University of Florida
Sweet Corn and Potato Breeding and Genomics Lab
CANVAS – Salt Lake City, 2025

Enhancing Breeding Efficiency: Prediction and Optimization of Breeding Crosses for Long-term Genetic Gain and Diversity

MATE
ALLOCATION
of breeding crosses

Marco Antonio Peixoto* and Marcio Resende

Rationale

- **Genomic selection**: the use of molecular markers and historical phenotypes to predict new unseen individuals.
- It has **revolutionized** animal/plant breeding programs.

1. Selection accuracy
2. Shorten breeding cycles

▼

High performance

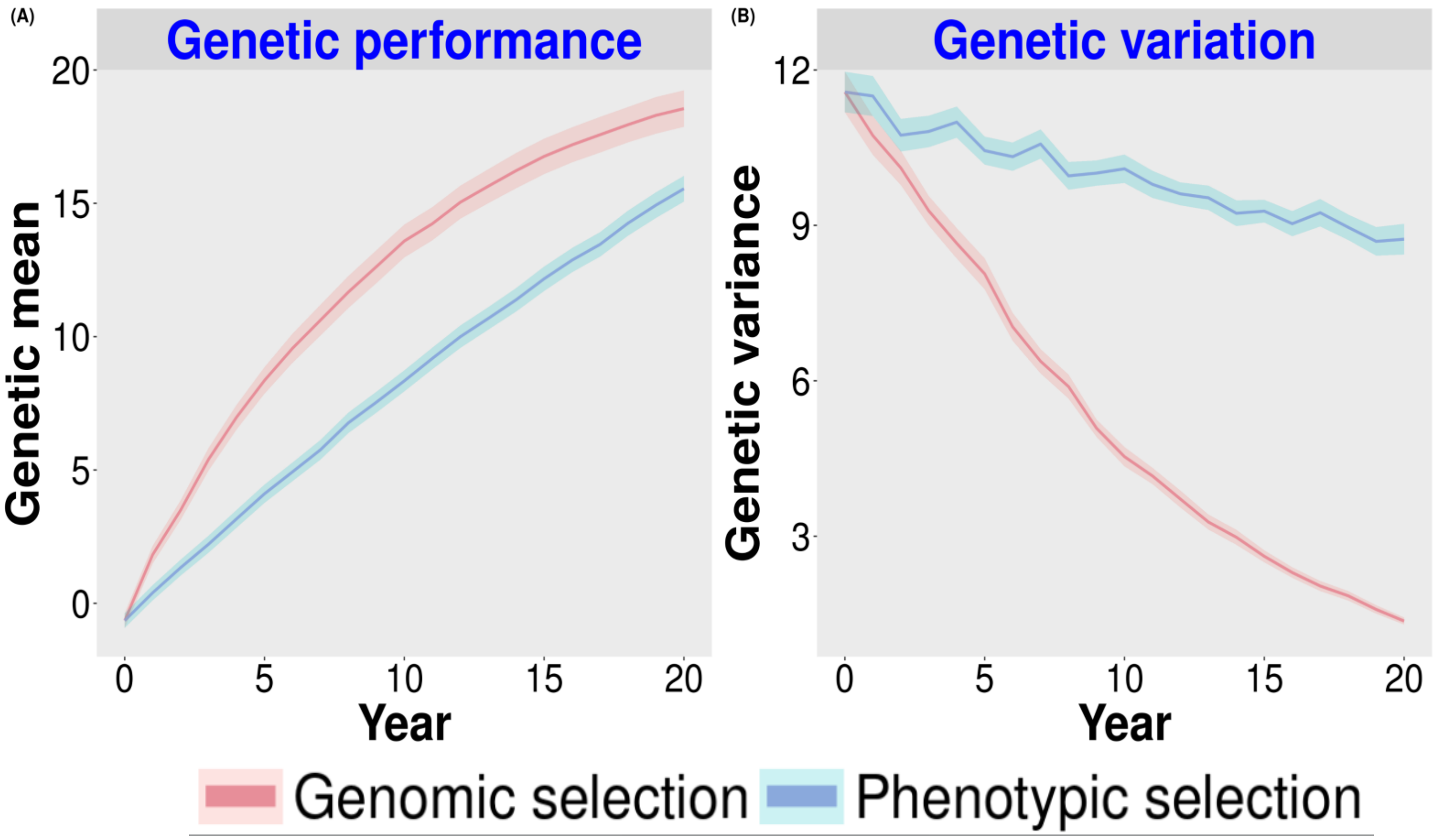
Rationale

- **Genomic selection**: the use of molecular markers and historical phenotypes to predict new unseen individuals.
- It has **revolutionized** animal/plant breeding programs.

1. Selection accuracy
2. Shorten breeding cycles

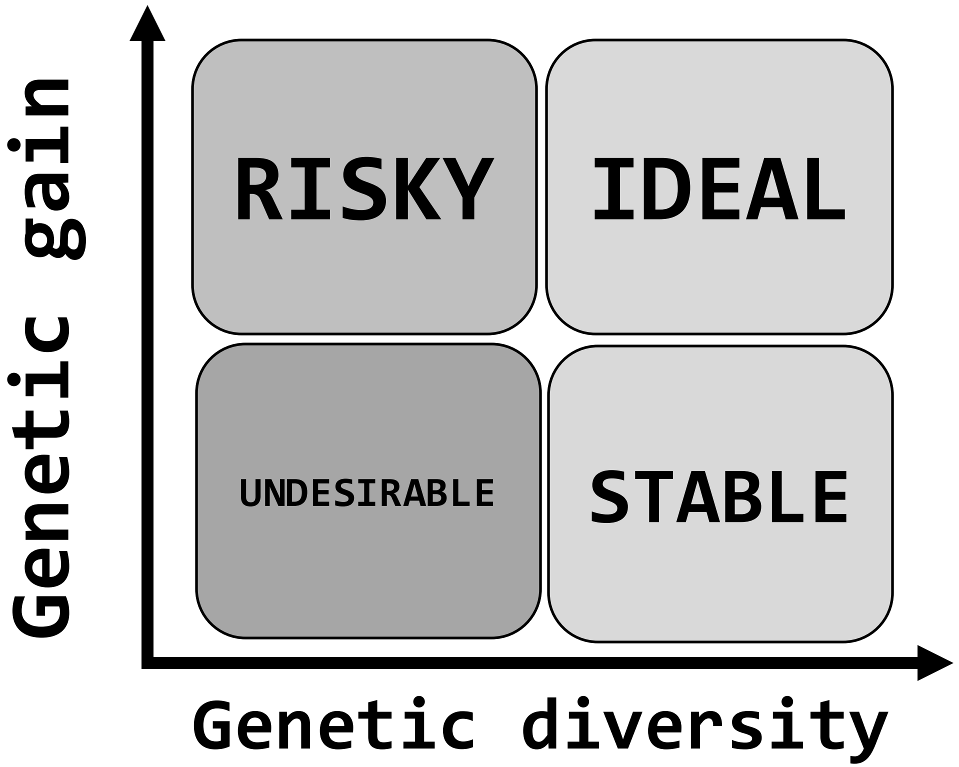
▼

High performance



Rationale

Problem



Genetic gain

RISKY

IDEAL

UNDESIRABLE

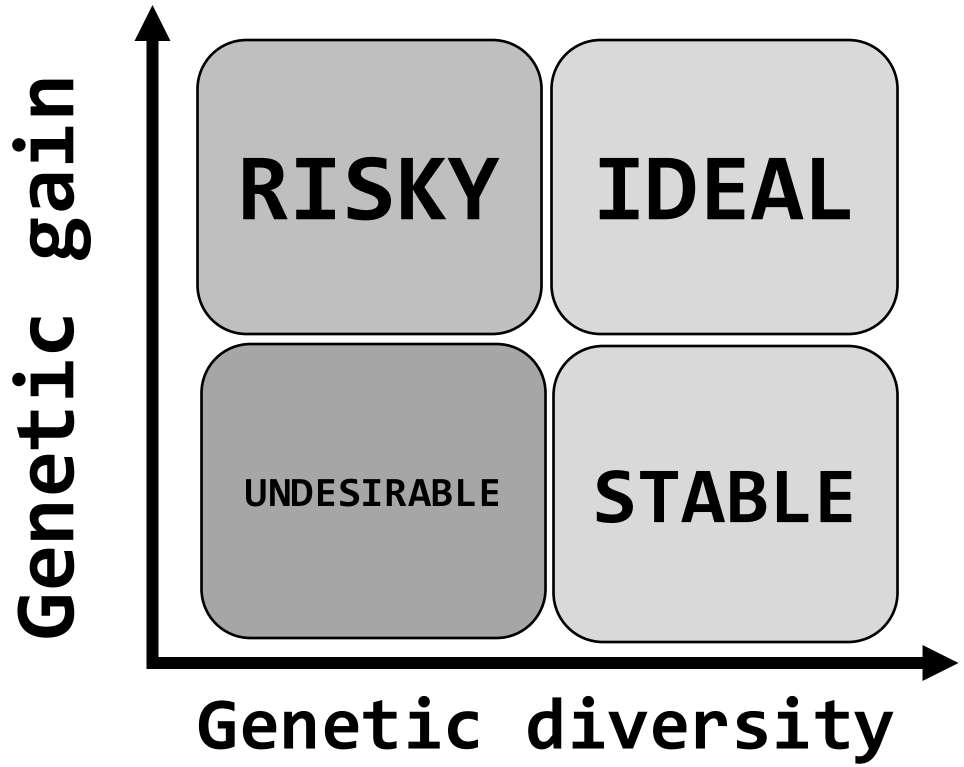
STABLE

Genetic diversity

Rationale

MATE ALLOCATION
of breeding crosses

Problem

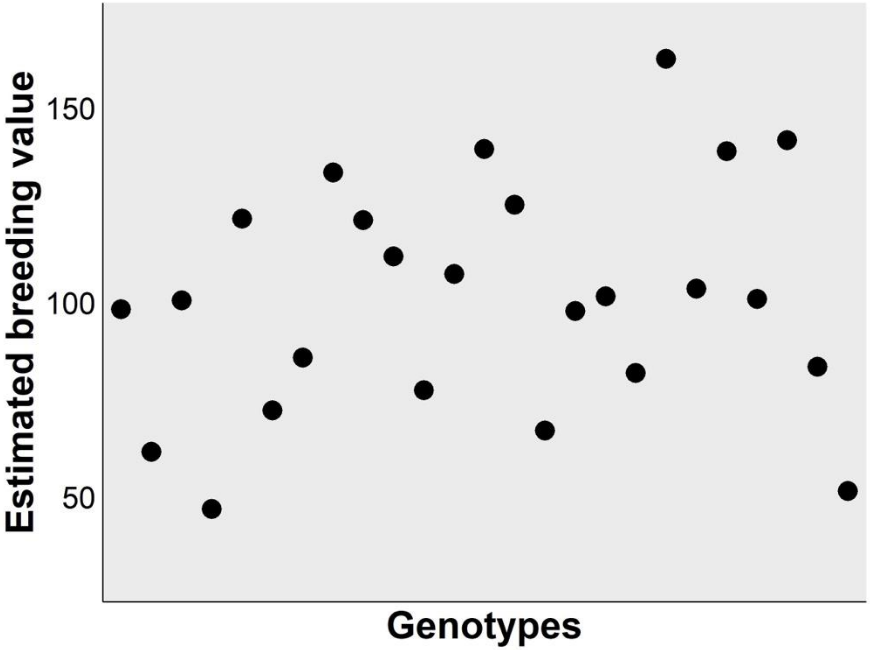


How do we balance rapid improvement with long-term sustainability in breeding programs?

