

Updating Training Data for Long-Term Genomewide Selection

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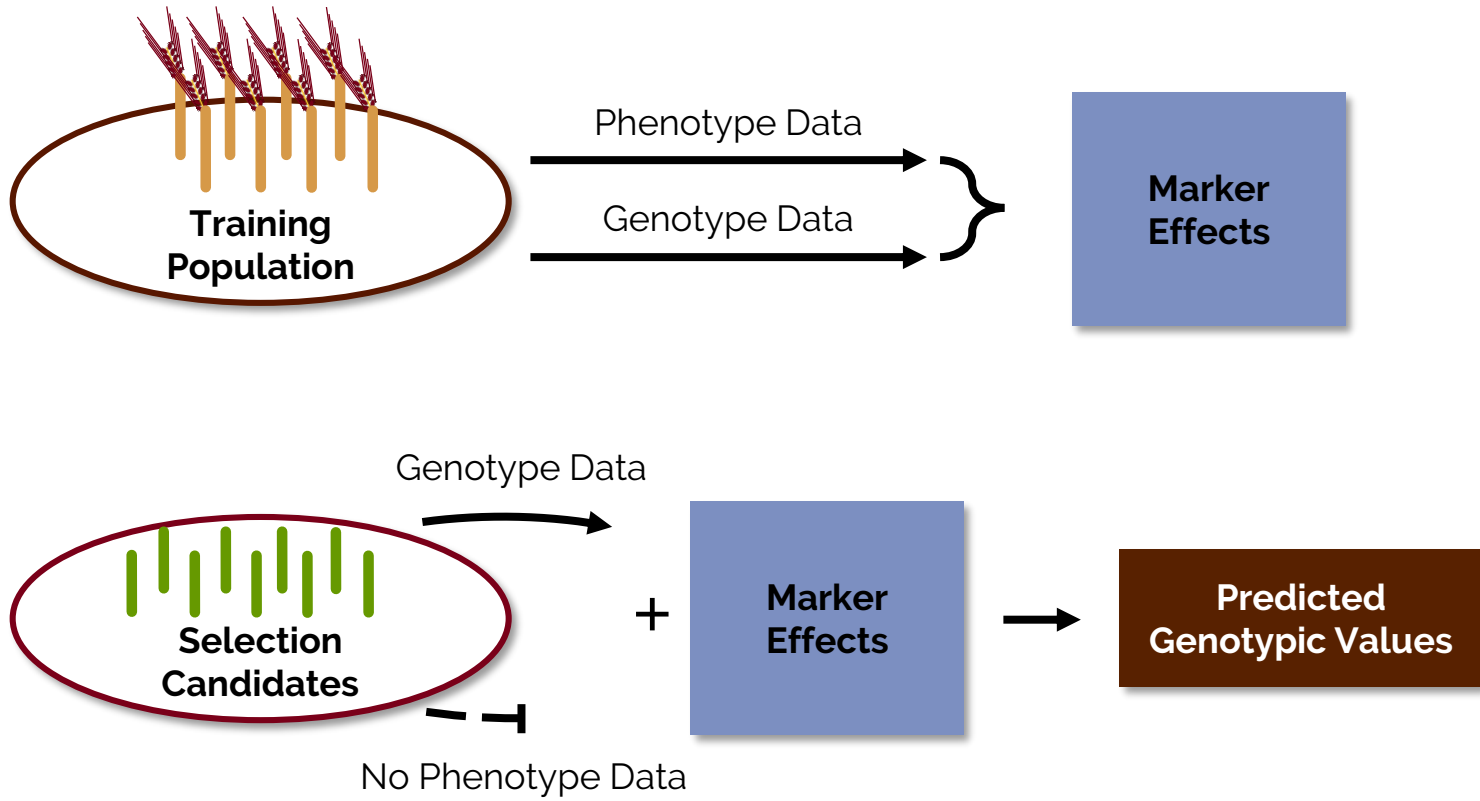
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slides: z.umn.edu/jnucdpss



