Note:

Slide 2-38 are for 1-hr research talk

Slide 39-63 are for 1-hr teaching talk

Shuffling Genetic Diversity for Crop Improvement

CJ Yang

Dec 7th, 2022

Talk outline

1. Introduction
2. Previous/current work
3. Research vision @UNL
4. Short term research plan
5. Long term research plan
6. Diversity, Equity, Inclusion (DEI) commitment

Introduction

Wisconsin
2012–2018
PhD Genetics

Edinburgh
2019–now
Postdoc

Freising
2018–2019
Postdoc

Indiana
2009–2012
BSc Biotechnology, Mathematics

Malaysia
1990–2009

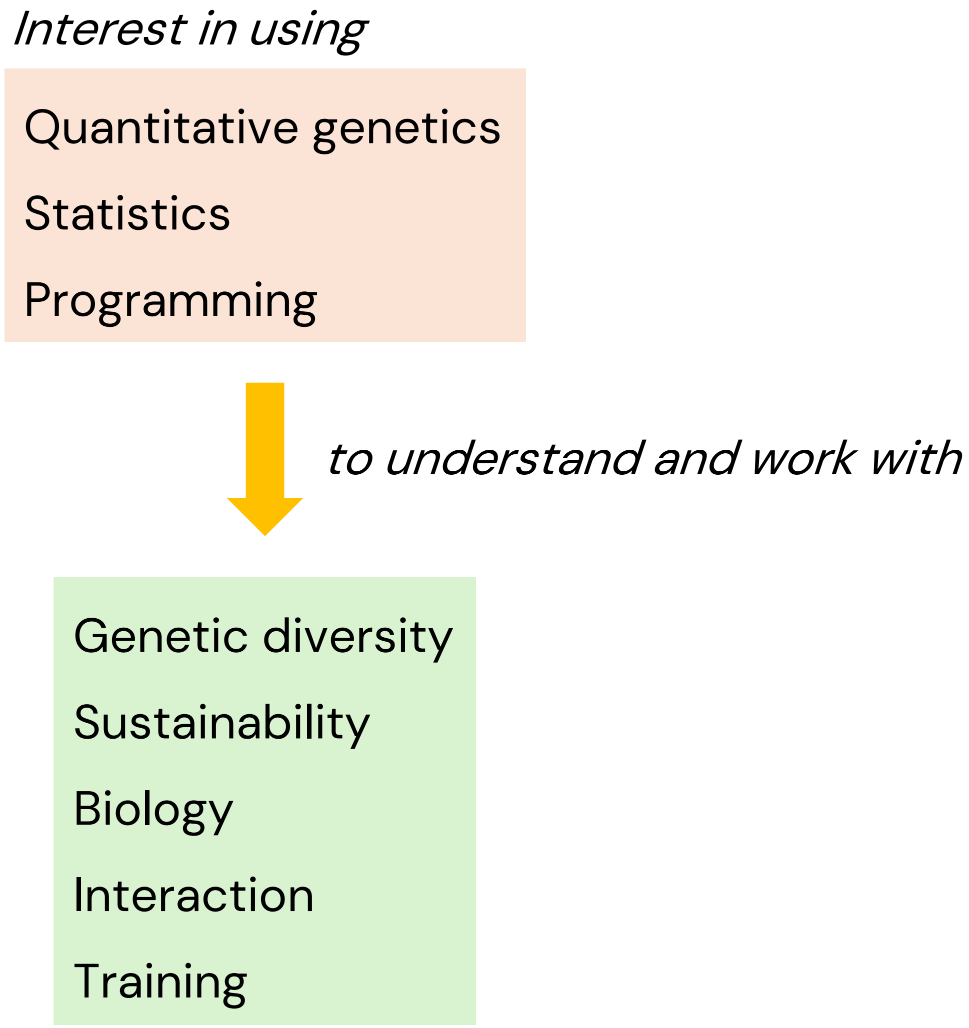
Research experience and interest

Graduate

- Maize, teosinte, domestication
- QTL mapping, fine-mapping
- Molecular biology
- Quantitative genetics

Postdoc

- Genomic selection
- Crop registration system
- Population design
- Selection mapping
- Breeding



Interest in using

Quantitative genetics

Statistics

Programming

to understand and work with

Genetic diversity

Sustainability

Biology

Interaction

Training

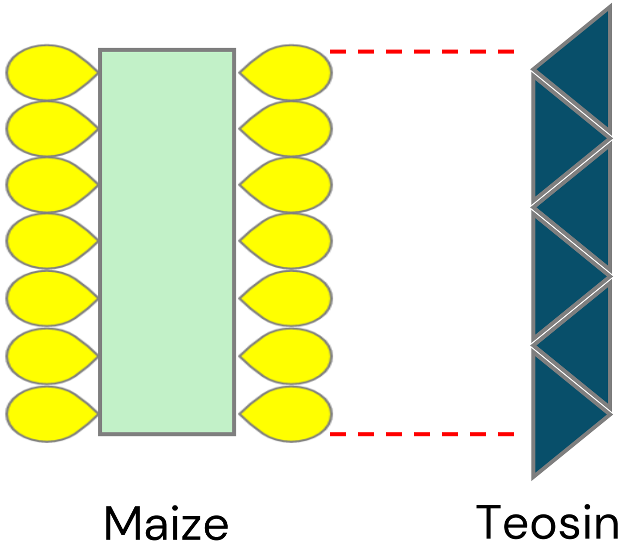
Previous work: QTL fine-mapping

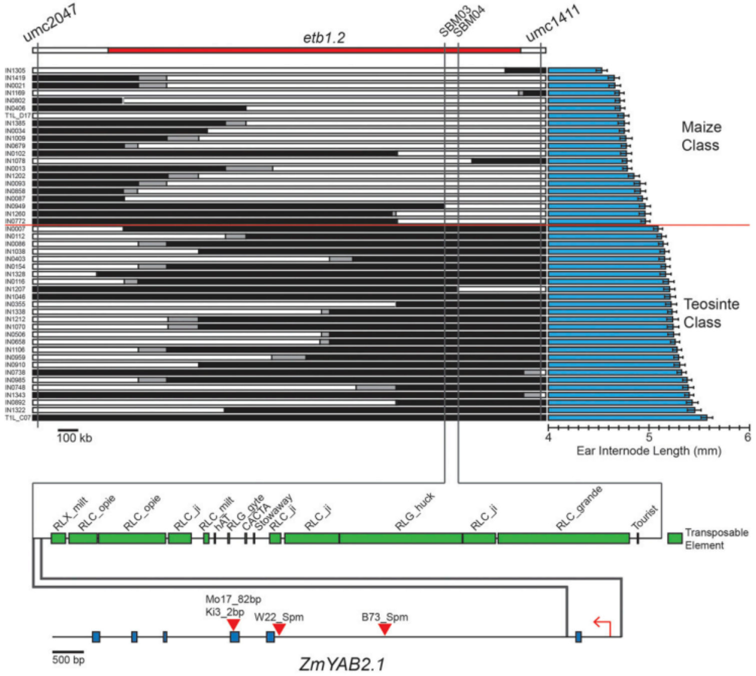
Ear internode length

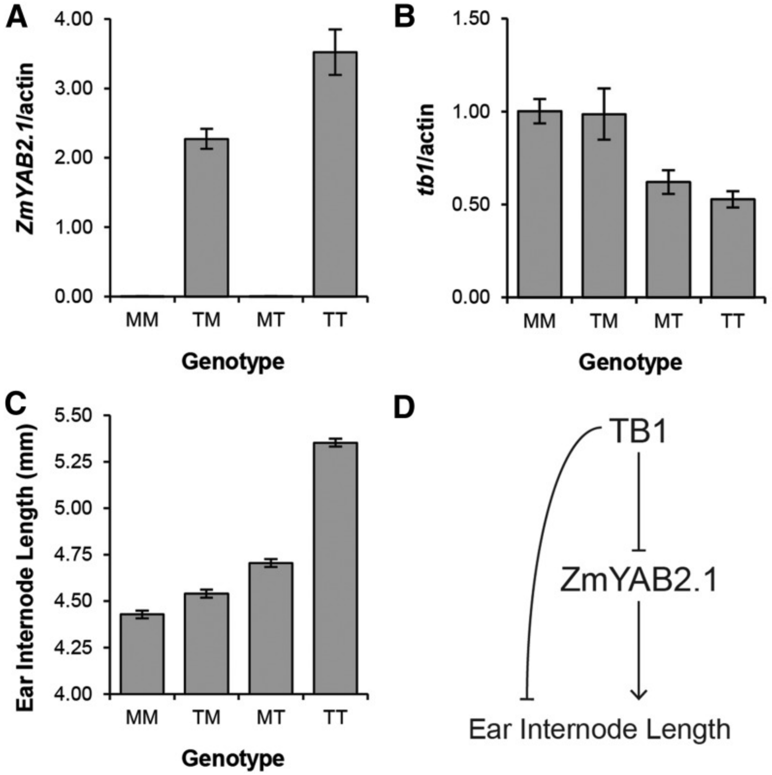
- Measure of kernel compactness
- *ZmYAB2.1* Transcription Factor

A gene for genetic background in *Zea mays*: fine-mapping *enhancer of teosinte branched1.2* to a YABBY class transcription factor

Yang CJ, Kursel LE, Studer AJ, Bartlett ME, Whipple CJ, Doebley JF





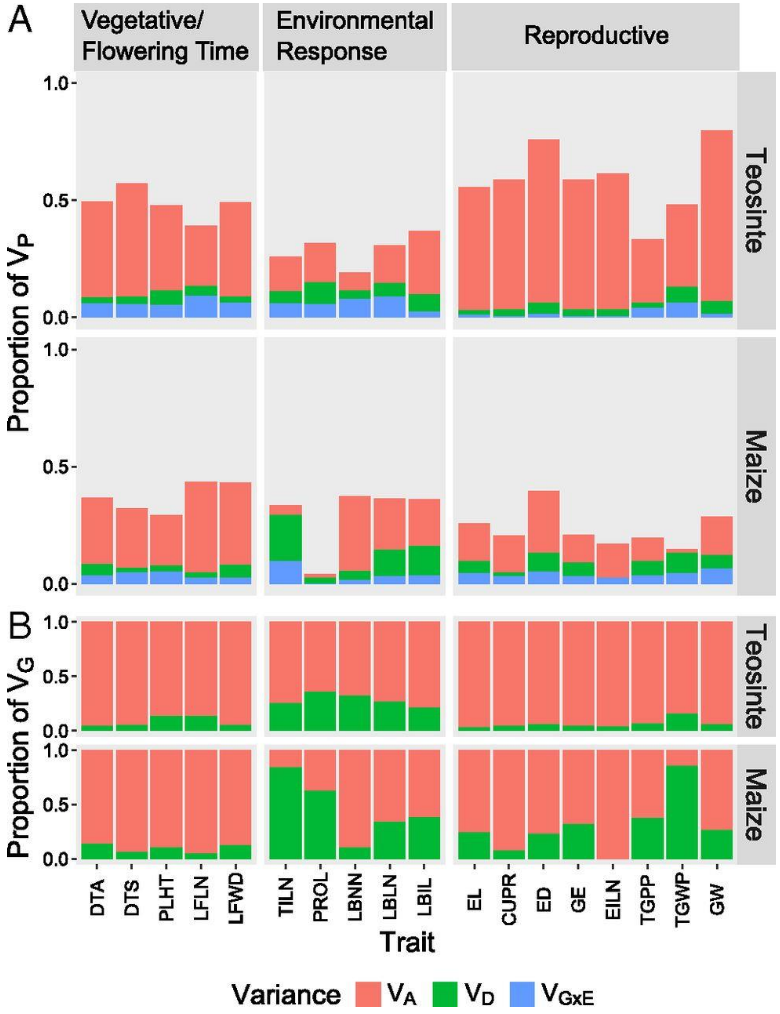


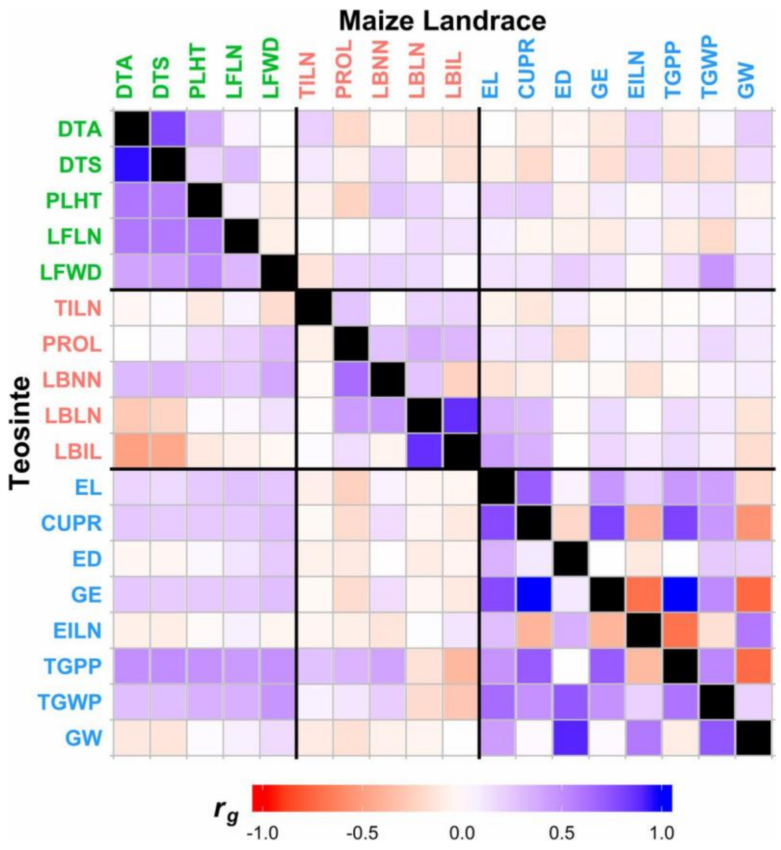
Previous work: QG of domestication

The genetic architecture of teosinte catalyzed and constrained maize domestication

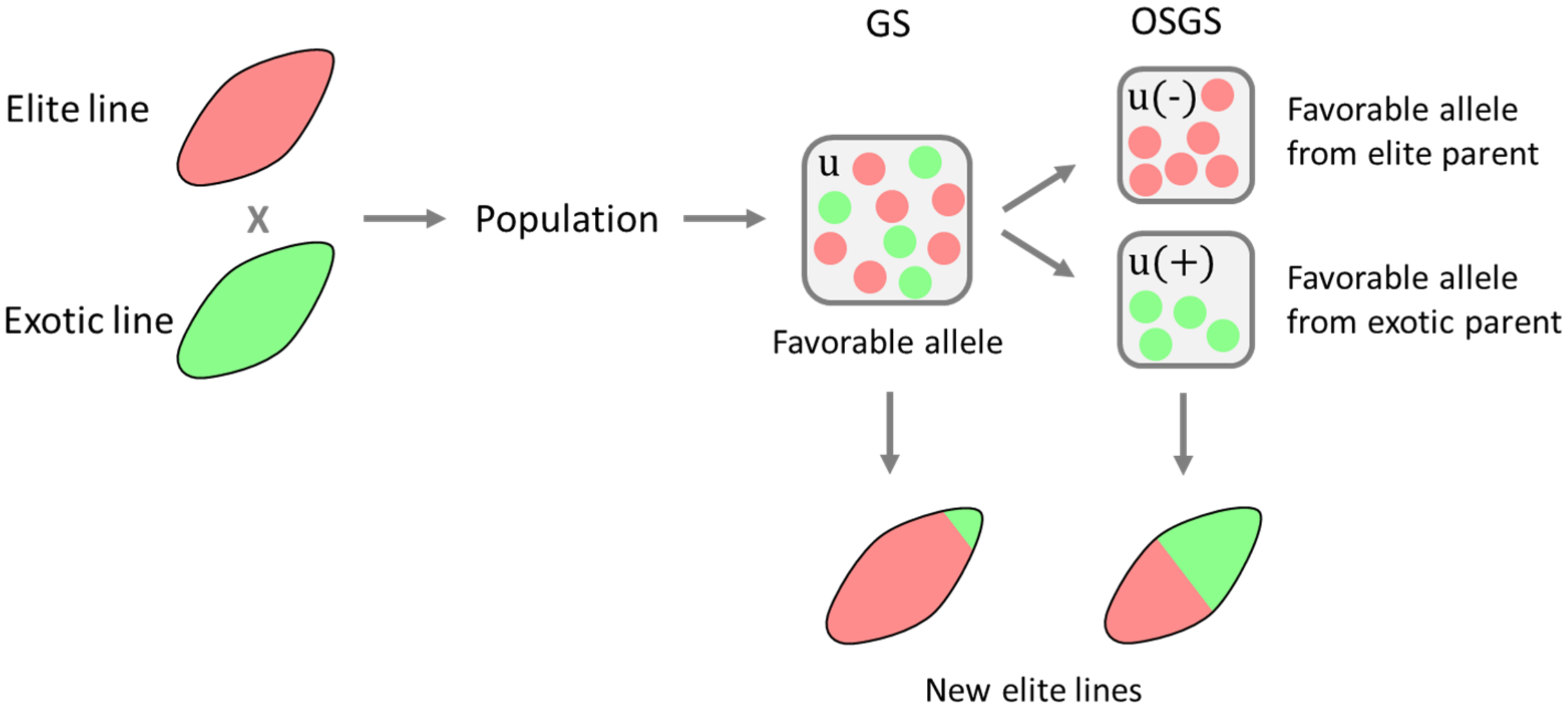
Yang CJ, Samayoa LF, Bradbury PJ, Olukolu BA, Xue W, York AM, Tuholski MR, Wang W, Daskalska L, Neumeyer MA, Sanchez-Gonzalez J, Romay MC, Glaubitz JC, Sun Q, Buckler ES, Holland JB, Doebley JF

Conservation and changes in genetic variances and correlations





Previous work: Origin Specific Genomic Selection (OSGS)

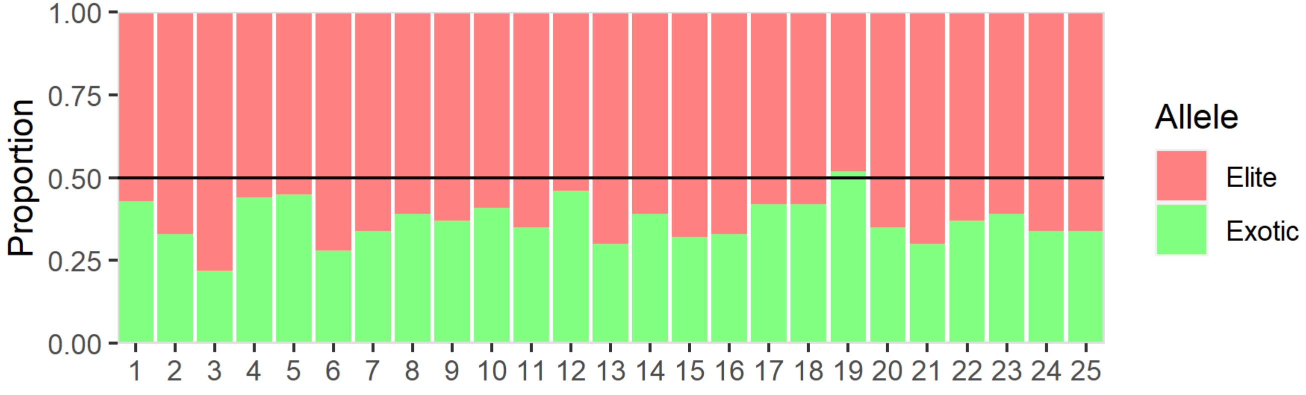


Origin Specific Genomic Selection: a simple process to optimize the favorable contribution of parents to progeny

