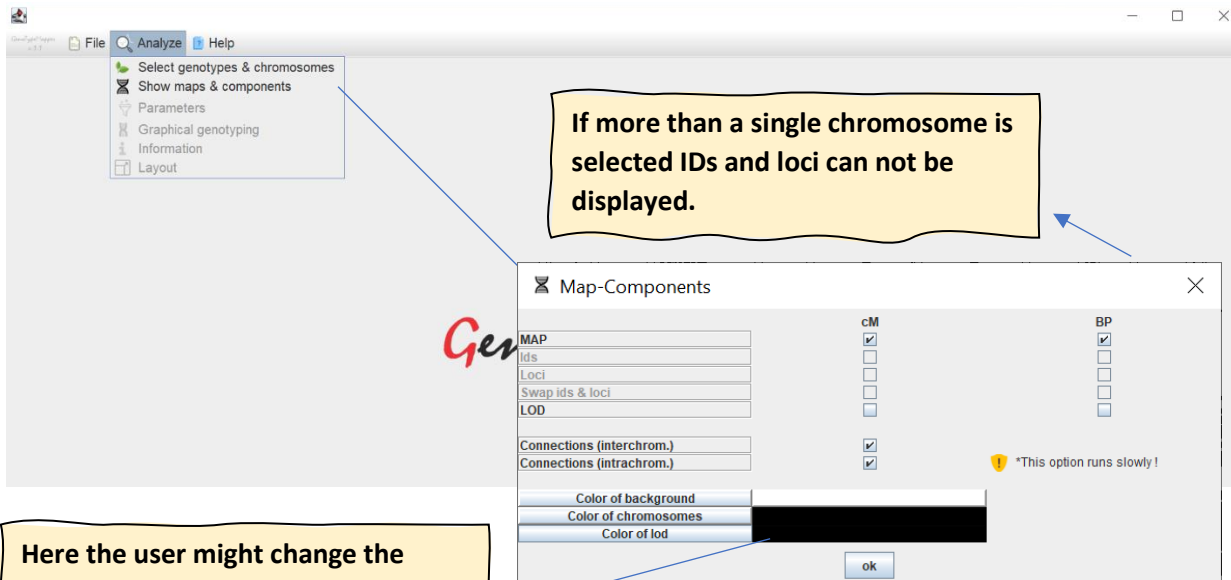


3. Finally - if all the information were provided correctly - the user can select the genotypes and the chromosomes that are of interest.



