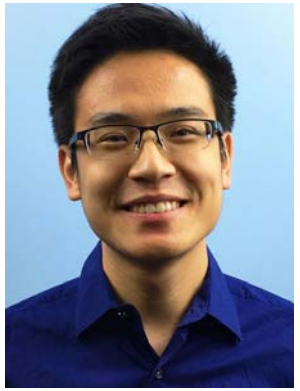
Workshop of Gene Mapping by Segregation

Sunday, January 14, 2024
4:00 PM - 6:10 PM, Town & Country, Pacific C

Zhiwu Zhang (**Organizer**)

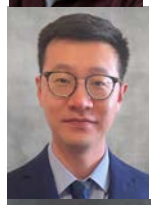


Hao Cheng (**Chair**)

Raluca Mateescu

Cesar Medina

Haipeng Yu



Alper Adak

Gabriel De Siqueira

Chansong Qian

Ignacy Misztal

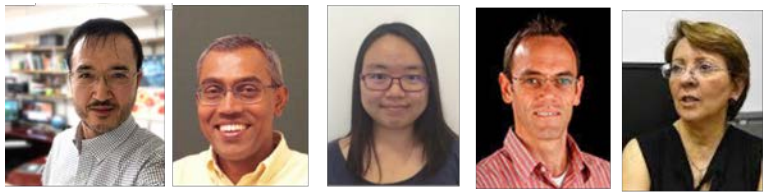
https://pag.confex.com/pag/31/meetingapp.cgi/Session/9207

2018

Patrick Schnable | Mike Olsen | Ghanasyam Rallapalli | Yongping Fu

Silvio Salvi | Haixiao Dong | Alexandre Fournier-Level | James Chen

2019



Zhiwu Zhang | Rohan Fernando | Lanshuan Shuang | Todd Dezwaan | Anete Pereira de Souza

Chiedozie Egesi | Ismail Rabbi | Jianli Chen | Endang Septiningsih | James Schnable

2020

Iulian Gabur | Alex Ogbonna | Yang Hu

Iulian Gabur | Longxi Yu | Jean-Luc Jannink

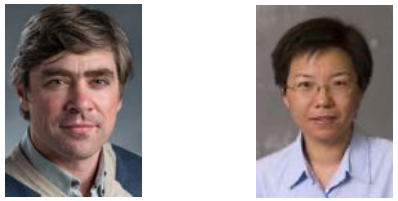
2022

Hao Cheng | Alexander Lipka | Jason Wallace

Atit Parajuli | Daniela Lourenco | Nidhi Rawat

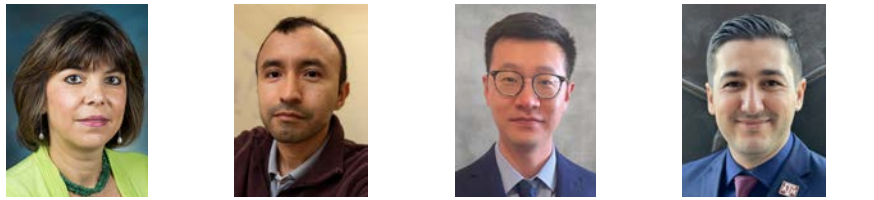
2023

Jiayi Qu | Hillel Brukental



Juan Steibel | Min Zhang

2024



Raluca Mateescu | Cesar Medina | Haipeng Yu | Alper Adak

Zhiwu Zhang | Gabriel De Siqueira | Changsong Qian | Ignacy Misztal

Zhiwu Zhang Laboratory

for Statistical Genomics

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Five ingredients to succeed: CS-VMV

Culture: Trying to understand.

Strategy: Solve biological problems with analytical and computational challenges.

Vision: Genomic and phenomic stream data is stationary water for organisms.

Mission: You get data, we help with our analytical methods, tools, and expertise.

Value: Every idea makes sense.