Yang CJ, Sharma R, Gorjanc G, Hearne S, Powell W, Mackay I

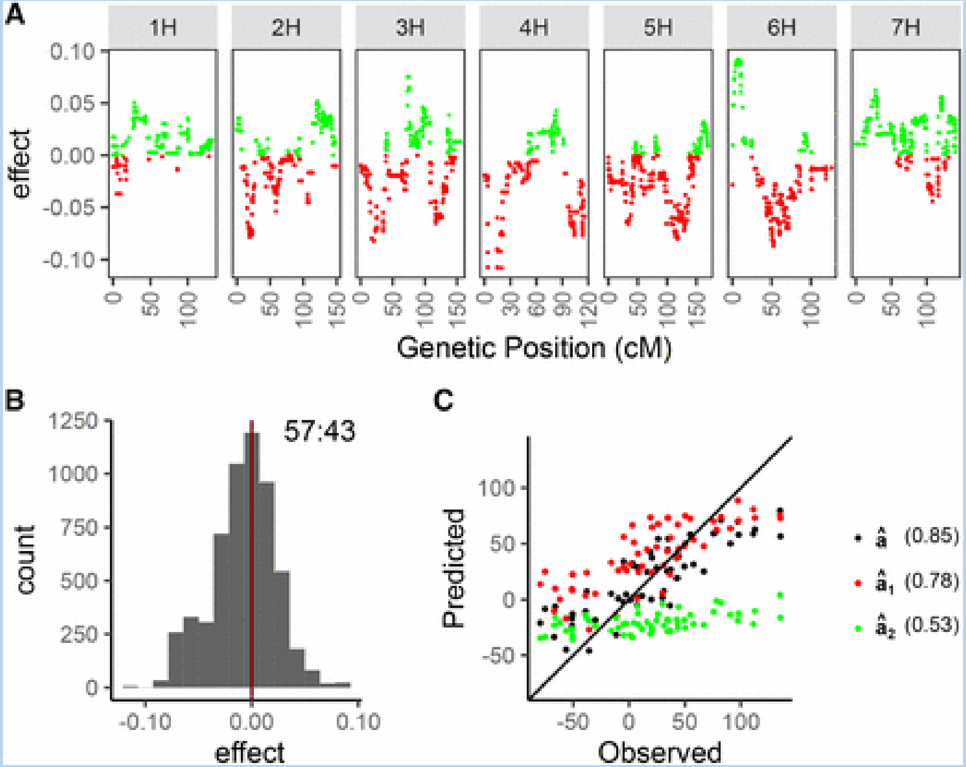
Previous work: Origin Specific Genomic Selection (OSGS)

- Dataset: Yield from HEB-25 barley NAM (Maurer et al. 2015).
- *Hordeum vulgare* ssp. *vulgare* (Barke) x ssp. *spontaneum*.
- Unequal proportions of favorable alleles (elite > exotic).



Yang et al (2020)

Case study in one NAM family



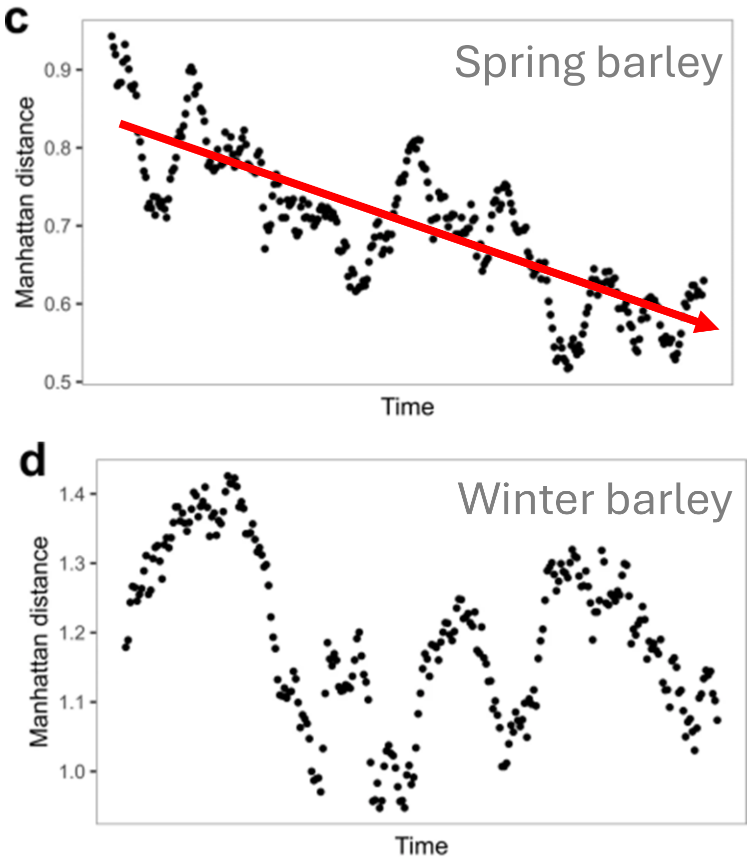
A: Partition the effects into favorable elite (negative) and exotic (positive).

B: Unequal proportions of favorable alleles (elite > exotic).

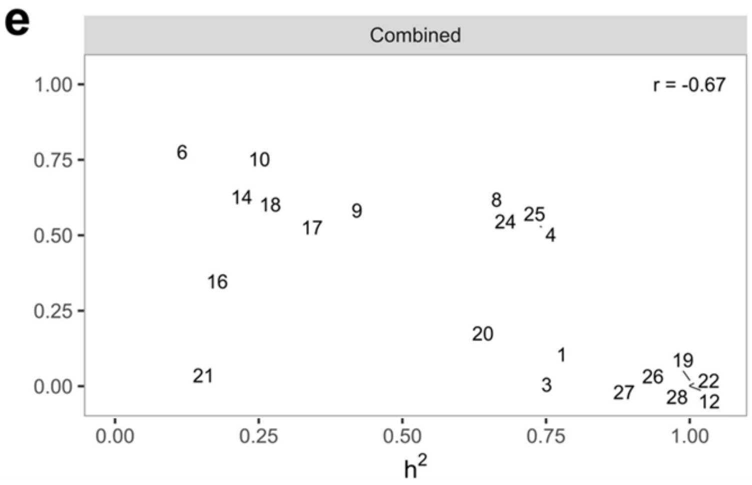
C: Trait predictions using all markers, elite-only and exotic-only favorable markers.

Previous work: Distinctness, Uniformity, Stability (DUS)

- DUS is a Plant Variety Rights (PVR) granting system by UPOV (International Union for the Protection of New Varieties of Plants).
- DUS for barley in the UK uses 28 morphological traits (e.g. season type, row number, pigmentation, etc…).



UK spring barley varieties are getting increasingly similar in their DUS traits (declining distance).



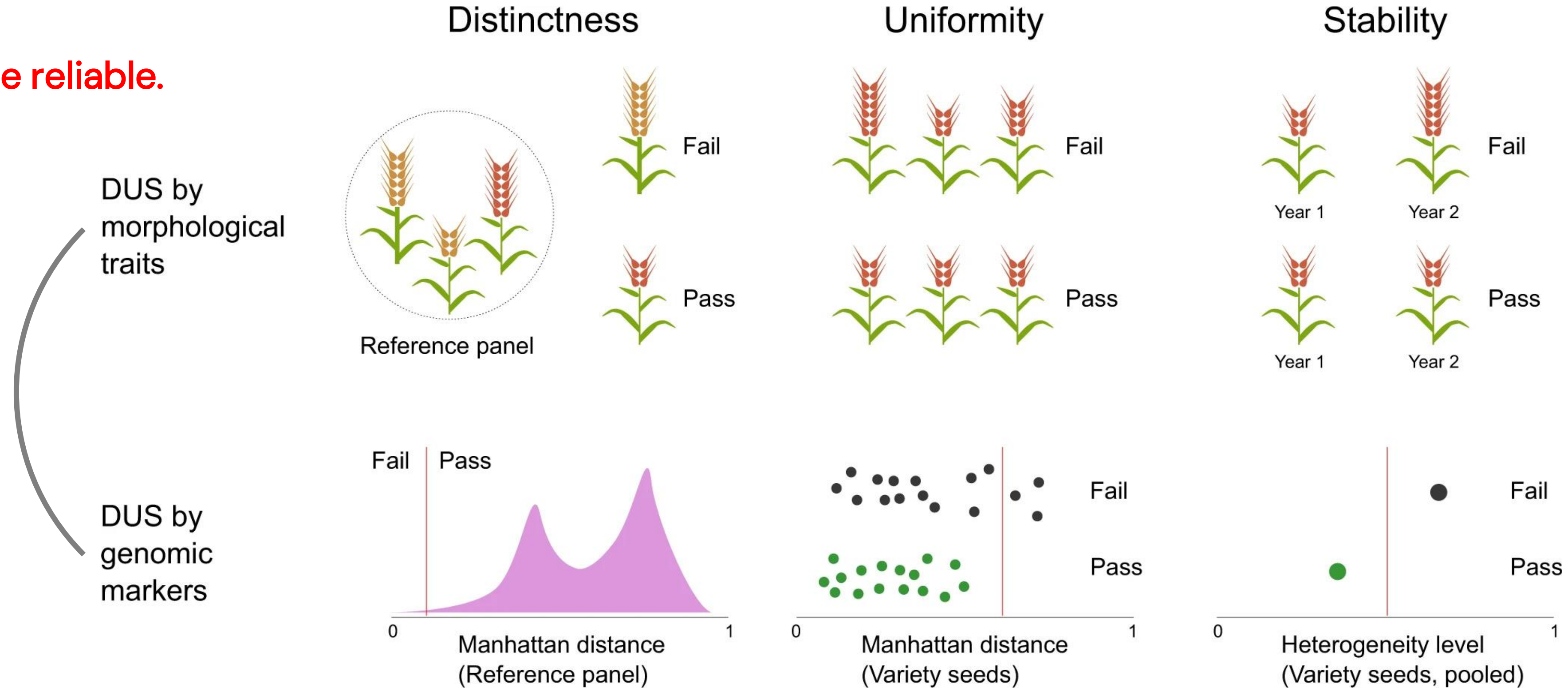
- Y-axis: proportion of DUS trait inconsistencies across organizations.
- X-axis: trait heritabilities.
- **DUS traits: low heritabilities, inconsistent across environments.**

Overcoming barriers to the registration of new plant varieties under the DUS system
Yang CJ, Russell J, Ramsay L, Thomas W, Powell W, Mackay I

Previous work: Distinctness, Uniformity, Stability (DUS)

Genomic DUS is cheaper and more reliable.

- E.g. barley 50k iSelect SNP array, £40 for 40k markers (Darrier et al 2019).
- Removes the needs for DUS field trials.
- Removes inconsistent traits (low heritabilities).



DUS by morphological traits

DUS by genomic markers

An example of how genomic DUS can be implemented.

Yang et al (2021)

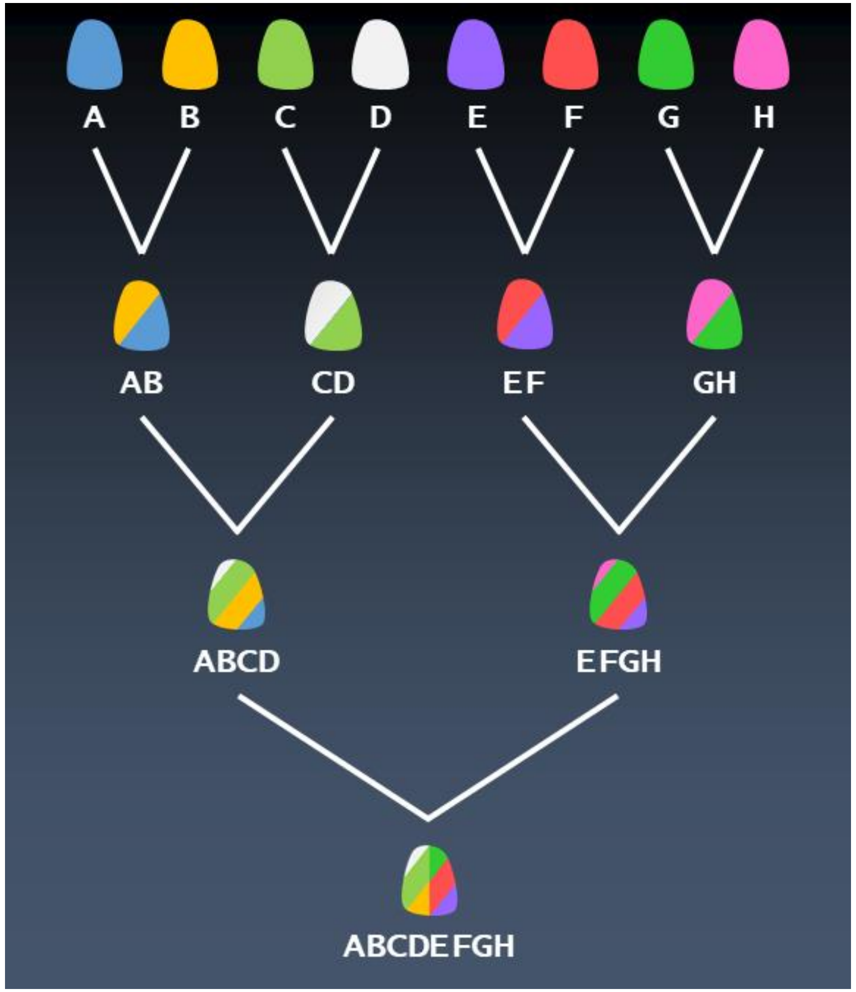
Previous work: R/magicdesign

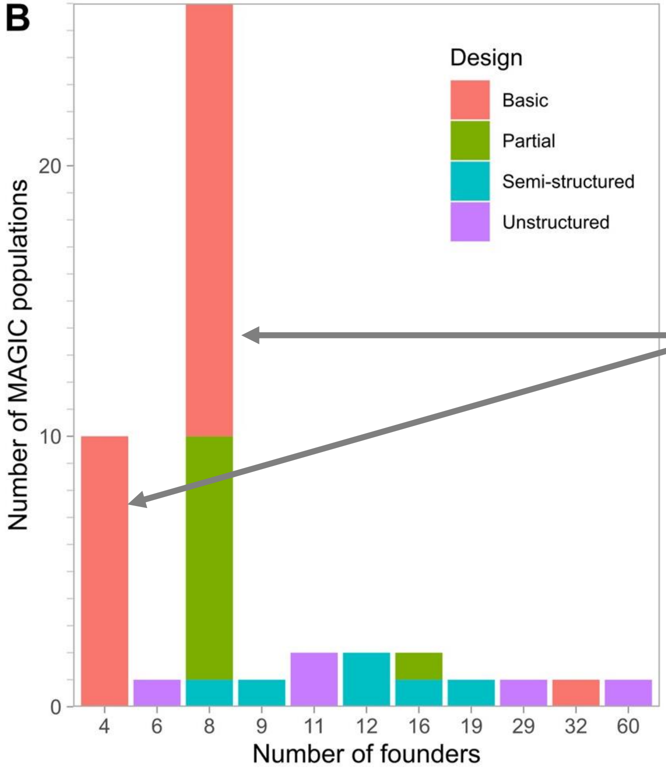
Crafting for a better MAGIC: systematic design and test for Multiparental Advanced Generation Inter-Cross population

Yang CJ, Edmondson RN, Piepho H-P, Powell W, Mackay I

Multiparental Advanced Generation Inter Cross (MAGIC)

- Population with a rich recombination landscape.
- Create novel genetic/haplotype diversity.
- Multi-purpose: QTL (gene) mapping, genomic selection, genetic resource.

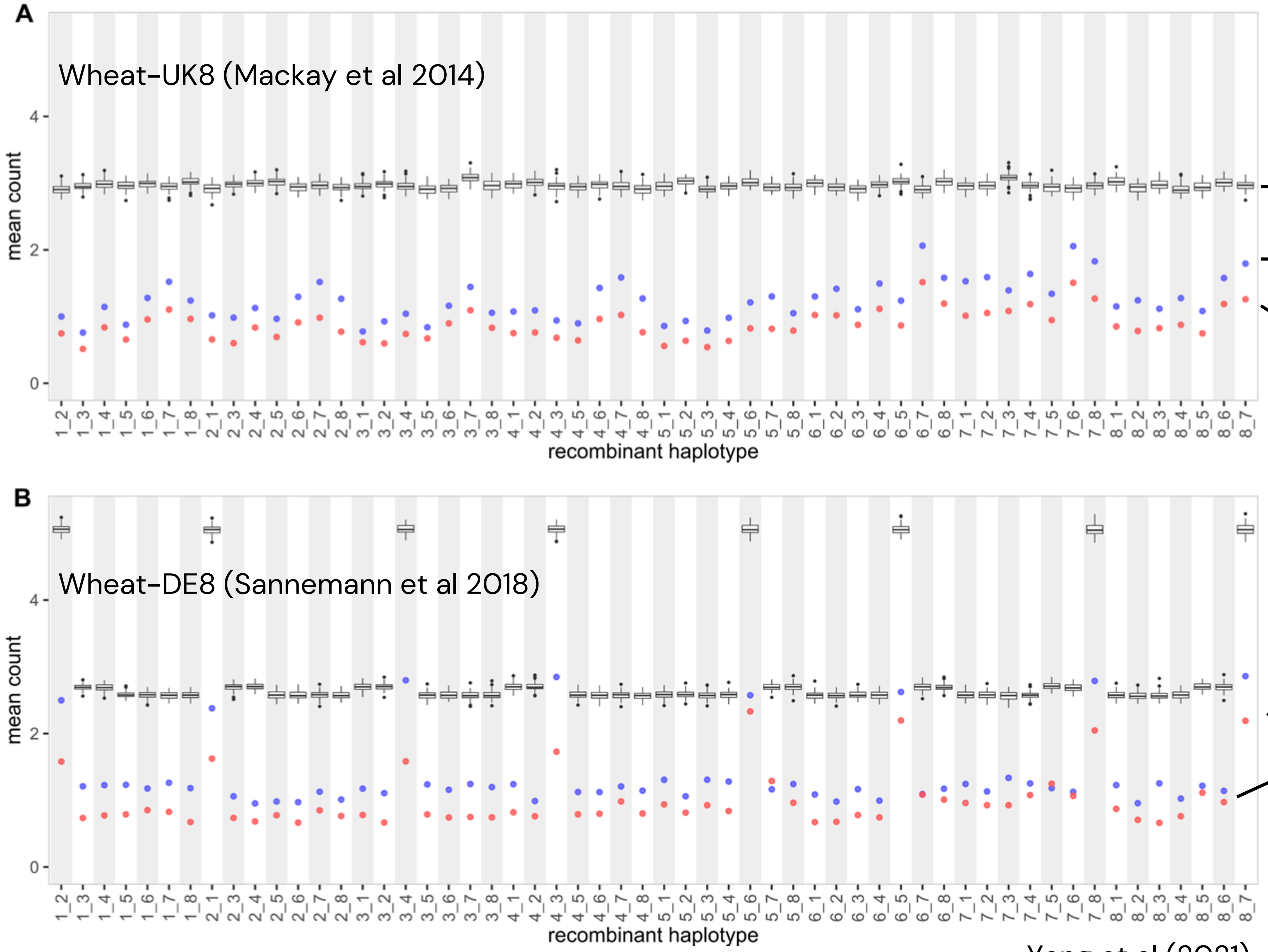




Despite having many ways to construct the crossing schemes, many populations use the same, single-funnel crossing scheme (as shown in the pedigree on the left).

