

# PARTITIONING OF GENOMIC VARIANCE USING PRIOR BIOLOGICAL INFORMATION

---

Stefan McKinnon Edwards, Per Madsen & Peter Sørensen

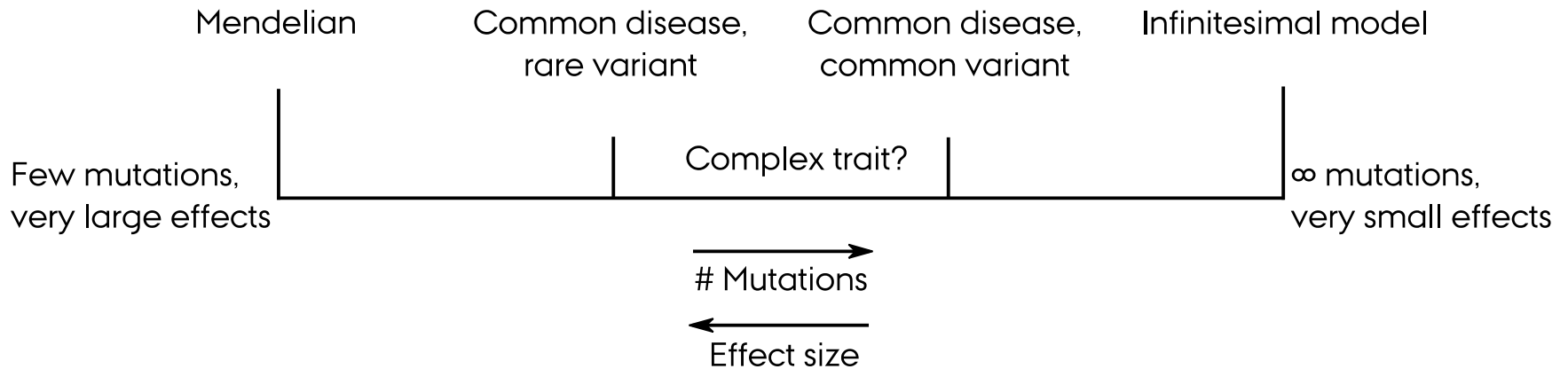
# Aim

---

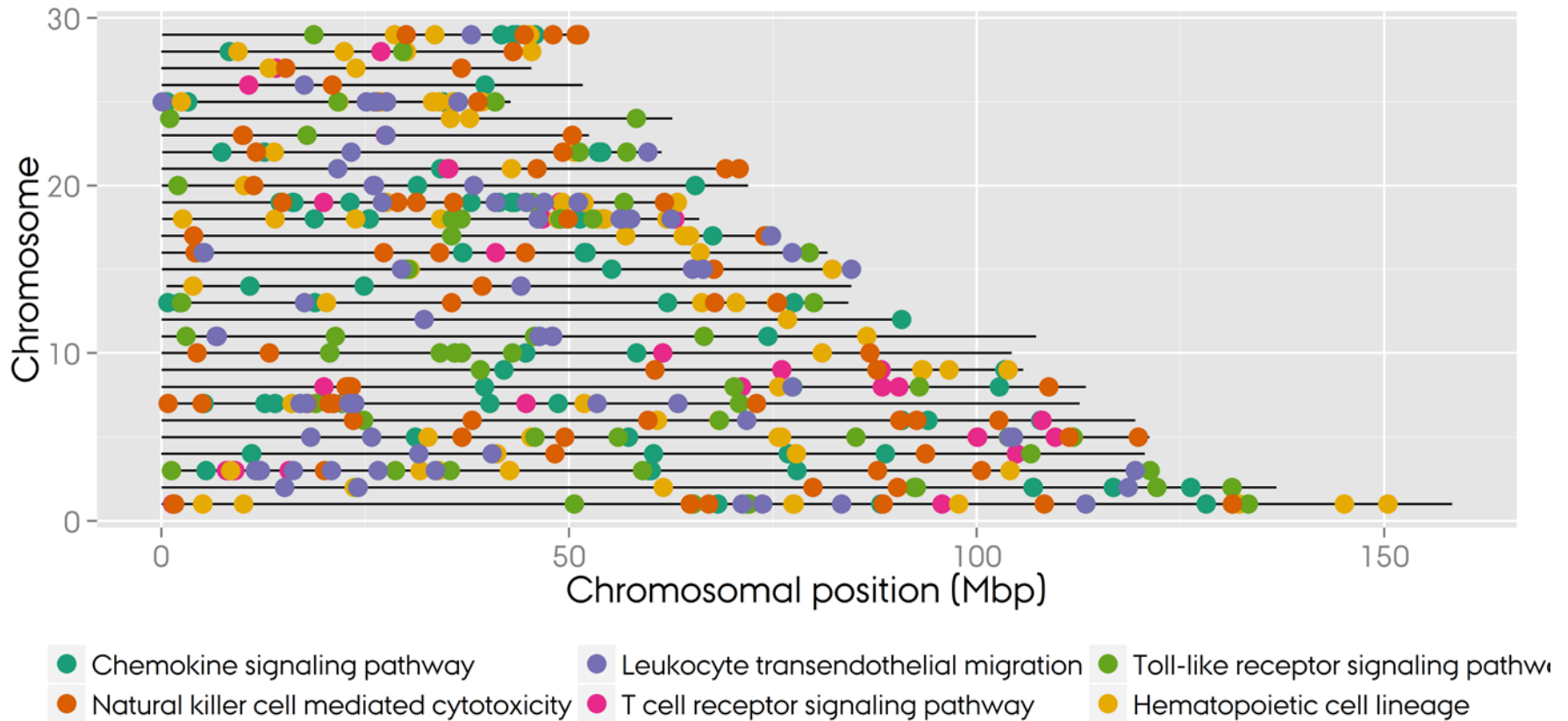
- "Develop an integrative genomics approach for evaluating the joint contribution of scattered genetic variants on complex traits."

