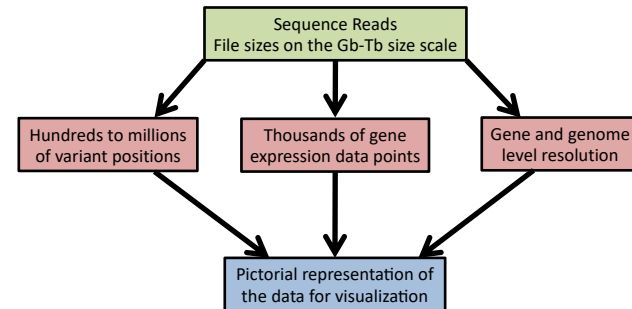
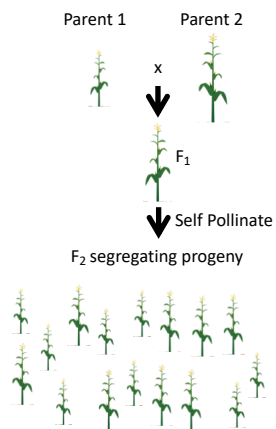


Data Visualization in R – Exercise 1

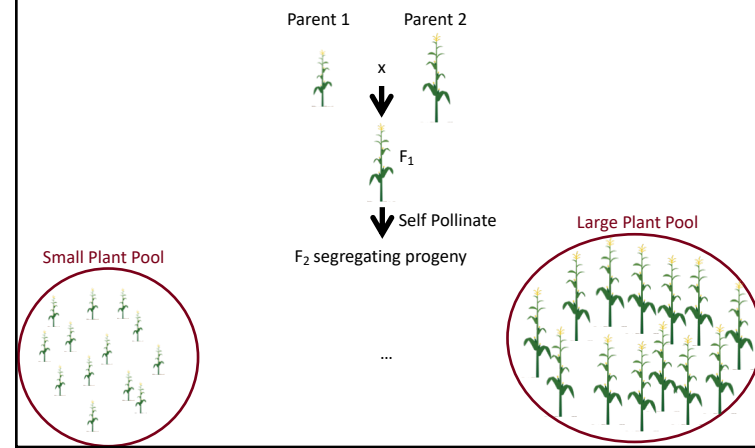
Visualizing Genomic Data



Bulk Segregant Analysis Dataset



Bulk Segregant Analysis Dataset



Bulk Segregant Analysis Dataset

Parent 1 Parent 2

Analysis Output:
Allele Frequencies
Significant Regions

In Groups: What are ways we could visualize this data?

Small Plant Pool ... Plant Pool

Data Visualization in R – Exercise 2

TE Insertional Polymorphisms

OXFORD G3 Genes | Genomes | Genetics

G3, 2021, 11(10), jkab238
DOI: 10.1093/g3journal/11/kab238
Advance Access Publication Date: 29 June 2021
Investigation

Whole-genome variation of transposable element insertions in a maize diversity panel

Yinjie Qiu^{1,2}, Christine H. O'Connor^{1,2,3}, Rafael Della Coletta¹, Jonathan S. Renk¹, Patrick J. Monahan^{1,2}, Jaclyn M. Noshay^{1,2}, Zhikai Liang², Amanda Gilbert¹, Sarah N. Anderson², Suzanne E. McGaugh², Nathan M. Springer^{1,3}, and Candice N. Hirsch^{1,4}

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²Department of Ecology, Evolution and Behavior, University of Minnesota, St. Paul, MN 55108, USA
³Department of Plant and Microbial Biology, University of Minnesota, St. Paul, MN 55108, USA
⁴Department of Genetics, Development, and Cell Biology, Iowa State University, Ames, IA 50011, USA

Also on course GitHub

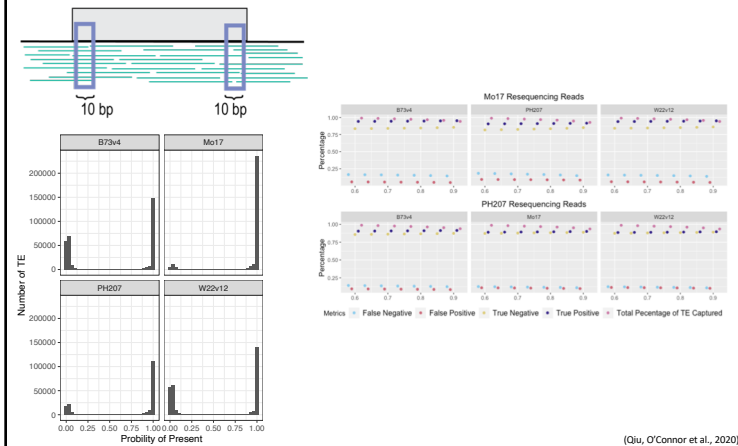
TE Insertional Polymorphisms

Yinjie Qiu

- Subset of ~500 lines
- Selected to flower within a two week window

(Qiu, O'Connor et al., 2020)

TE Insertional Polymorphisms



Let's look at all of the manuscript figures...

Lets check out the code...

Data Availability: All sequence data is available on the NCBI SRA (BioProject PRJNA661271, Table S1). Code for this study is available at https://github.com/HirschLabUMN/TE_variation.

RESULTS AND DISCUSSION

Using short read sequence data to identify TE presence/absence: For this study, we

https://github.com/HirschLabUMN/TE_variation

Breakout Groups

- Pick out a plot from the paper
- Go to the GitHub repository
- Explore the code used to generate that plot!