This creates a bias toward recombinations from earlier crosses.

Previous work: R/magicdesign



Wheat-UK8 (Mackay et al 2014)

Wheat-DE8 (Sannemann et al 2018)

True founder genotype (sim)

Inferred founder genotype (sim)

Inferred founder genotype (real)

Inferred founder genotype produced about half of the recombinant haplotypes identified from true founder genotypes.

Bias toward 2-way recombinant haplotypes

Yang et al (2021)

Previous work: R/magicdesign

- R package for designing and testing various MAGIC population designs by simulations.
- Available at https://github.com/cjyang-work/magicdesign
- R/magicdesign allows us to explore more crossing schemes.

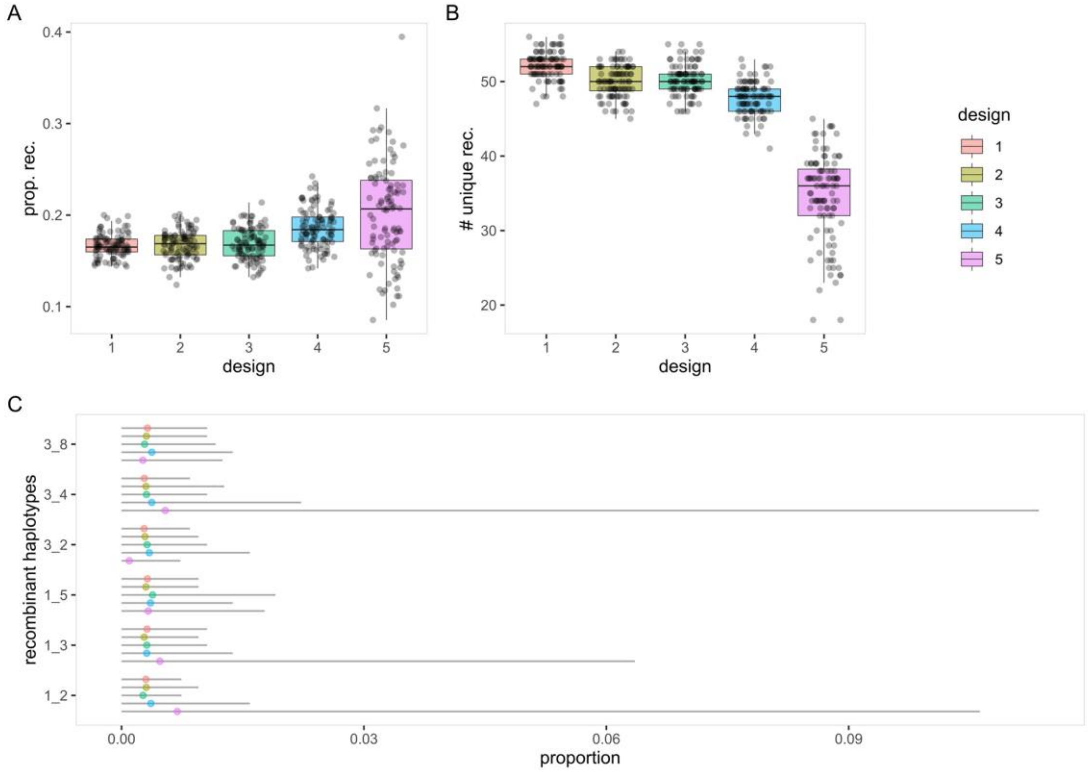
Sample codes in R/magicdesign:

8 founders, 49 (7 x 7) funnels, 1 x 3 x 4 replicates, and 4 selfing generations = 588 RILs.

```
magic.eval(n=8,
           m=7,
           reps=c(1,3,4),
           self=c(0,0,4),
           chr.len=c(3.37, 2.89, 2.50, 2.11, 1.94),
           n.sim=100)
```

Sample output to evaluate 5 different crossing scheme.

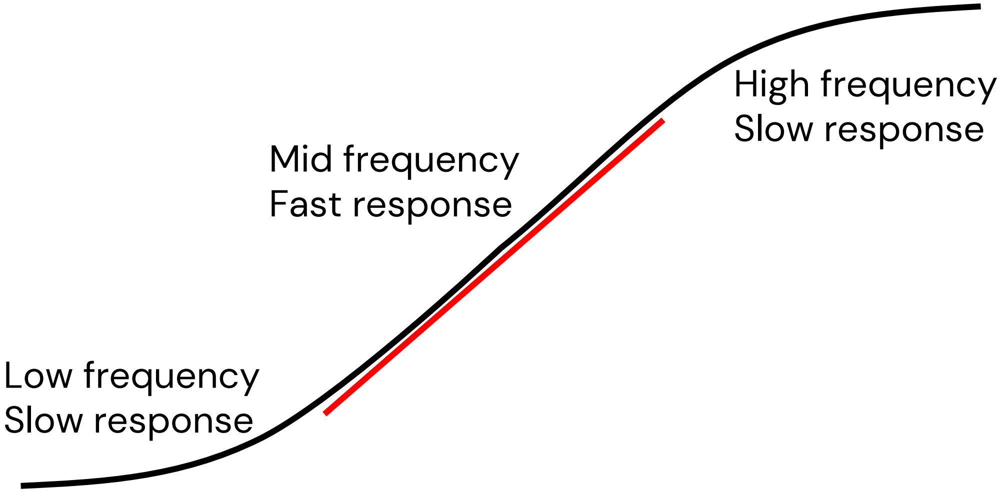
e.g. proportion of recombinant haplotypes within an interval.



Yang et al (2021)

Previous work: Regression of Alleles on Years (RALLY)

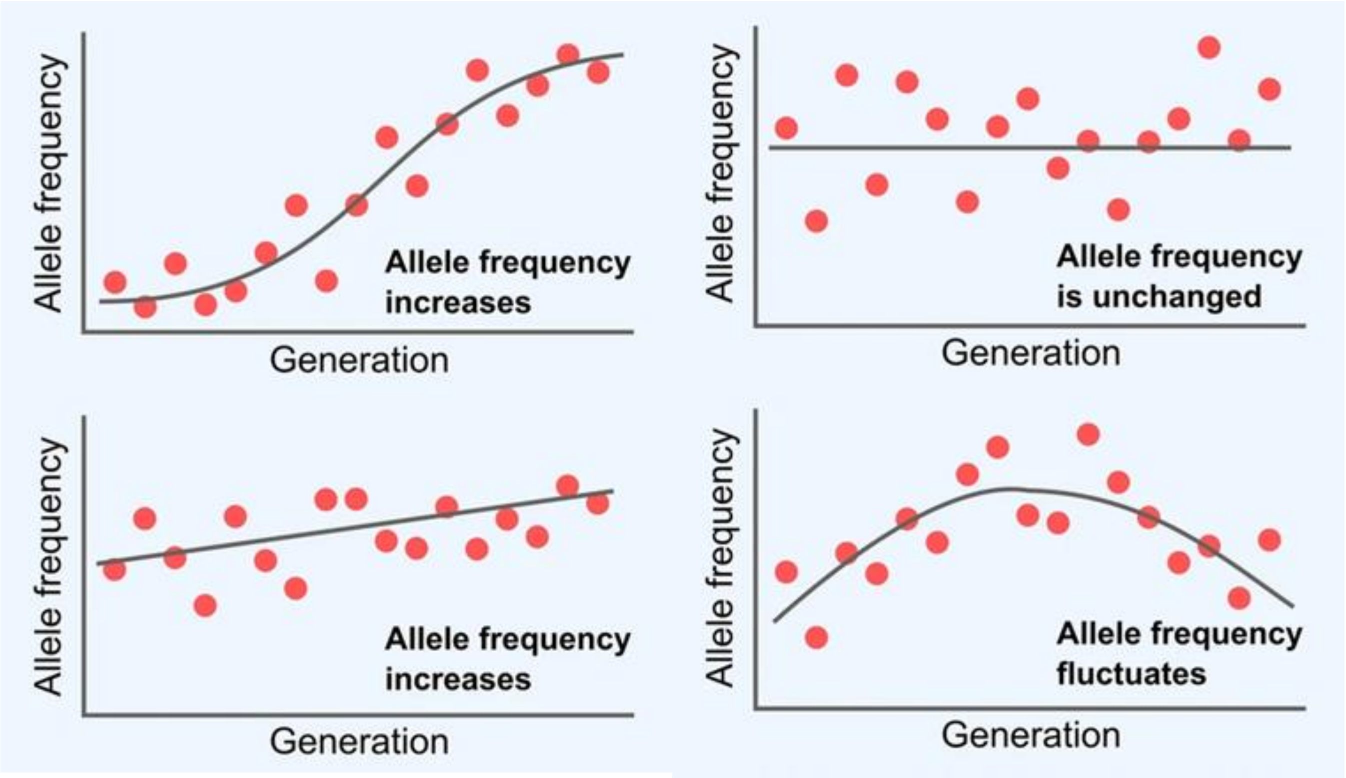
Logistic regression to model allele frequency changes



Low frequency
Slow response

Mid frequency
Fast response

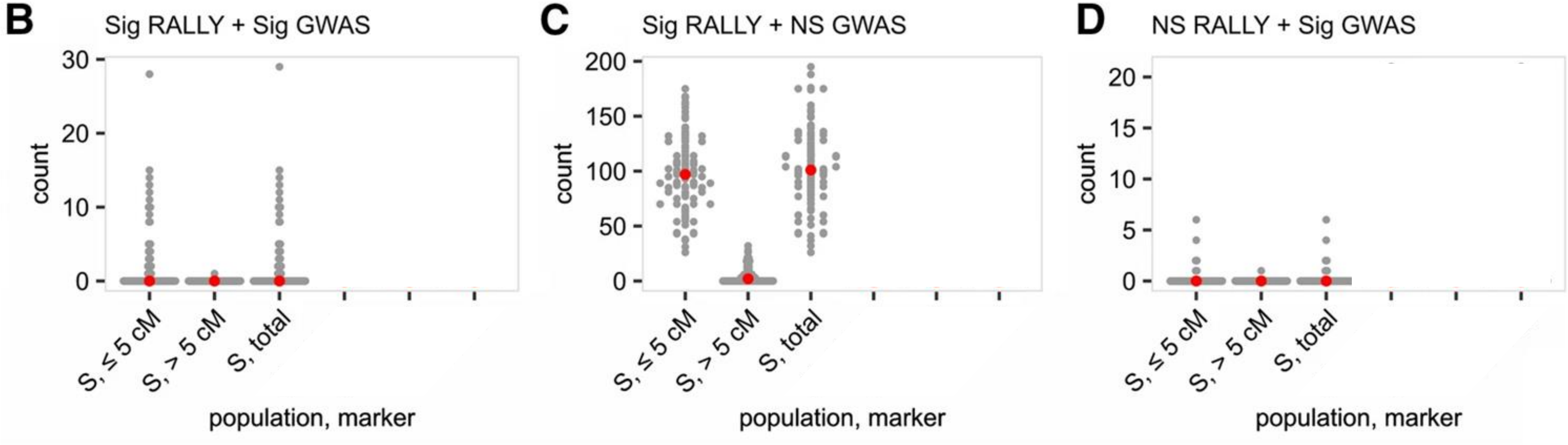
High frequency
Slow response



Analysis of historical selection in winter wheat
Yang CJ, Ladejobi O, Mott R, Powell W, Mackay I

Previous work: Regression of Alleles on Years (RALLY)

Simulate 50 generations of selection (S) – repeat 100X.

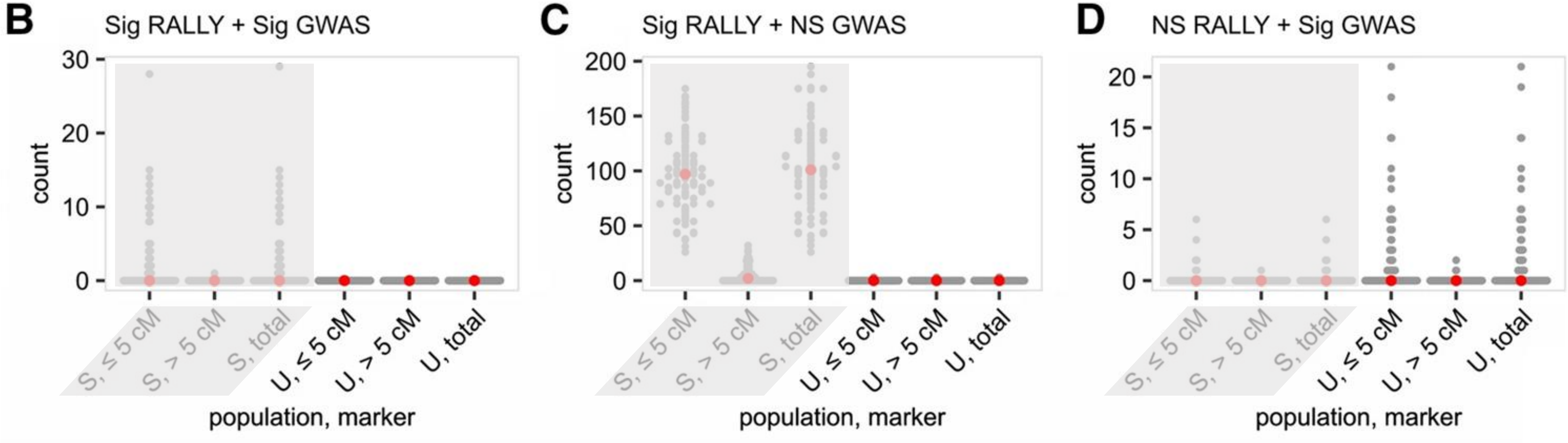


Yang et al (2022)

In the presence of selection, RALLY has more mapping power than GWAS.

Previous work: Regression of Alleles on Years (RALLY)

Similarly, simulate 50 generations of control, i.e. no selection (U).



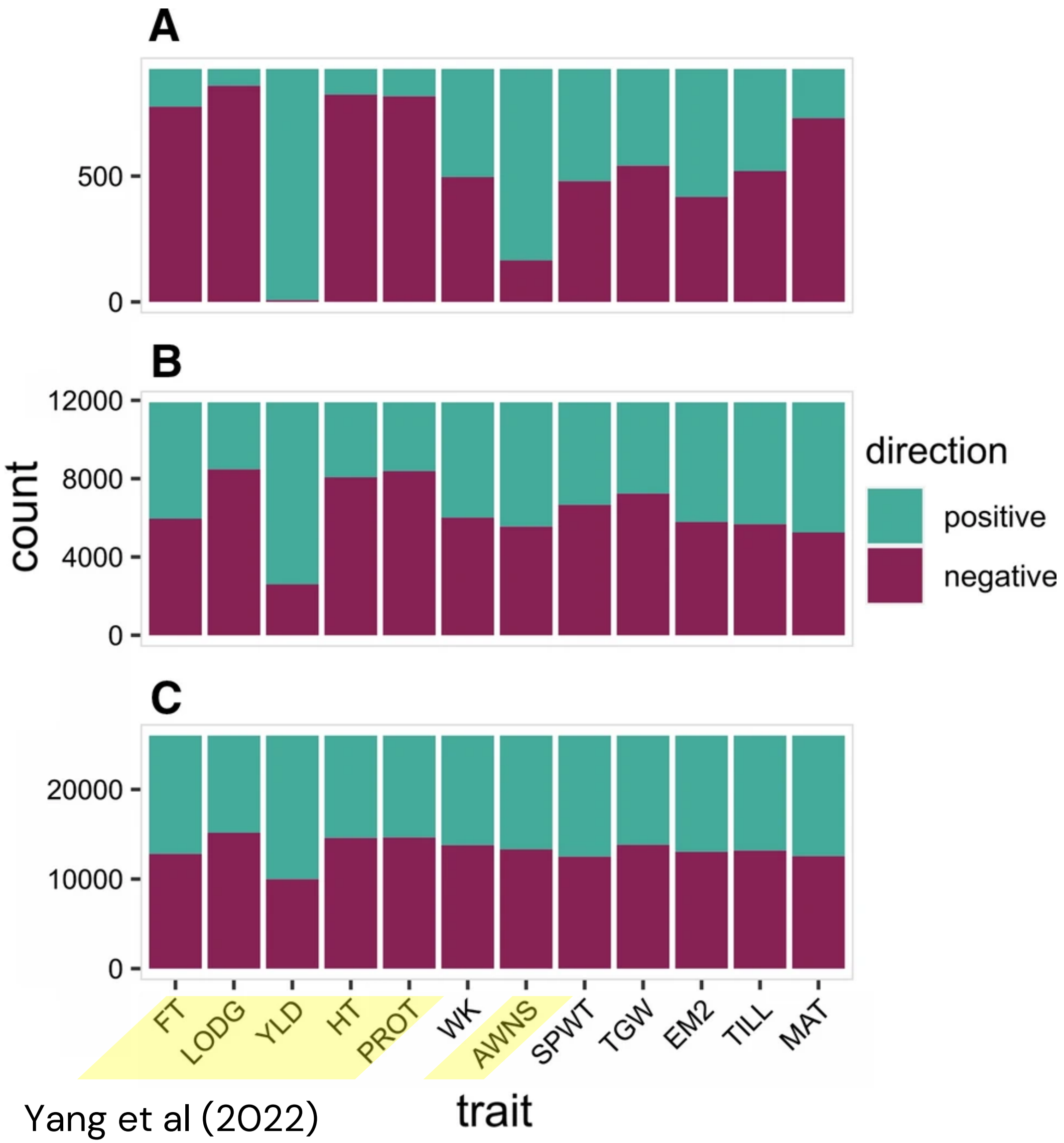
Yang et al (2022)

In the absence of selection, RALLY finds no significant markers.

False positive control in RALLY uses Parametric Control = Genomic Control + Delta Control.

Previous work: Regression of Alleles on Years (RALLY)

- Analysis in the Triticeae Genome (TG) dataset.
- 333 winter wheat varieties, DE/FR/UK, 1948–2007.
- 38,852 GBS markers (m).
- Fit standard ridge regression BLUP model.
- Match marker effect directions to RALLY directions.
- Partition the markers into sets.
- **A**: markers with RALLY $p < 0.05/m$.
- **B**: markers with RALLY $0.05/m < p < 0.05$.
- **C**: markers with RALLY $p > 0.05$.



Yang et al (2022)

Current work: Phantom epistasis and heterosis

A quantitative genetic framework highlights the role of epistatic effects for grain-yield heterosis in bread wheat.
Jiang et al (2017)

Negative dominance and dominance-by-dominance epistatic effects reduce grain-yield heterosis in wide crosses in wheat.
Boeven et al (2020)

Within the genetic variance (V_G) accounting for heterosis:

16/11% Dominance (V_D)

50/61% Additive x additive (V_{AA})

21/17% Additive x dominance (V_{AD})

13/11% Dominance x dominance (V_{DD})

This is contradictory to the conventional expectation of “heterosis is caused by dominance”.

