

Improving the efficiency of selecting for nut traits using genomic data

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Rationale

- Phenotypic selection is resource intensive
- Genotypic information could help improve efficiency of breeding, since it is relatively cheap
- Goal: selecting better parents in crosses, screening larger families, & increasing selection intensity at the seedling stage

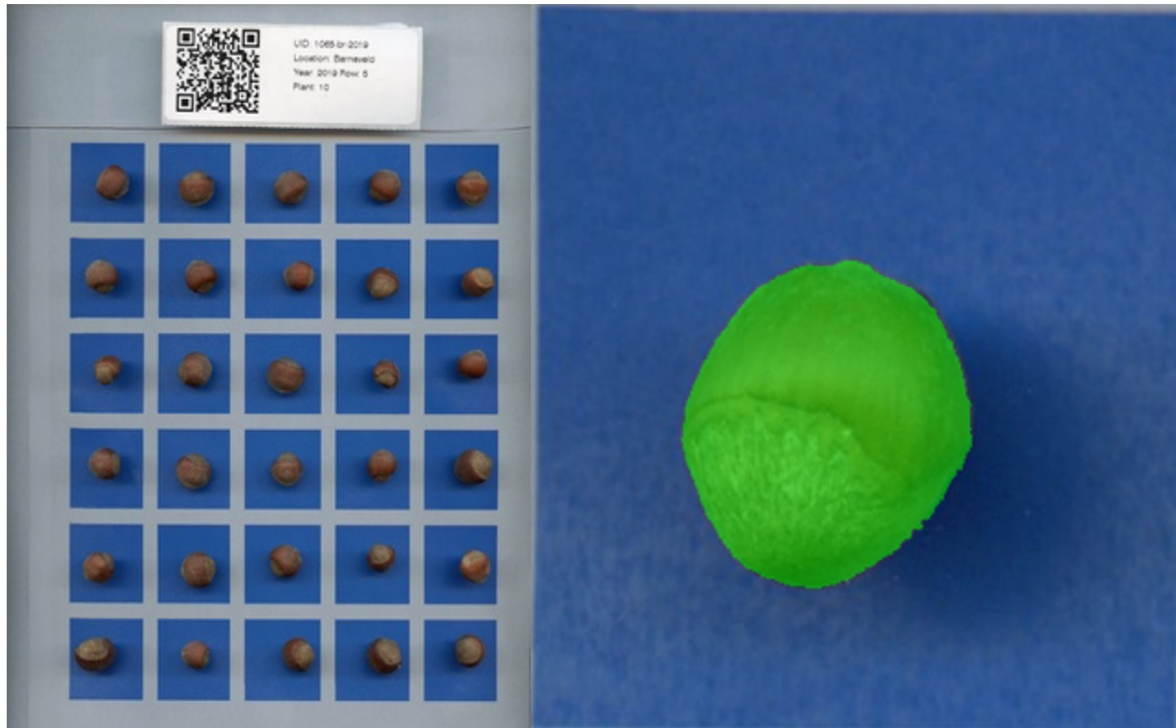
Traits that we are targeting

1. Direct measurements of size and shape of in-shell nuts and kernels
2. Indirect measurements of shell thickness / percent kernel

