

QTL mapping in multi-parent populations

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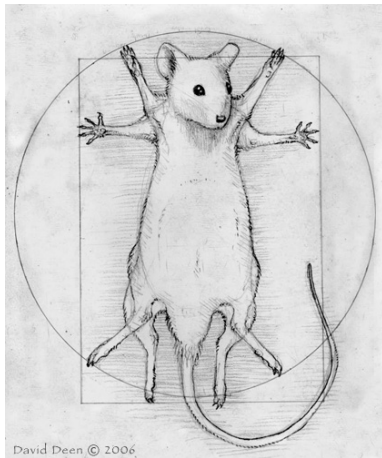
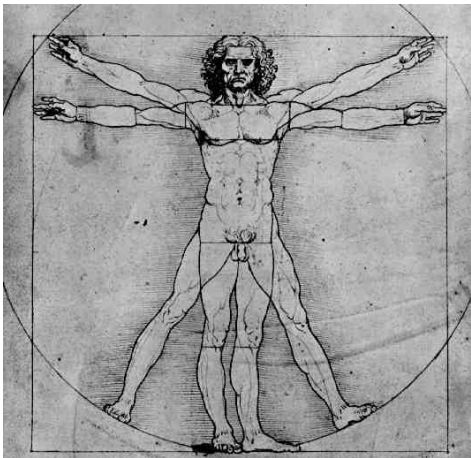
github.com/kbroman

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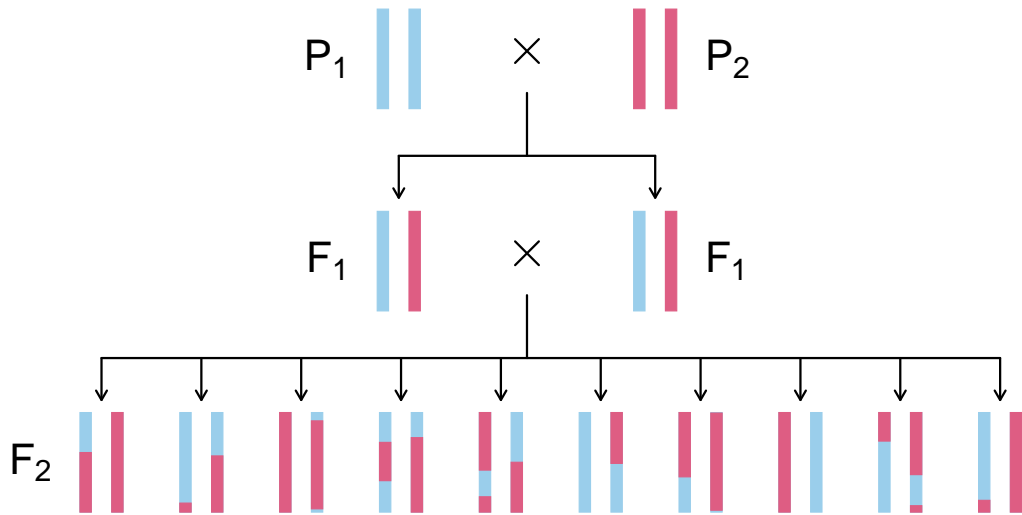