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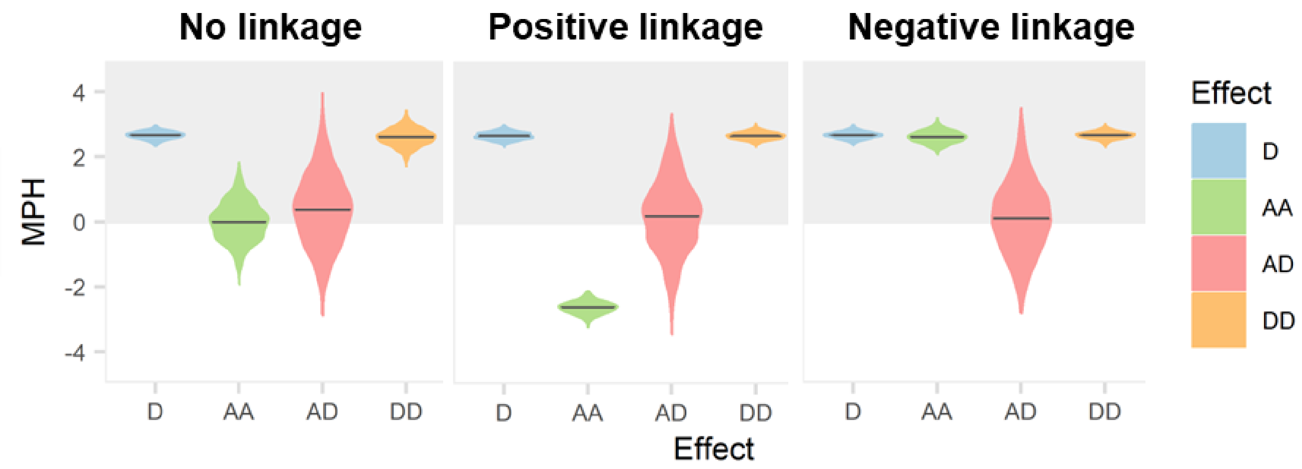
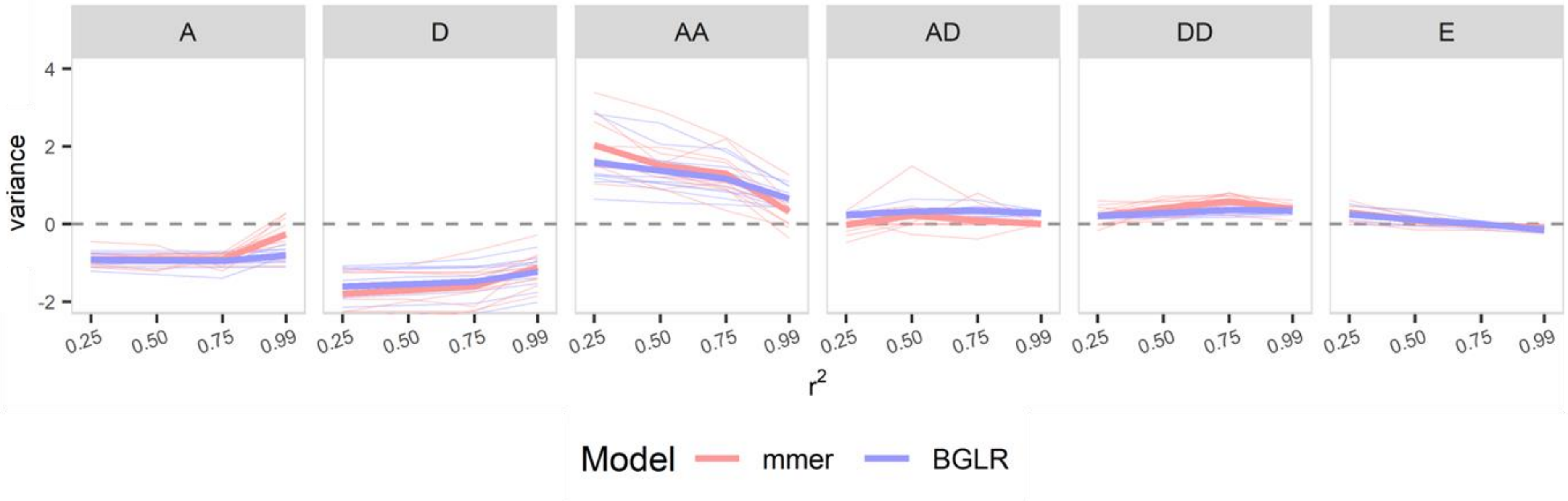


Linkage is needed for non-zero MPH due to AA.

Current work: Phantom epistasis and heterosis



- Use wheat hybrid marker data (Zhao et al 2015, 120 + 15 parents, 1604 hybrids, 2701 markers).
- Simulate trait with A + D (V_A = 1 and 0 < D < 2A).
- Thin marker data according to its linkage with simulated QTLs.
- Estimate variance components.

Full talk is available at the Roslin CGDG YouTube channel

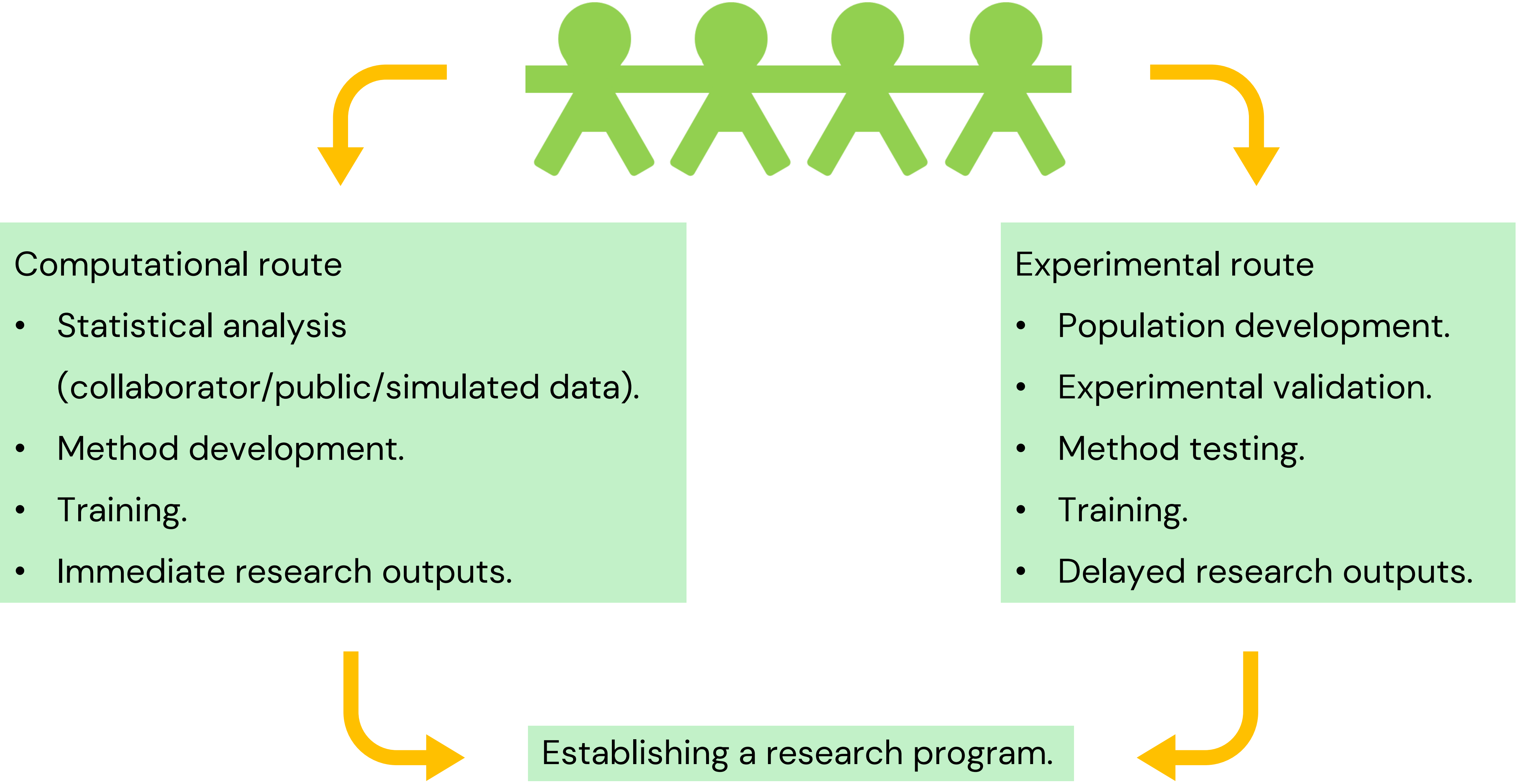
https://youtu.be/ThbKA6VzG0U

Research vision @UNL

1. Improved genetic diversity management for sustainable crop breeding.
2. Development of major and minor/novel crop breeding.
3. Holistic research training.
4. Contribution toward UNL N2025 aims.

Aim	**Strategy**
Increasing research impact.	Training, innovative research, collaboration, publications, funding.
Interdisciplinary collaboration.	Teamwork, Center of Plant Science Innovation, IANR communities.
Broadening stakeholders' engagement.	Knowledge exchange and transfer, participatory breeding.
Fostering professional development.	Training, alternative opportunities, progress tracking.
Promoting diversity, equity and inclusion.	Training, recruitment, respect, well-being.
Enhancing student experience.	Research experience.

Short-term research plan



Computational route

- Statistical analysis (collaborator/public/simulated data).
- Method development.
- Training.
- Immediate research outputs.

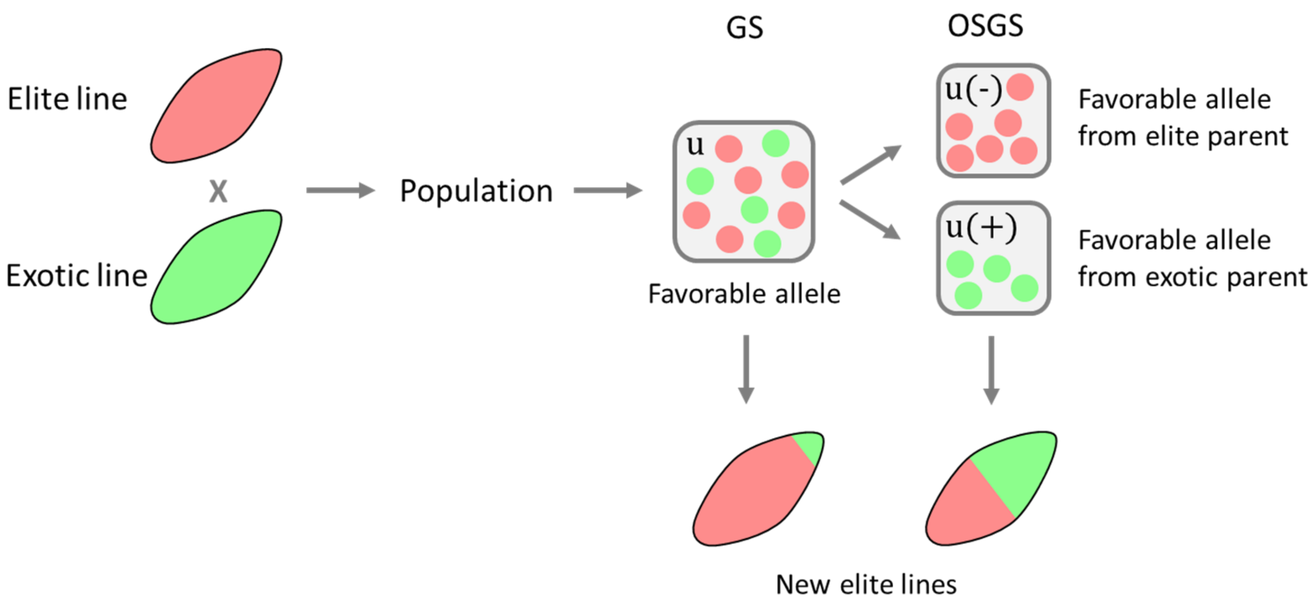
Experimental route

- Population development.
- Experimental validation.
- Method testing.
- Training.
- Delayed research outputs.

Establishing a research program.

Plan 1: multivariate OSGS (mvOSGS)

Recall previously that we can partition the favorable parental contributions using OSGS.



However, this only works with in a single trait, bi-parental setting.

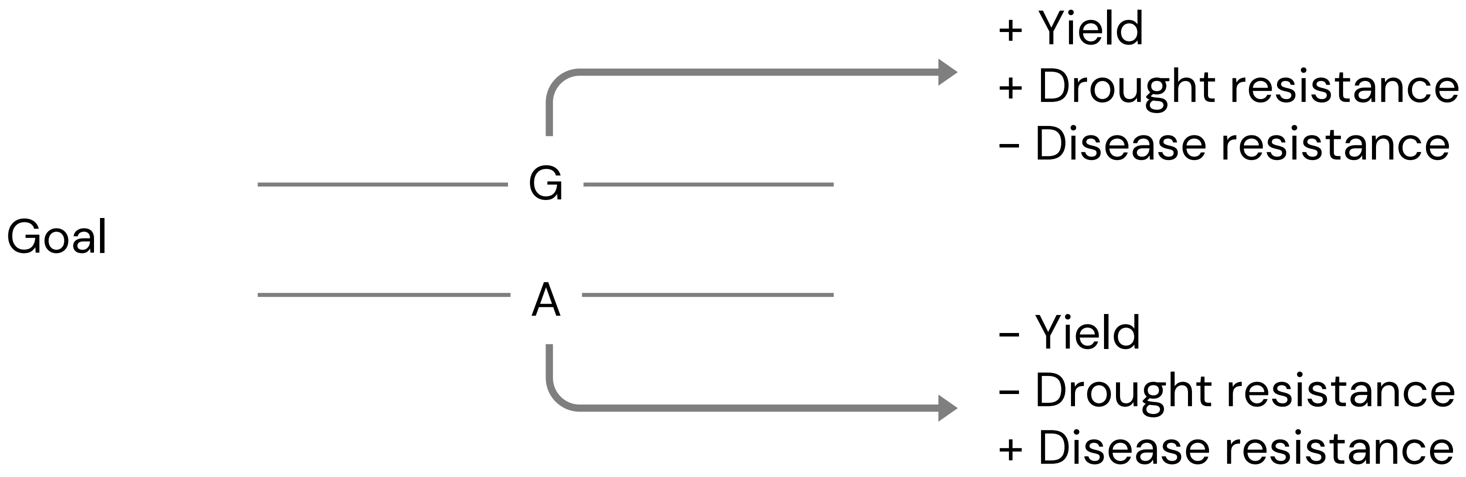
An upgrade is necessary to make it more practical.

Plan 1: multivariate OSGS (mvOSGS)

First, how do we deal with multi-trait?

There are 3 immediate options:

1. Fit each trait by itself – assumes no covariances among traits.
2. Fit all traits at once using SNP-BLUP model, e.g. ridge regression, elastic net, LASSO.
3. Fit all traits at once using G-BLUP model, then apply linear transformation of $u_i = Z_i' K^{-1} g$ (Ning et al 2018).



+ Yield
+ Drought resistance
- Disease resistance

Goal

G

A

- Yield
- Drought resistance
+ Disease resistance

Plan 1: multivariate OSGS (mvOSGS)

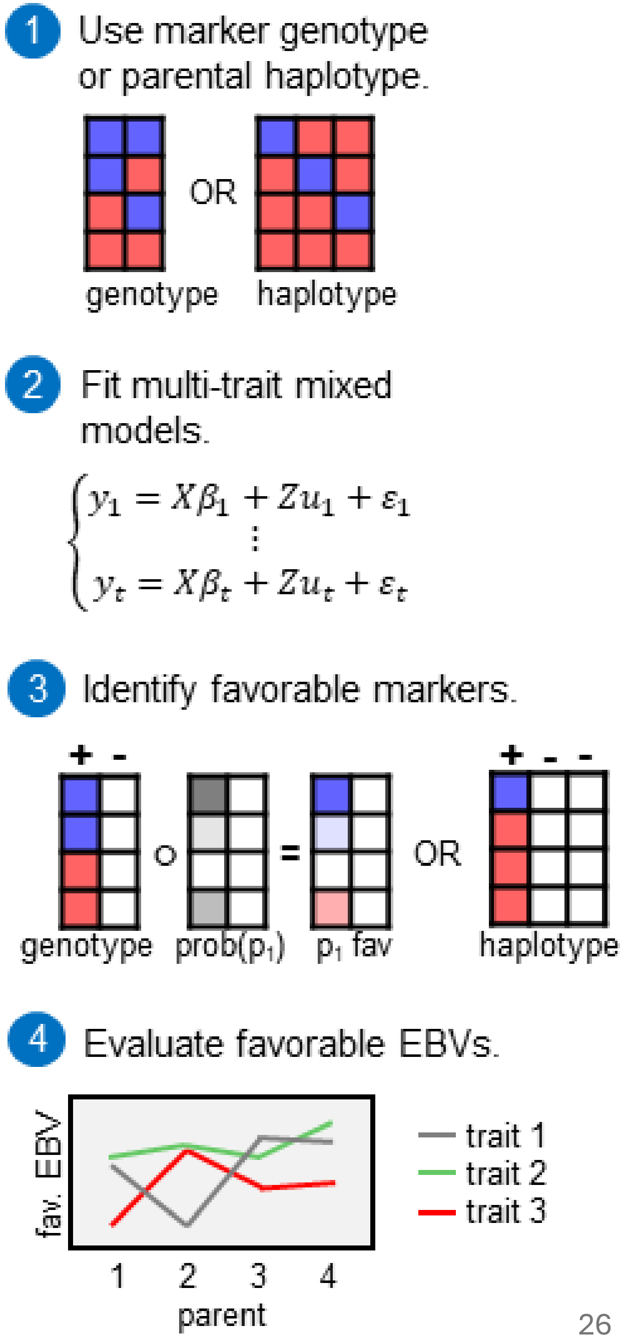
Next, how do we deal with multi-parent?

There are two immediate options:

1. Fit genotype matrix.

```
          ID Allele P(P1) P(P2) P(P3) Fav-P1
   Parent-1      1   1.0     0     0     NA
   Parent-2      1     0   1.0     0     NA
   Parent-3     -1     0     0   1.0     NA

  Progeny-1      1   0.8   0.2     0    0.8
  Progeny-2     -1     0     0   1.0      0
  Progeny-3      1   0.1   0.9     0    0.1
```



① Use marker genotype or parental haplotype.

② Fit multi-trait mixed models.

$$\begin{cases} y_1 = X\beta_1 + Zu_1 + \varepsilon_1 \\ \vdots \\ y_t = X\beta_t + Zu_t + \varepsilon_t \end{cases}$$

③ Identify favorable markers.

④ Evaluate favorable EBVs.

