The Genotype Visualisation Tool (GVT)

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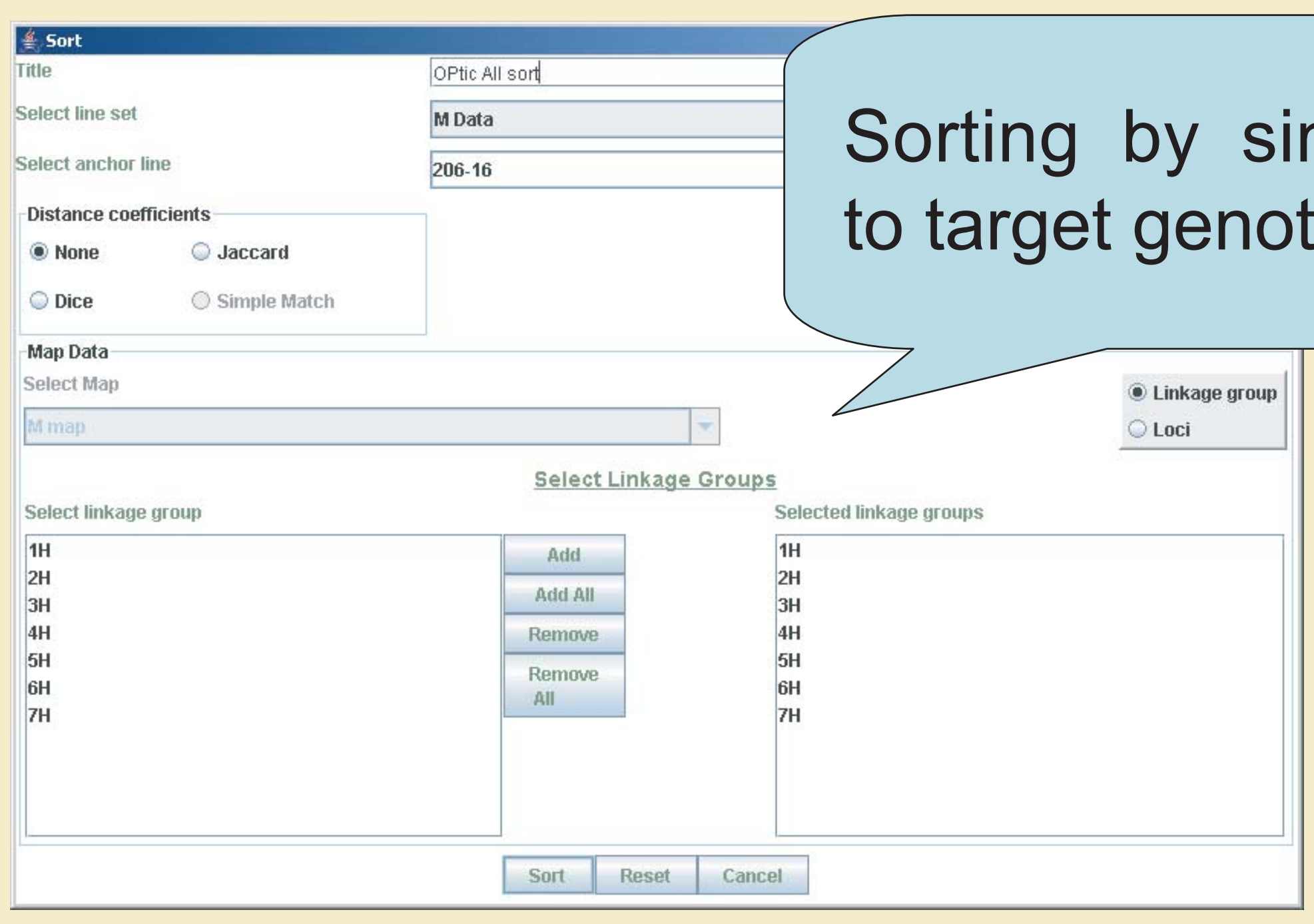
The Genotype Visualisation Tool (GVT is a Java application designed for the visualisation and analysis of plant genotype data in the form of graphical genotypes. It has been designed to support a range of genotyping technologies, including SSRs, SNPS, AFLPs and RBIPS. We anticipate that it should be extendable to other technolgies.