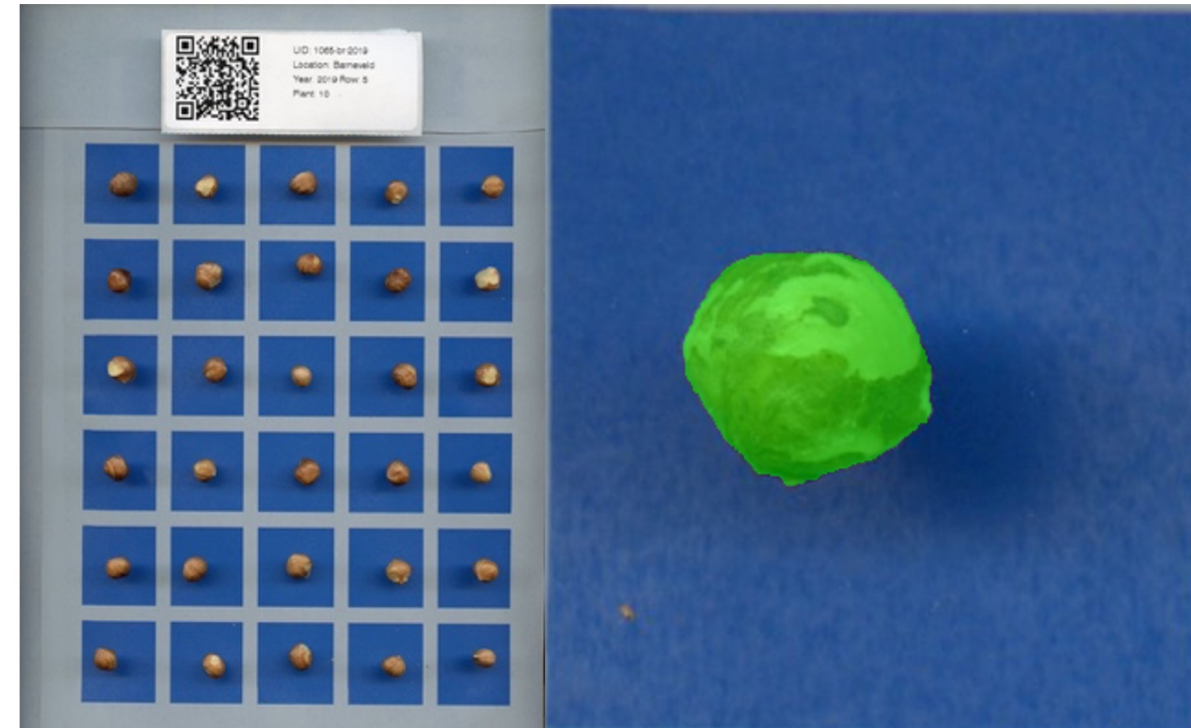


Digital image analysis

A. In-shell

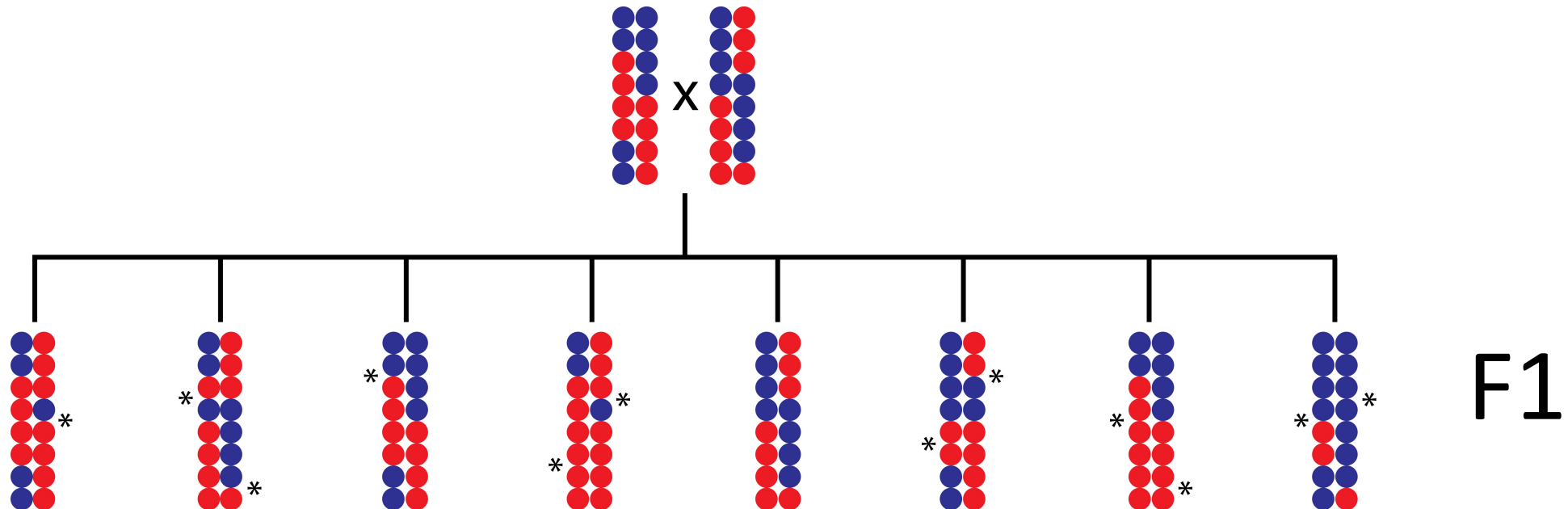


B. Kernel



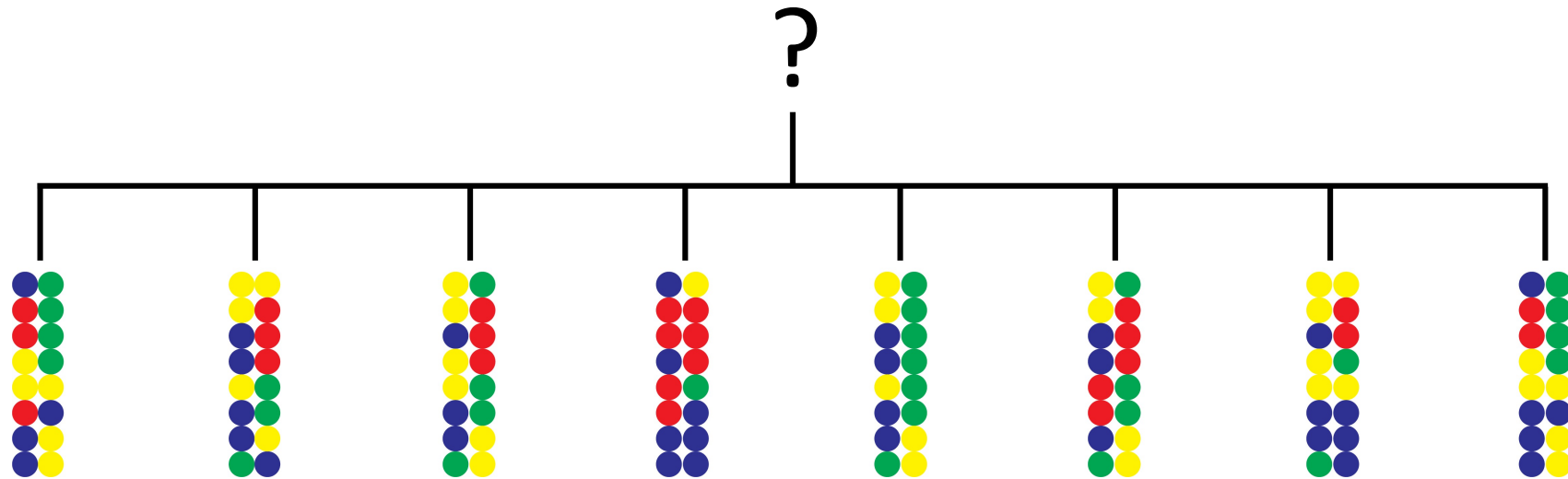
Populations that we are targeting

1. F1 populations descended from controlled crosses between specific parents, growing in Stoughton, WI (~250 bushes / family), and in Rosemount, MN (~100 bushes / family)