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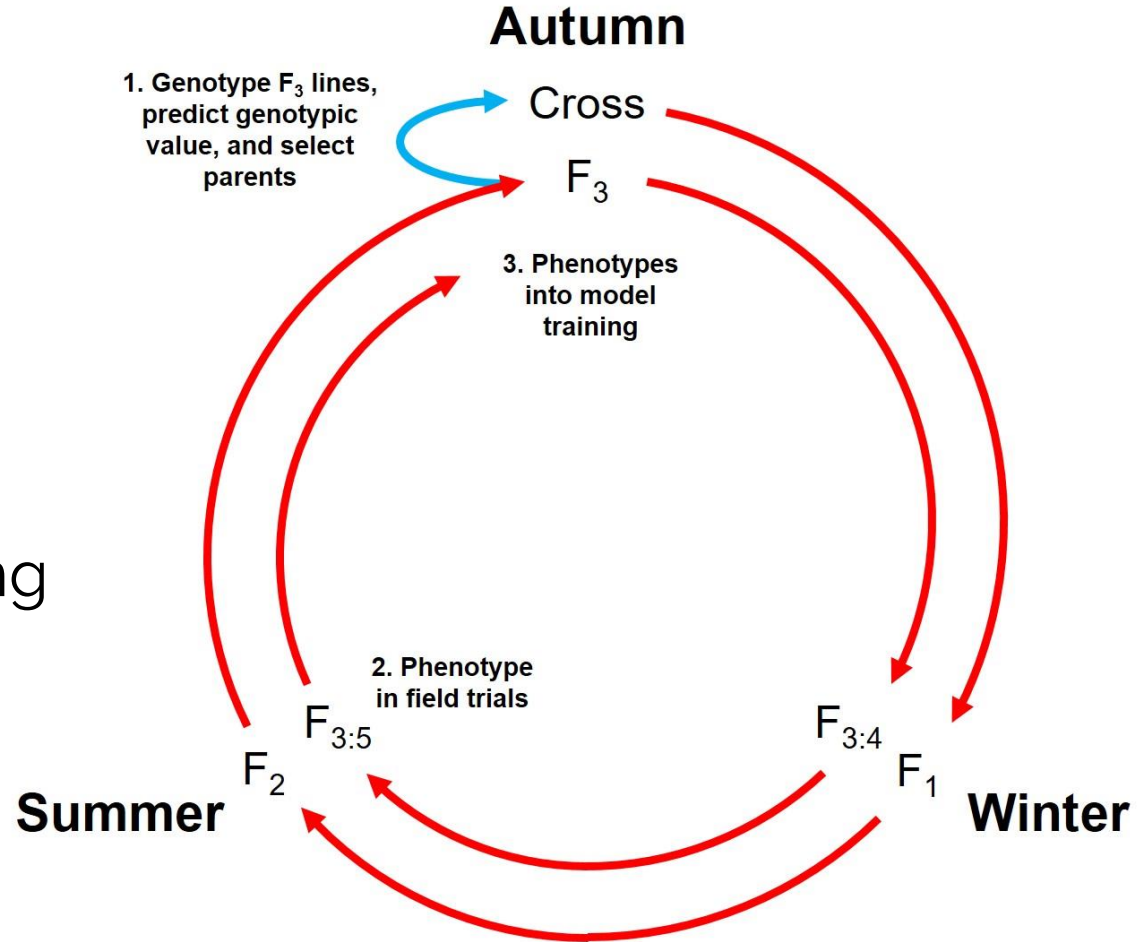
Driven to DiscoverSM