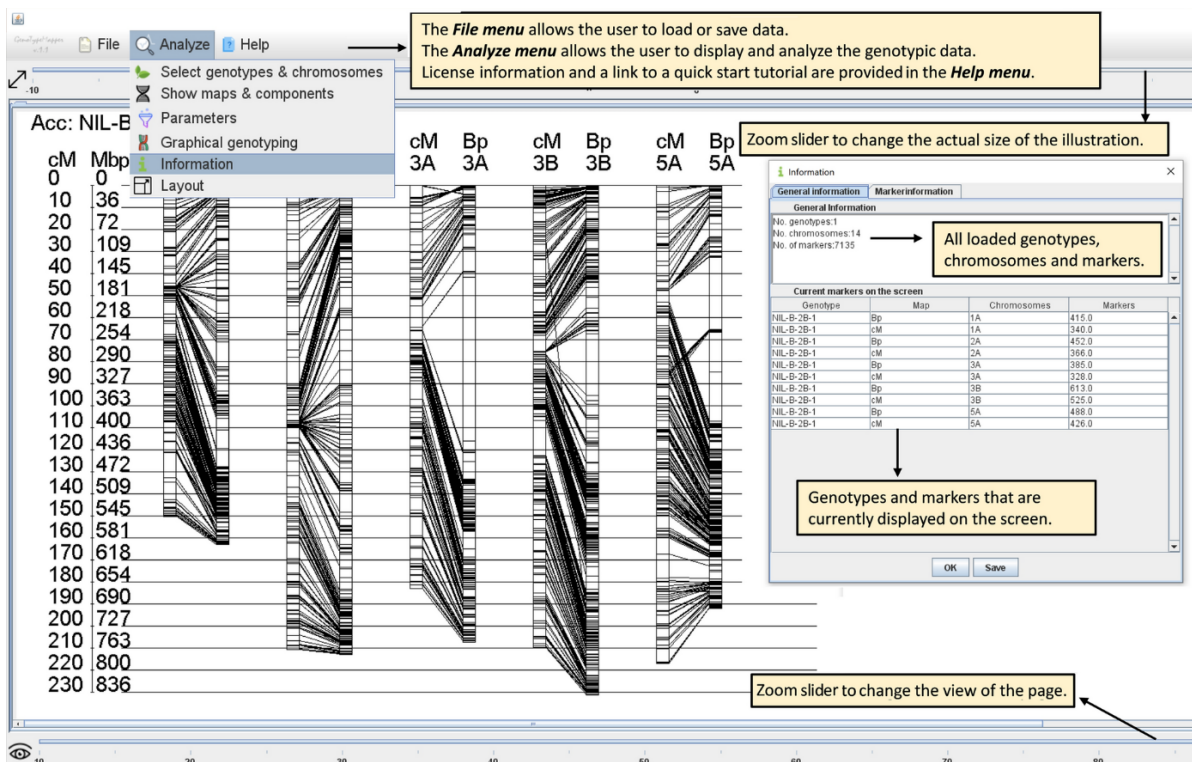


4. In the „Analyze menu“ the map components can be selected. The information of both maps might be illustrated together or independently