# Complex traits

---



# KEGG pathway: Immune System



# Linear mixed models

---

$$\mathbf{y} = \mathbf{g} + \mathbf{e}$$

$$\mathbf{y} = \mathbf{g}_1 + \mathbf{g}_2 + \mathbf{e}$$

Empirical statistics:

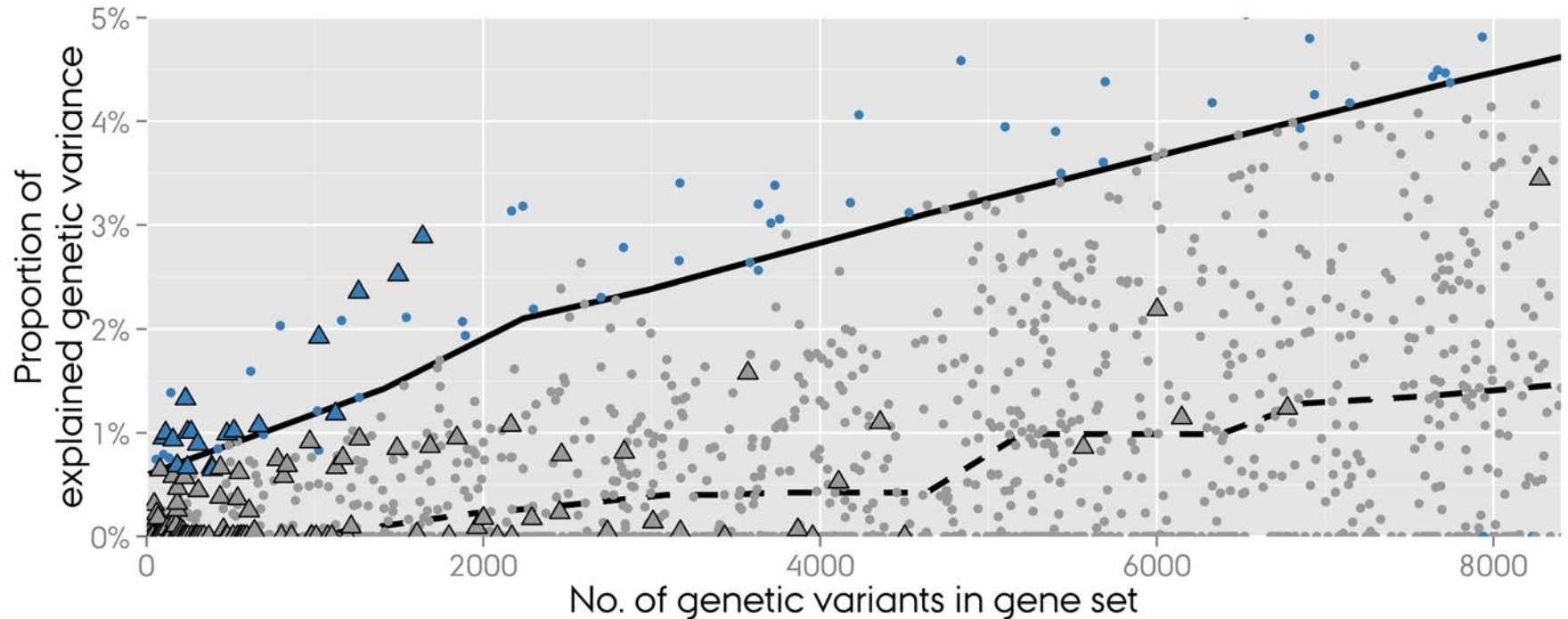
- Likelihood ratio (LR)
- Proportion of explained genetic variance

# Data

---

- 4,497 genotyped bulls.
- 637,951 markers per bull.
- Health traits derived from daughters.