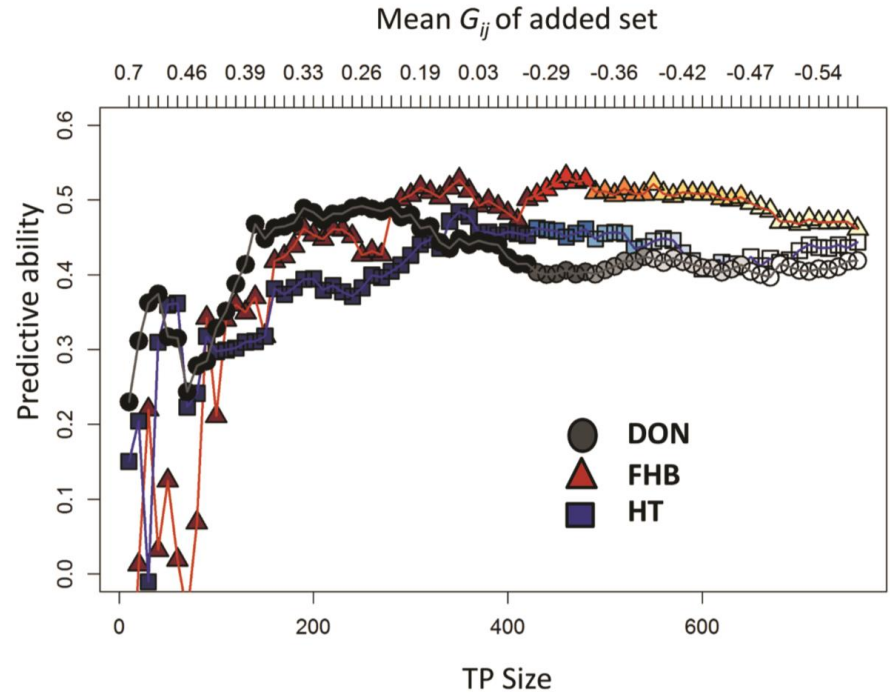
Genomewide selection to rapidly
improve Minnesota spring two-
row barley



A barley breeding program using genomewide selection can complete a breeding cycle in 1 year



Prediction accuracy depends on several factors, including *training population design*



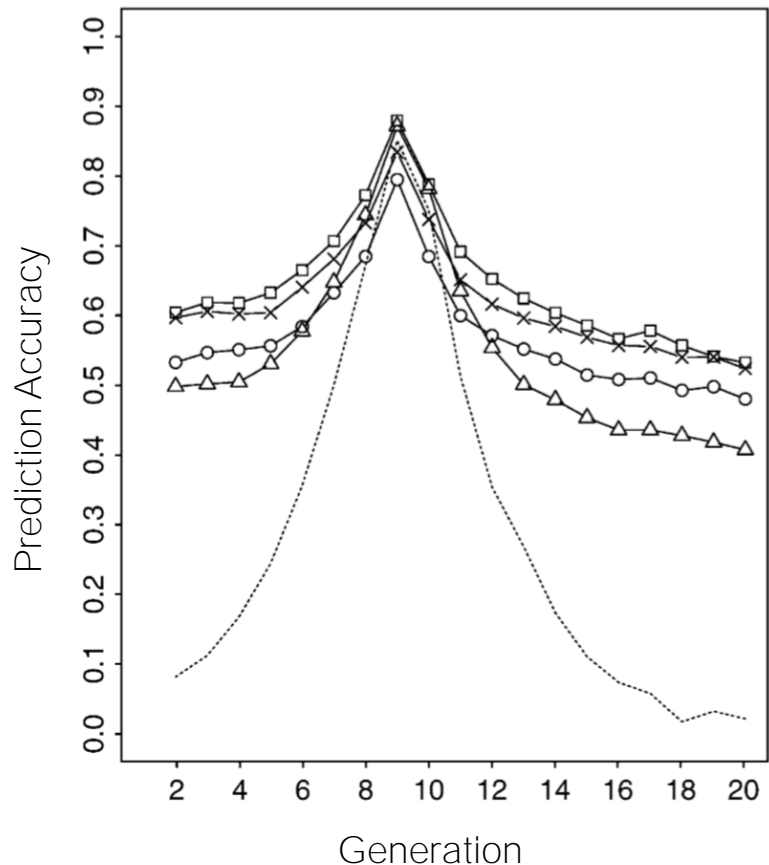
Modified from Lorenz and Smith 2015 *Crop Science*

Properties of recurrent selection will alter prediction accuracy

Recombination breaks marker-QTL linkage disequilibrium

Training population becomes more distant to selection candidates

What are efficient methods to update the training population?