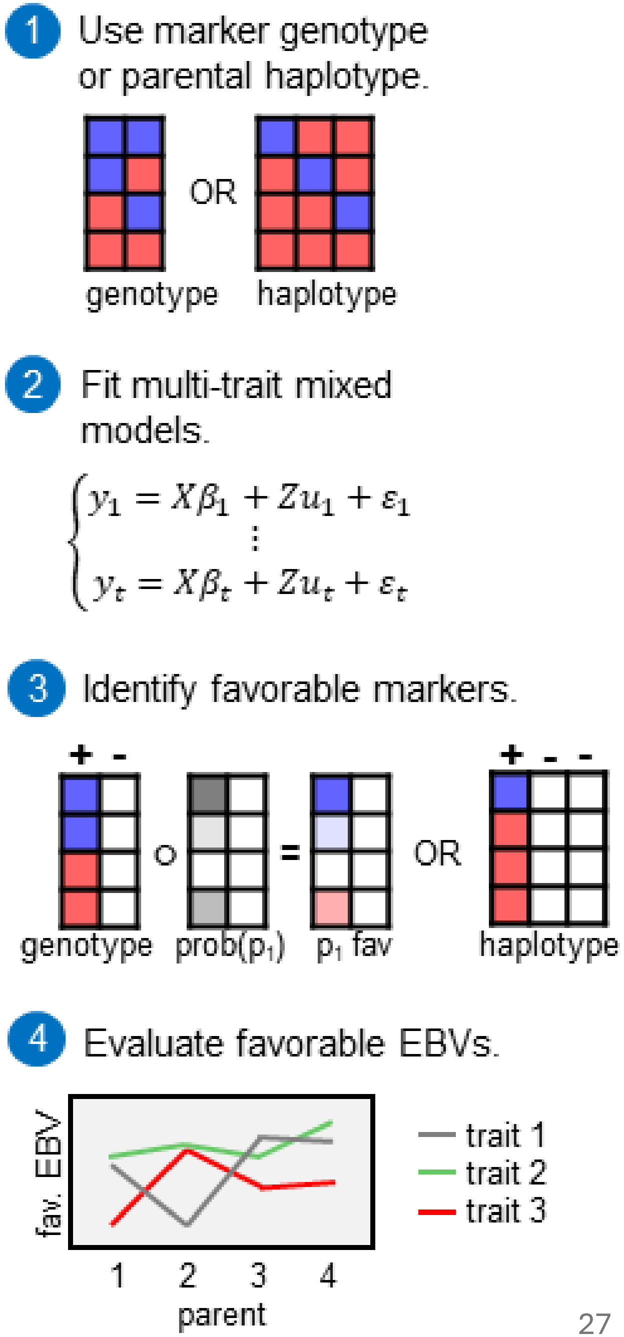
Plan 1: multivariate OSGS (mvOSGS)

Next, how do we deal with multi-parent?

There are two immediate options:

2. Fit parental haplotype matrix.

ID	M1	M2	H1	H2	H3	Fav-H1
Parent-1	G	T	1	-1	-1	NA
Parent-2	G	C	-1	1	-1	NA
Parent-3	A	T	-1	-1	1	NA
Parent-4	A	C	-1	-1	-1	NA
Progeny-1	G	C	-1	1	-1	0
Progeny-2	A	C	-1	-1	-1	0
Progeny-3	G	T	1	-1	-1	1



1 Use marker genotype or parental haplotype.

2 Fit multi-trait mixed models.

$$\begin{cases} y_1 = X\beta_1 + Zu_1 + \varepsilon_1 \\ \vdots \\ y_t = X\beta_t + Zu_t + \varepsilon_t \end{cases}$$

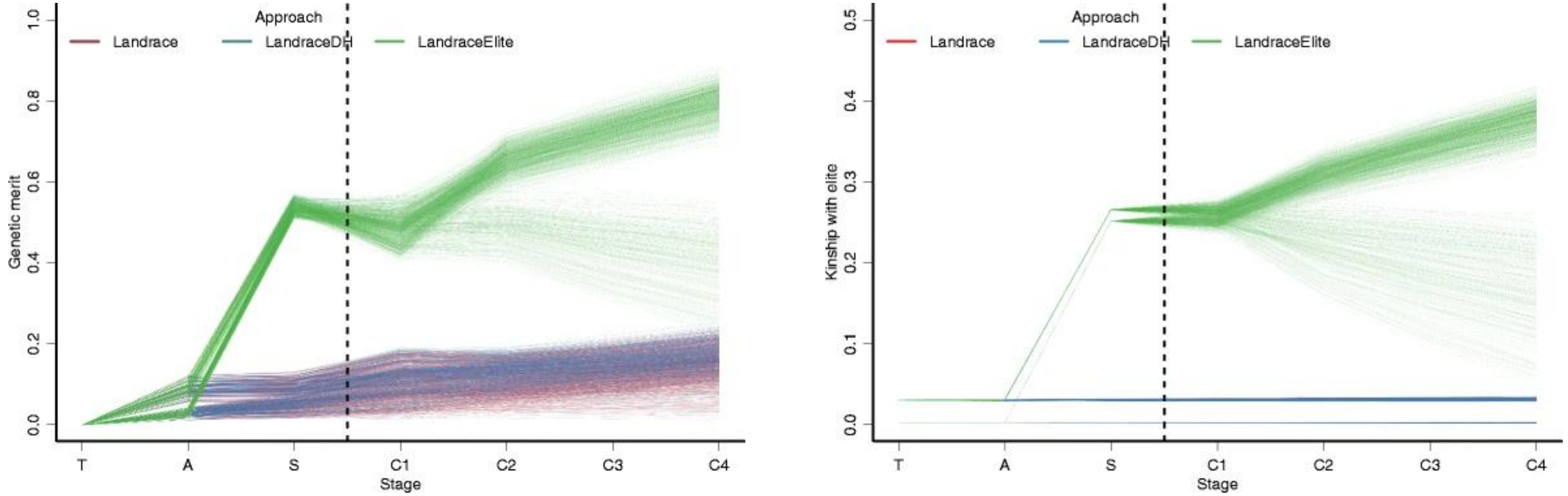
3 Identify favorable markers.

4 Evaluate favorable EBVs.

Plan 1: multivariate OSGS (mvOSGS)

What is mvOSGS useful for?

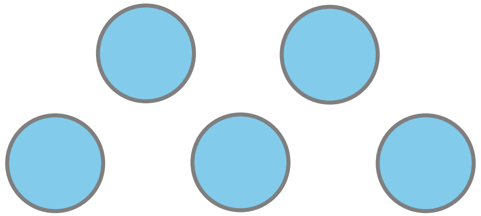
- Just like OSGS, it can be used to introgress novel alleles from exotic.
- Just like OSGS, it prevents reconstitution of elite genome.



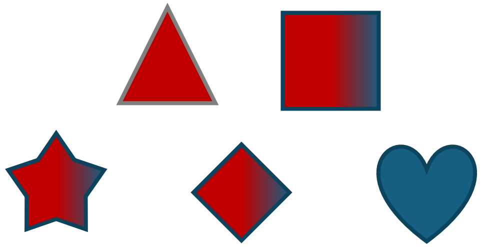
Gorjanc et al (2016)

- Unlike OSGS, it accounts for multiple founders and traits.

Elite population



Exotic population



Mildly favorable

Strongly favorable

Strongly unfavorable

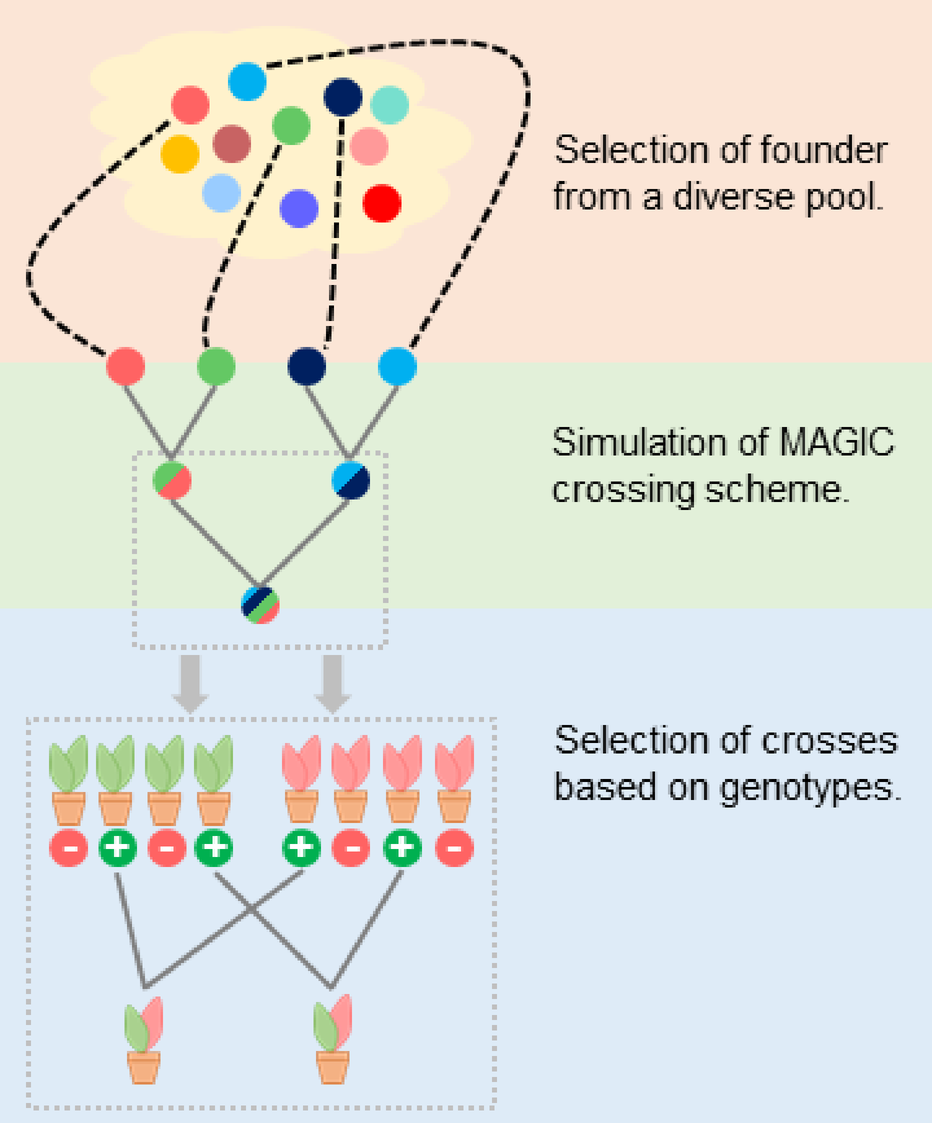
Plan 2: R/magicdesign

Founders' information >>> Create funnels >>> Simulate

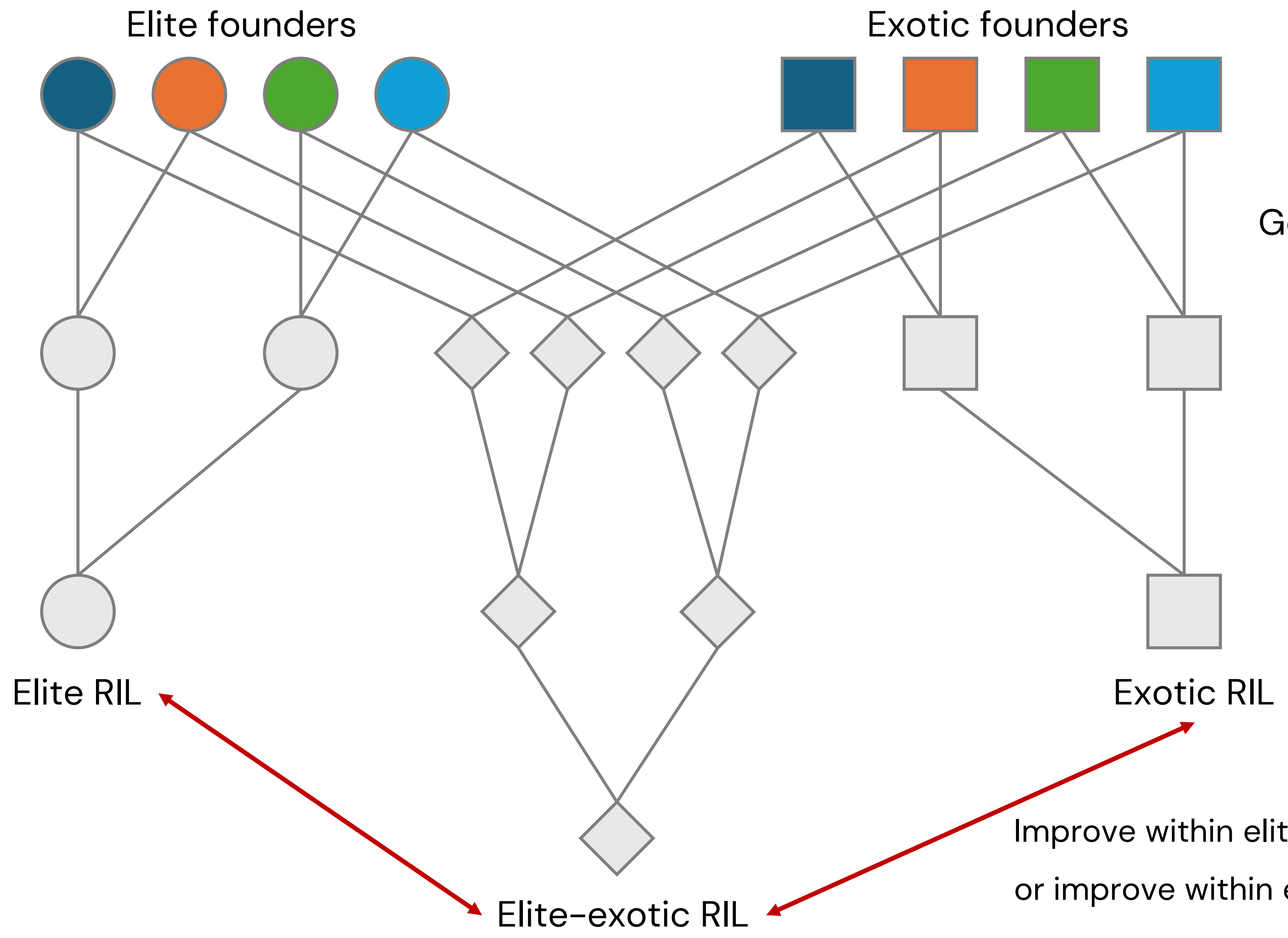
It is currently very basic and would benefit from including additional functions.

1. Founder selection – diversity measures, e.g. Manhattan distance, F_{ST}, simulated annealing (Kirkpatrick et al 1983).
2. Crosses' genotypes – identify and select for crosses that would maximize unique recombinations.

Training opportunity for group members.



Plan 3: Elite-exotic MAGIC

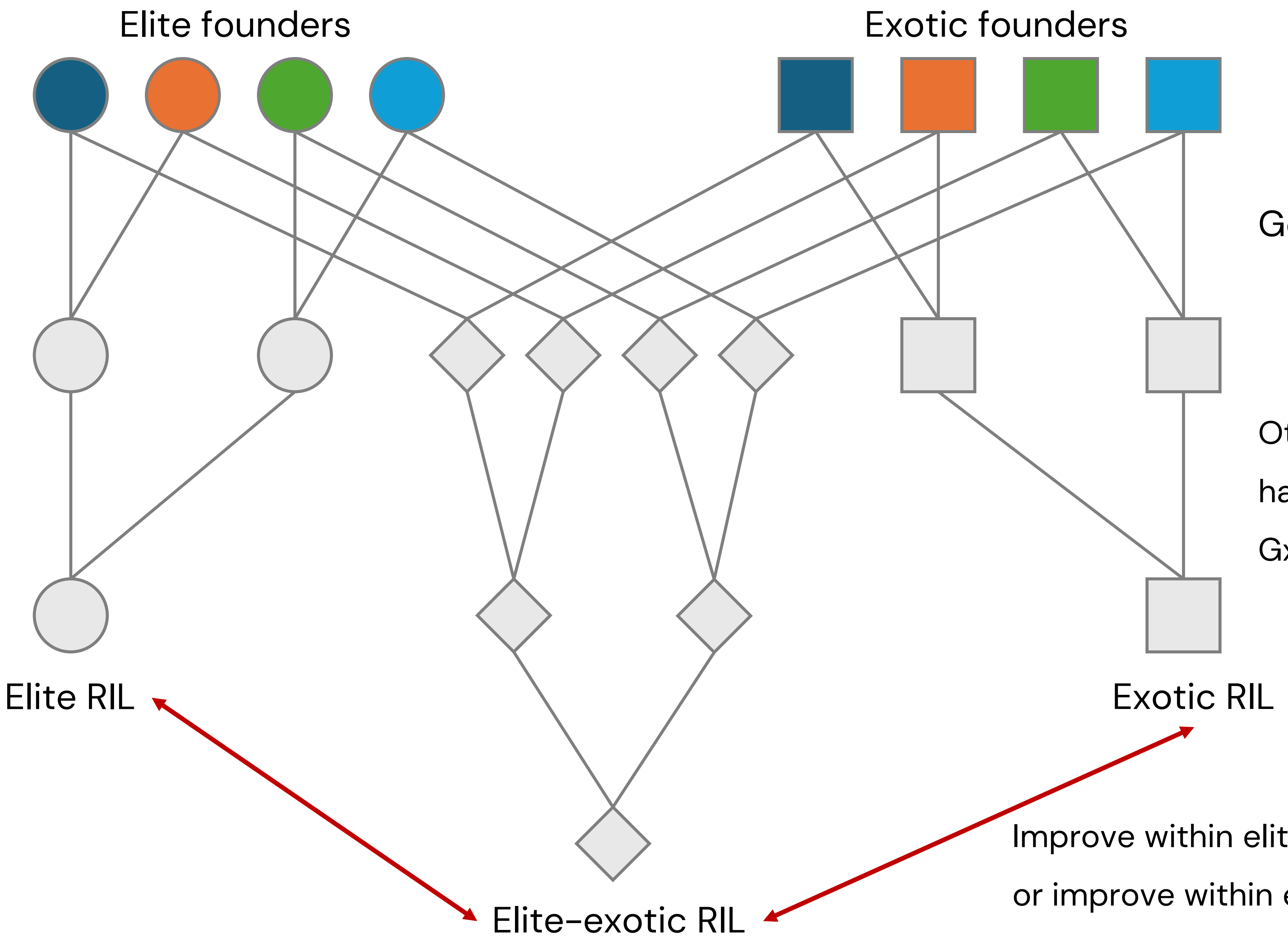


General approach for any species.

Improve within elite-exotic RILs (using mvOSGS)

or improve within exotic RILs?