Rationale

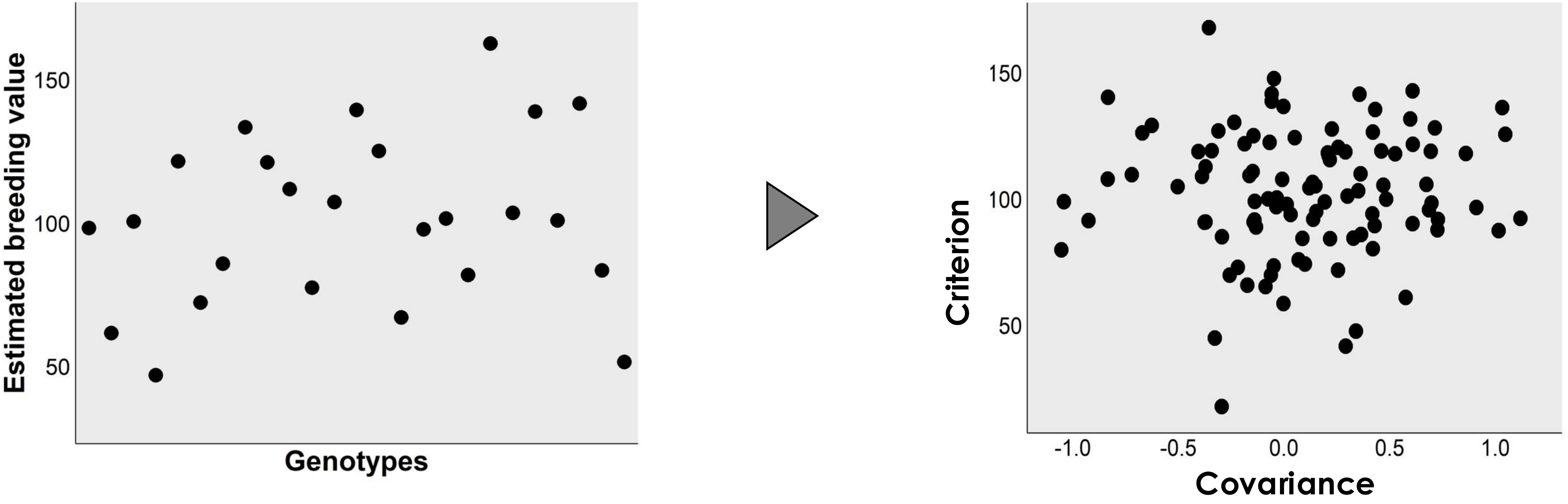
MATE ALLOCATION
of breeding crosses

Selection of parental combinations: optimal cross selection



Rationale

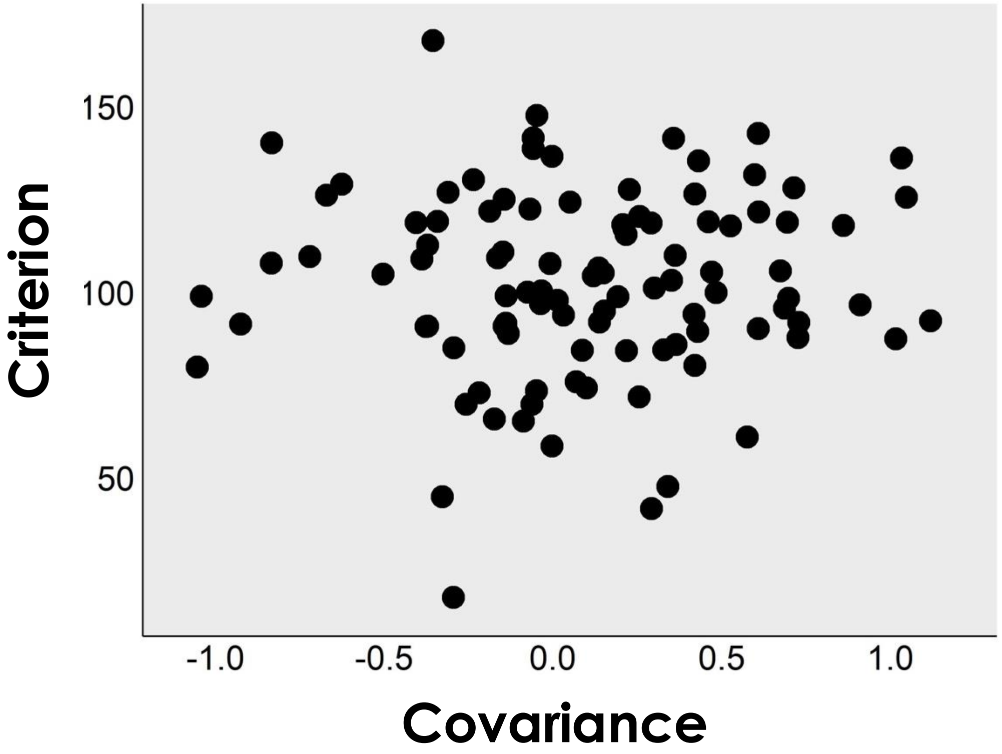
Selection of parental combinations: optimal cross selection



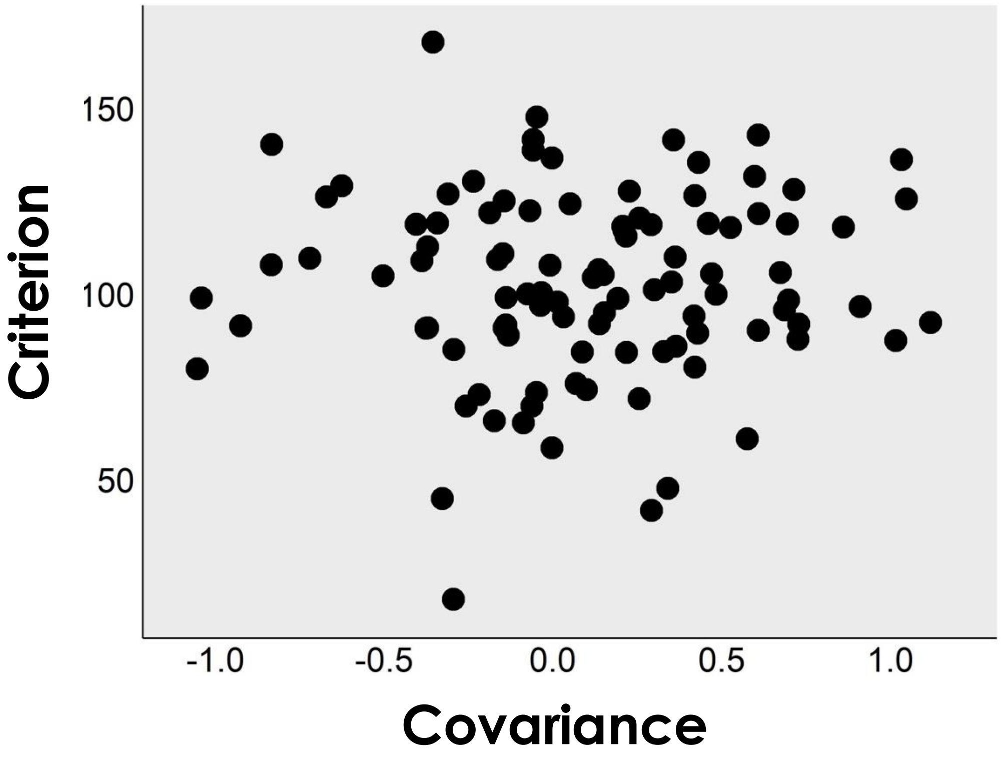
$$\mu_{ebv} = \frac{EBV_{p1} + EBV_{p2}}{2}$$

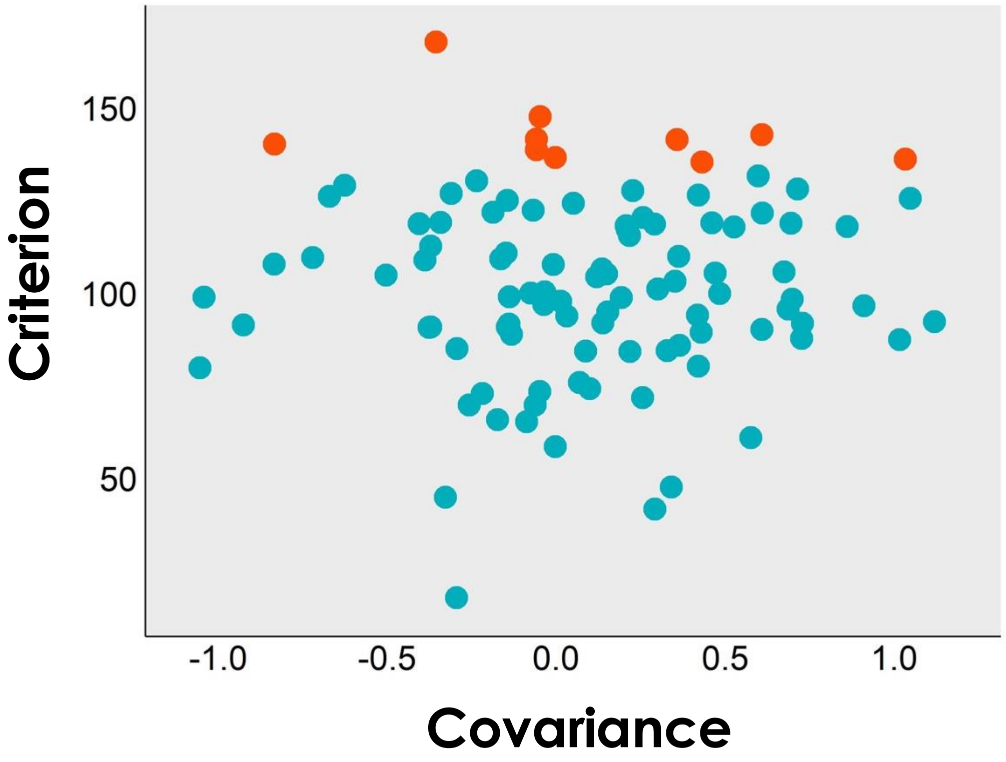
Akdemir et al. 2016, Gorjanc et al. 2018, Kinghorn, 1999