zzlab.net/share

Zhiwu Zhang Laboratory
for Statistical Genomics

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GAPIT

Blink

GRID

GridFree

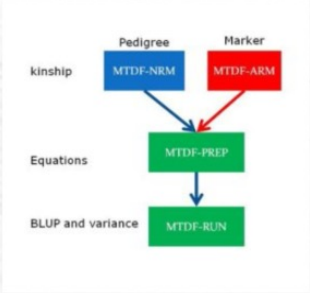
iPat

FarmCPU

Rooster

LADDER

mMAP



MTDFREML

Audio4EDU

AI4EVER

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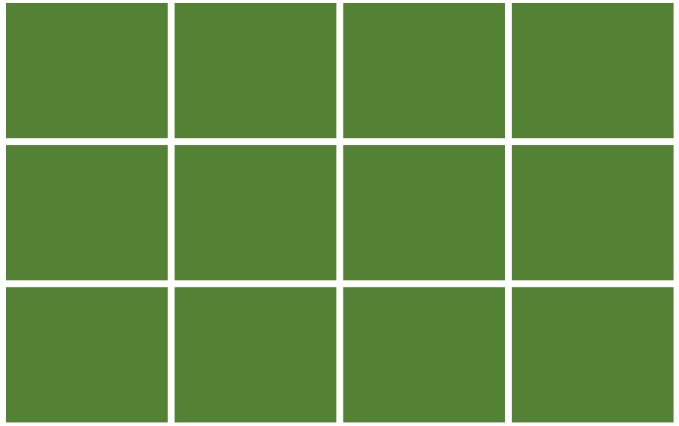
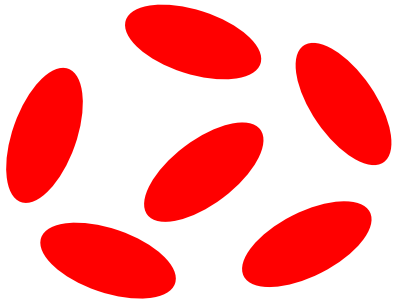
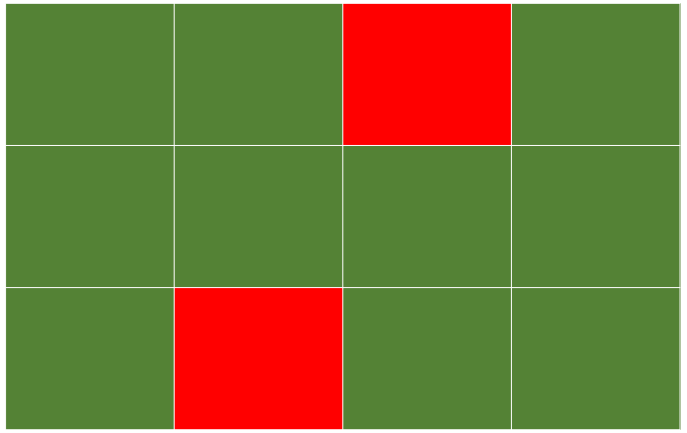
GRID

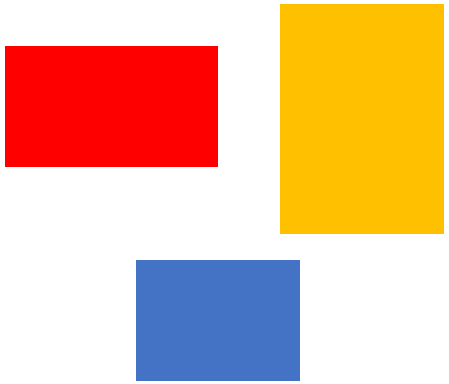




GridFree

Mosaic





MosaicFree

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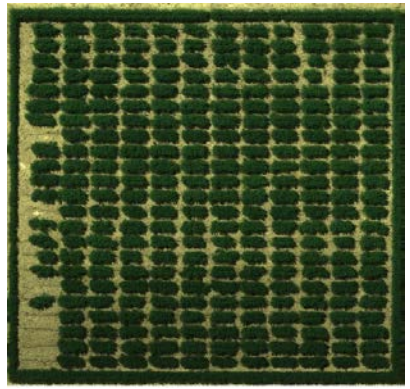
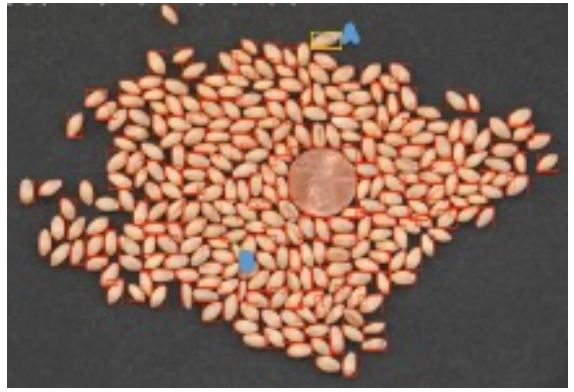


Grid



GridFree

Mosaic

MosaicFree

Model

GRID

GridFree

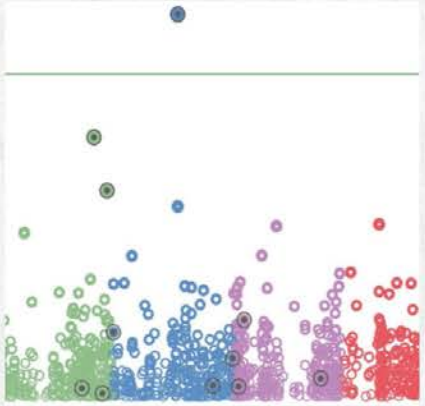
Rooster

LADDER

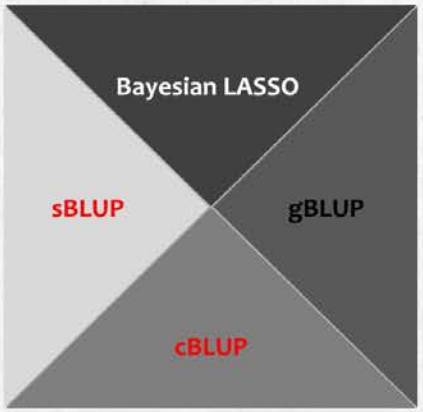
AI4EVER

Zhiwu Zhang Laboratory
for Statistical Genomics

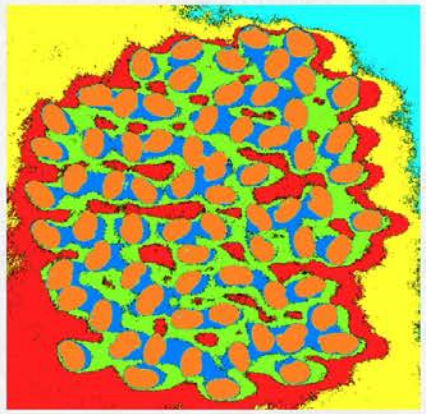
Home People Publication Research Teaching Software Outreach Jobs