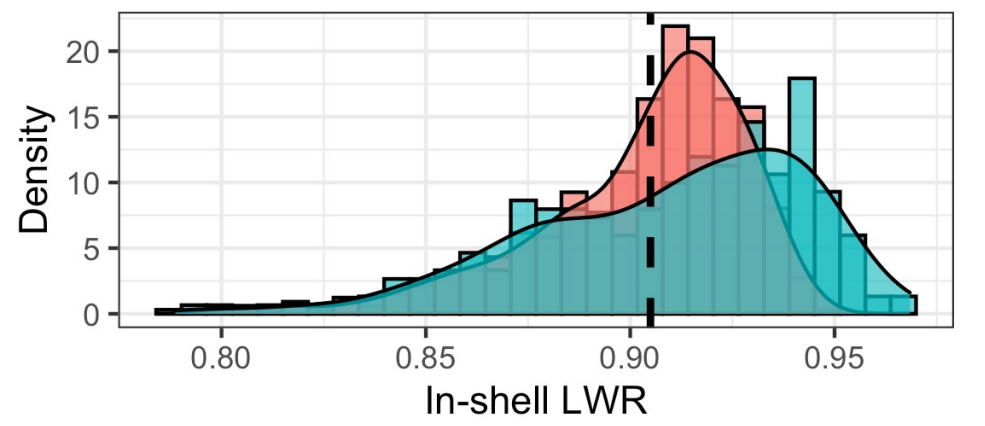
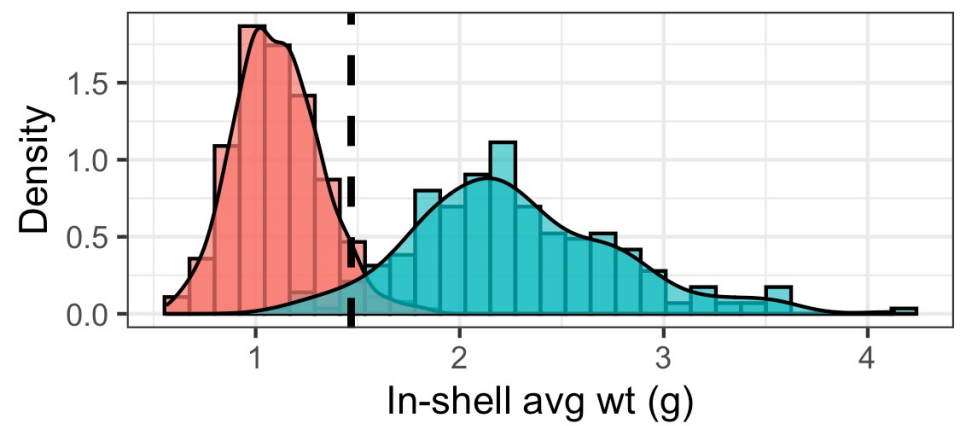
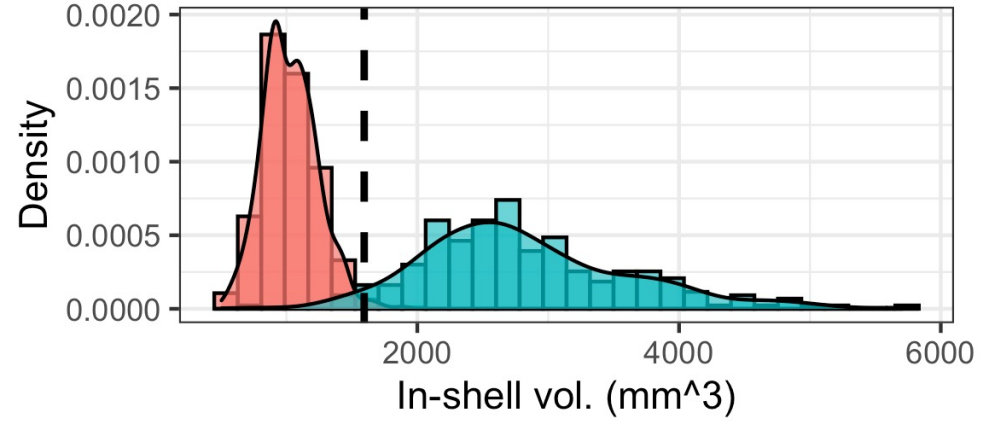
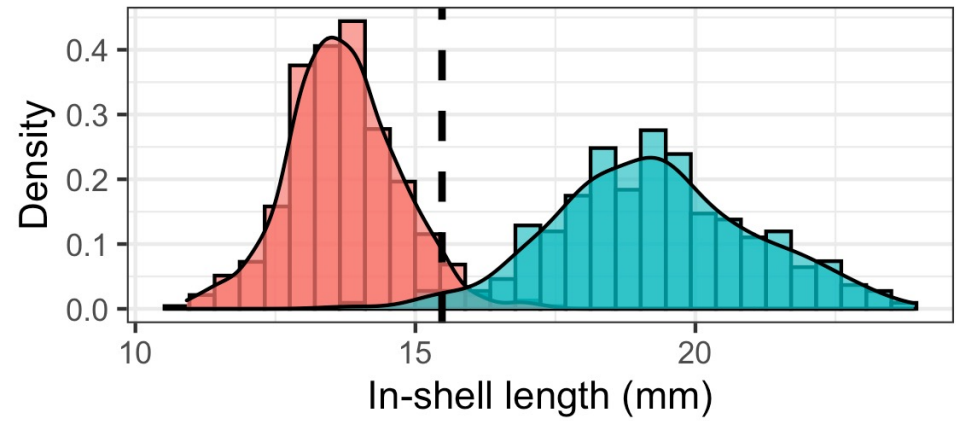