Optimal cross selection



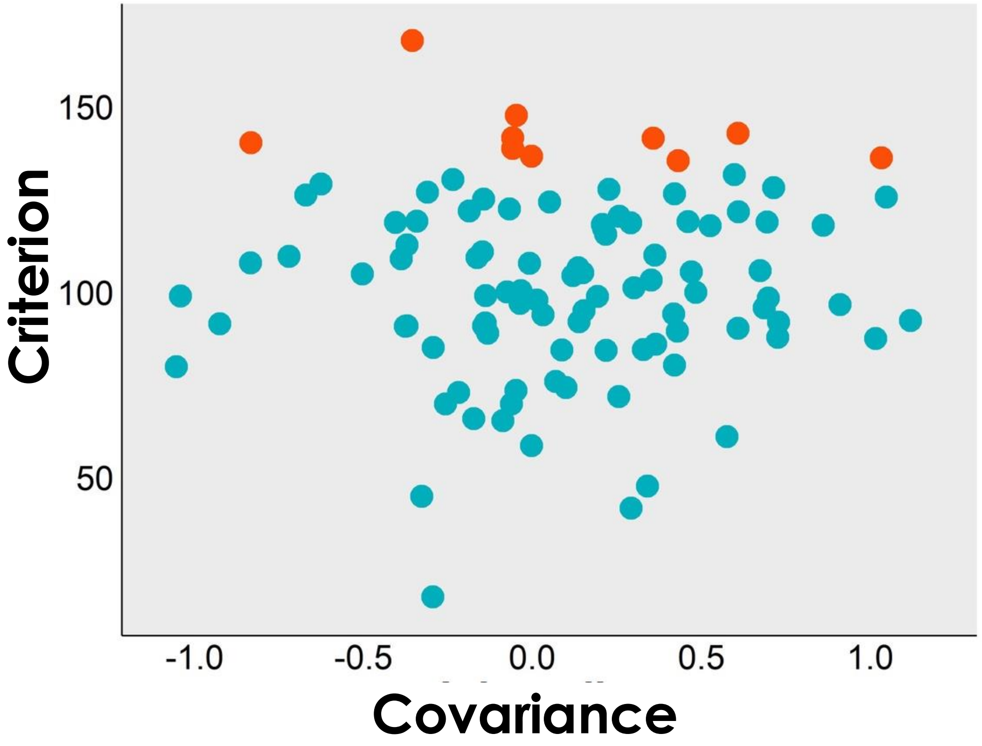
Optimal cross selection

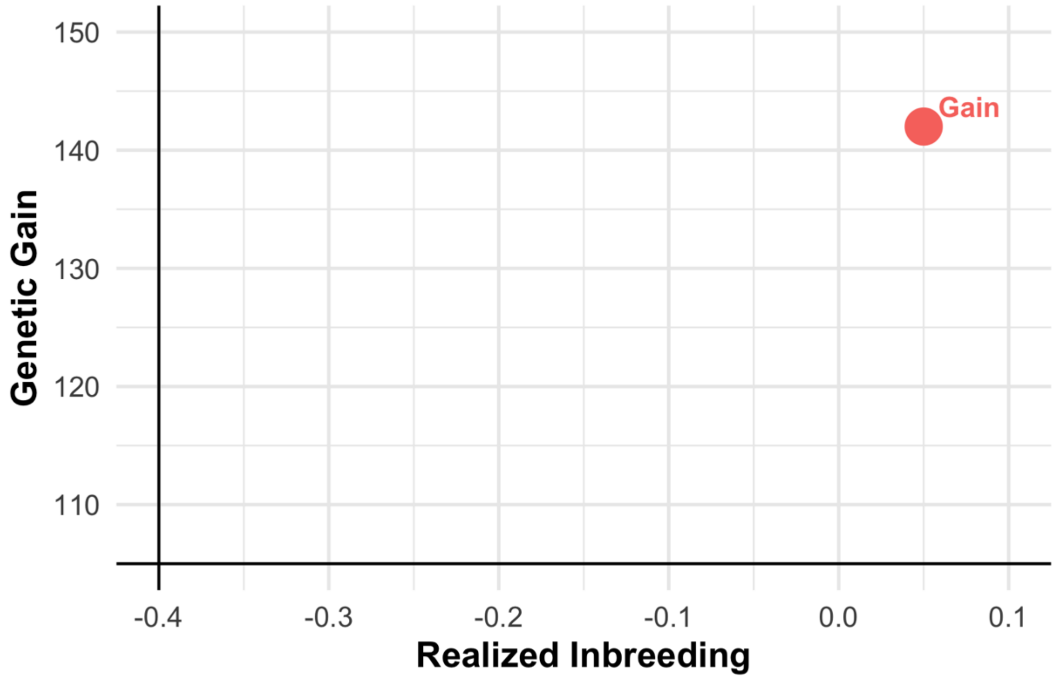




Optimal cross selection

MATE
ALLOCATION
of breeding crosses





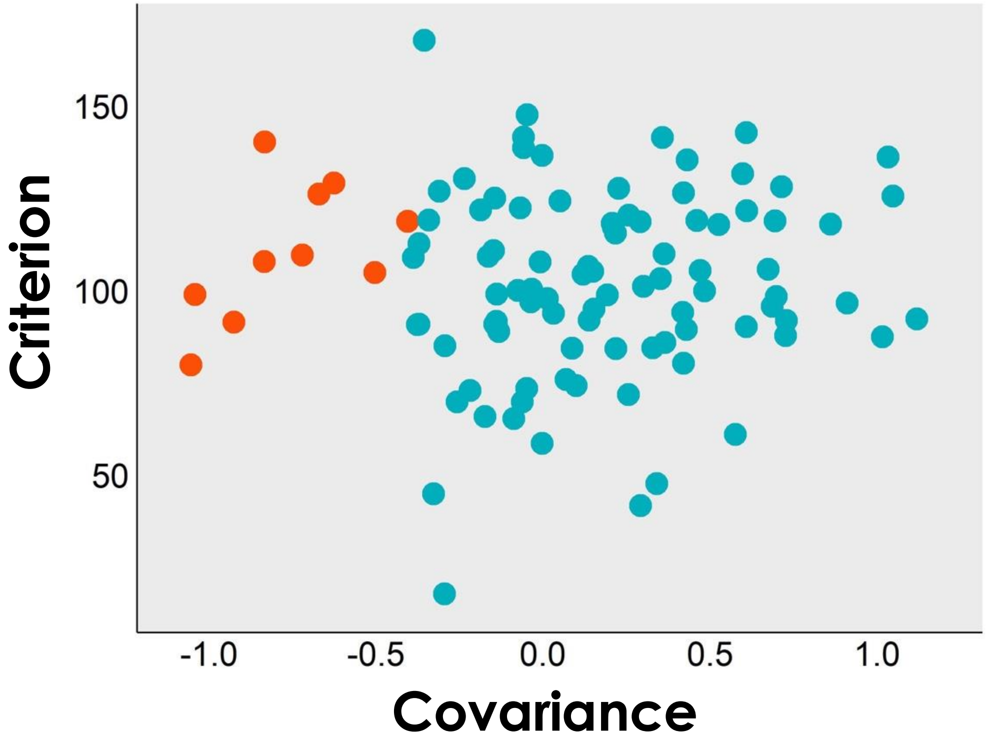
$$\frac{A}{2} = \text{Coancestry}$$

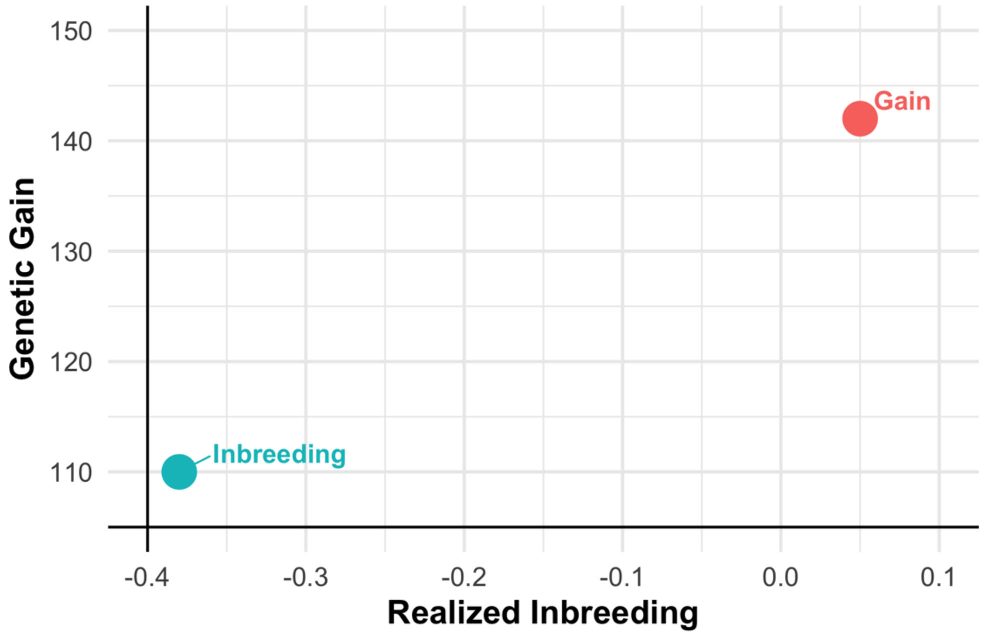
Coancestry (t) = Inbreeding (t+1)

