

Genetic partitioning of the genome

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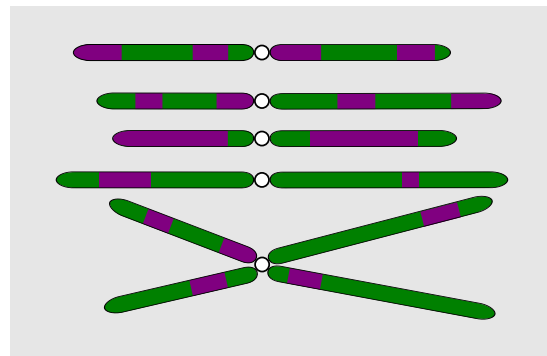
Problem

Is it possible to partition a genome's markers into those that have a high marker effect vs. those with low marker effect.

Conclusion

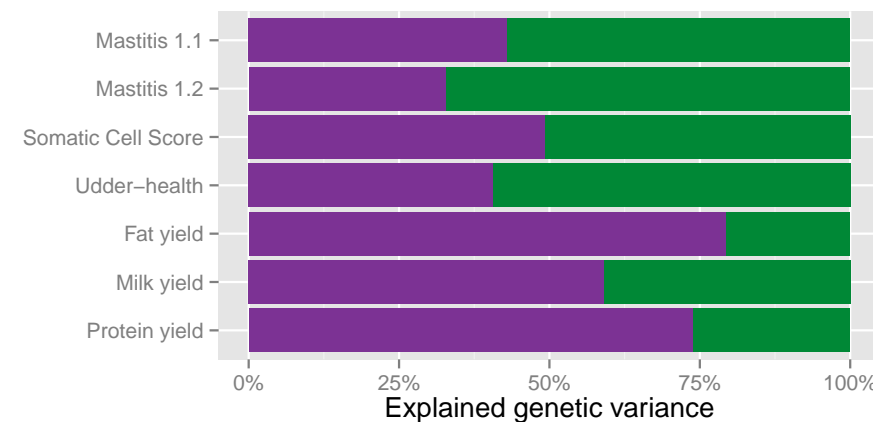
- Splitting markers into those with higher or low marker effect improves model fitting.
- Something to do with the infinitesimal model.
- Generated results here indicate it also improves prediction of new genotypes.
- Excel charts are to graphical design what bricks are to poetry.

Genomic partitioning



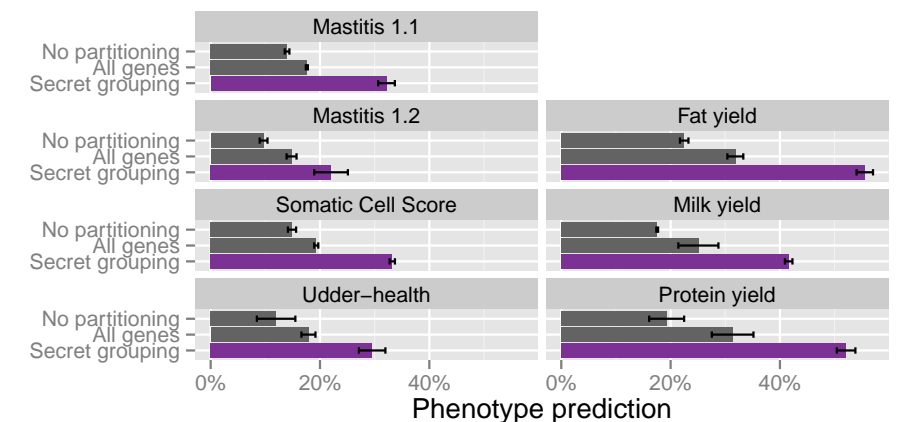
By including using any kind of external information, e.g. KEGG pathways, we can partition the genome into two sets, purple (S) and green ($\neg S$).

Explained genetic variance



Amount of genetic variance explained by markers in purple and green areas of the genome for seven different phenotypic traits.

Prediction ability



Comparison of prediction reliabilities for no partitioning, partitioning by all genes and by a selected partitioning for seven phenotypic traits.

References

- Albert, Leonard. "Gnomonology: Joyce's 'The Sisters'." *James Joyce Quarterly* 27.2 (1990): 355–364. PDF.
- Aristotle. *The Poetics*. Trans. W. Hamilton Frye. Cambridge: Harvard UP, 1927. Print. Loeb Classical Library 199, Aristotle 23.
- Guererro, Frank. *Giraffes in the Wild*. Philadelphia: Philadelphia Publishing Inc, 2002.

Model

$$\mathbf{y} = \mu + \mathbf{Z}_S \mathbf{b}_S + \mathbf{Z}_{\neg S} \mathbf{b}_{\neg S} + \mathbf{e}$$

where \mathbf{y} is a vector of phenotypes, \mathbf{Z}_S a marker-incidence matrix for the markers in set S , \mathbf{b}_S marker effects for ditto markers, $\neg S$ indicates markers *not* belonging to set S and \mathbf{e} model residuals.

Variance components for \mathbf{b}_S , $\mathbf{b}_{\neg S}$ and \mathbf{e} were estimated using the AI-REML algorithm in the software DMU.

Acknowledgements

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