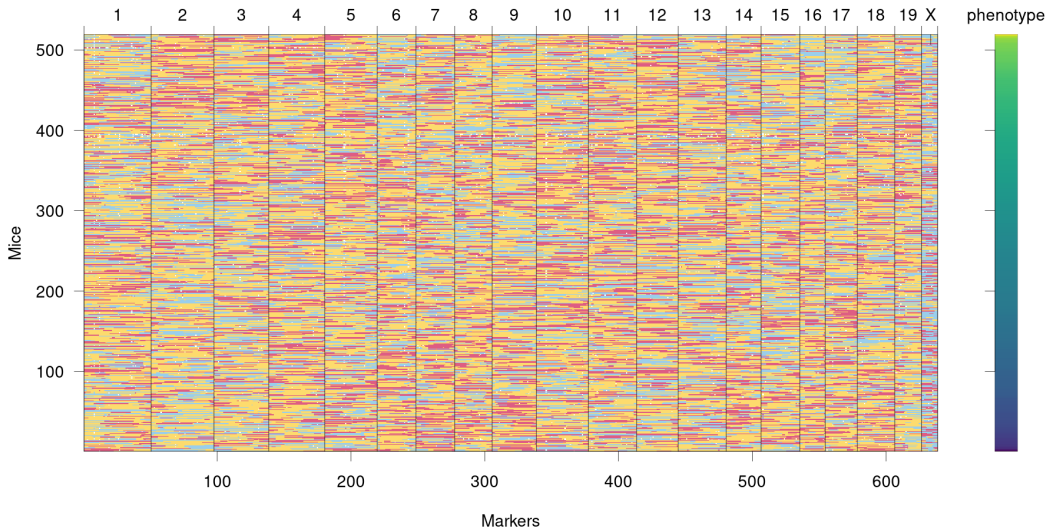


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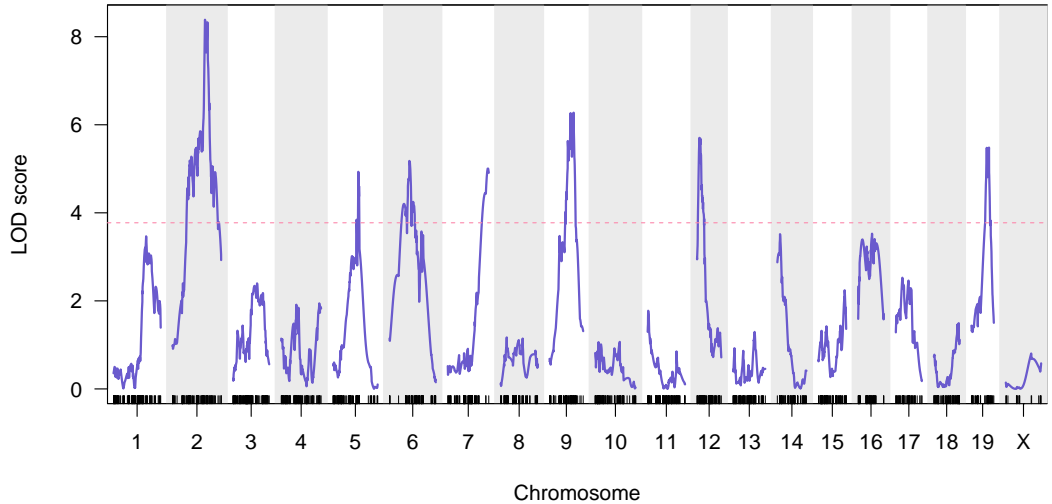
Intercross