Akdemir et al. 2016, Gorjanc et al. 2018, Kinghorn, 1999

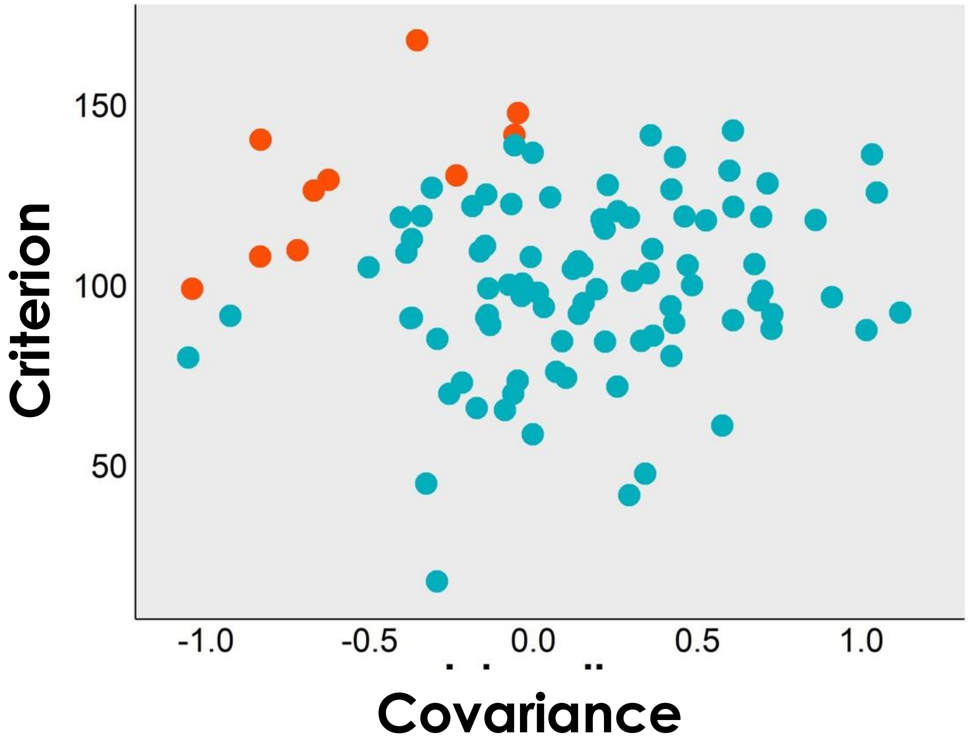
Optimal cross selection

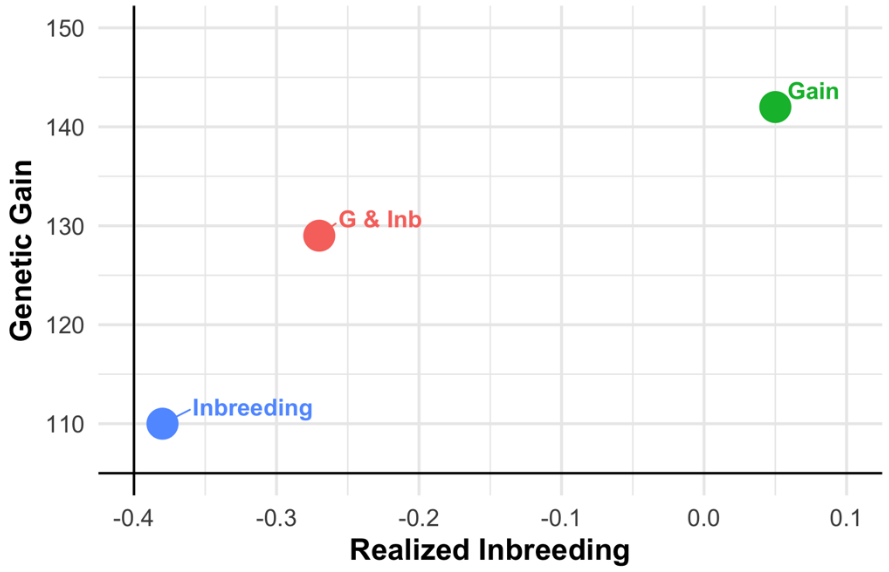
MATE ALLOCATION
of breeding crosses





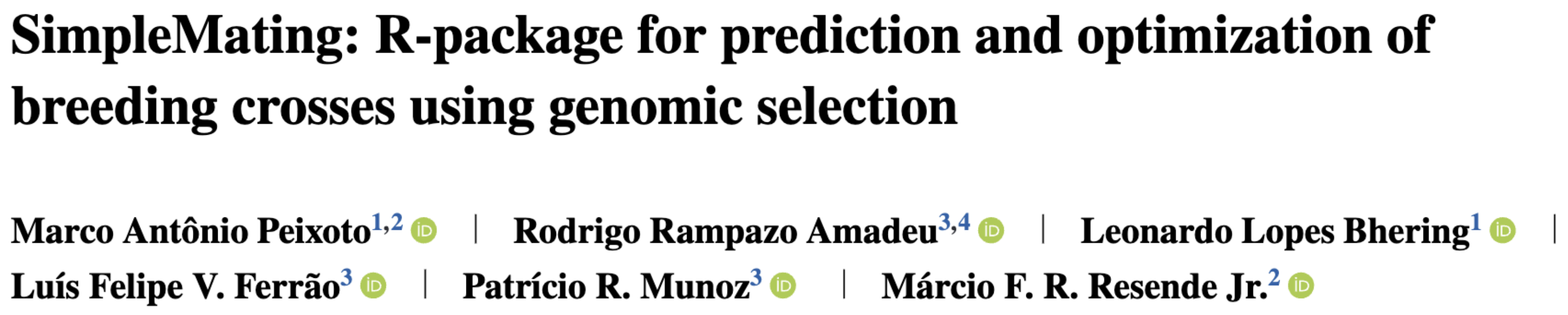
Optimal cross selection





SimpleMating

- Cross prediction and optimization



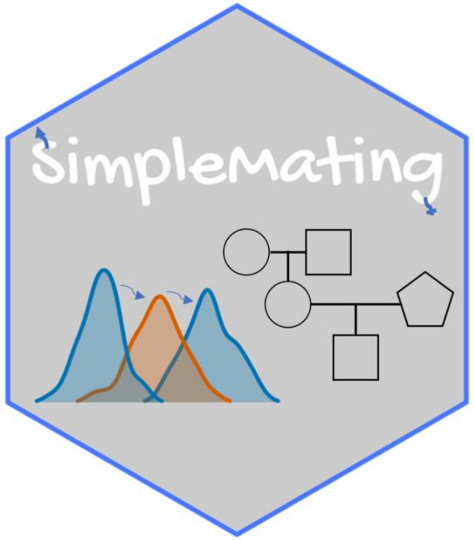
SimpleMating: R-package for prediction and optimization of breeding crosses using genomic selection

Marco Antônio Peixoto[1,2] | Rodrigo Rampazo Amadeu[3,4] | Leonardo Lopes Bhering[1] | Luís Felipe V. Ferrão[3] | Patrício R. Munoz[3] | Márcio F. R. Resende Jr.[2]

- Two module package

  i. Prediction of cross performance

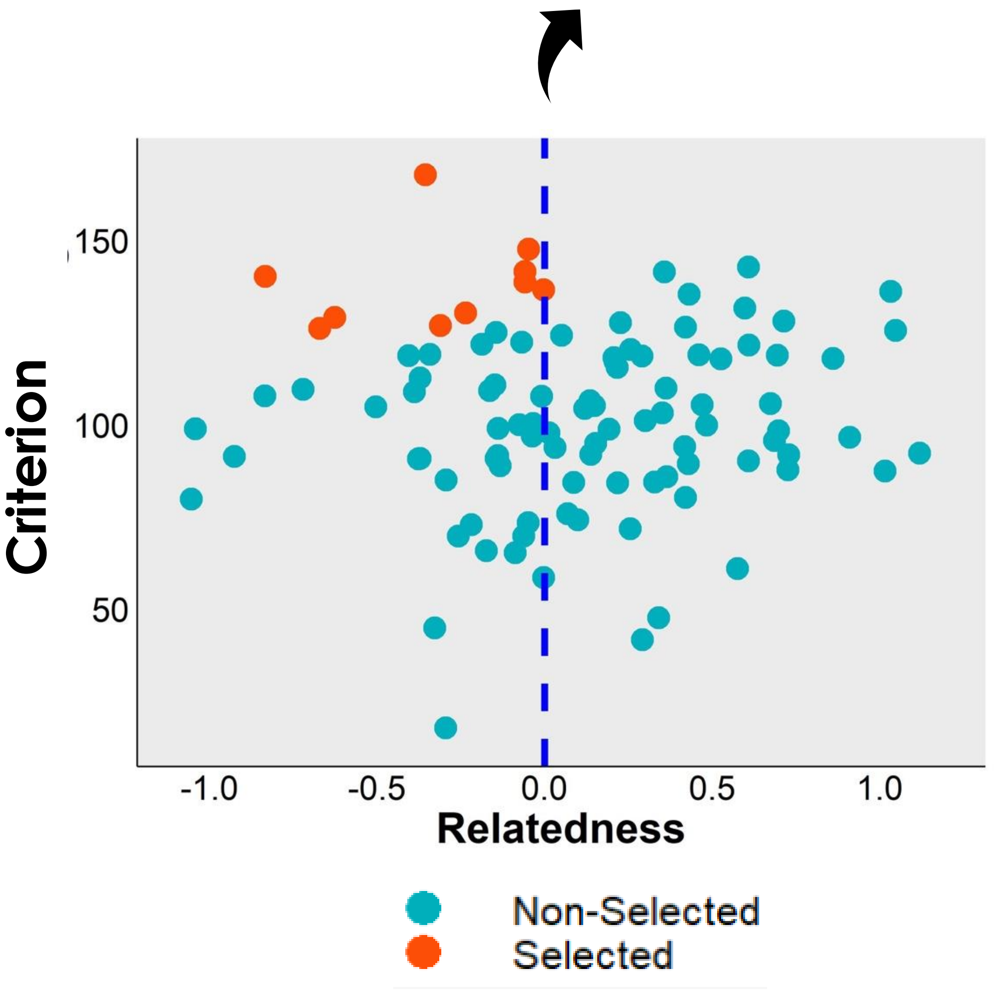
  ii. Optimization of crosses

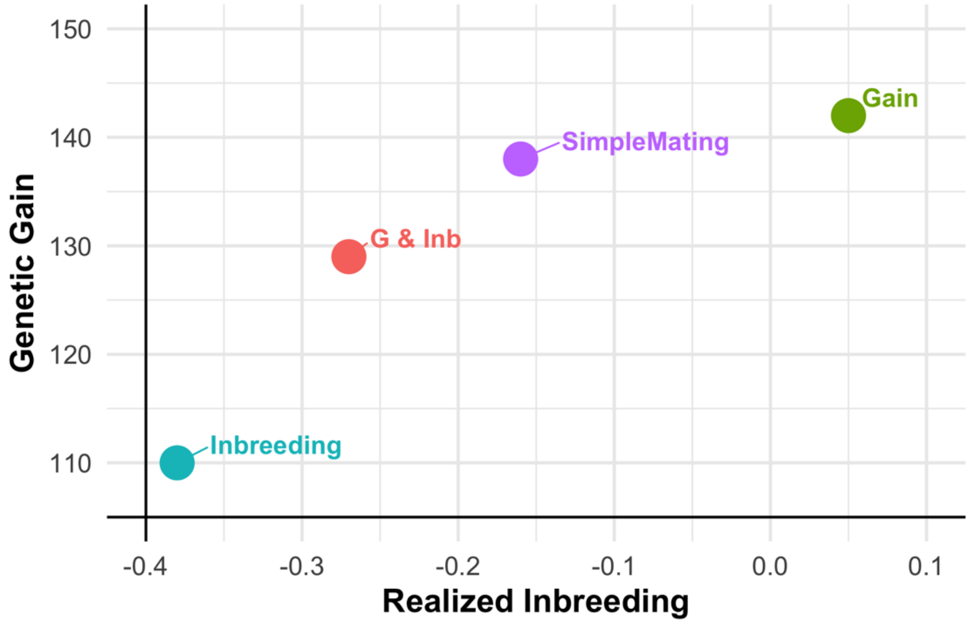


Peixoto et al. 2025

Optimal cross selection

MATE
ALLOCATION
of breeding crosses


Truncated threshold



Peixoto et al. 2025

SimpleMating: cross performance

① **Mid-parental value**

$$\mu_{ebv} = \frac{ebv_{p1} + ebv_{p2}}{2}$$

③ **Usefulness (A/AD)**

$$UC = \mu + i\sigma$$

② **Total genetic value**

$$\mu_{gv} = \sum_{i=1}^{n} [a_i(p_i - q_i - y_i) + d_i[2p_i q_i + y_i(p_i - q_i)]]$$