Objectives

Simulate a barley genomewide selection program

Determine optimal methods to update training data

Suggest implications for a breeding program

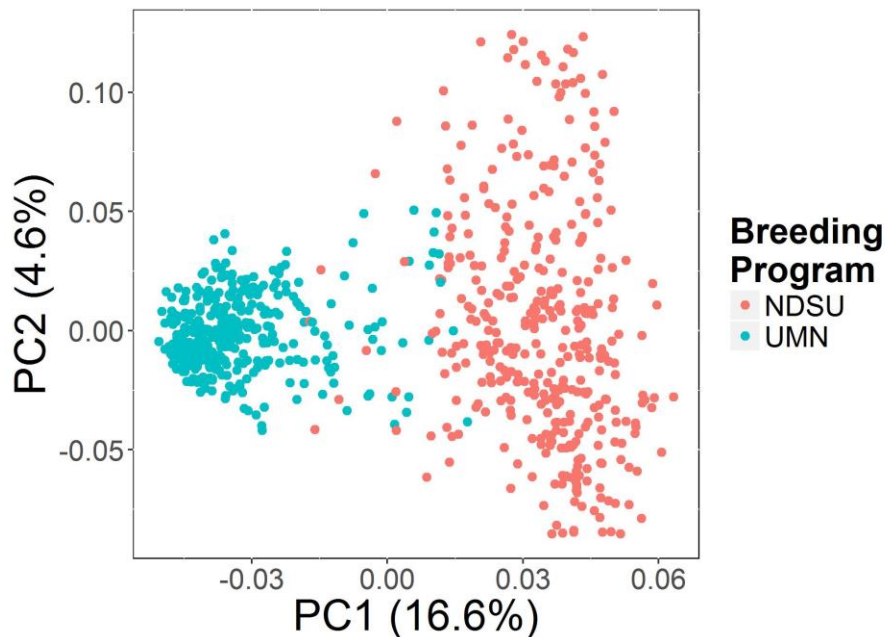


Starting material

Historical genotype data on 764
barley breeding lines

Simulated a trait controlled by 100
QTL and $h^2 = 0.5$

15 cycles of genomewide
recurrent selection



Three streams per cycle

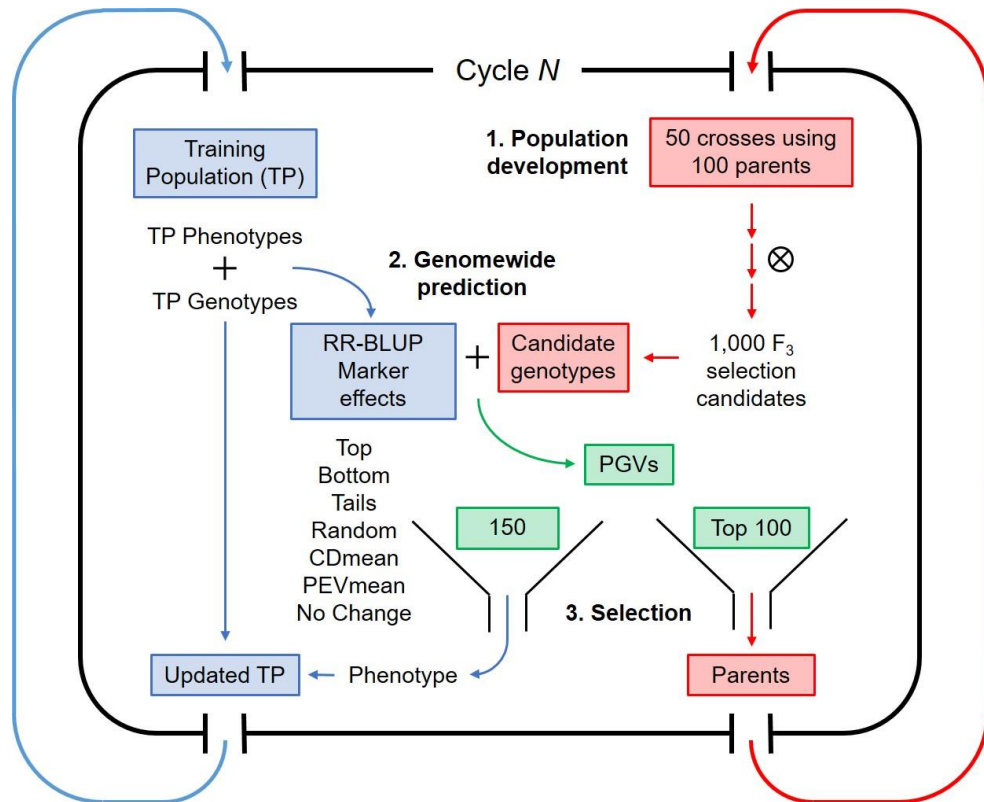
Blue: steps to manage the training population