Populations that we are targeting

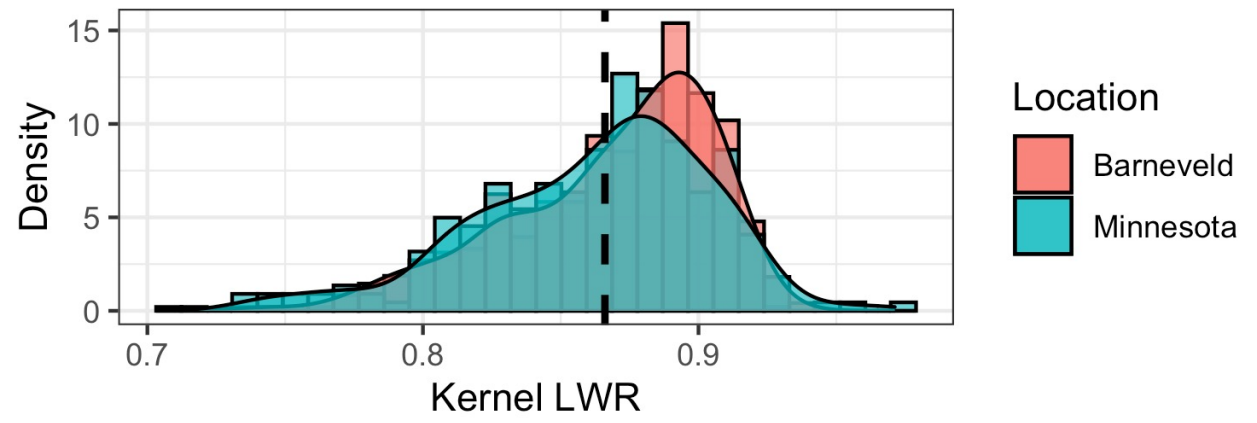
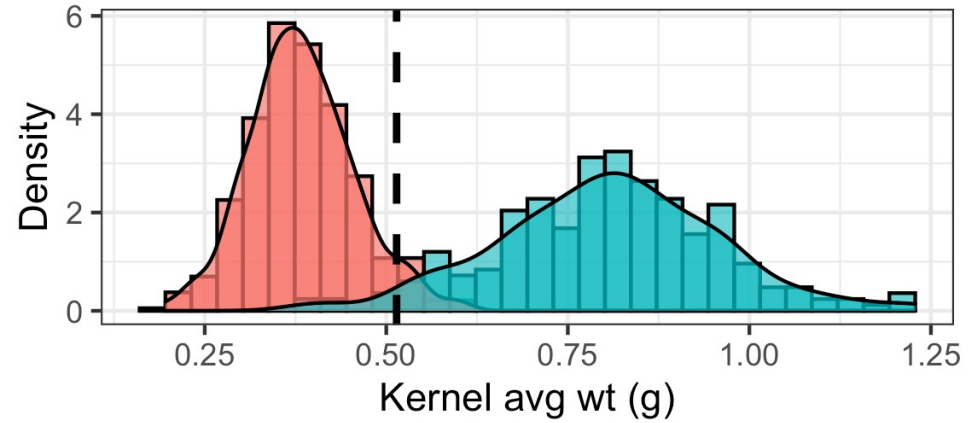
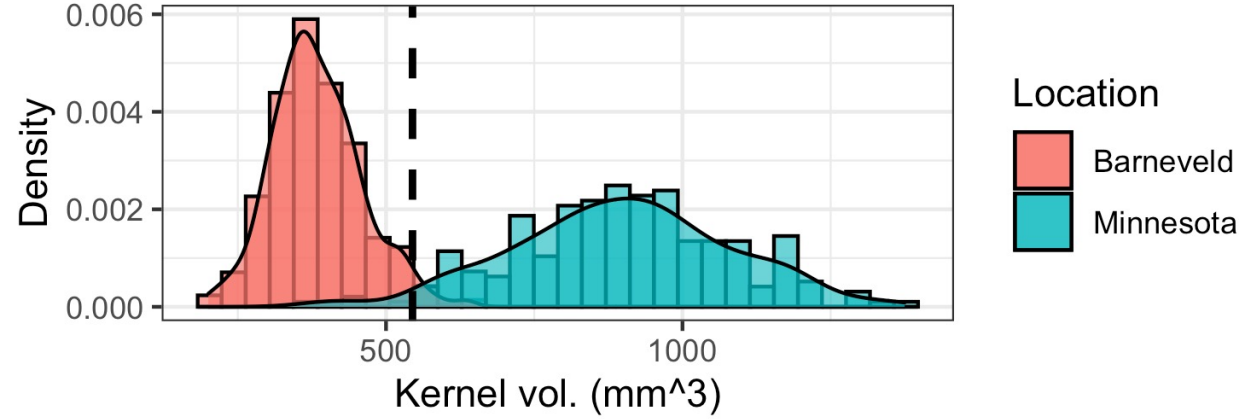