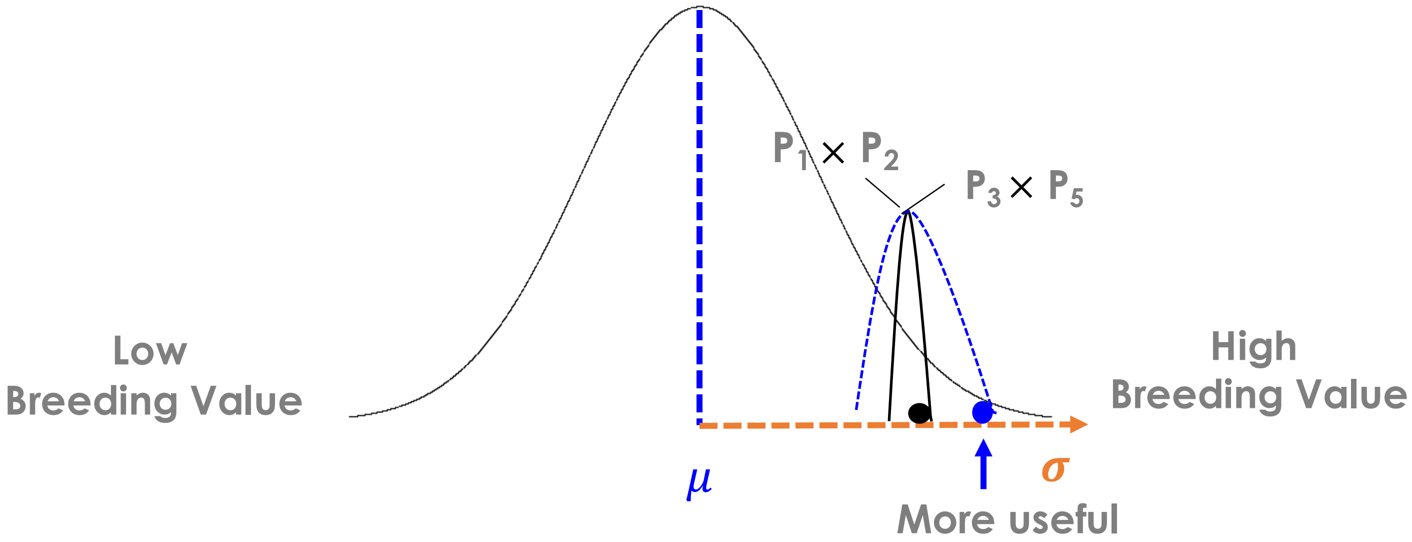
④ **Multi-trait for all above**

Mate allocation of breeding crosses
Canvas - 2025
Marco Peixoto | Marcio Resende

Falconer & Mackey, 1996, Wolfe et al. 2021, Lehermeier et al. 2017, Allier et al. 2019, Peixoto et al. 2025

SimpleMating – Cross performance

Prediction of cross performance: Usefulness



$$UC = \mu + i\sigma$$

μ = progeny mean
i = selection intensity
σ = progeny standard deviation

Schnell and Utz (1975)

Falconer & Mackey, 1996, Wolfe et al. 2021, Lehermeier et al. 2017, Allier et al. 2019, Peixoto et al. 2025

Prediction of cross performance

Output

```
### ----- 1. Performance prediction
ST_tgv2 <- getTGV(MatePlan = CrossPlan,
                  Markers = Markers,
                  addEff = addEff,
                  domEff = domEff,
                  K = relMat,
                  ploidy = 2)
```

```
### ----- 1. Performance prediction
usefAdd <-  getUsefA(MatePlan = CrossPlan,
                     Markers = Markers,
                     addEff = effAdd,
                     K = relMat,
                     Map.In = Map, # Genetic map
                     linkDes = NULL,
                     propSel = 0.05,
                     Type = "DH",
                     Generation = 1)
```

Peixoto et al. 2025

SimpleMating Module 2

MATE ALLOCATION
of breeding crosses

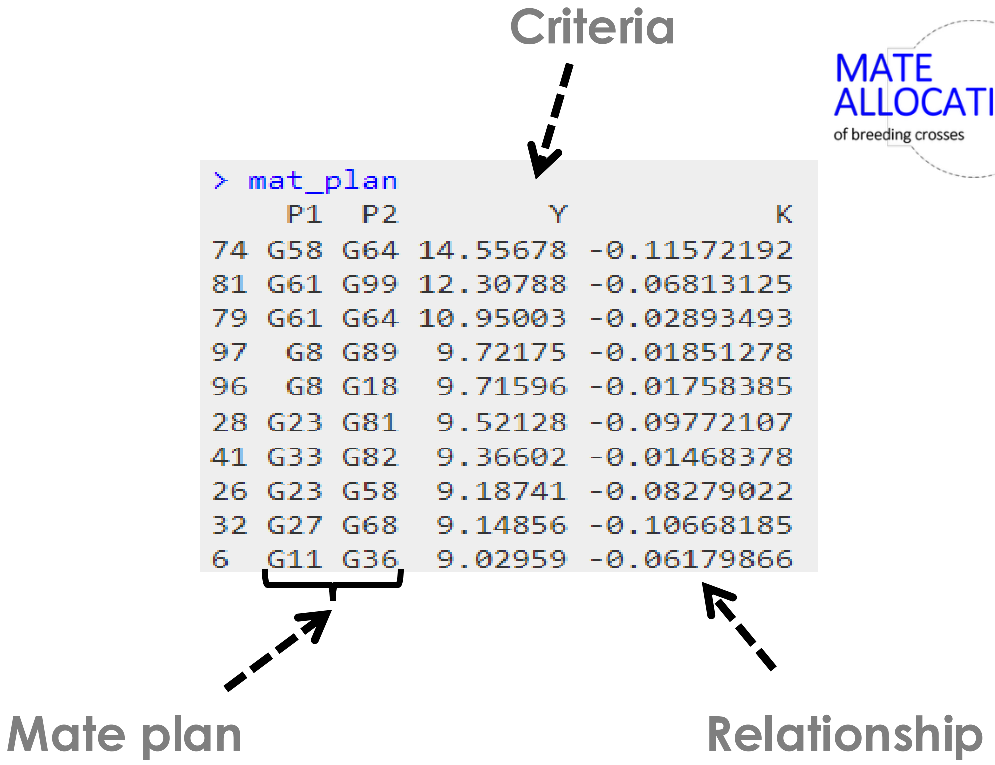
Output

```r
### ----- 2. Optimization
MatePlan = selectCrosses(data = ST_tgv4,
                         n.cross = 20,
                         max.cross = 2,
                         min.cross = 1,
                         culling.pairwise.k = 0)


# stats
MatePlan[[1]]

# Plan
MatePlan[[2]]

# Plot
MatePlan[[3]]
```

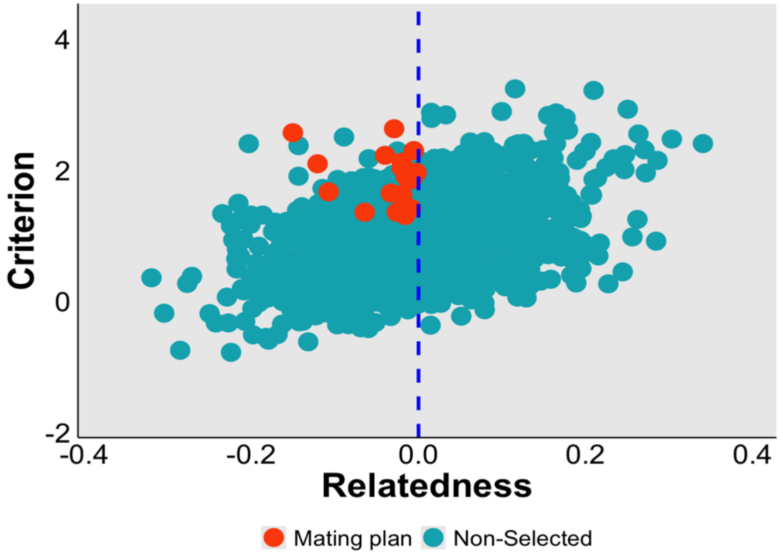


Criteria

```
> mat_plan
    P1  P2        Y           K
74 G58 G64 14.55678 -0.11572192
81 G61 G99 12.30788 -0.06813125
79 G61 G64 10.95003 -0.02893493
97  G8 G89  9.72175 -0.01851278
96  G8 G18  9.71596 -0.01758385
28 G23 G81  9.52128 -0.09772107
41 G33 G82  9.36602 -0.01468378
26 G23 G58  9.18741 -0.08279022
32 G27 G68  9.14856 -0.10668185
6  G11 G36  9.02959 -0.06179866
```