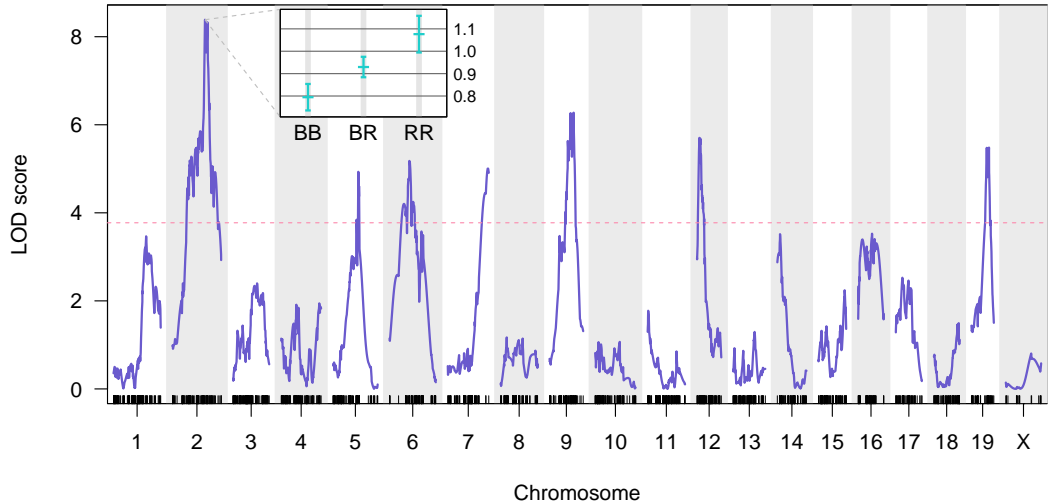
Data



Genome scan



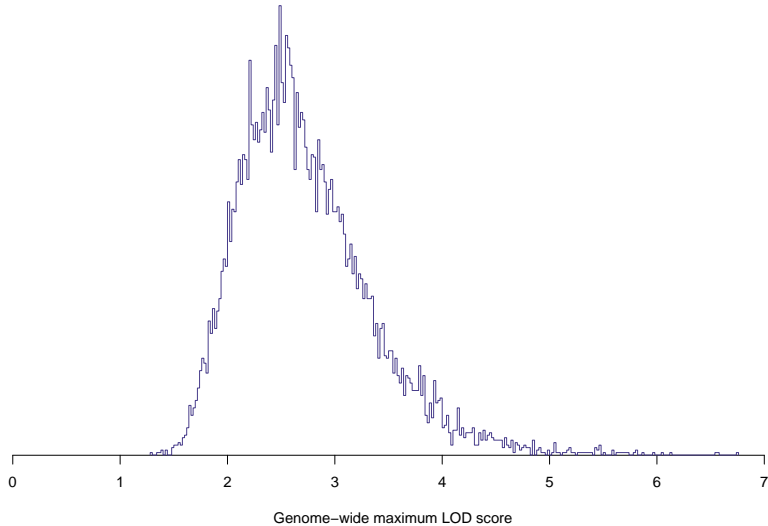
Genome scan



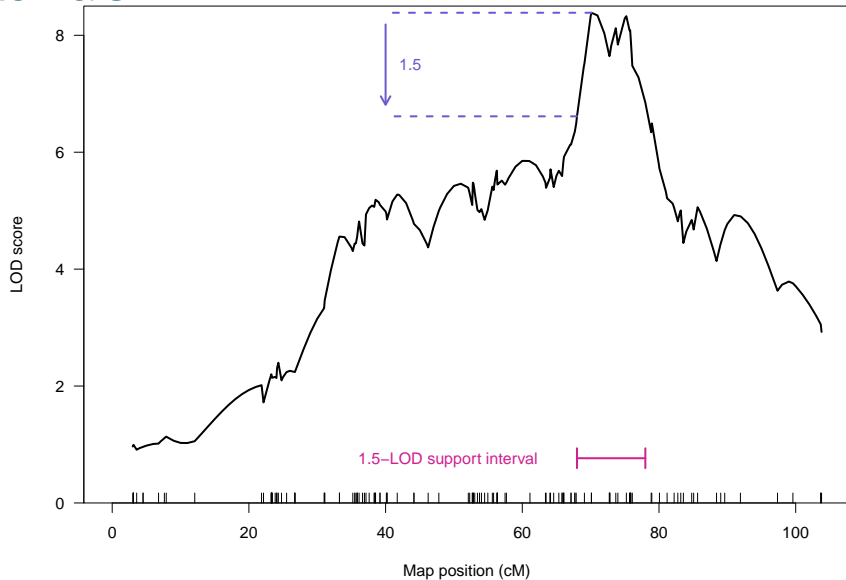
Permutation test



Permutation distribution