Red: steps to create populations

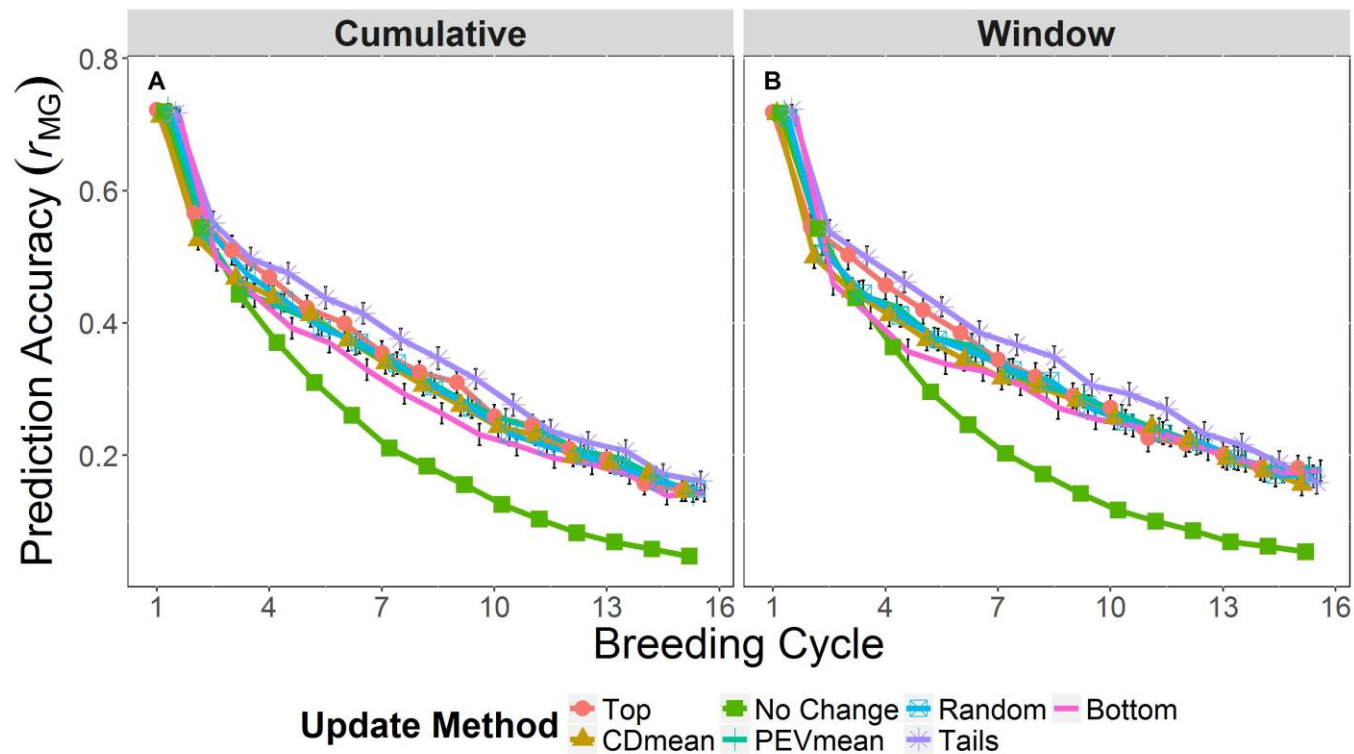
Green: steps to select parents and lines to update the training population