GWAS

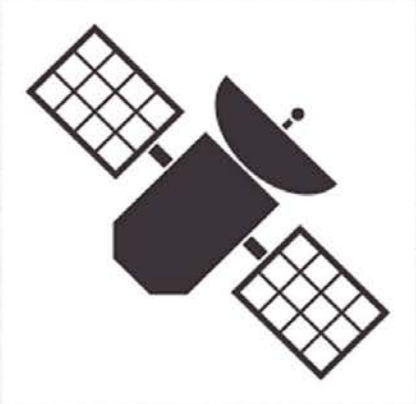


GS



Alfalfa Inbreds

UAV Phenomics



Satellite Assisted Breeding

Cloud Computing

All the versions have been implemented to GAPIT with R

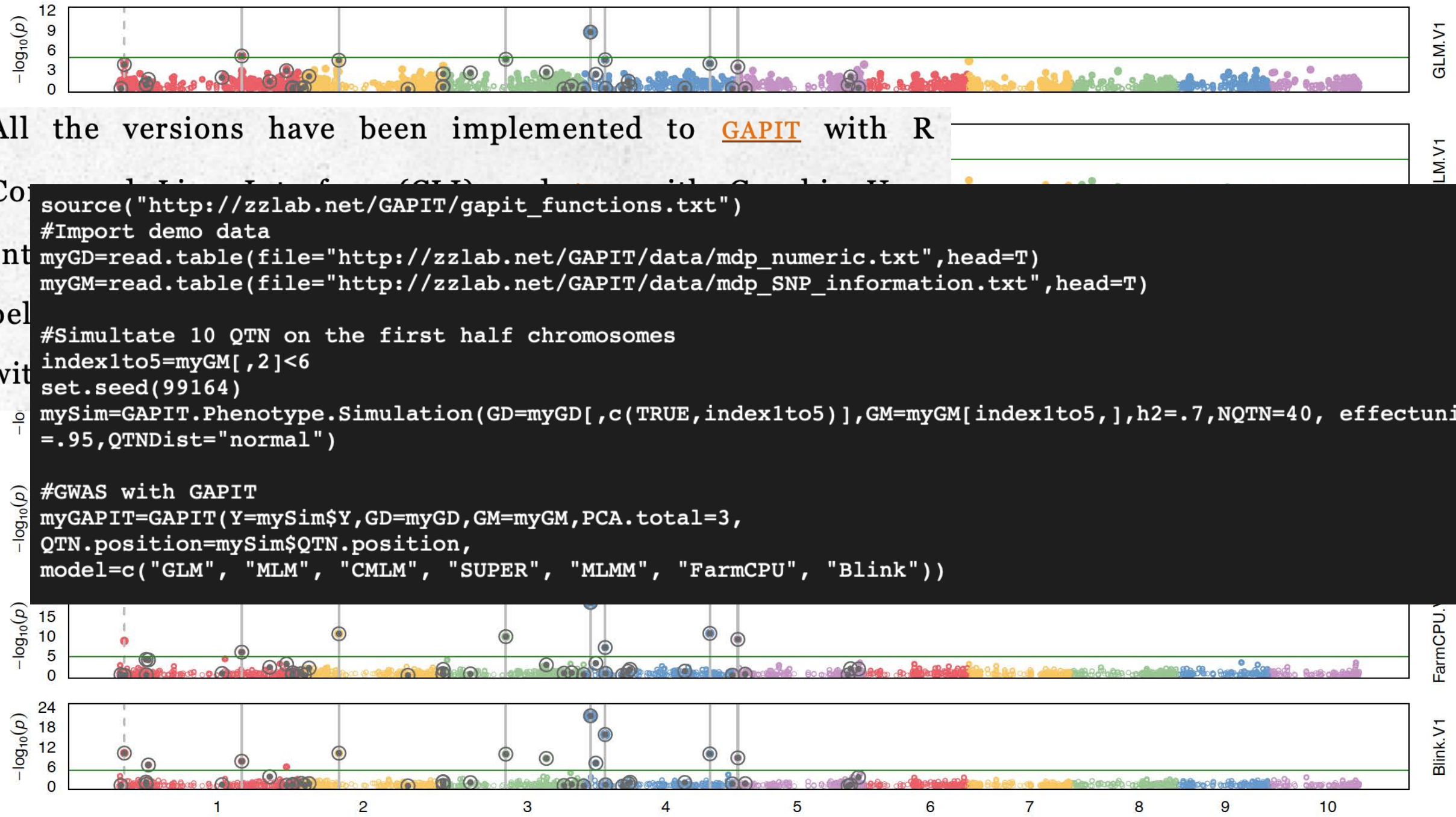
Co

Int

bel

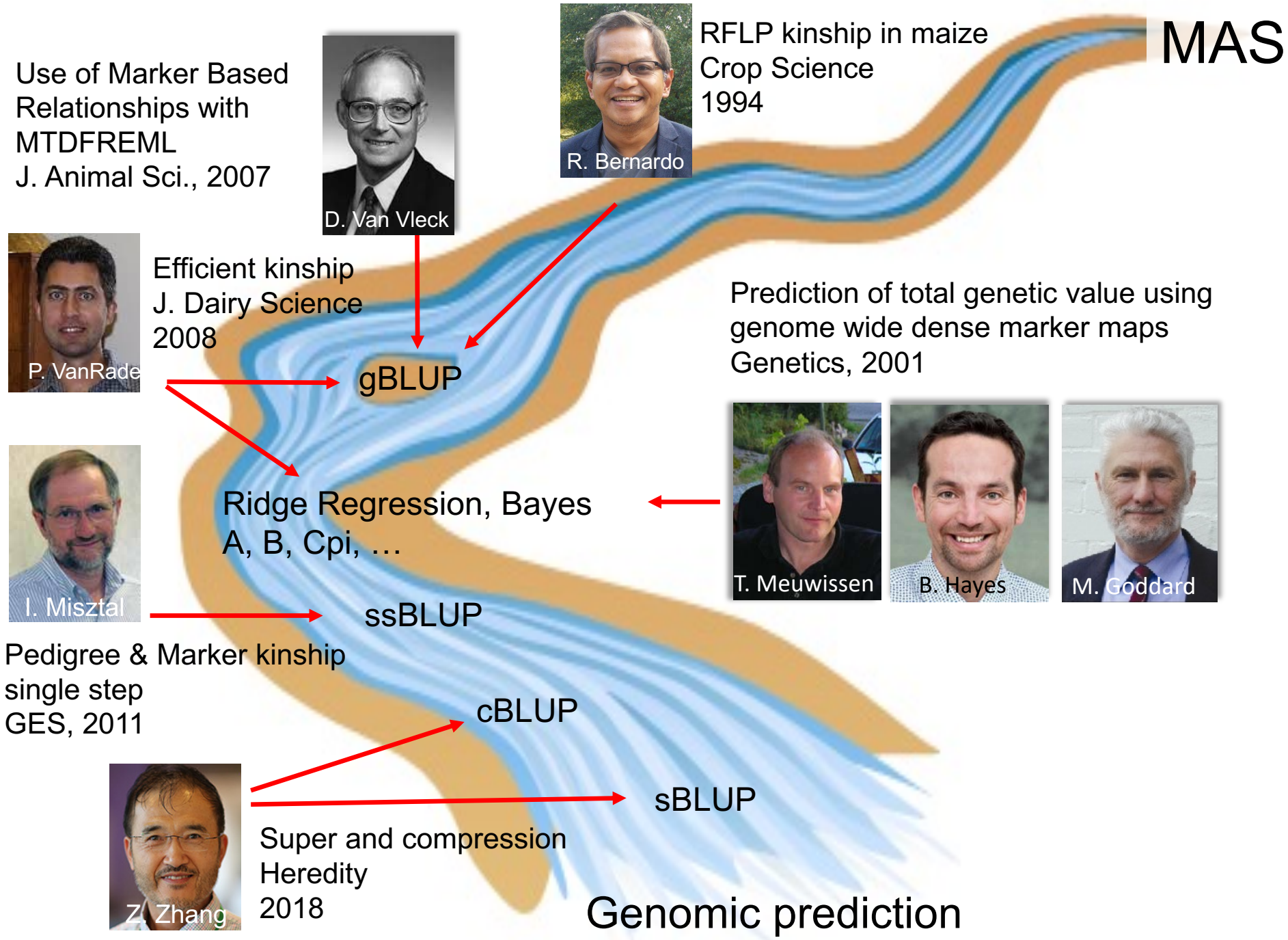
wit

```
source("http://zzlab.net/GAPIT/gapit_functions.txt")
#Import demo data
myGD=read.table(file="http://zzlab.net/GAPIT/data/mdp_numeric.txt",head=T)
myGM=read.table(file="http://zzlab.net/GAPIT/data/mdp_SNP_information.txt",head=T)

#Simultate 10 QTN on the first half chromosomes
index1to5=myGM[,2]<6
set.seed(99164)
mySim=GAPIT.Phenotype.Simulation(GD=myGD[,c(TRUE,index1to5)],GM=myGM[index1to5,],h2=.7,NQTN=40, effectunit
=.95,QTNDist="normal")

#GWAS with GAPIT
myGAPIT=GAPIT(Y=mySim$Y,GD=myGD,GM=myGM,PCA.total=3,
QTN.position=mySim$QTN.position,
model=c("GLM", "MLM", "CMLM", "SUPER", "MLMM", "FarmCPU", "Blink"))
```