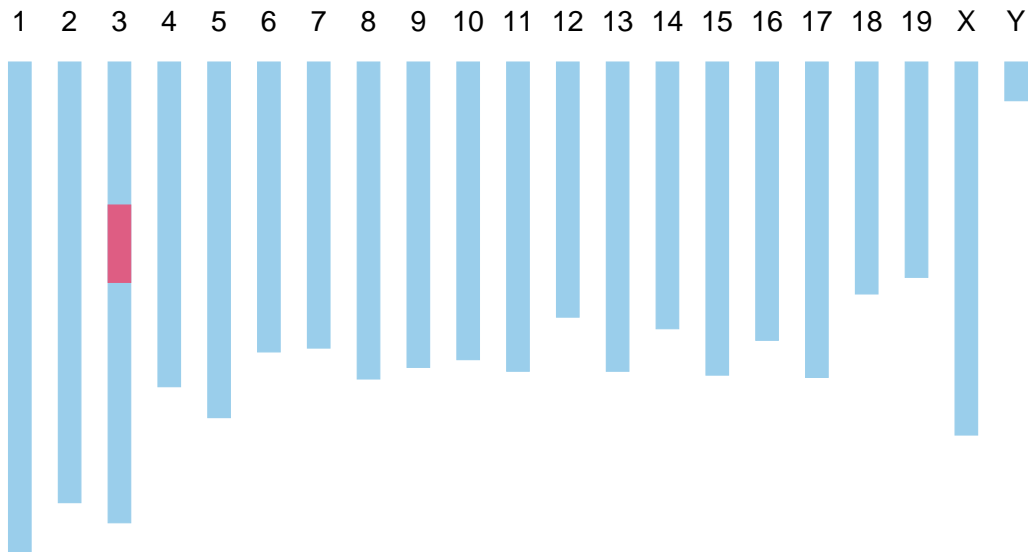
QTL intervals



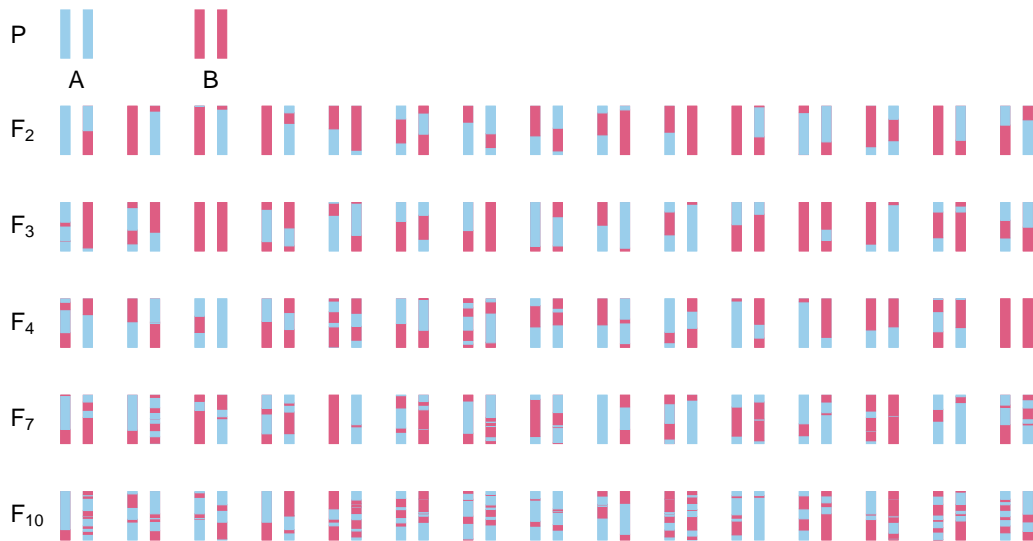
Multiple QTL models

- ▶ Reduce residual variation \longrightarrow greater power
- ▶ Separate linked QTL
- ▶ Identify interactions (epistasis)