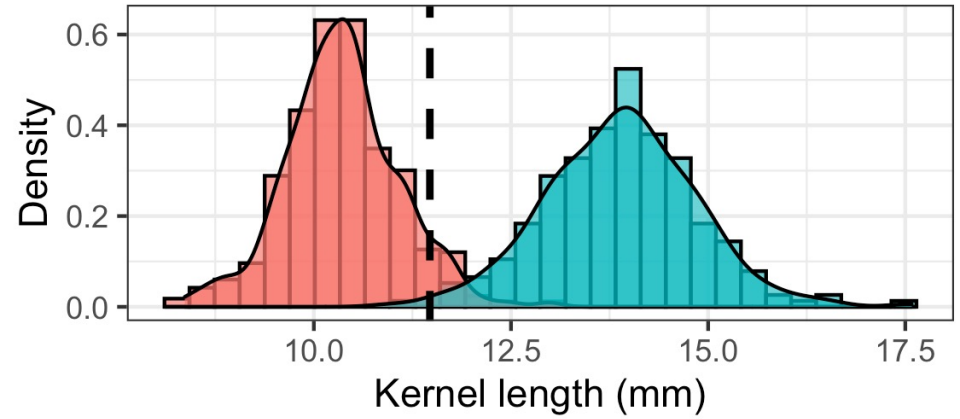
2. A population of wild American hazelnuts from the Department of Natural Resources, that are growing near Barneveld, WI (~500 bushes)



