

Rare alleles and the genetic basis of crop phenotypes

Thinking about population demography and effects on genetic architecture of traits.

intro to quantitative traits

understanding them is key

traditionally, QTL has been used

recently GWAS, potential to identify individual genes

missing heritability

rare alleles of large negative effect often missed (Thornton et al., 2013)

demographic effects can impact deleterious allele distro

V_a influenced by demography (Lohmueller, 2014)

These guys did crap (Gazave et al., 2013). But Thornton (2014) did more.

For designing breeding strategies, for utilizing diversity from wild relatives, for understanding variation in phenotype, for engineering new traits (GMOs, CRISPR).

References

- Gazave, E., Chang, D., Clark, A. G., and Keinan, A. (2013). Population growth inflates the per-individual number of deleterious mutations and reduces their mean effect. *Genetics*, 195(3):969–978.
- Lohmueller, K. E. (2014). The impact of population demography and selection on the genetic architecture of complex traits. *PLoS Genetics*, 10(5):e1004379.
- Thornton, K. R. (2014). A c++ template library for efficient forward-time population genetic simulation of large populations. *Genetics*, 198:157–166.
- Thornton, K. R., Foran, A. J., and Long, A. D. (2013). Properties and modeling of gwas when complex disease risk is due to non-complementing, deleterious mutations in genes of large effect. *PLoS genetics*, 9(2):e1003258.

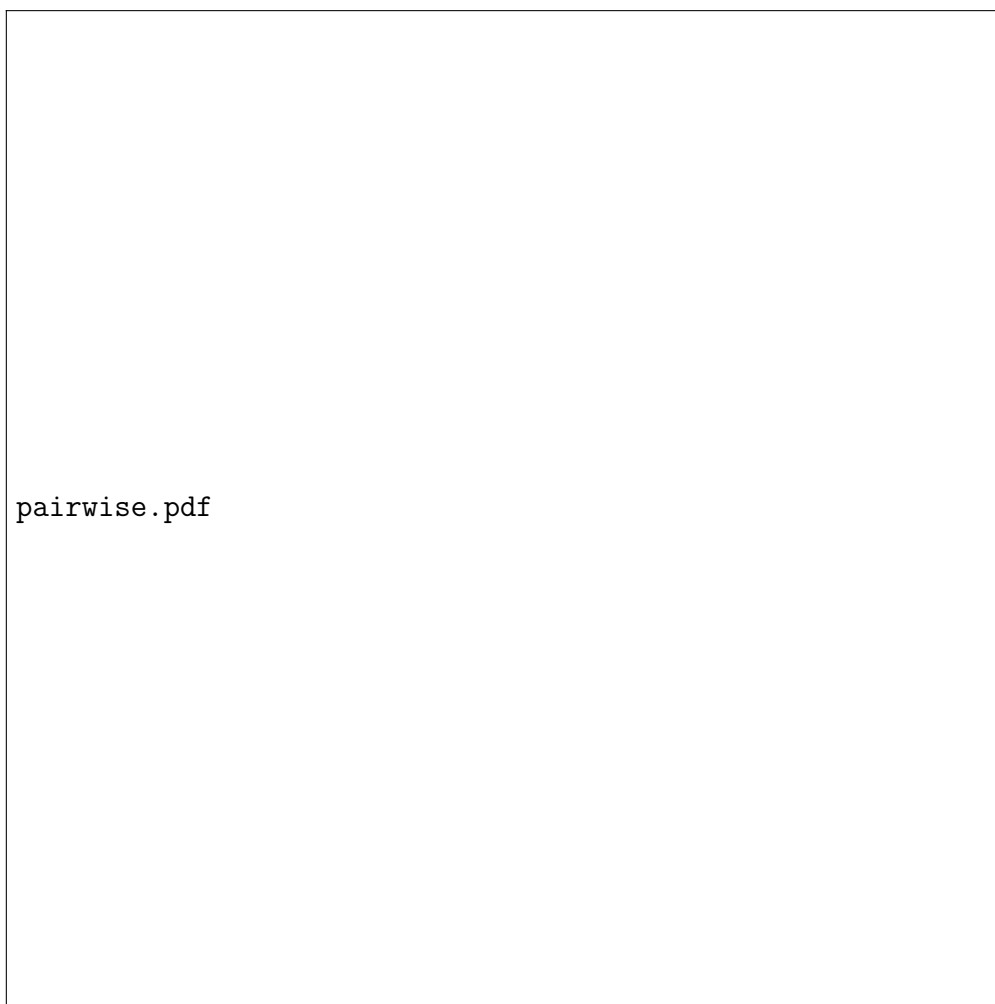


Figure 1: All polymorphisms