Mate plan

Relationship



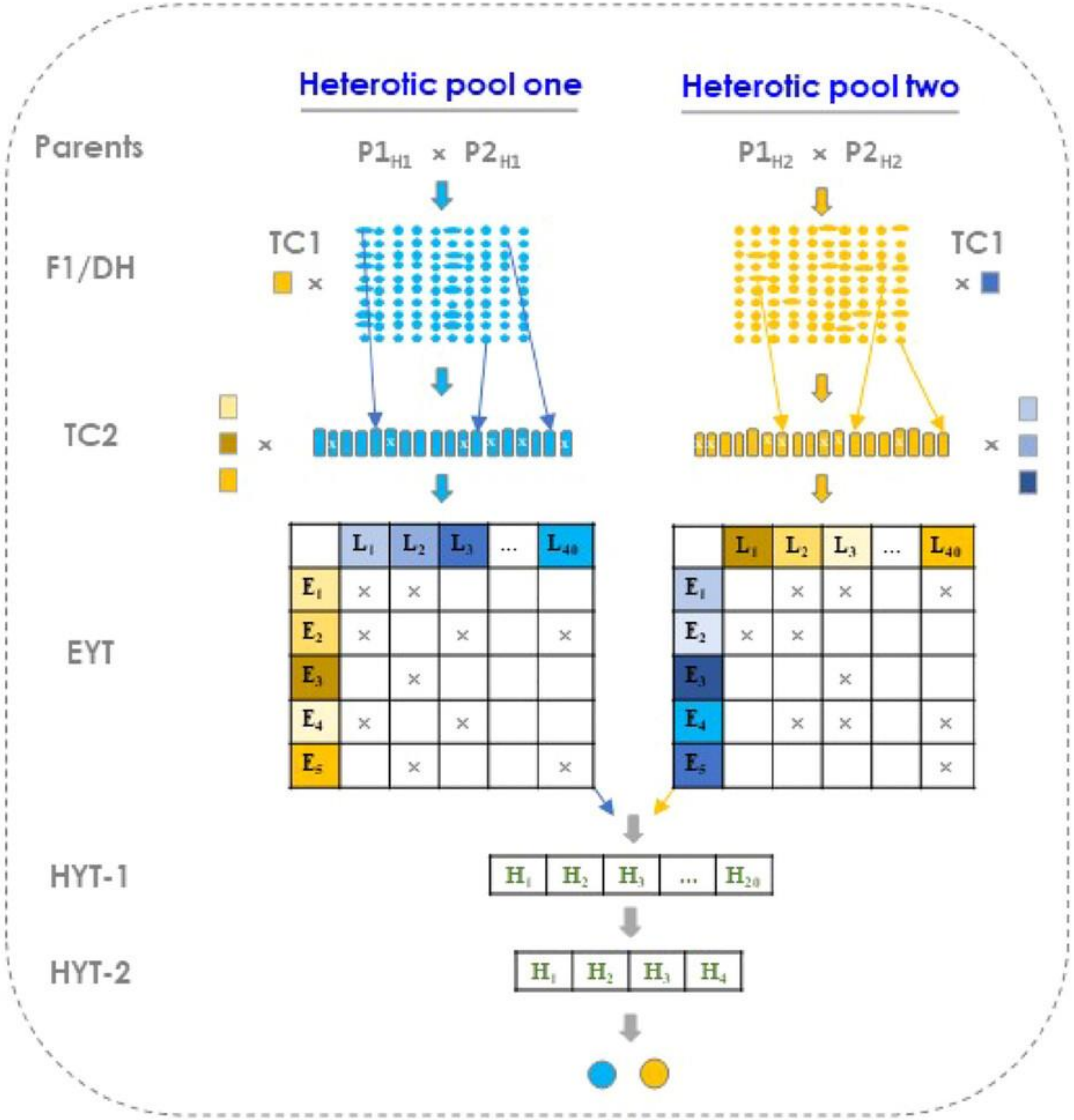
Peixoto et al. 2025

Example one: Hybrid breeding program

- Maize breeding program with two heterotic groups;
- Recurrent reciprocal selection scheme;

- PS: selection only using phenotypes;
- GS: Truncated selection via estimated breeding values;
- OCS: Optimal cross selection with usefulness as criterion (SimpleMating);

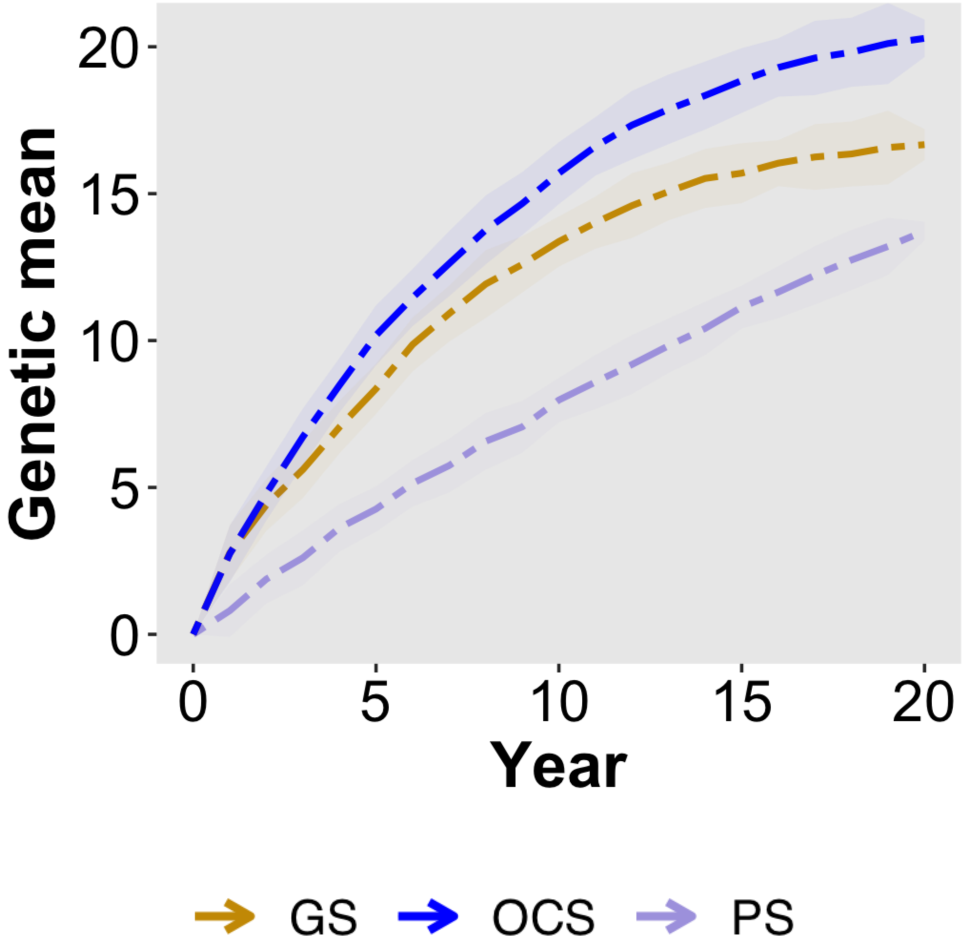
- 20 years of simulations (AlphasimR).