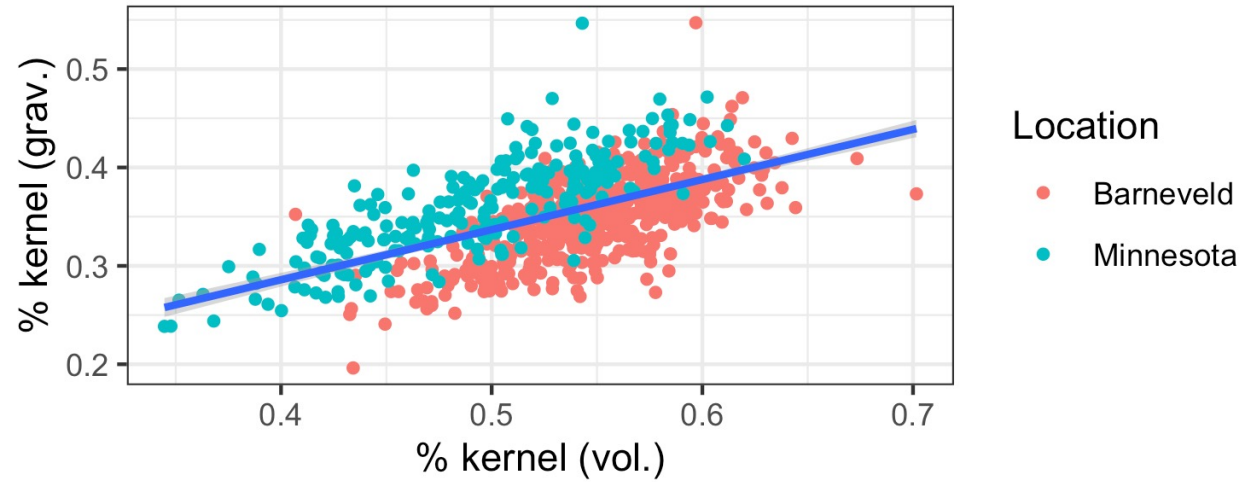
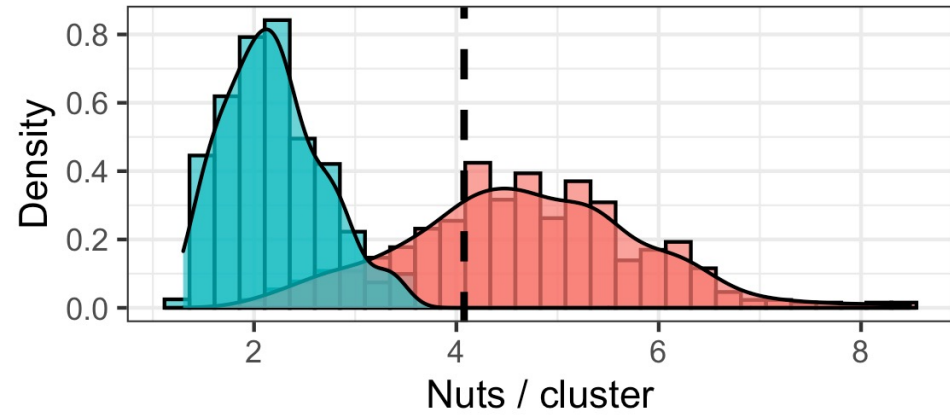
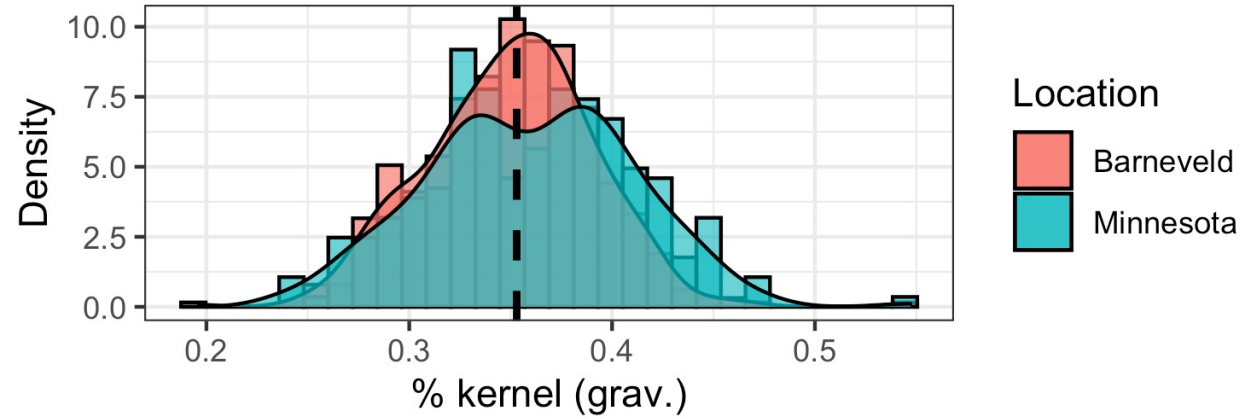
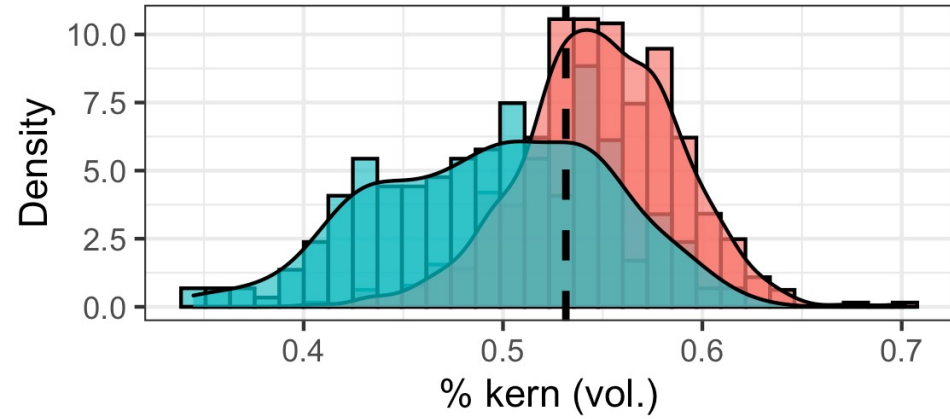
In-shell traits