GWAS Stream

EMMAx
EMMA
PC+K
PC
CMLM
Q+K
Q
P3D
GCTA
SELECT
MLMM
ECMLM
SUPER
FST-LMM
GEMMA
GenAbel
FarmCPU
BLINK


MAS
RFLP kinship in maize
Crop Science
1994
R. Bernardo
Use of Marker Based
Relationships with
MTDFREML
J. Animal Sci., 2007
D. Van Vleck
P. VanRade
Efficient kinship
J. Dairy Science
2008
gBLUP
Prediction of total genetic value using
genome wide dense marker maps
Genetics, 2001
T. Meuwissen
B. Hayes
M. Goddard
Ridge Regression, Bayes
A, B, Cpi, …
I. Misztal
ssBLUP
Pedigree & Marker kinship
single step
GES, 2011
cBLUP
sBLUP
Z. Zhang
Super and compression
Heredity
2018
Genomic prediction

PBG Seminar Series- FINAL (View Only)

Cornell CALS
College of Agriculture and Life Sciences

Plant Breeding and Genetics Section Seminar Series PLSCI 7000

Tuesdays, 12:20 - 1:10 PM

Seminar Date	Seminar Time	Seminar Location	**Speaker Name**	Speaker Affiliation	Title	Host
Tuesday, January 23, 2024	12:20 PM	135 Emerson Hall	**Zhiwu Zhang**	*Department of Crop and Soil Science* *Washington State University*	**Confusion and Prospection of Genomic Prediction to Incorporate Genome-Wide Association Study**	Ed Buckler
Tuesday, January 30, 2024	12:20 PM	135 Emerson Hall	**Special Seminar**			
Tuesday, February 6, 2024	12:20 PM	135 Emerson Hall	**Merritt Khaipho-Burch**	*SIPS- Plant Breeding and Genetics* *Edward Buckler's research group* *Cornell University*	**Small Effect, Big Picture: Understanding the Role of Pleiotropy, Transposable Elements, and Single-Genes on Maize Genetics and Yield**	Ed Buckler
Tuesday, February 13, 2024	12:20 PM	135 Emerson Hall	**Reserved for Lightening Talks**	*Lightening Talk Speakers: Gaurav Dilip Moghe, Lori Huberman, Yu Jiang*		

BLINK Adaptation to Complex Data

- Multiple alleles
- Additive and dominant effects
- Multiple environments/traits
- Models (e.g., different number of PCs)
- Rice example

Multiple Alleles

Marker	Allele	Ind1	Ind2	Ind3	Ind4	...	Indn
1	A/C/T	AC	AT	AA	CT	...	TT
2	C/G/T	CC	GG	TT	CG	...	GT
...	...	...	...	...	...	...	...
m	A/G/T	AA	GG	TT	AT	...	GT

Marker	Genotype	IND1	IND2	IND3	IND4	...	INDn
11	AA			1			
12	AC	1					
13	AT		1				
14	CC						
15	CT				1		
16	TT						1
21	CC	1					
22	CG				1		
23	CT						
24	GG		1				
25	GT						1
26	TT			1			

Cutoff=1%/6m

Additive and Dominant Effects

	Additive				Dominant			
Y	S1	S2	...	Sm	S1	S2	...	Sm
Y1	1	2	0	2	0	0	0	0
Y2	1	0	2	0	0	0	0	0
Y3	0	1	0	2	0	0	0	0
Y4	0	1	0	0	0	0	0	0
Y5	2	0	1	0	0	0	0	0
Y6	0	0	1	0	0	0	0	0
Y7	2	2	0	1	0	0	0	0
Y8	0	0	0	1	0	0	0	0
..	..	..	..	..	..	..	..	..
Yn	1	0	2	0	0	0	0	0
Y1	0	0	0	0	1	0	0	0
Y2	0	0	0	0	1	0	0	0
Y3	0	0	0	0	0	1	0	0
Y4	0	0	0	0	0	1	0	0
Y5	0	0	0	0	2	0	1	0
Y6	0	0	0	0	0	0	1	0
Y7	0	0	0	0	0	0	0	1
Y8	0	0	0	0	0	0	0	1
..	..	..	..	..	..	..	..	..
Yn	0	0	0	0	1	0	0	0

Cutoff=1%/2m

Multiple Locations/Years/Traits

	Year1				Year2			
Y	S1	S2	...	Sm	S1	S2	...	Sm
Y1	1	2	0	2	0	0	0	0
Y2	1	0	2	0	0	0	0	0
Y3	0	1	0	2	0	0	0	0
Y4	0	1	0	0	0	0	0	0
Y5	2	0	1	0	0	0	0	0
Y6	0	0	1	0	0	0	0	0
Y7	2	2	0	1	0	0	0	0
Y8	0	0	0	1	0	0	0	0
..	..	..	..	..	..	..	..	..
Yn	1	0	2	0	0	0	0	0
Y1	0	0	0	0	1	2	0	2
Y2	0	0	0	0	1	0	2	0
Y3	0	0	0	0	0	1	0	2
Y4	0	0	0	0	0	1	0	0
Y5	0	0	0	0	2	0	1	0
Y6	0	0	0	0	0	0	1	0
Y7	0	0	0	0	2	2	0	1
Y8	0	0	0	0	0	0	0	1
..	..	..	..	..	..	..	..	..
Yn	0	0	0	0	1	0	2	0