Plan 3: Elite-exotic MAGIC



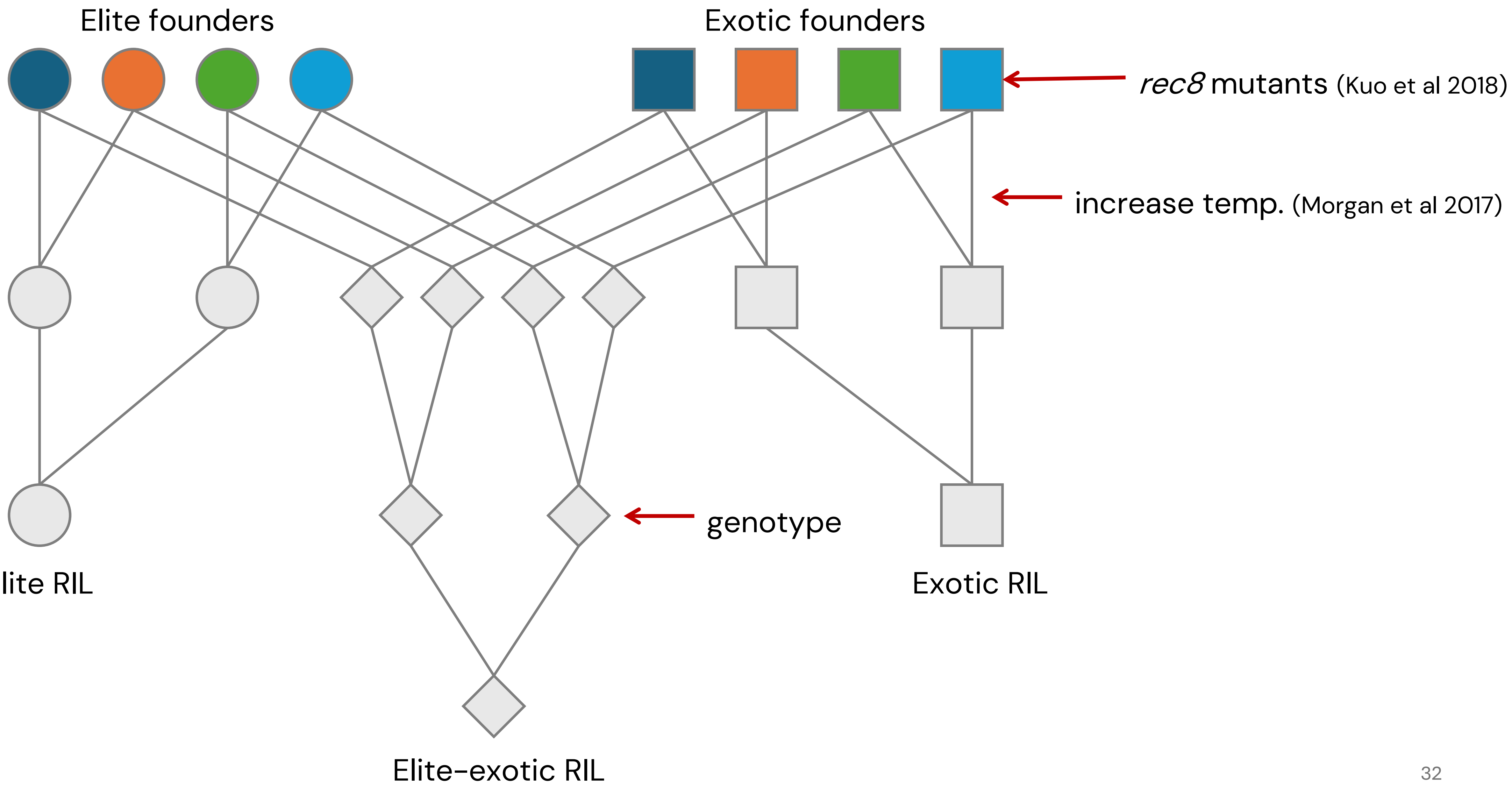
General approach for any species.

Other uses: QTL mapping, novel haplotypes (transgressive segregation, GxE, phenomics, animal feed, etc)

Improve within elite-exotic RILs (using mvOSGS) or improve within exotic RILs?

Plan 3: Elite-exotic MAGIC

playing with recombinations



Plan 3: Elite-exotic MAGIC

playing with recombinations

Elite founders

Exotic founders

If it ain't broke, don't fix it: evaluating the effect of increased recombination on response to selection for wheat breeding

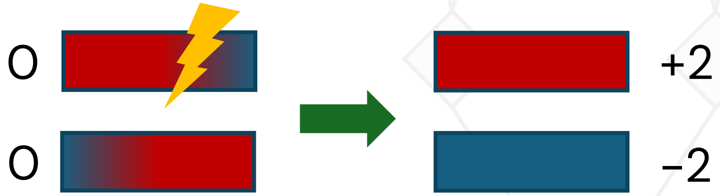
Ella Taagen ✉, Katherine Jordan, Eduard Akhunov, Mark E Sorrells, Jean-Luc Jannink

G3 Genes|Genomes|Genetics, Volume 12, Issue 12, December 2022, jkac291, https://doi.org/10.1093/g3journal/jkac291

rec8 mutants (Kuo et al 2018)

increase temp. (Morgan et al 2017)

Due to GS training model failing to catch up with the disrupted dispersion.



genotype

Elite RIL

Exotic RIL

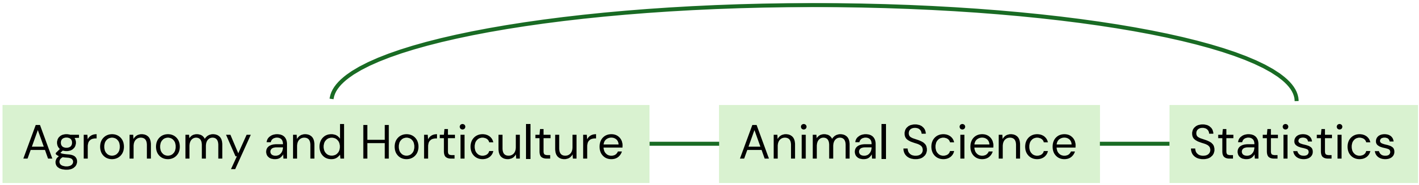
Not a problem in MAGIC – new haplotypes are captured in the GS training model.

Elite-exotic RIL

Collaboration opportunities

See a strong commitment toward collaboration at UNL.

- **IANR communities:** Computational science, Economic vitality, Healthy humans, Healthy systems, Stress biology, Science literacy.
- **Center for Plant Science Innovation:** combines genetics, genomics, phenomics, microbiome, immunology, bioinformatics.



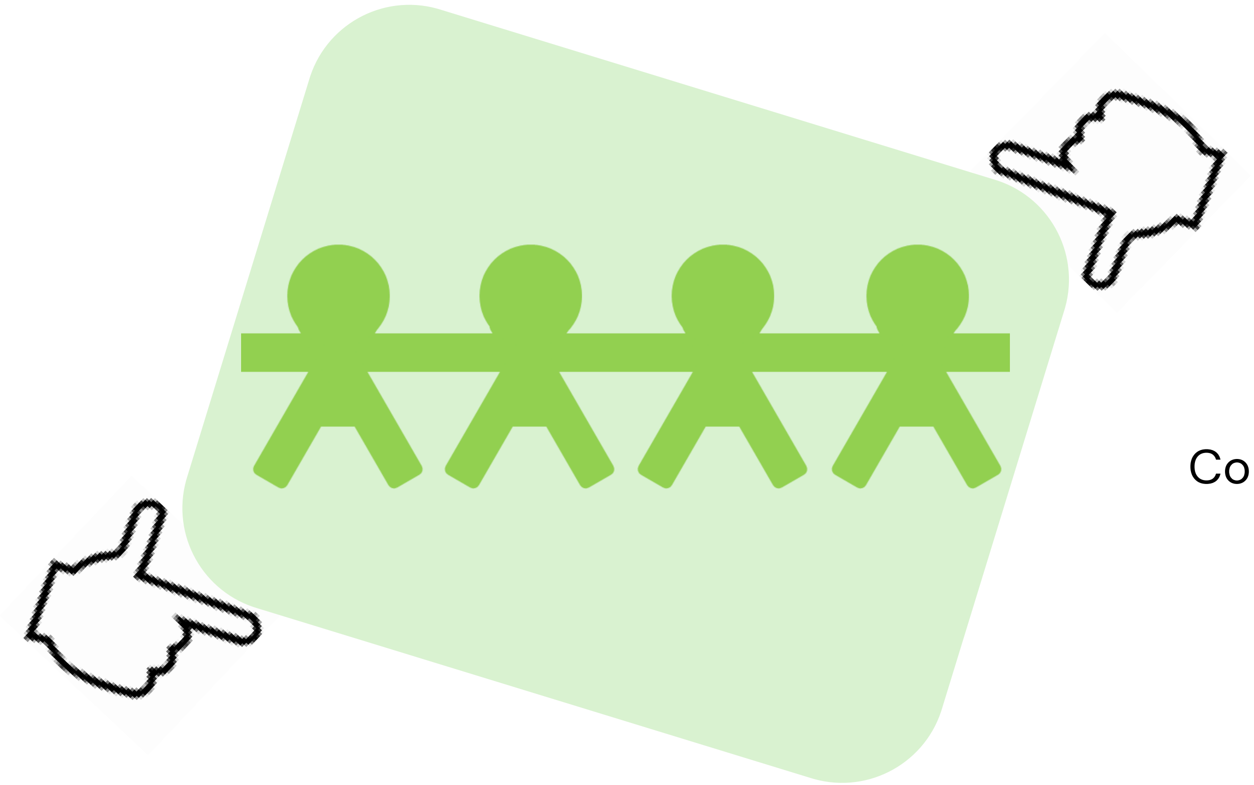
Various exciting research in breeding and genetics.

- Genomics, phenomics, microbiome, animal nutrition, mixed model, experimental design.
- Knowledge exchange (we can offer those developed in the short-term plans).

Extension - deliver direct impact.

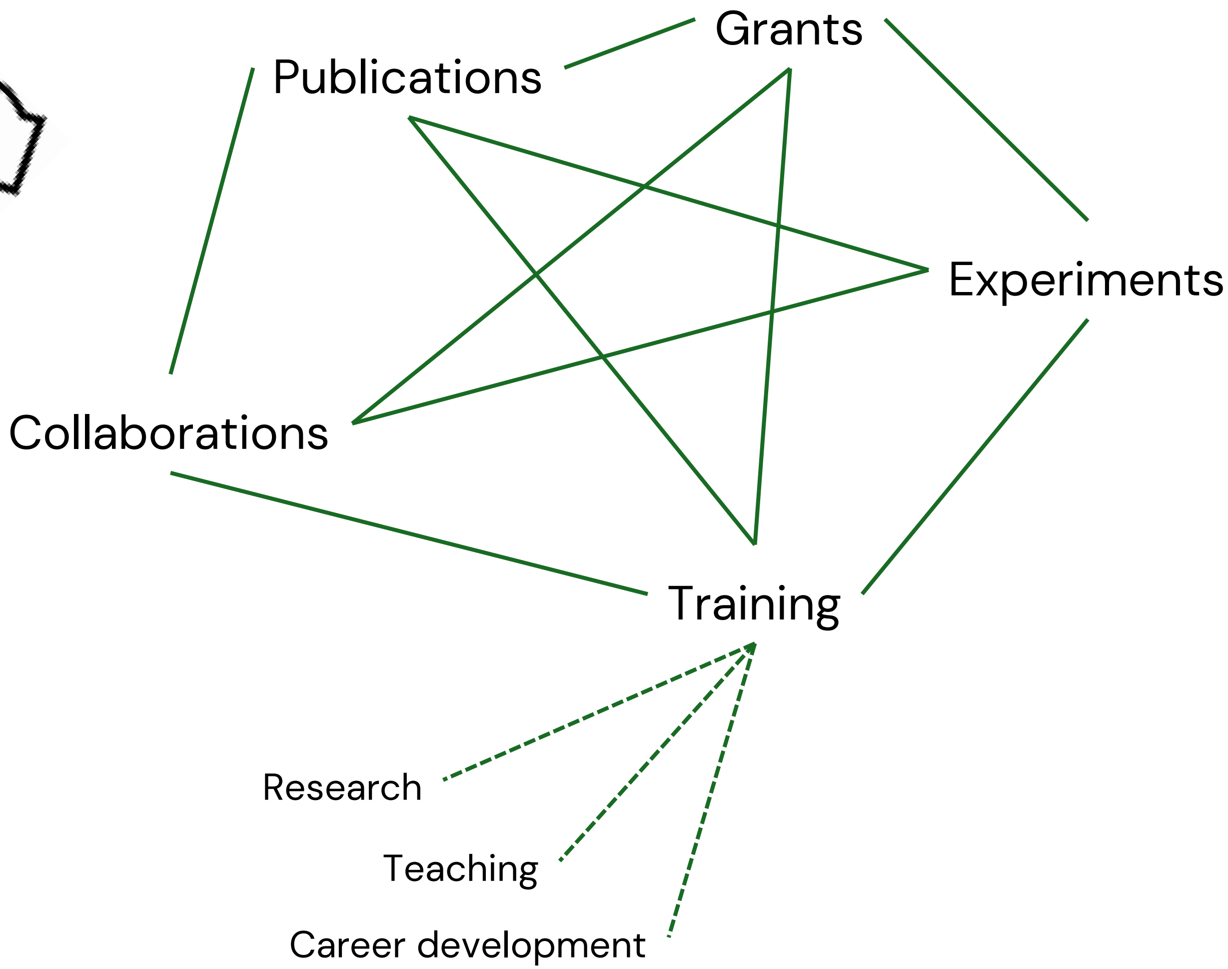
Training – plenty of opportunities.

Long-term research plan



What is in the future for us

as a research group?



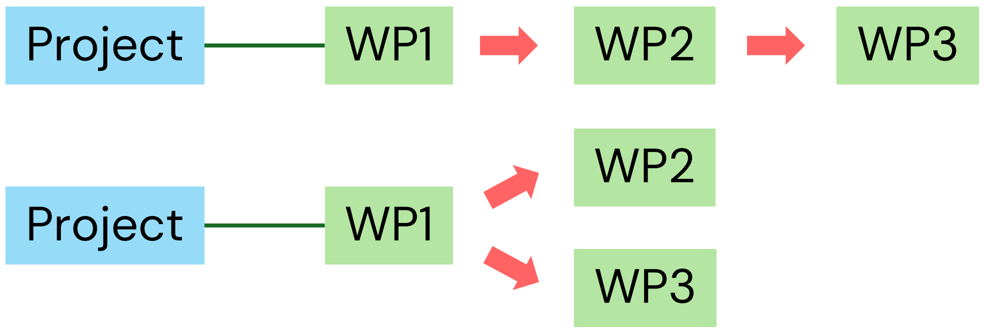
Long-term research plan

External grant funding is the key to keep the research group going.

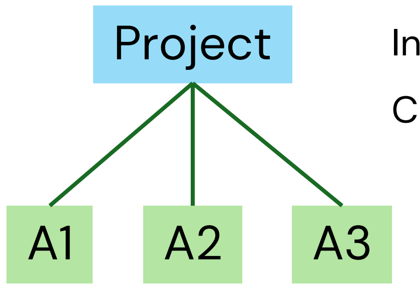
Grant experience

- MAGS: Mutation breeding for quantitative traits with genomic selection (IAEA, 2022-2027).
- BARGAIN: Mobilizing untapped genetic diversity (RESAS, 2022-2027).
- The impact of novel crops and farming practices on the Scottish agricultural landscape (RESAS, 2022-2027).
- Development of high-value bio-products from wild-harvested and farmed Scottish seaweed (IBioIC, 2022-2023).
- Rapid domestication of purslane in a vertical farm environment (EASTBIO, student pending).
- Development of a data-driven breeding program for sugar kelp (SAIC, submitted).

EU model


Project
WP1
WP2
WP3
Project
WP1
WP2
WP3

NA model


Project
A1
A2
A3

Federal : NSF, USDA, DoE

Industry

Commodity board

Commitment toward Diversity, Equity and Inclusion (DEI)

Past experience

- Mentoring of a diverse group of undergraduates.
- Assistance in scientific presentations.
- Meetings, symposiums, conferences, publications.
- Various supports.

Going forward

DEI Vision

D: open door to diversity (women, PoC, LGBT+, disabled, first-gen, more).

E: support in all areas, be aware and act on invisible disadvantages.

I: communication, cultural exchange, be accommodating, well-being.

Every person and every interaction matters – UNL N2025 Strategic Plan

Acknowledgement

Many thanks to you all for joining today!

And big thanks to:

- UNL IANR Search Committee for the opportunity to present.
- Kay McClure-Kelly for organizing and scheduling.
- Past and current mentors for their continuous guidance and support.
- All collaborators as none of the work would have been possible without them.

Teaching students to learn effectively

CJ Yang

Dec 8th, 2022

Talk outline

1. Introduction
2. Teaching experience
3. Teaching vision/philosophy
4. Teaching approaches
5. Teaching examples
6. Diversity, Equity, Inclusion (DEI) commitment

Introduction

Education & Research

2009 – 2012	Indiana University Bloomington (IU)	BSc Biotechnology, Mathematics
2012 – 2018	University of Wisconsin (UW)-Madison	PhD Genetics
2018 – 2019	Technical University of Munich (TUM)	Postdoc
2019 – now	Scotland's Rural College (SRUC)	Postdoc

Teaching

2013	Teaching Assistant (TA)	General genetics	UW-Madison
2021	Guest lecturer	Plant genetics, genomics and breeding	CIHEAM Zaragoza
2022	Guest lecturer	Genetics improvement of crops	University of Edinburgh

Teaching experience: TA for General Genetics

Just as many of you are familiar with:

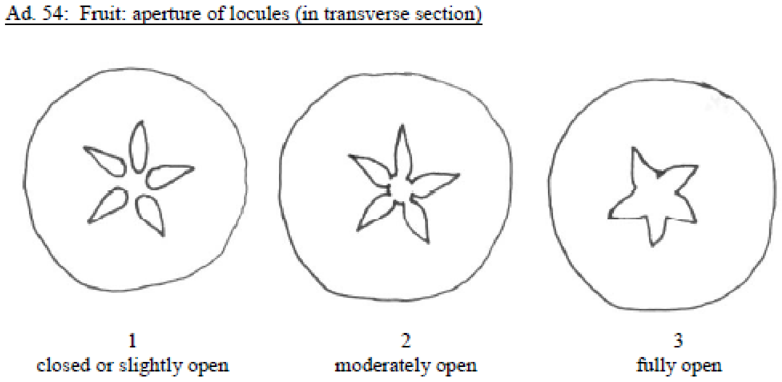
- Provide support to the students in understanding lecture materials through discussions.
- Maintain two-way communications to assess the students’ understanding.
- Made myself flexible with the students.
- Good introduction into teaching (for me).

Teaching experience: Plant Genetics, Genomics and Breeding

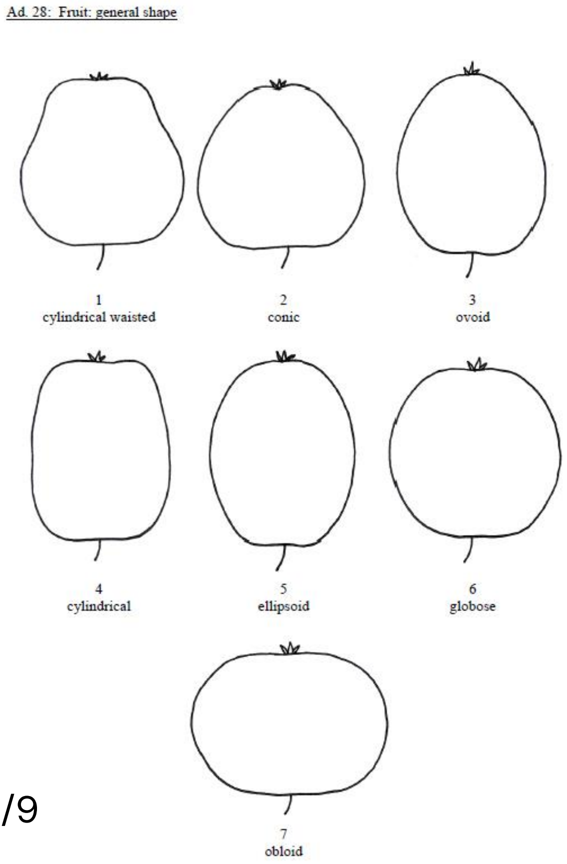
- Guest lecturer for the section on “IBD, IBS, Genetic Distance, Population Structure”.
- 30 students with strong background in plant genetics and breeding.
- Online teaching – meant to take place in Zaragoza, Spain in early 2021.
- 4 hours of lecture + 4 hours of lab practical.
- Lack of visual interaction – encouraged the students to speak out or type in the chat boxes or emails.
- Had computational analyses in R for the lab practical (not easy…., need to debug).
- Spent extra time to divide up the analyses to make sure everyone was on the same page.
- Take home exercise with short answer questions – with a focus on justifications to stimulate thinking.
- Happy to see students coming with questions on their own datasets.