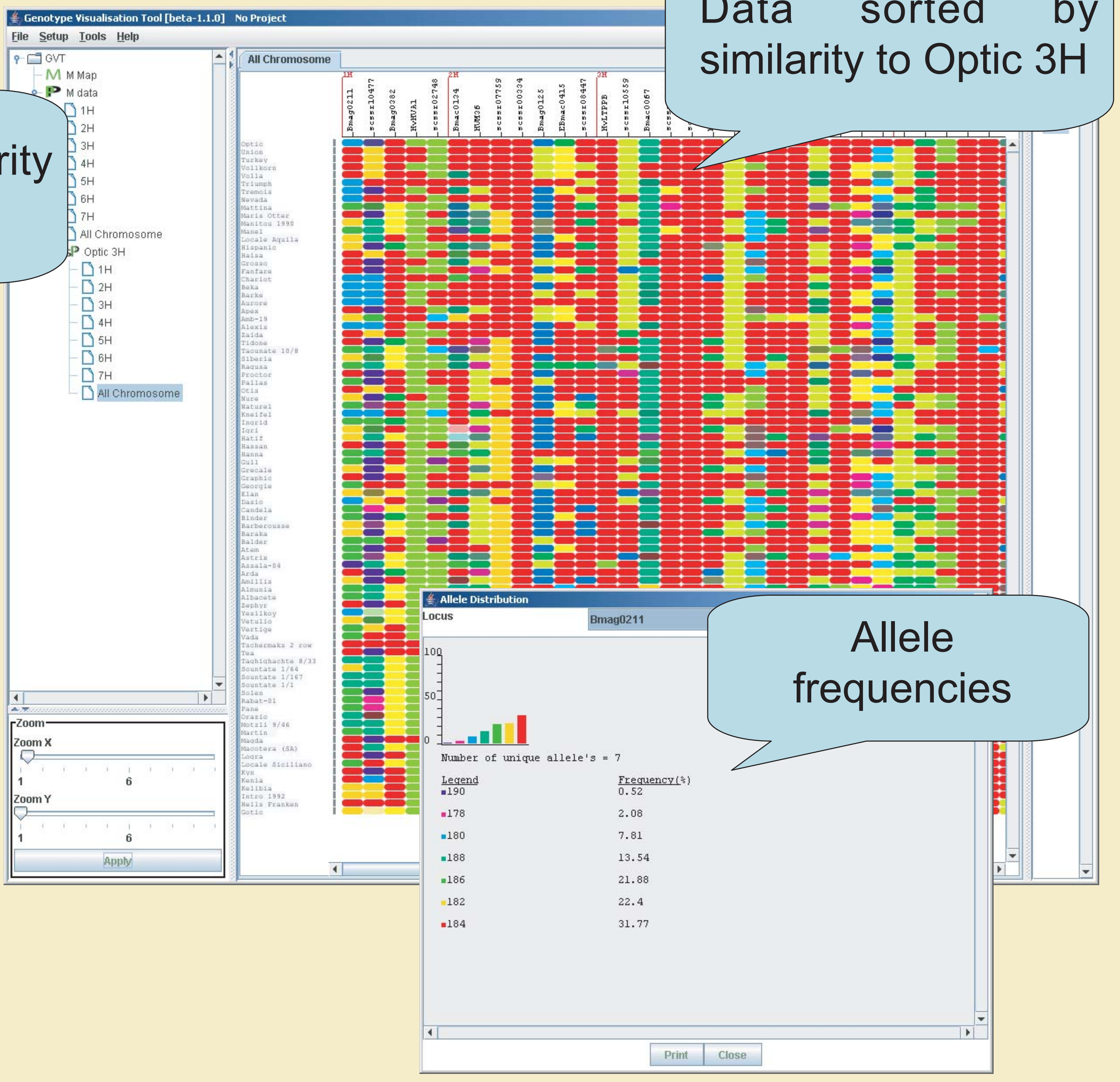
Choosing your colour model

GVT currently has two colour models, plus custom options, to maximise the visibility of alleles based on frequency or other measures of value. Irrespective of the genotyping technology used, we have developed a colouring engine that assigns a unique colour to each allele value; our colouring engine is optimised to select the set of most contrasting colours in the HSB colour model for the list of allele values at a locus.