Two updating scenarios

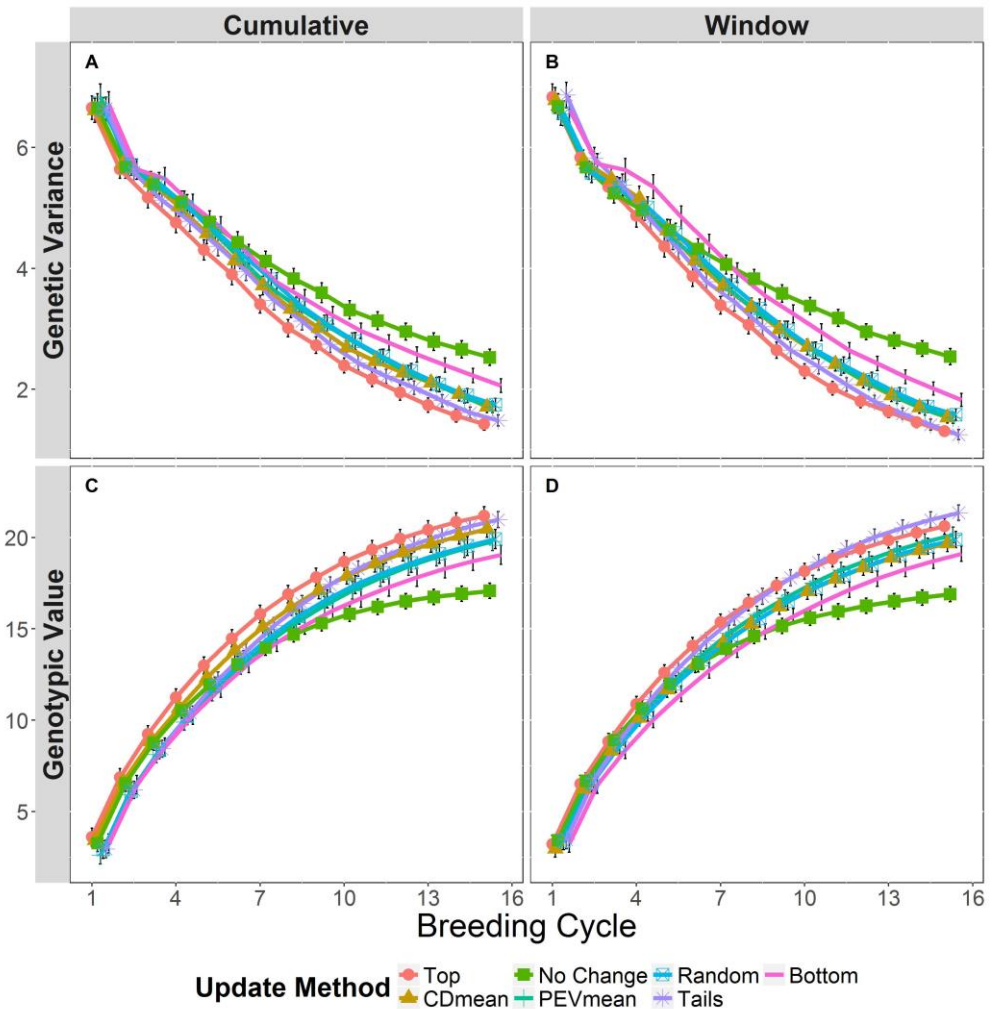
- Cumulative
- Window



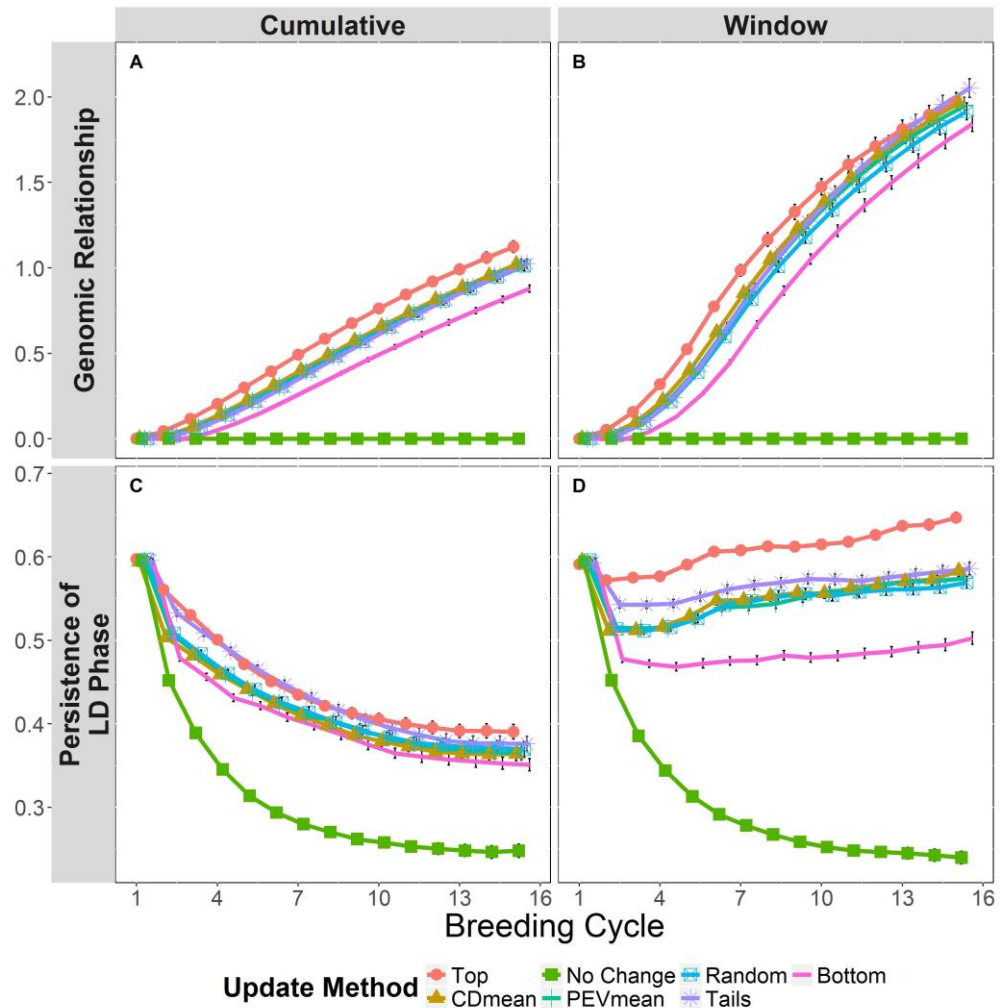
Updating with something is better than nothing



Patterns of genetic variance and response to selection reflect prediction accuracy



Training populations updated via *Top* or *Tails* are more closely related to selection candidates and maintain LD phase



Implications

Training data must be updated

Breeders can update using data from typical selections

More recent data is informative



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Questions?

Early online paper in G3: Genes|Genomes|Genetics
doi: *10.1534/g3.117.040550*

Data access

github.com/UMN-BarleyOatSilphium/GSSimTPUpdate