Peixoto et al. 2025

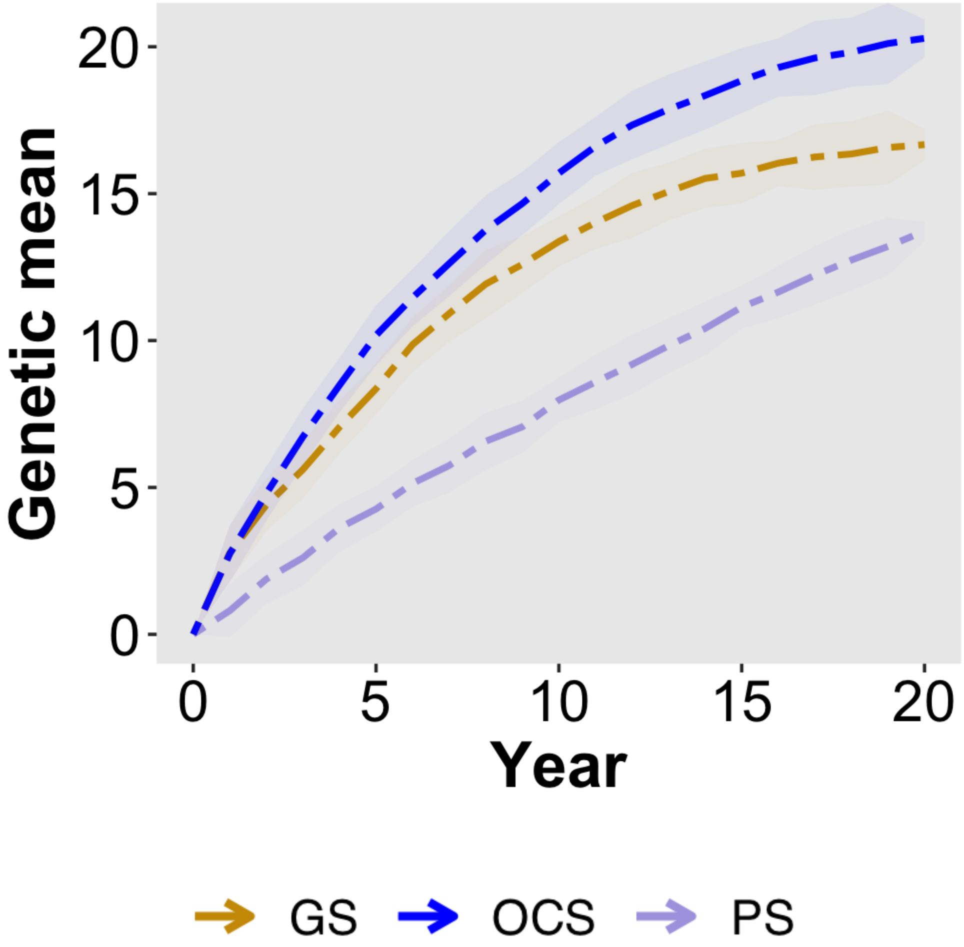
Example one: Hybrid breeding program

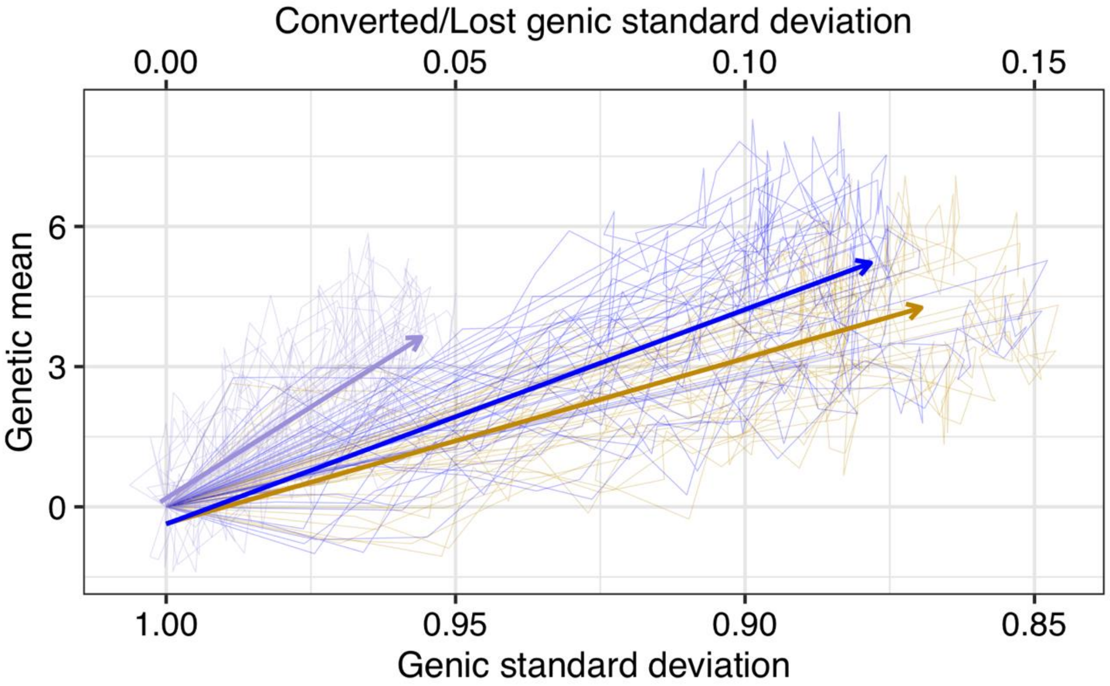
MATE
ALLOCATION
of breeding crosses



Example one: Hybrid breeding program

MATE
ALLOCATION
of breeding crosses



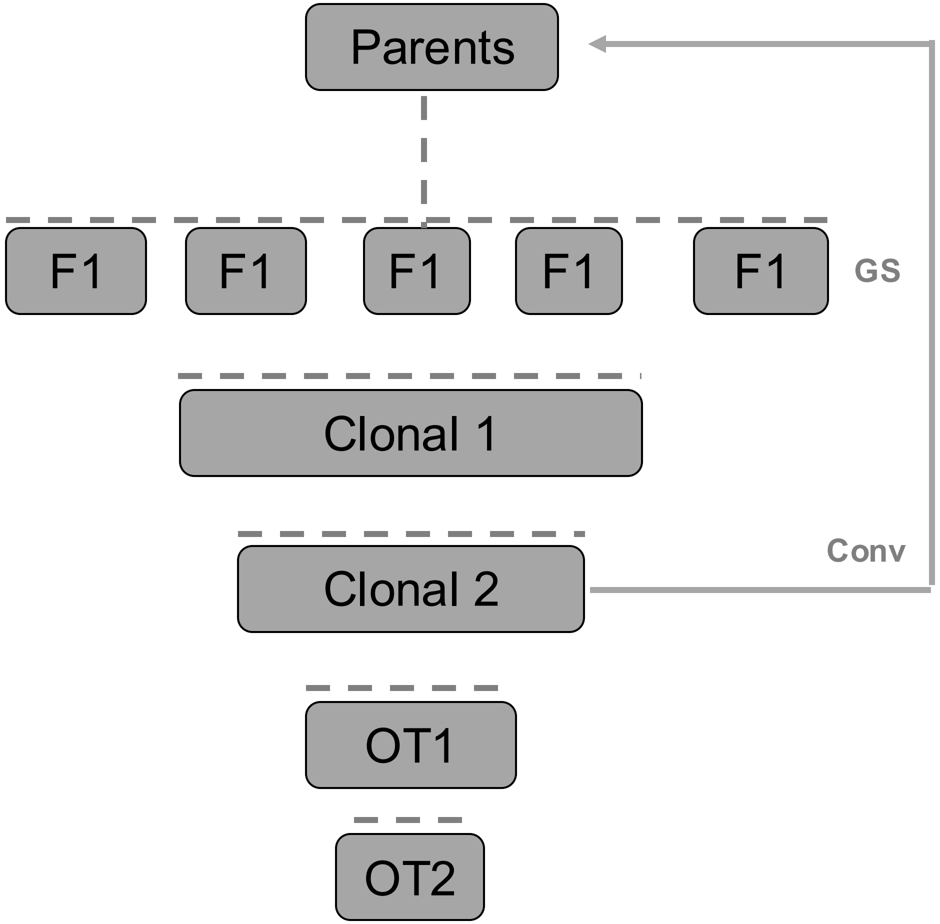


Example Two: Clonal breeding program

- Clonal breeding program (potato UF);
- Recurrent reciprocal selection scheme;

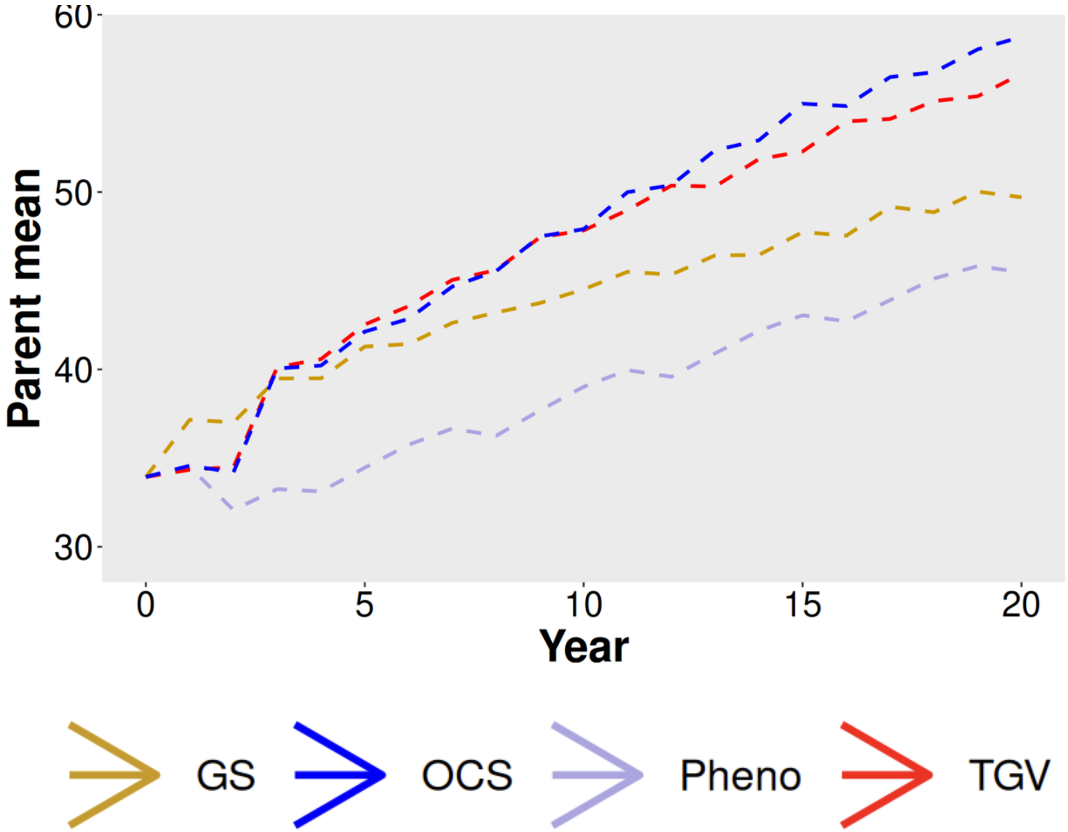
- PS: selection only using phenotypes;
- GS: Truncated selection via estimated breeding values;
- TGV: Truncated selection via total genetic value (A+D);
- OCS: Optimal cross selection with TGV as criterion (SimpleMating);

- 20 years of simulations (AlphasimR);
- Dominance deviation: 0.4.