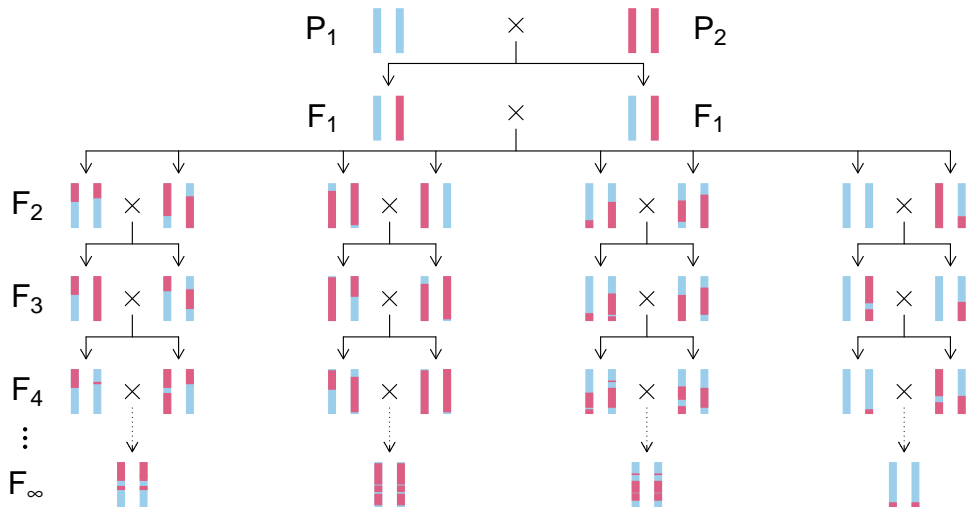
Congenic line



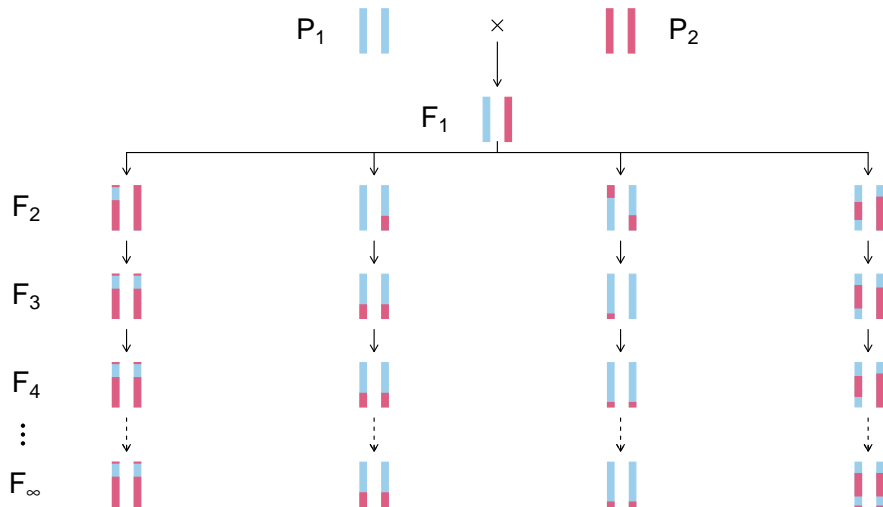
Advanced intercross lines



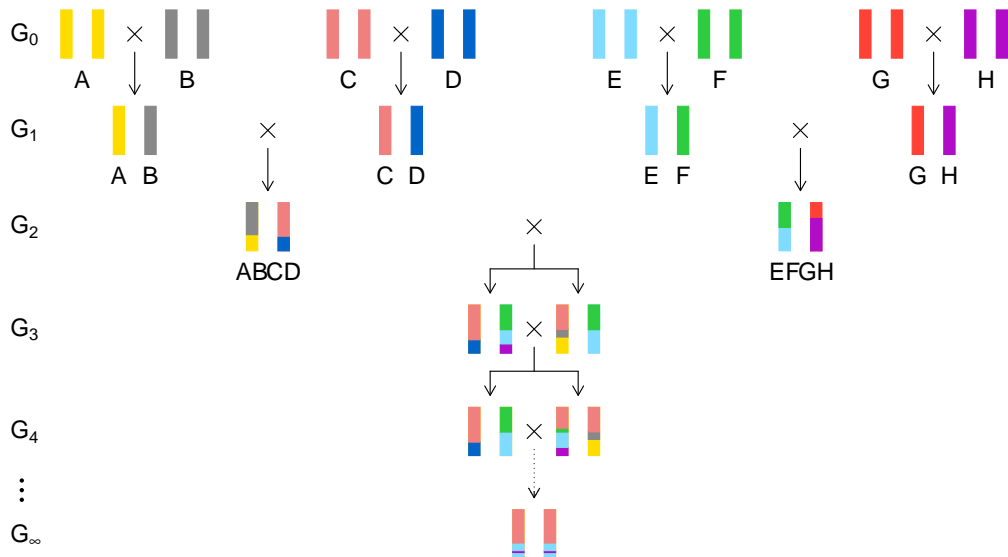
Recombinant inbred lines



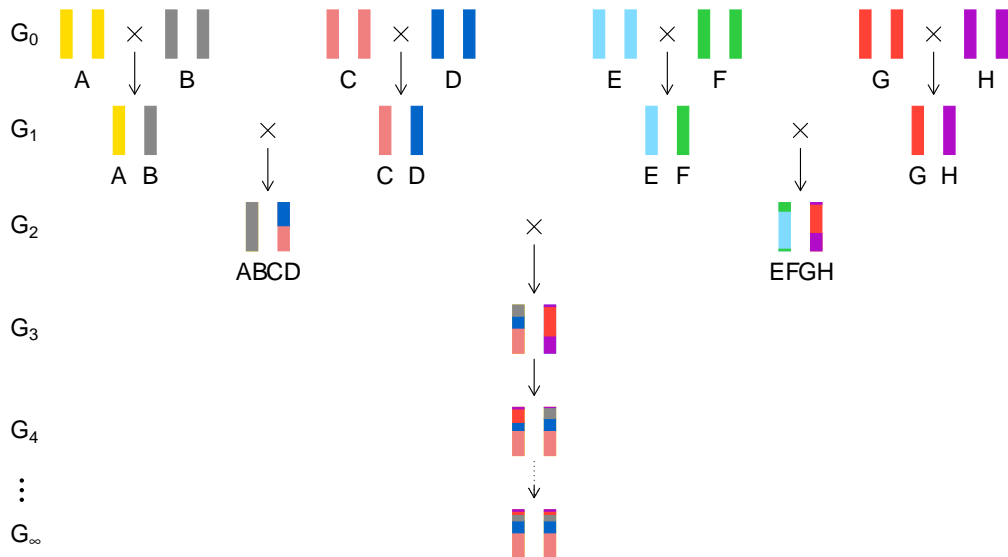
Recombinant inbred lines (selfing)