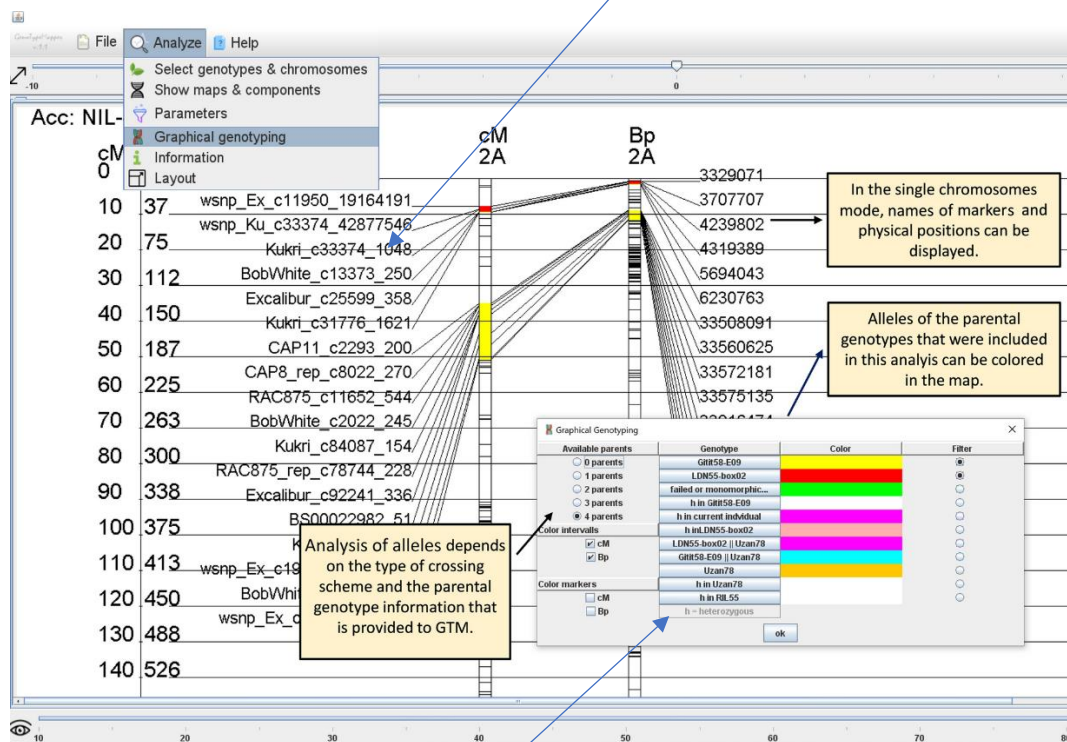
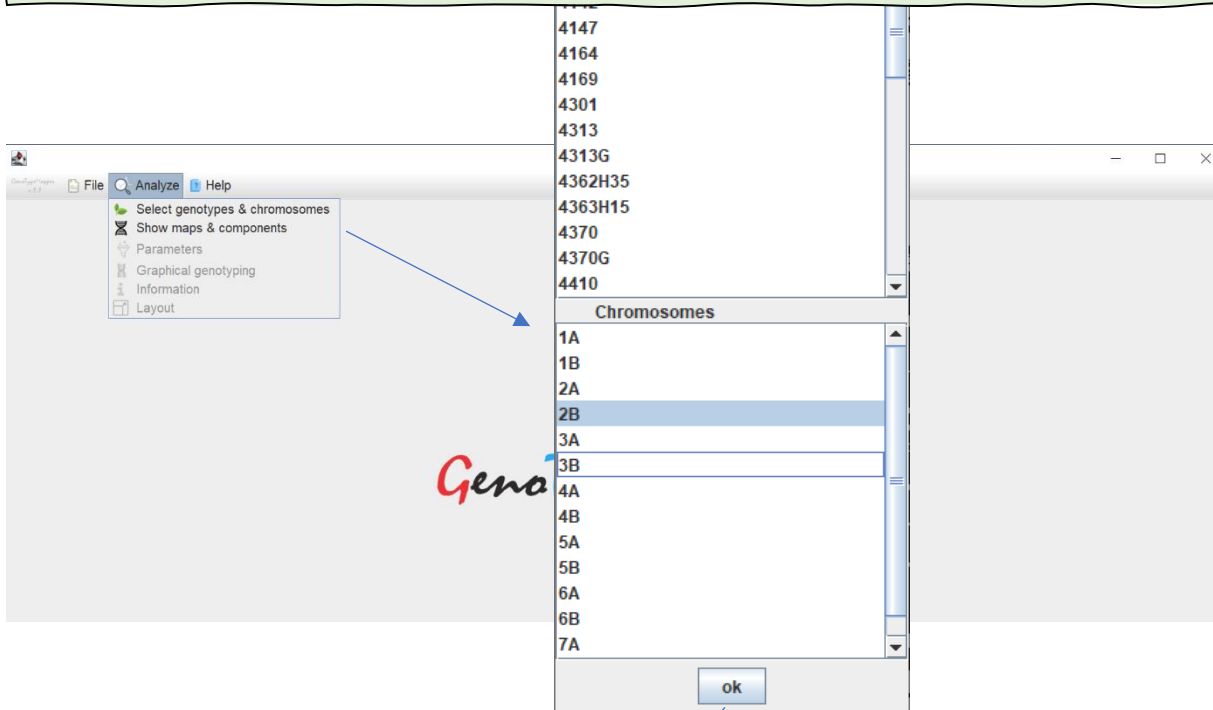
Here the user might change the color of the chromosomes, the lod curves or the background

5. The requested information will be displayed on the screen and can subsequently be modified. The view (e.g. the distance between the chromosomes, the width of the chromosomes etc.) might be adapted in the „parameters“ menu.





6. If the user selects a single chromosome, markernames and loci can be displayed via the components menu.



In the single chromosomes mode, names of markers and physical positions can be displayed.

Alleles of the parental genotypes that were included in this analysis can be colored in the map.

Analysis of alleles depends on the type of crossing scheme and the parental genotype information that is provided to GTM.

Please note that genotypic data can be selected, colored and displayed via the „Graphical genotyping menu“. Please read our article for more detailed information.



7. The picture of the chromosome and marker and allelic data displayed on the screen can be exported as *.png file or *.text file respectively via the „File“ menu.