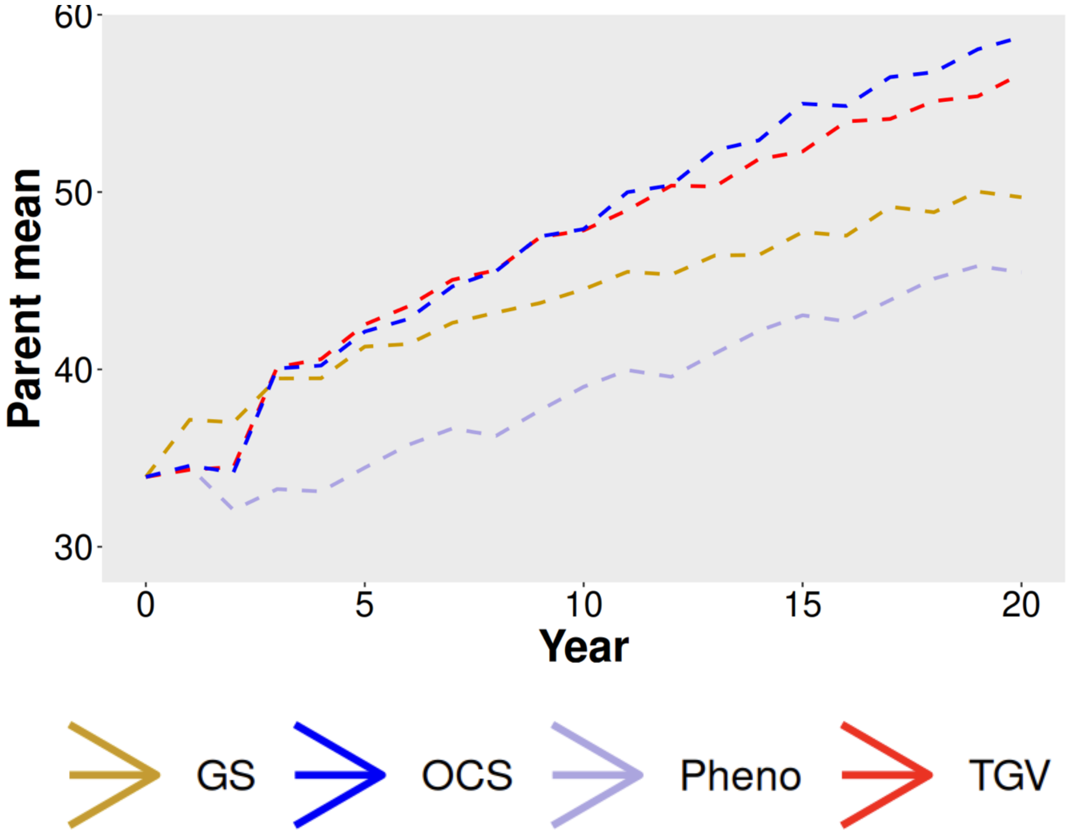


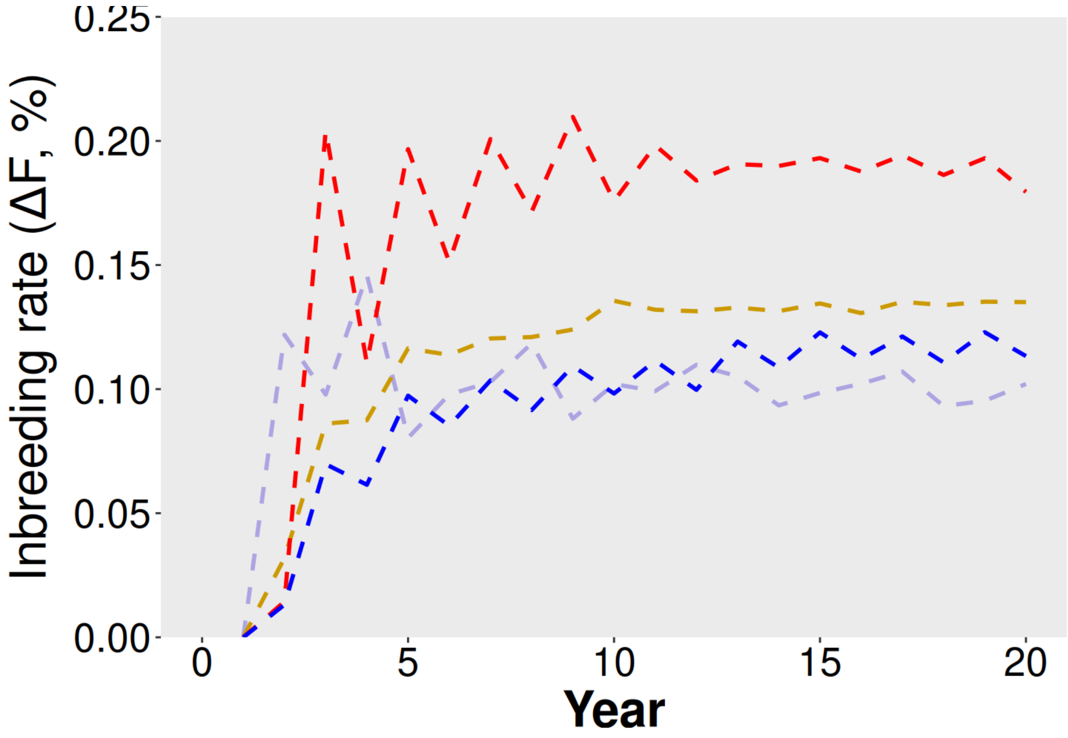
Peixoto et al. unp.

Example Two: Clonal breeding program

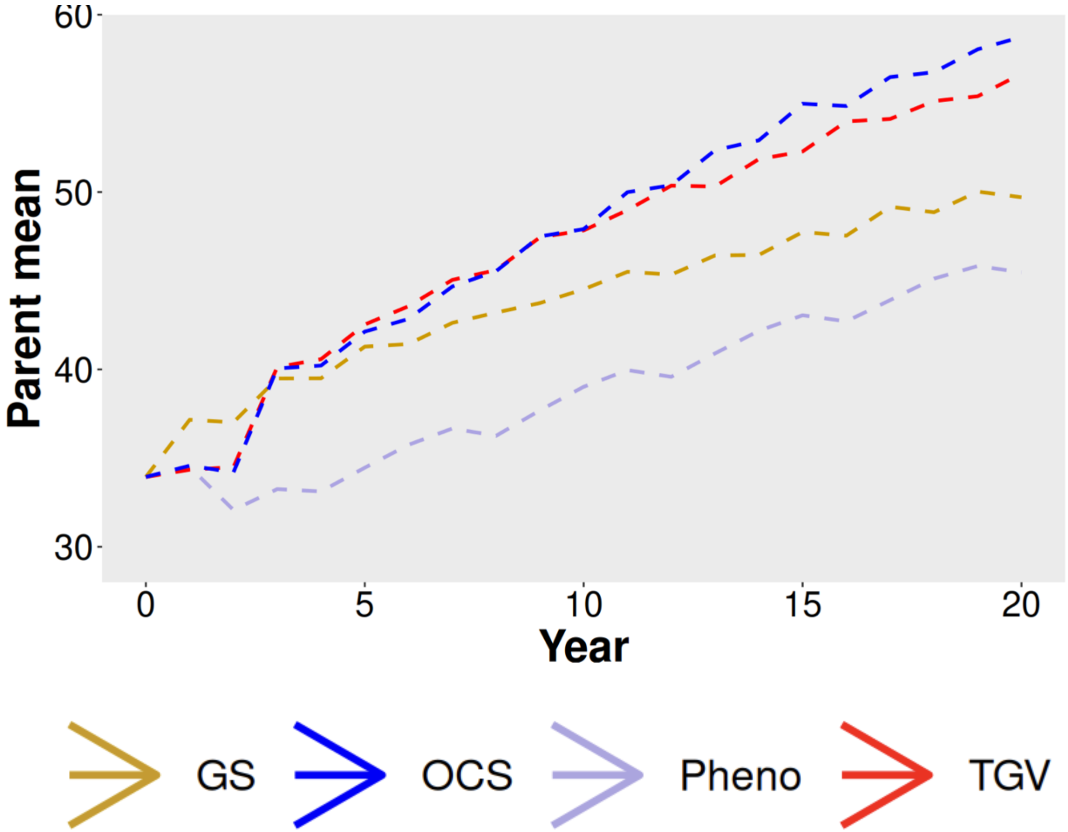


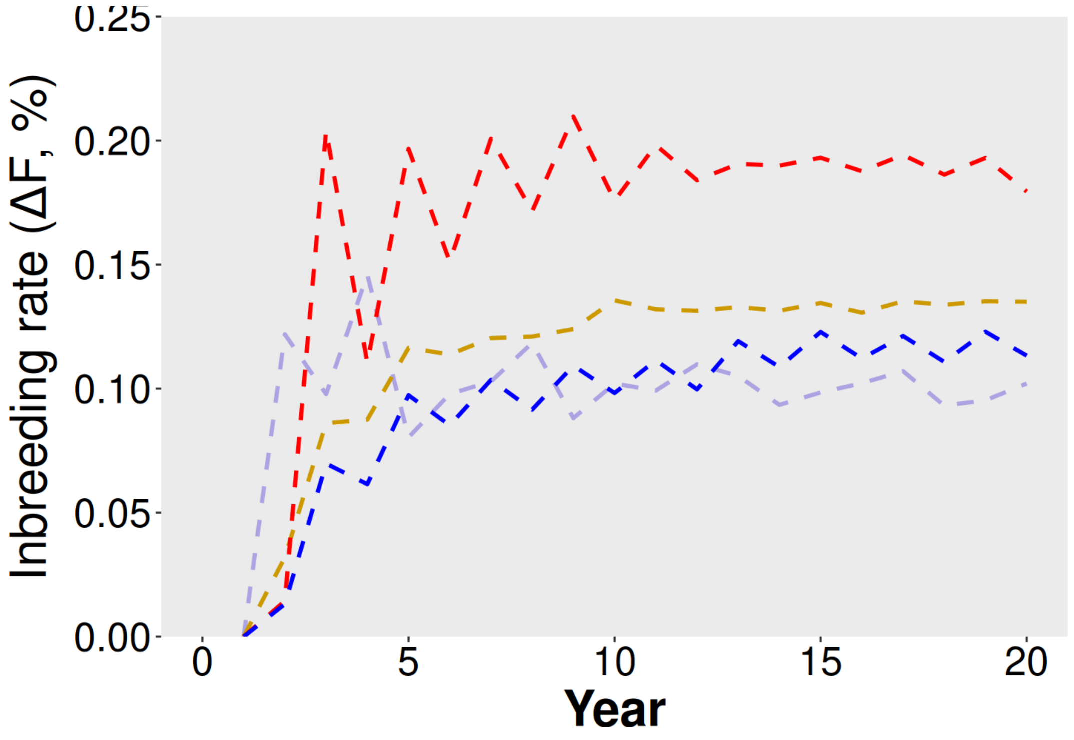
Example Two: Clonal breeding program

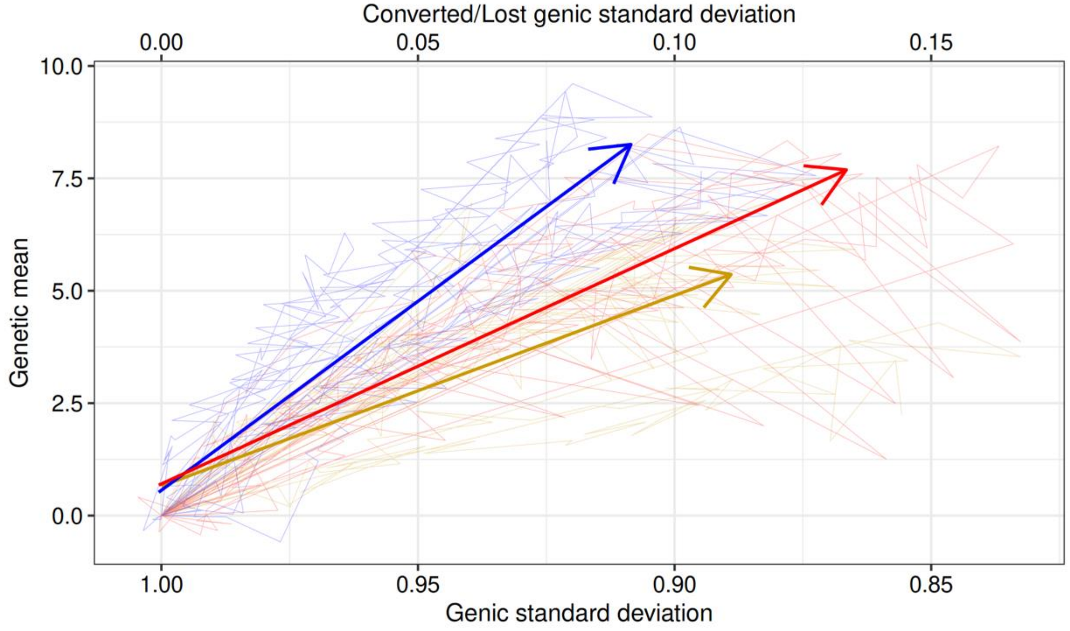




Example Two: Clonal breeding program







Take home notes

MATE
ALLOCATION
of breeding crosses

Use of **optimal cross selection** is an efficient implementation in various genomic selection-based breeding programs

SimpleMating provides an efficient framework for optimizing crosses and improving selection decisions in breeding programs

Acknowledgments

UNIVERSITY of FLORIDA

Sweet Corn & Potato Breeding and Genonnomics

USDA NIFA: 2024-67013-42584

USDA NIFA: 2023-34141-40975

NIFA-SCRI 2018–51181-28419

AFRI 2019–05410

USDA-NIFA 2022–51181-38333

CANVAS

deamorimpeixotom@ufl.edu

https://marcopxt.github.io/