Additional facilities include a query interface to search for genotypes based on logical combinations of alleles, together with facilities to sort by similarity to an anchor genotype or to generate a subset of the population. The resulting graphical genotypes



Sorting by similarity to target genotype



Data sorted by similarity to Optic 3H

Allele frequencies

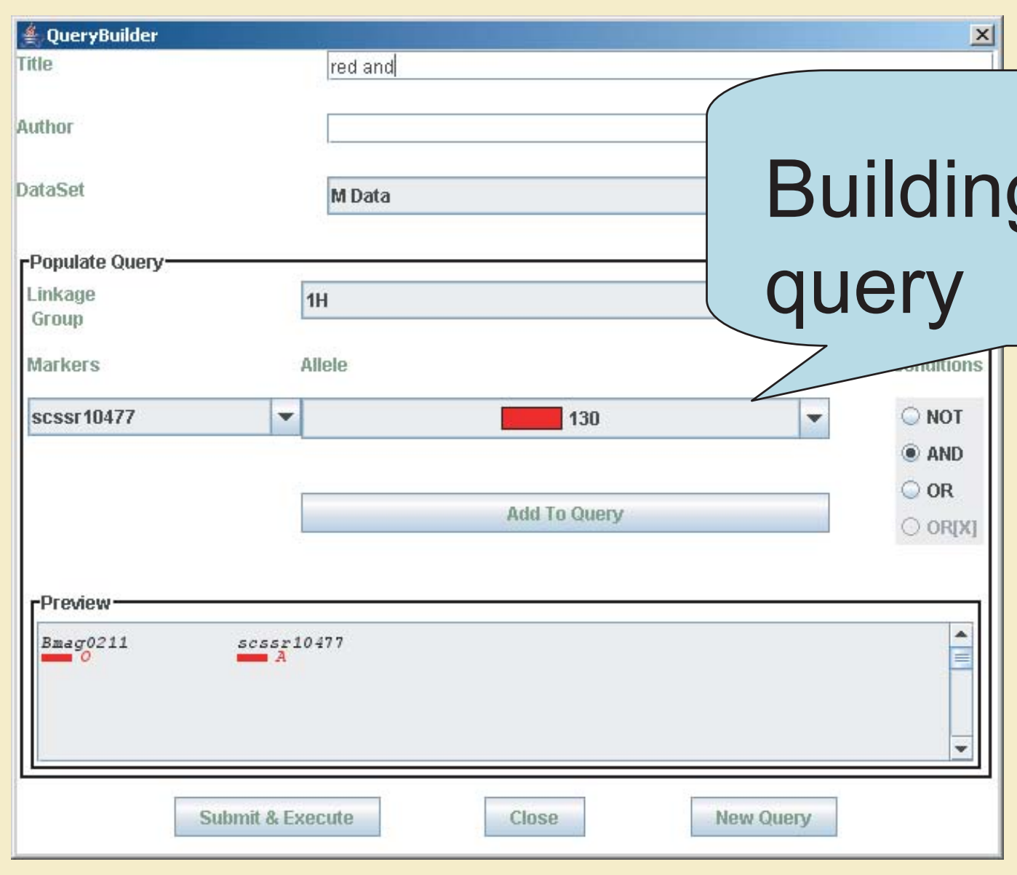
Allele Distribution

Locus: Bmag0211

Number of unique allele's = 7

Legend	Frequency(%)
■190	0.52
■178	2.08
■180	7.81
■188	13.54
■186	21.88
■182	22.4
■184	31.77

Data can be loaded into the GVT platform through the GERMINATE database (see Poster 865) or similar GDPC enabled databases or from a local Excel spreadsheet based on a supplied template. GVT is a Java 1.5 application and currently we are working to develop additional analysis tools as well as the visualisation of genotypes in both pedigree and clustering contexts into the GVT framework.



Building a visual query

Subset of lines which contain chosen alleles at 2 loci

We are currently working to expand the number of analytical and visual functions available in GVT, including different clustering options, one or more haplotype block algorithms and a range of rporting tools.

Related Work

Please also see posters no 865 (Germinate) and 847 (Barley SNPs etc.)

Acknowledgements

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