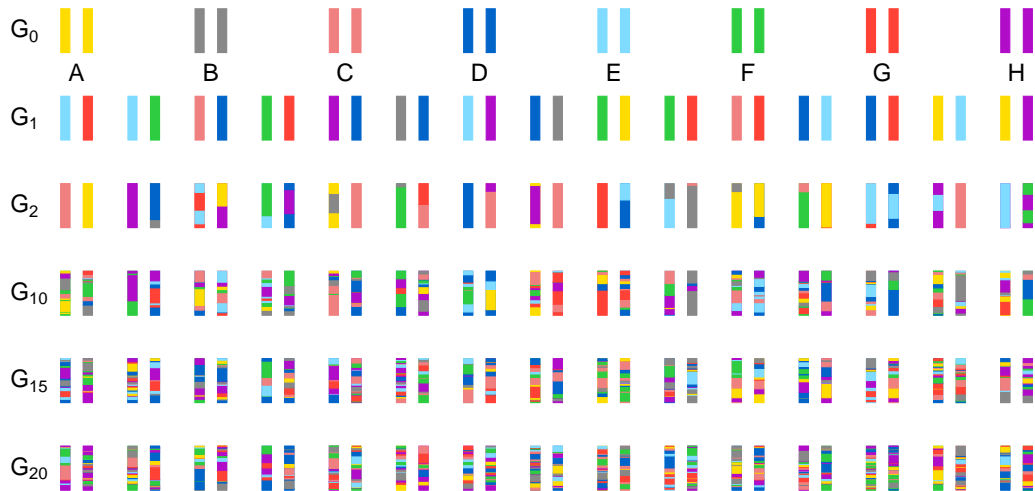
Collaborative Cross



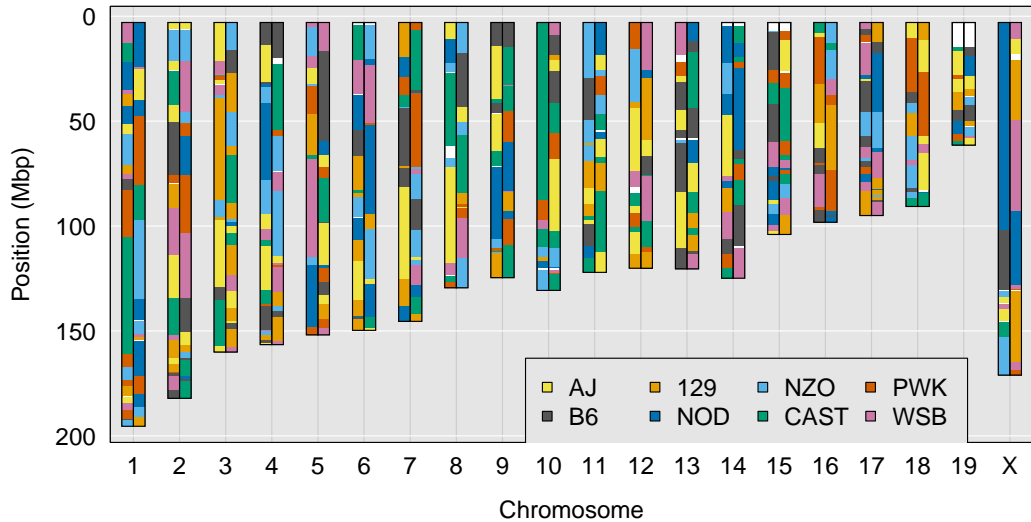
MAGIC lines



Heterogeneous Stock/Diversity outbreeds



DO genome



QTL analysis in DO

- ▶ Genotype reconstruction
- ▶ Kinship correction
- ▶ Treatment of QTL genotype

Genotype reconstruction

Linear mixed model

Treatment of QTL genotypes

Research topics

- ▶ Identifying the causal polymorphisms
- ▶ Joint analysis of high-dimensional outcomes
- ▶ Use of intermediate biochemical traits
- ▶ Cross-species analyses

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