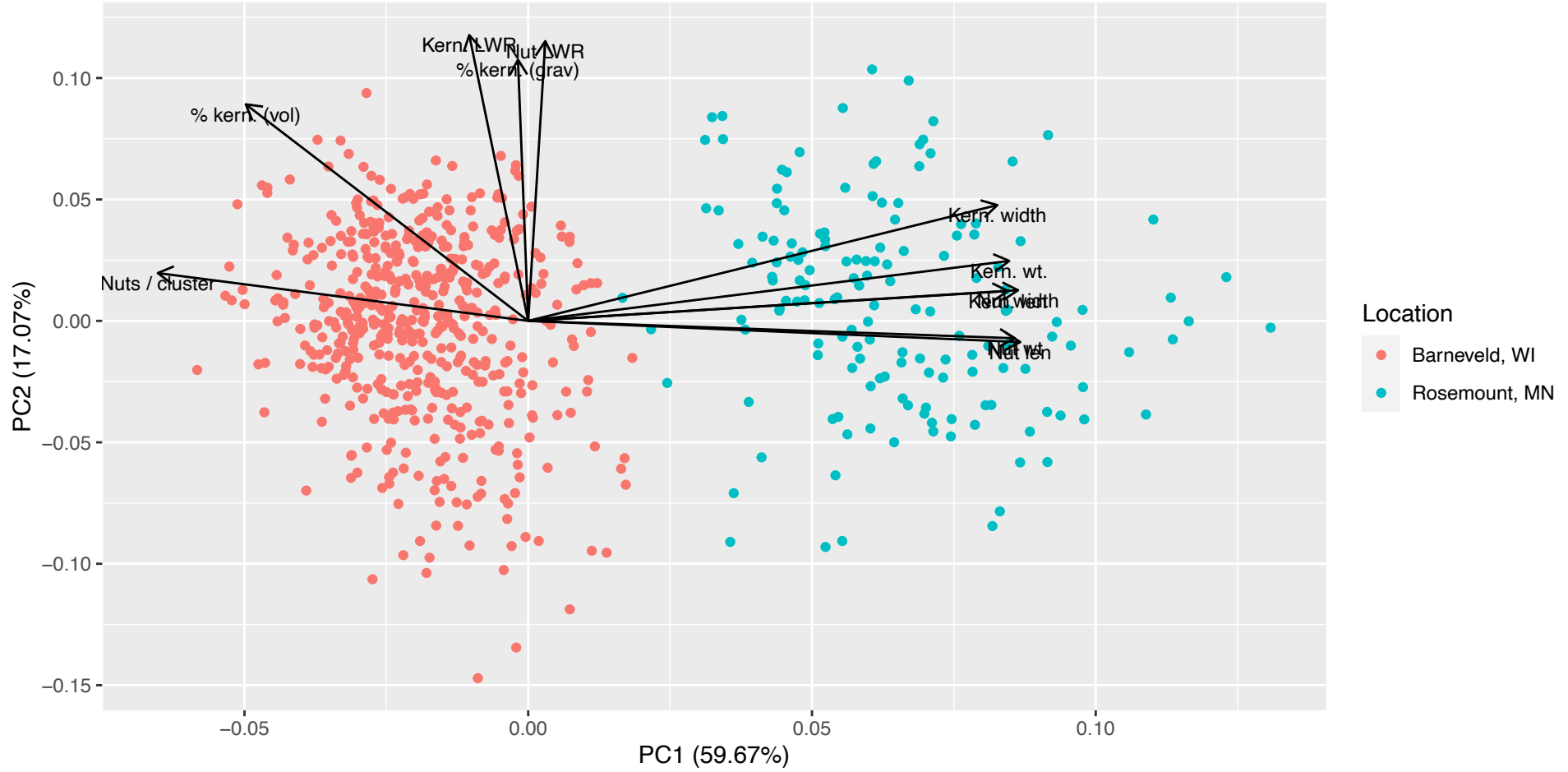
Kernel traits



Nut traits



PCA



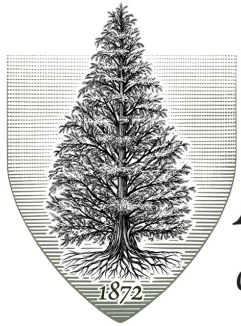
Timeline

1. Phenotype harvests from 2019, 2020, 2021: complete
2. Genotype all plants: underway
3. Build models to understand genetic control of key traits (single gene vs. polygenic): summer 2022
4. Use models to make about parents to use in crosses: in time for 2023 crosses!

Funding



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