Multiple Models

Model 1: y=SNP+PC1+PC2+PC3+e

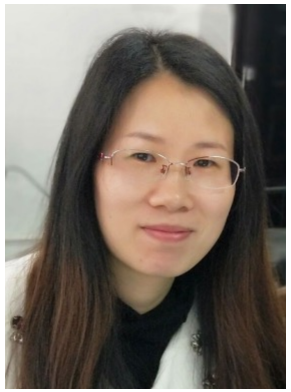
Model 2: y=SNP+PC1 +PC2+PC3 +PC4+PC5+e

							G1				G2			
	Y	PC1	PC2	PC3	PC4	PC5	S1	S2	...	Sm	S1	S2	...	Sm
Model 1	Y1	0.00831	0.1491	0.91112	0	0	1	2	0	2	0	0	0	0
	Y2	0.13958	0.76769	0.41248	0	0	1	0	2	0	0	0	0	0
	Y3	0.33252	0.9203	0.2509	0	0	0	1	0	2	0	0	0	0
	Y4	0.12217	0.49453	0.33911	0	0	0	1	0	0	0	0	0	0
	Y5	0.82962	0.40827	0.21138	0	0	2	0	1	0	0	0	0	0
	Y6	0.9544	0.78745	0.82685	0	0	0	0	1	0	0	0	0	0
	Y7	0.40486	0.56716	0.74141	0	0	2	2	0	1	0	0	0	0
	Y8	0.21303	0.69876	0.50728	0	0	0	0	0	1	0	0	0	0
	..	..	..	..	..	..	..	..	..	..	..	..	..	..
	Yn	0.71394	0.51623	0.46755	0	0	1	0	2	0	0	0	0	0
Model 2	Y1	0.00831	0.1491	0.91112	0.06458	0.28215	0	0	0	0	1	2	0	2
	Y2	0.13958	0.76769	0.41248	0.41029	0.93074	0	0	0	0	1	0	2	0
	Y3	0.33252	0.9203	0.2509	0.63312	0.44412	0	0	0	0	0	1	0	2
	Y4	0.12217	0.49453	0.33911	0.04205	0.61255	0	0	0	0	0	1	0	0
	Y5	0.82962	0.40827	0.21138	0.8459	0.0085	0	0	0	0	2	0	1	0
	Y6	0.9544	0.78745	0.82685	0.07227	0.76632	0	0	0	0	0	0	1	0
	Y7	0.40486	0.56716	0.74141	0.62386	0.67831	0	0	0	0	2	2	0	1
	Y8	0.21303	0.69876	0.50728	0.63005	0.92204	0	0	0	0	0	0	0	1
	..	..	..	..	..	..	..	..	..	..	..	..	..	..
	Yn	0.71394	0.51623	0.46755	0.41246	0.02482	0	0	0	0	1	0	2	0

Joint analysis of phenotype-effect-generation identifies loci associated with grain quality traits in rice hybrids

Lanzhi Li, Xingfei Zheng, Jiabo Wang, Xueli Zhang, Xiaogang He, Liwen Xiong, Shufeng Song, Jing Su, Ying Diao, Zheming Yuan, Zhiwu Zhang & Zhongli Hu

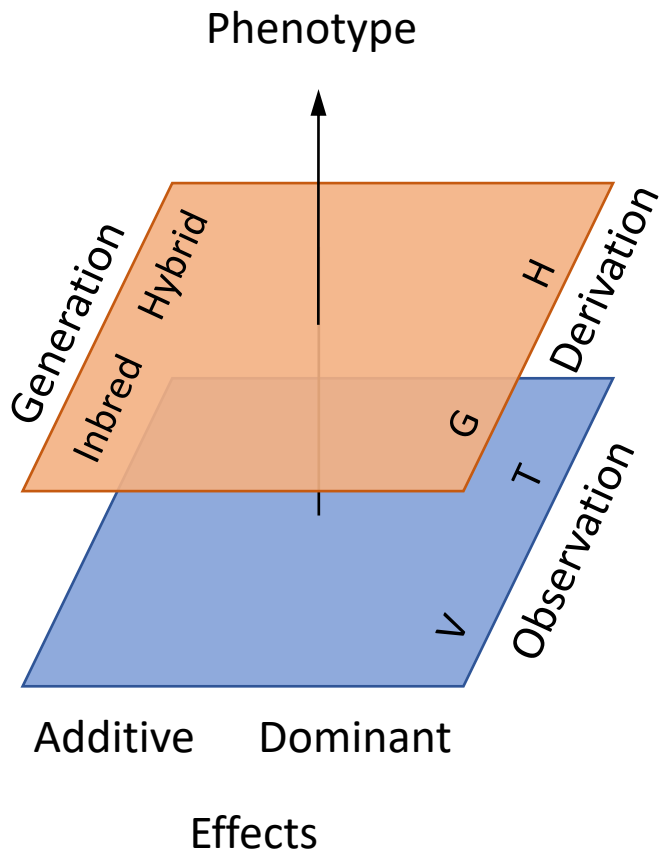
Nature Communications **14**, Article number: 3930 (2023) | Cite this article