Teaching experience: Genetic Improvement of Crops

- Guest lecturer for “Conventional vs Advanced Breeding Methods” and “Variety Identification”.
- 3 students – had more chance to be interactive.
- 2 hours of lecture + 3 hours of lab practical.
- Breeding exercise – simulate a single cycle of selection in R.
- Challenging – walk the students through.
- Identify apple varieties according to the UPOV standards.



UPOV TG/14/9

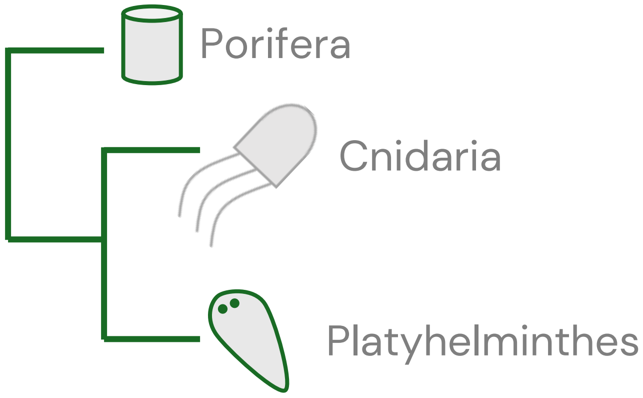


Teaching vision/philosophy - backstory

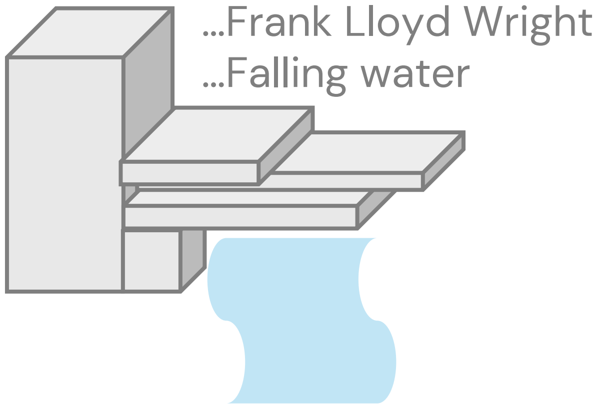
Undergraduate time at IU

Variable courses – need to adapt to learn quickly.

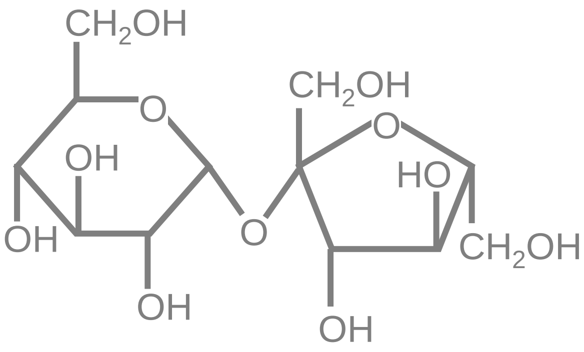
9:00 am Biology Building



1:00 pm Ballantine Hall



11:00 am Woodburn Hall



3:00 pm Swain Hall

$$\frac{dy}{dx} = y + xy$$

$$y^{-1}dy = (x+1)dx$$

$$\int y^{-1}dy = \int (x+1)dx$$

$$\ln(y) = \frac{x^2}{2} + x + C$$

Teaching vision/philosophy

Teaching students to learn effectively.

↓

Relevance to the UNL N2025 aims.

↓

- Enhancing student experience.
- Promoting diversity, equity and inclusion.

↓

- Learning never ends.
- Improve students' learning skills.
- Everyone is unique – space to develop personal learning style.
- Everyone should have the rights to learn – outreach.

Teaching approaches

Adaptation: adjust teaching style and course contents to match the needs.

Analogy: use of prior knowledge (example) to understand unfamiliar topics.

Assessment: gauge students’ needs and interests.

Teaching approaches: Adaptation

Motivation

- Everyone is unique.
- Space for everyone to develop their strengths in learning.

Examples

- Small vs large class – how much can we deviate from the core syllabus?
- Students' interest – is there any alternative teaching material that fit better? e.g. scientific literature.
- Students' background – how advanced can we go? level-appropriateness of resources.
- Nature of the class – is there any non-class component? e.g. field trip.
- Individual vs group work – can we have both?

Teaching approaches: Analogy

Motivation

- More relatable and attractive.
- Clearer framework to understand and evaluate.

Examples

- Genotype imputation – predicting weather from cloud cover and wind direction.
- CRISPR – Photoshop, Find & Replace, …, Bomb Removal Tool (https://www.statnews.com/2017/12/08/crispr-analogies-ranked/)
- After introducing the analogy,
  - highlight the core features
  - identify the parallel points
  - if needed, improve the analogy for next time

Ledford (2015)

Teaching approaches: Assessment

Motivation

- Identify students’ progress, strength/weakness, issue, misconception, need, interest.
- Circulate back to adjust pace and adapt course plan.

Examples

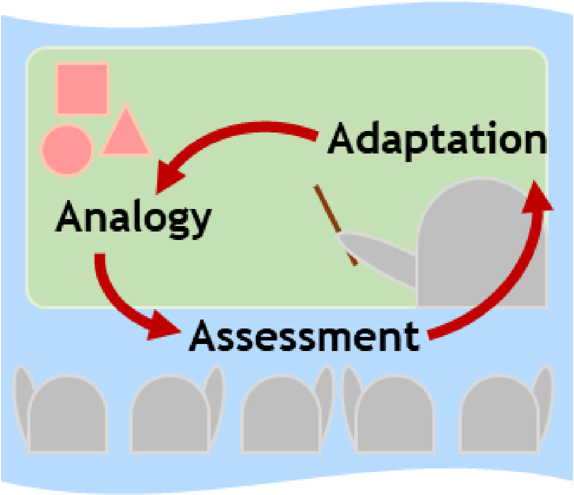
- Final exam
- Mid-term exam
- Project report
- Survey
- Quiz
- Clicker question

In-depth probe, minimal opportunity to act.

Understanding > Answer

Shallow probe, plenty of opportunity to act.

Teaching approaches: 3A



- Adaptation, Analogy and Assessment form a loop.
- Stimulate students’ critical thinking.
- Learning skill that extends beyond the class.
- As an instructor, be ready to improve.
- Improvement never ends – go beyond any semester.
- Continuous curriculum update, e.g. Genomic Selection, CRISPR.

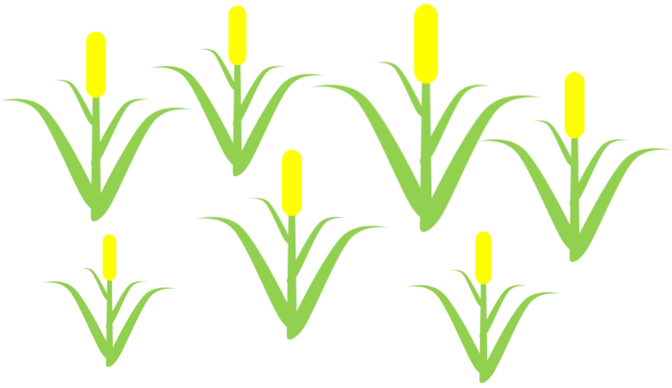
Teaching examples

The next few slides are examples of my teaching slides.

They will be presented as how I would when I am teaching.

And then I will highlight the relevant points and possible improvement.

IBD in QTL mapping



Genotype a bi-parental population →

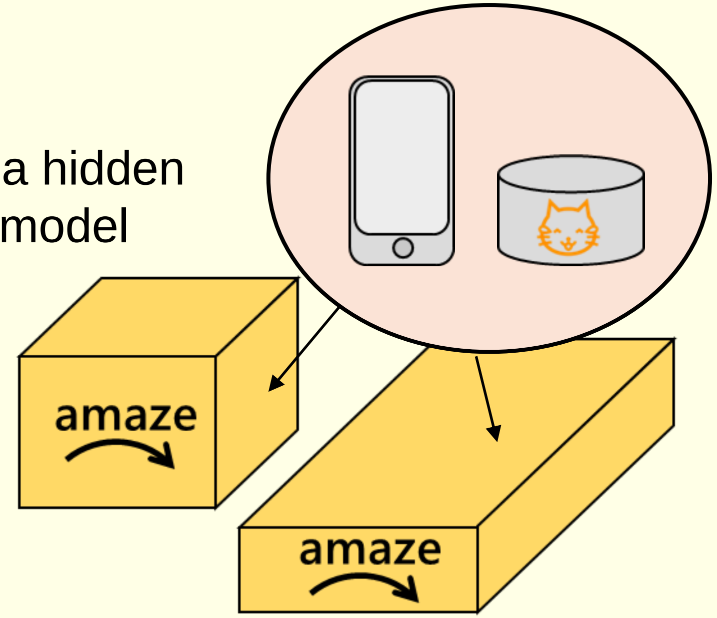
ID1	A	G	C	A
ID2	A	C	C	T
ID3	G	C	C	T

Obtain P(IBD) using hidden Markov model →

P(IBD) with founder 1

ID1	1	1	.5	1
ID2	1	0	.5	0
ID3	0	0	.5	0

What is a hidden Markov model (HMM)?



Suppose you receive a package every day. How would you tell which item is in which package?

Assume the packages form a Markov chain (i.e. today’s package depends on yesterday’s), open the packages every day, keep track of the contents, make an educated guess.

Package = marker genotype
Content = P(IBD)

A short detour – what is a matrix?

Bluntly speaking, a matrix is a rectangle of numbers…

$$\begin{vmatrix} 1 & 4 & 2 \\ 5 & 2 & 3 \end{vmatrix} \qquad \begin{vmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{vmatrix} \qquad \begin{vmatrix} 2 & 3 \end{vmatrix}$$

A square matrix is … square!

$$\begin{vmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{vmatrix}$$

This specific example is also a diagonal matrix and identity matrix.

A matrix has row and column.

$$\begin{array}{cc} & \text{Column} \\ \text{Row} & \begin{vmatrix} 1 & 4 & 2 \\ 5 & 2 & 3 \end{vmatrix} \end{array}$$

An $n \times m$ matrix has n rows and m columns.

Elements of matrix $\boldsymbol{M}$ are referred as M_{ij}

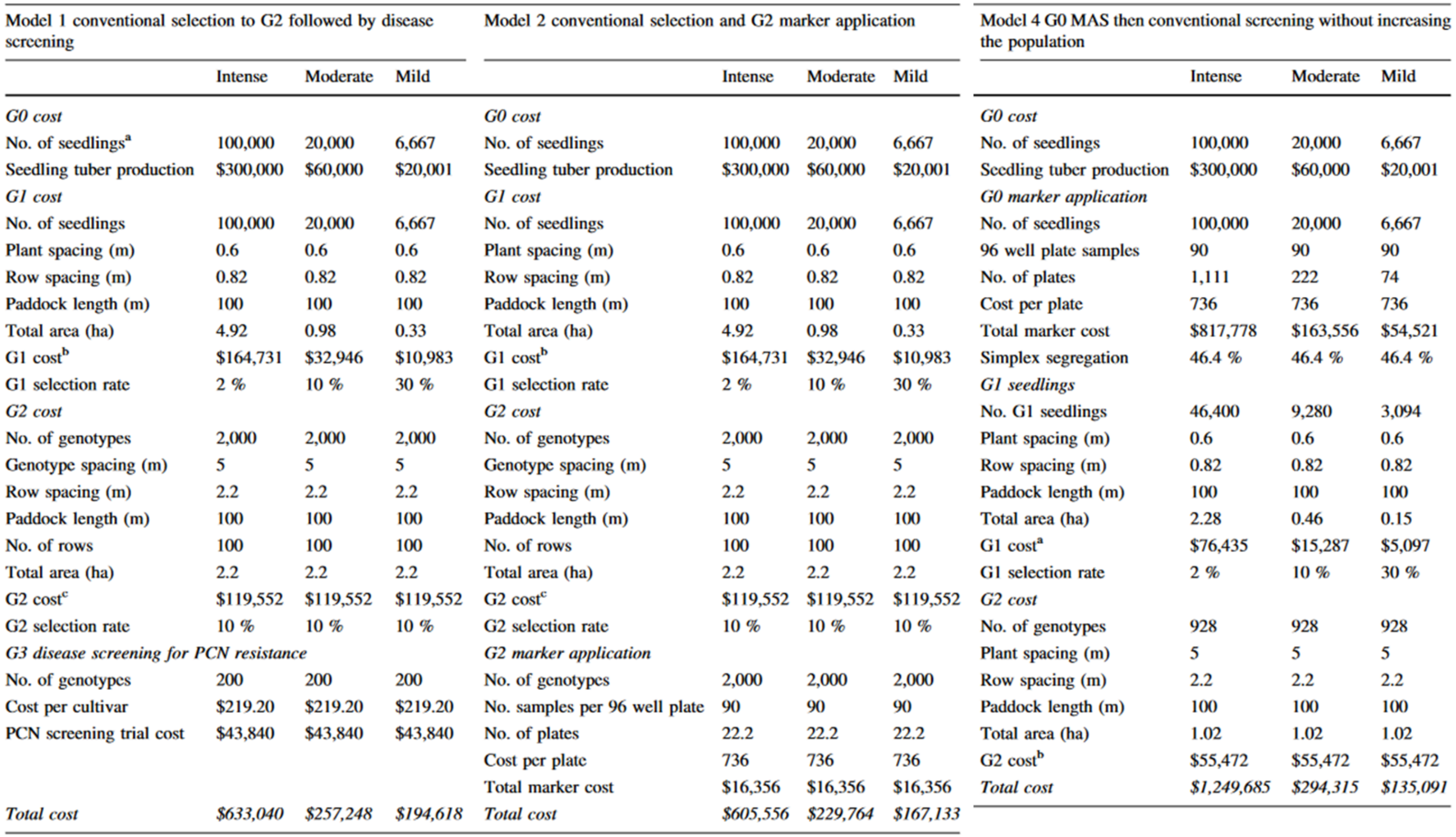
$$\begin{vmatrix} M_{11} & M_{12} & M_{13} \\ M_{21} & M_{22} & M_{23} \end{vmatrix}$$

Time and cost (an example in potato breeding)

Cost analysis of the application of marker-assisted selection in potato breeding

Anthony T. Slater, Noel O. I. Cogan & John W. Forster

Molecular Breeding **32**, 299–310 (2013) | Cite this article



Model 1 conventional selection to G2 followed by disease screening	Intense	Moderate	Mild
G0 cost			
No. of seedlings[a]	100,000	20,000	6,667
Seedling tuber production	$300,000	$60,000	$20,001
G1 cost			
No. of seedlings	100,000	20,000	6,667
Plant spacing (m)	0.6	0.6	0.6
Row spacing (m)	0.82	0.82	0.82
Paddock length (m)	100	100	100
Total area (ha)	4.92	0.98	0.33
G1 cost[b]	$164,731	$32,946	$10,983
G1 selection rate	2 %	10 %	30 %
G2 cost			
No. of genotypes	2,000	2,000	2,000
Genotype spacing (m)	5	5	5
Row spacing (m)	2.2	2.2	2.2
Paddock length (m)	100	100	100
No. of rows	100	100	100
Total area (ha)	2.2	2.2	2.2
G2 cost[c]	$119,552	$119,552	$119,552
G2 selection rate	10 %	10 %	10 %
G3 disease screening for PCN resistance			
No. of genotypes	200	200	200
Cost per cultivar	$219.20	$219.20	$219.20
PCN screening trial cost	$43,840	$43,840	$43,840
Total cost	*$633,040*	*$257,248*	*$194,618*

Model 2 conventional selection and G2 marker application	Intense	Moderate	Mild
G0 cost			
No. of seedlings	100,000	20,000	6,667
Seedling tuber production	$300,000	$60,000	$20,001
G1 cost			
No. of seedlings	100,000	20,000	6,667
Plant spacing (m)	0.6	0.6	0.6
Row spacing (m)	0.82	0.82	0.82
Paddock length (m)	100	100	100
Total area (ha)	4.92	0.98	0.33
G1 cost[b]	$164,731	$32,946	$10,983
G1 selection rate	2 %	10 %	30 %
G2 cost			
No. of genotypes	2,000	2,000	2,000
Genotype spacing (m)	5	5	5
Row spacing (m)	2.2	2.2	2.2
Paddock length (m)	100	100	100
No. of rows	100	100	100
Total area (ha)	2.2	2.2	2.2
G2 cost[c]	$119,552	$119,552	$119,552
G2 selection rate	10 %	10 %	10 %
G2 marker application			
No. of genotypes	2,000	2,000	2,000
No. samples per 96 well plate	90	90	90
No. of plates	22.2	22.2	22.2
Cost per plate	736	736	736
Total marker cost	$16,356	$16,356	$16,356
Total cost	*$605,556*	*$229,764*	*$167,133*

Model 4 G0 MAS then conventional screening without increasing the population	Intense	Moderate	Mild
G0 cost			
No. of seedlings	100,000	20,000	6,667
Seedling tuber production	$300,000	$60,000	$20,001
G0 marker application			
No. of seedlings	100,000	20,000	6,667
96 well plate samples	90	90	90
No. of plates	1,111	222	74
Cost per plate	736	736	736
Total marker cost	$817,778	$163,556	$54,521
Simplex segregation	46.4 %	46.4 %	46.4 %
G1 seedlings			
No. G1 seedlings	46,400	9,280	3,094
Plant spacing (m)	0.6	0.6	0.6
Row spacing (m)	0.82	0.82	0.82
Paddock length (m)	100	100	100
Total area (ha)	2.28	0.46	0.15
G1 cost[a]	$76,435	$15,287	$5,097
G1 selection rate	2 %	10 %	30 %
G2 cost			
No. of genotypes	928	928	928
Plant spacing (m)	5	5	5
Row spacing (m)	2.2	2.2	2.2
Paddock length (m)	100	100	100
Total area (ha)	1.02	1.02	1.02
G2 cost[b]	$55,472	$55,472	$55,472
Total cost	*$1,249,685*	*$294,315*	*$135,091*

- Phenotypic screen for disease.
- 4 generations (G0 - G3).
- Cost = AUD 195k - 633k

- MAS at G2
- 3 generations.
- Cost = AUD 167k - 606k

- MAS at G0.
- 3 generations.
- Cost = AUD 135k – 1,250k

Bandwagon and hype

Bandwagons I, too, have known

Rex Bernardo

Theoretical and Applied Genetics **129**, 2323–2332 (2016) | Cite this article

5234 Accesses | **126** Citations | **35** Altmetric | Metrics

Abstract

Key message

Bandwagons come in waves. A plant breeder, just like a surfer, needs to carefully choose which waves to be on.