# Results: Random gene sets



△ KEGG pathways  
○ Random gene set

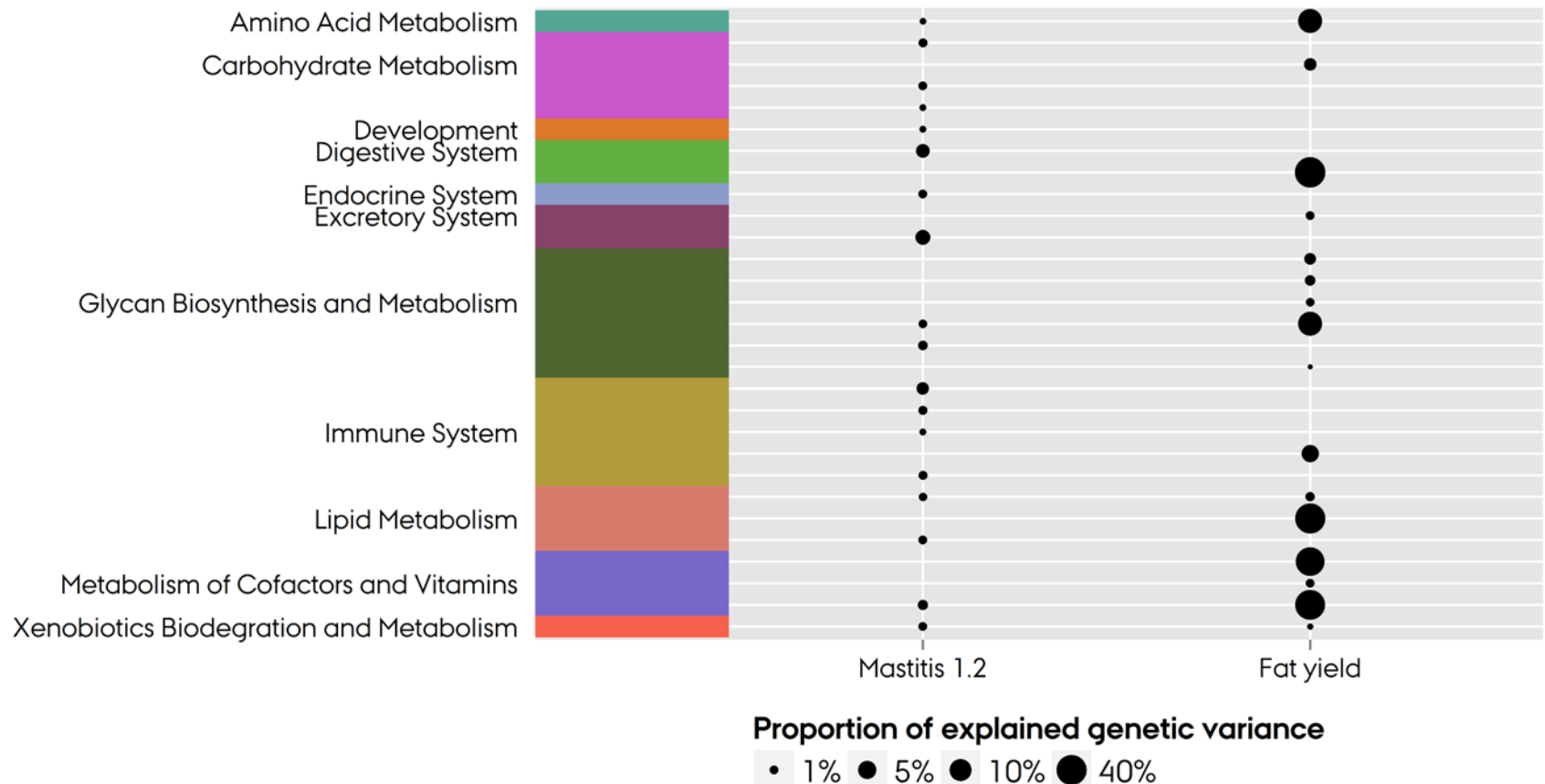
$LR \geq LR_{95}$

● No  
● Yes

Percentile

--- 50%  
— 95%

# Results: Significant KEGG pathways





# Conclusions

---

- 10-12% of pathways significant
- Results can be plugged into genetic prediction framework
- Opened the black box