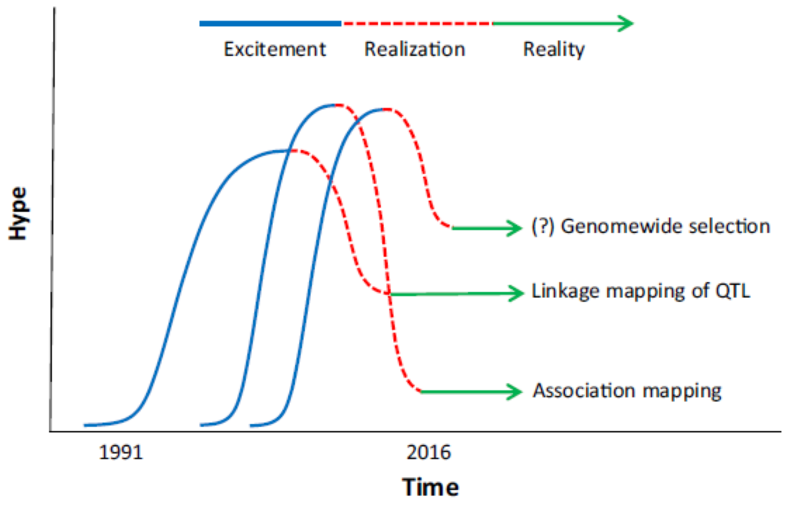
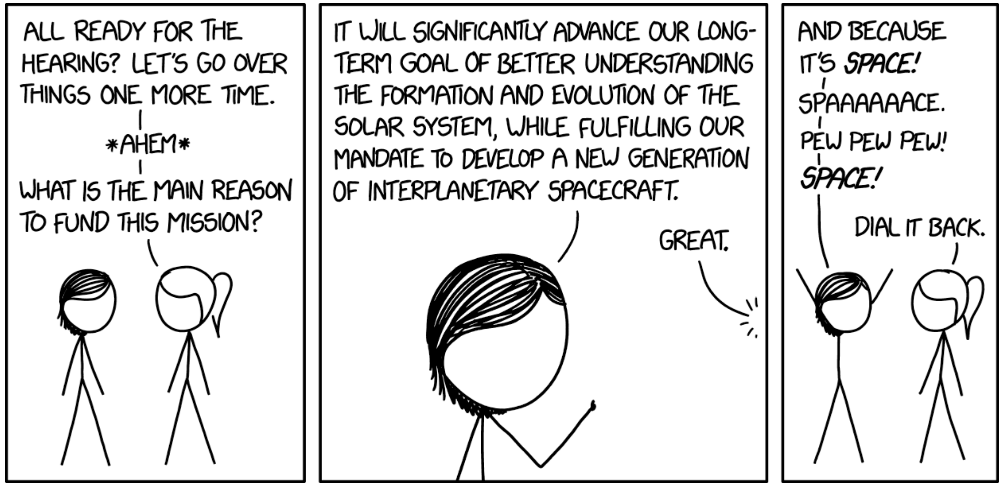


Fig. 1 Life cycle of a bandwagon, with QTL mapping, association mapping, and genomewide selection as examples. The reality level for association mapping is low, because the approach typically lacks power for detecting rare variants, which are what plant breeders most often seek. The (?) before genomewide selection indicates that the eventual level of usefulness of the procedure is still being discovered

- The hype (excitement) phase of a bandwagon is important.
- It is the best opportunity for getting funding.
- In a way, bandwagon pushes advanced breeding methods forward.

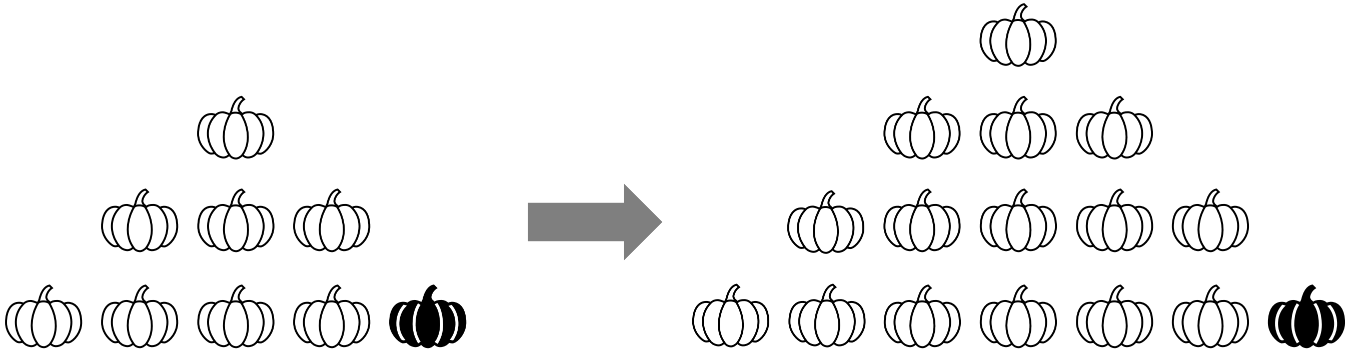


https://xkcd.com/2124

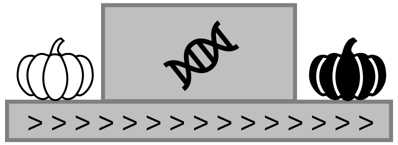
Selection intensity

We can increase selection intensity by:

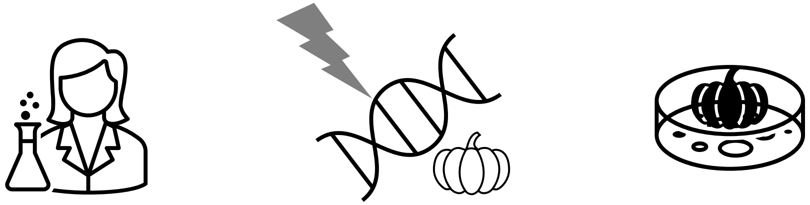
1. Increasing the population size (budget limitation!).



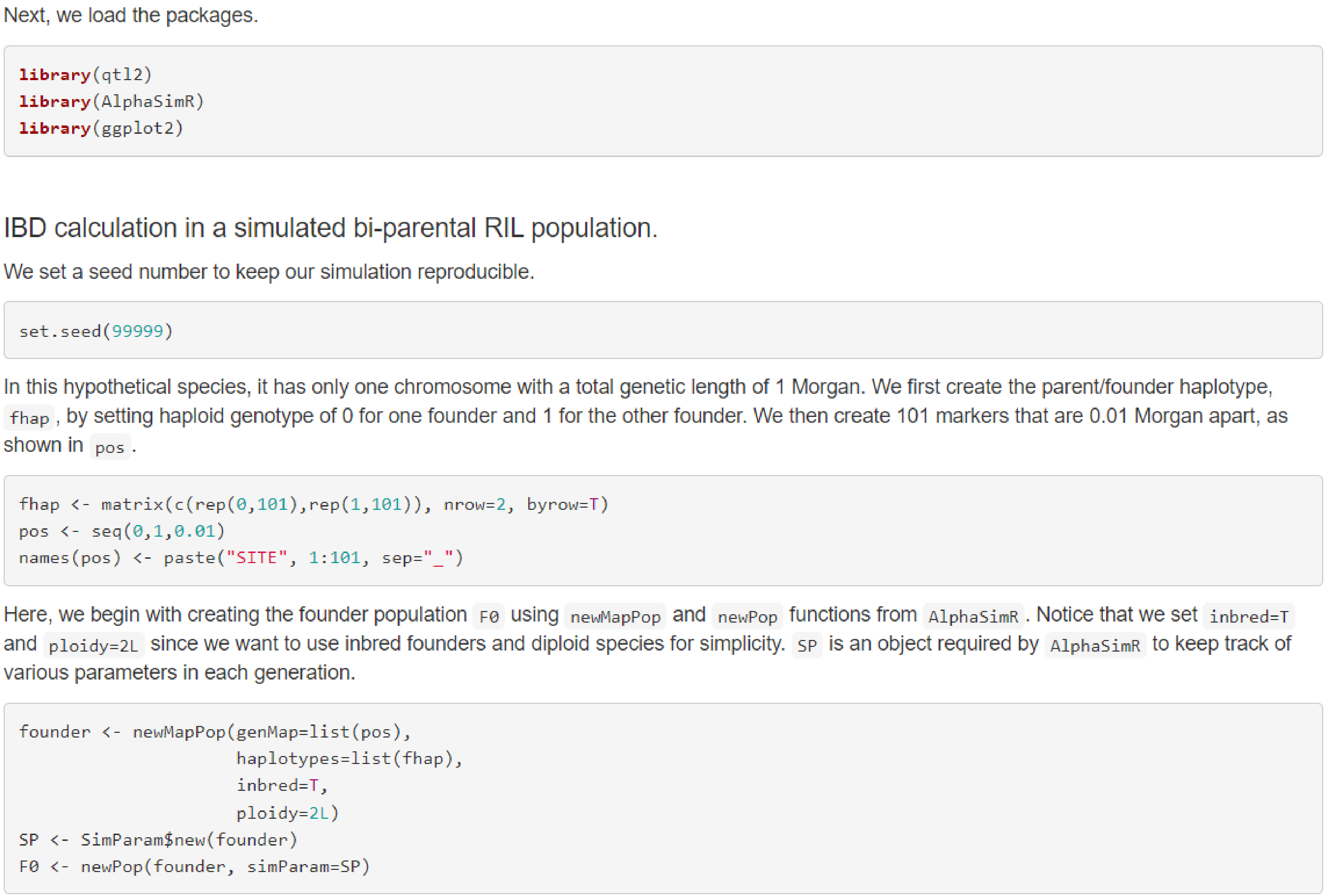
2. Reducing the cost of genotype evaluation (trial design, MAS, GS, phenomics).



3. Creating our target through GM/GE (maximum selection intensity).



Lab practical example



Next, we load the packages.

```
library(qtl2)
library(AlphaSimR)
library(ggplot2)
```

IBD calculation in a simulated bi-parental RIL population.

We set a seed number to keep our simulation reproducible.

```
set.seed(99999)
```

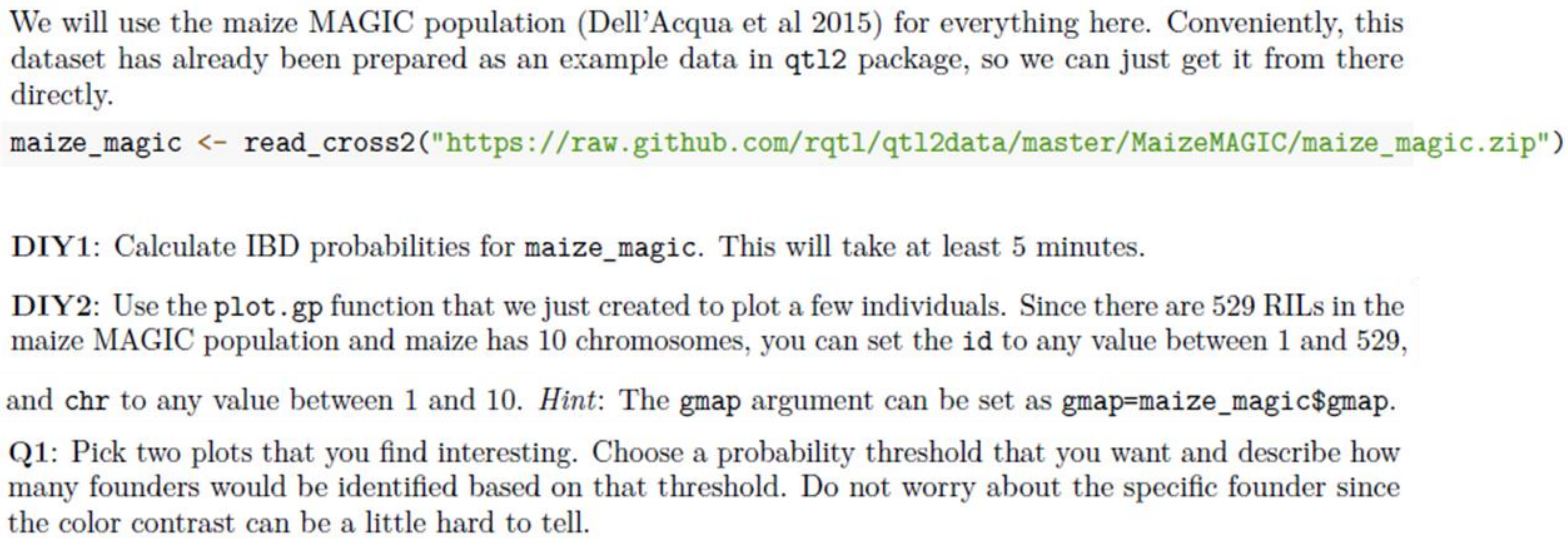
In this hypothetical species, it has only one chromosome with a total genetic length of 1 Morgan. We first create the parent/founder haplotype, `fhap`, by setting haploid genotype of 0 for one founder and 1 for the other founder. We then create 101 markers that are 0.01 Morgan apart, as shown in `pos`.

```
fhap <- matrix(c(rep(0,101),rep(1,101)), nrow=2, byrow=T)
pos <- seq(0,1,0.01)
names(pos) <- paste("SITE", 1:101, sep="_")
```

Here, we begin with creating the founder population `F0` using `newMapPop` and `newPop` functions from `AlphaSimR`. Notice that we set `inbred=T` and `ploidy=2L` since we want to use inbred founders and diploid species for simplicity. `SP` is an object required by `AlphaSimR` to keep track of various parameters in each generation.

```
founder <- newMapPop(genMap=list(pos),
                     haplotypes=list(fhap),
                     inbred=T,
                     ploidy=2L)
SP <- SimParam$new(founder)
F0 <- newPop(founder, simParam=SP)
```

Lab practical example



We will use the maize MAGIC population (Dell'Acqua et al 2015) for everything here. Conveniently, this dataset has already been prepared as an example data in `qtl2` package, so we can just get it from there directly.

```
maize_magic <- read_cross2("https://raw.github.com/rqtl/qtl2data/master/MaizeMAGIC/maize_magic.zip")
```

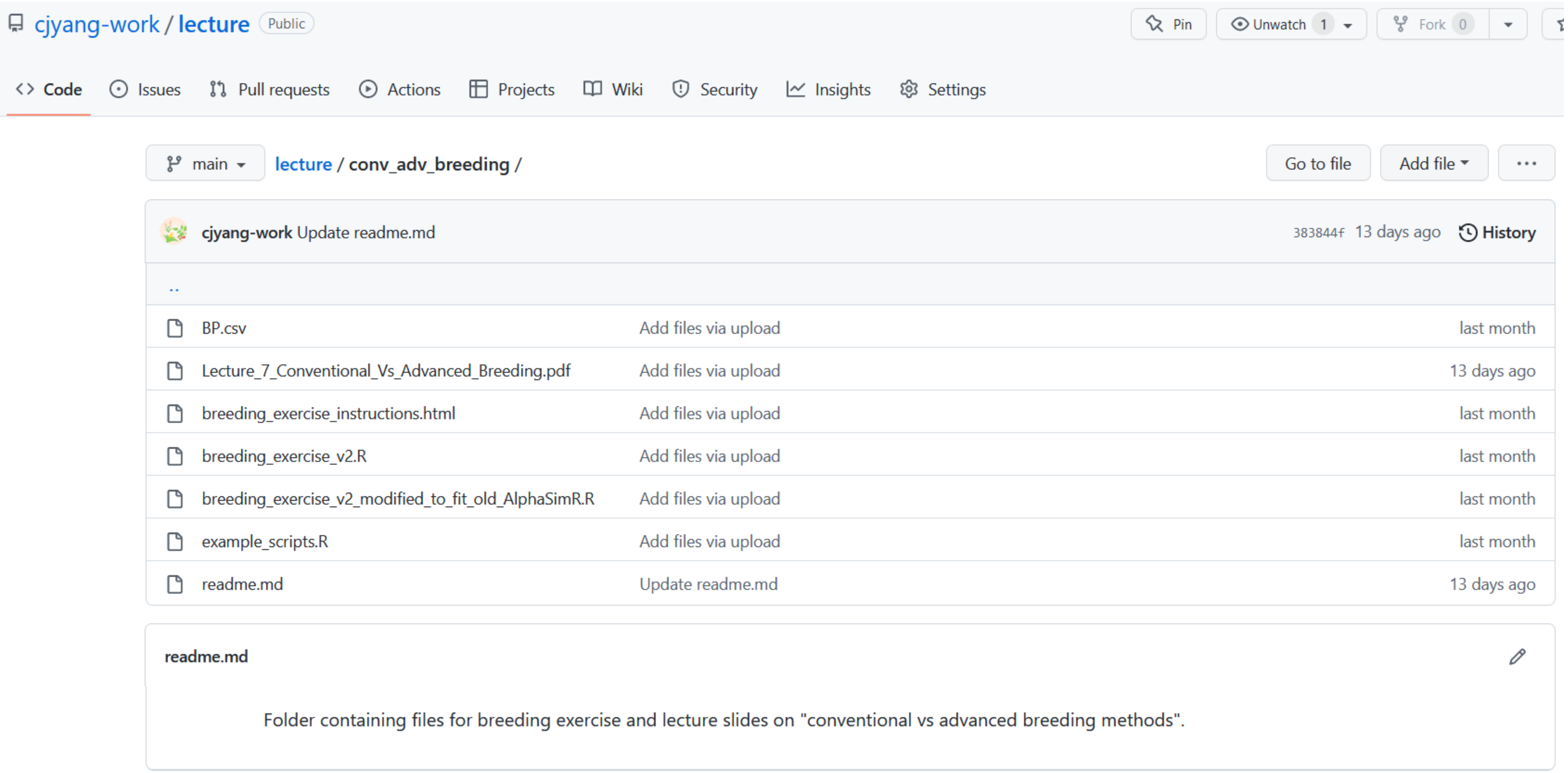
DIY1: Calculate IBD probabilities for `maize_magic`. This will take at least 5 minutes.

DIY2: Use the `plot.gp` function that we just created to plot a few individuals. Since there are 529 RILs in the maize MAGIC population and maize has 10 chromosomes, you can set the `id` to any value between 1 and 529, and `chr` to any value between 1 and 10. *Hint*: The `gmap` argument can be set as `gmap=maize_magic$gmap`.

Q1: Pick two plots that you find interesting. Choose a probability threshold that you want and describe how many founders would be identified based on that threshold. Do not worry about the specific founder since the color contrast can be a little hard to tell.

Online depository

Important to keep the class materials accessible!



lecture / conv_adv_breeding /

cjyang-work Update readme.md 383844f 13 days ago

..

BP.csv	Add files via upload	last month
Lecture_7_Conventional_Vs_Advanced_Breeding.pdf	Add files via upload	13 days ago
breeding_exercise_instructions.html	Add files via upload	last month
breeding_exercise_v2.R	Add files via upload	last month
breeding_exercise_v2_modified_to_fit_old_AlphaSimR.R	Add files via upload	last month
example_scripts.R	Add files via upload	last month
readme.md	Update readme.md	13 days ago

readme.md

Folder containing files for breeding exercise and lecture slides on "conventional vs advanced breeding methods".

Teaching opportunities at UNL

Current classes that might be relevant to my research group

- AGRO 815: Introduction to Plant Breeding and Cultivar Development
- AGRO 896: Molecular Plant Breeding
- AGRO 932: Biometrical Genetics and Plant Breeding

Opportunities for classes in:

- Introduction to plant breeding (undergraduate)
- Introduction to quantitative genetics (undergraduate)
- Case studies in plant breeding: breeding program design
- Sustainable crop production
- Novel crop breeding
- Online classes

Commitment toward Diversity, Equity and Inclusion (DEI)

Diversity

- Remove recruitment barrier into research and education.
- Participate in outreach programs – nurture scientific interest and bridge the gaps in HE.
- Be active in DEI committee.

Equity

- Be an observant educator – to some extent, make use of 3A.
- Act on students' needs – make sure everyone is on the same learning ground.

Inclusion

- Engage with students.
- Avoid "fitting the students into a box".

Important to maintain modesty and humility
DEI standards evolve over time – flexible and stay up to date

Acknowledgement

Many thanks to you all for joining today (and yesterday)!

And big thanks to:

- UNL IANR Search Committee for the opportunity to present.
- Kay McClure-Kelly for organizing and scheduling.
- Past and current mentors for their continuous guidance and support.