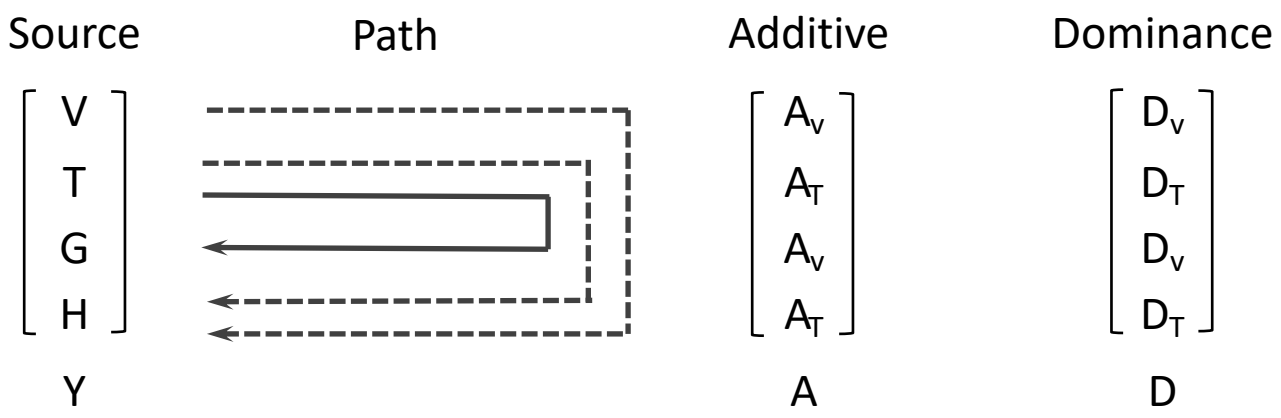
Lanzhi Li

Jiabo Wang

Three dimensions of data



Phenotype relationship

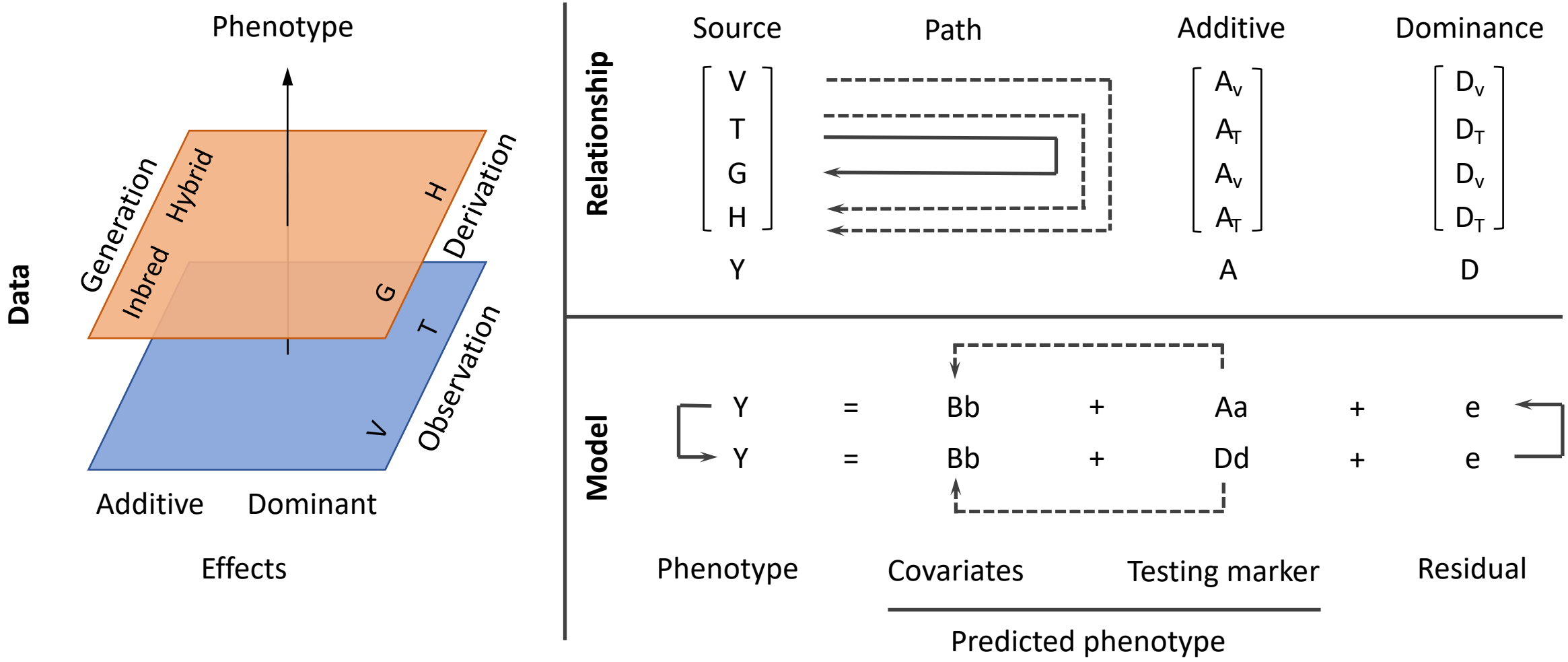


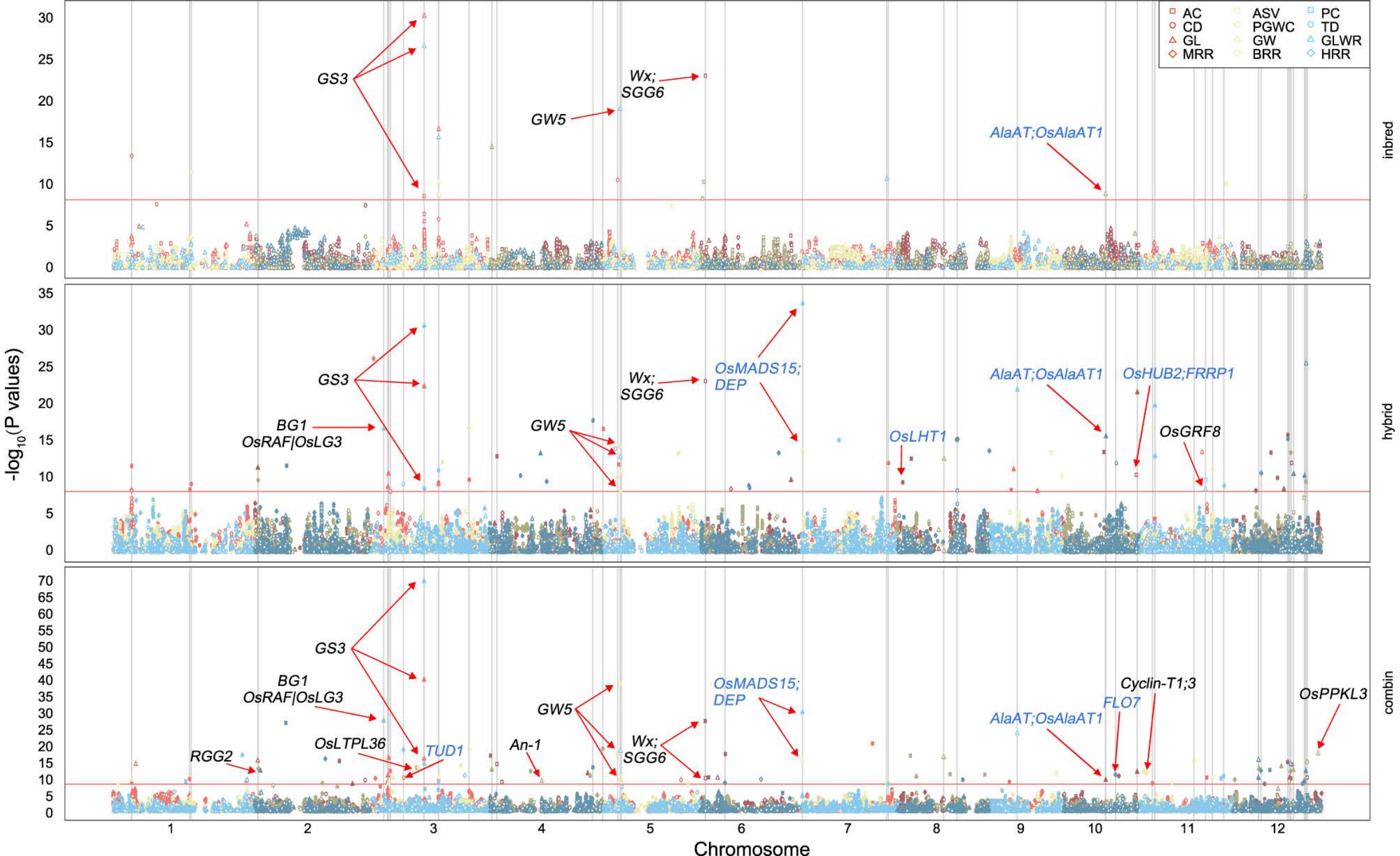
Statistical model

Model

Phenotype		Covariates		Testing marker		Residual
Y	=	Bb	+	Aa	+	e
Y	=	Bb	+	Dd	+	e

Predicted phenotype


Phenotype
Data
Generation
Hybrid
Inbred
H
Derivation
G
T
V
Observation
Additive
Dominant
Effects
Relationship
Source
Path
Additive
Dominance
V
T
G
H
Y
A_v
A_T
A_v
A_T
A
D_v
D_T
D_v
D_T
D
Model
Y = Bb + Aa + e
Y = Bb + Dd + e
Phenotype
Covariates
Testing marker
Residual
Predicted phenotype


AC
CD
GL
MRR
ASV
PGWC
GW
BRR
PC
TD
GLWR
HRR
inbred
hybrid
combin
-log10(P values)
Chromosome
GS3
Wx;
SGG6
GW5
AlaAT;OsAlaAT1
BG1
OsRAF|OsLG3
OsMADS15;
DEP
OsLHT1
OsHUB2;FRRP1
OsGRF8
RGG2
OsLTPL36
TUD1
An-1
FLO7
Cyclin-T1;3
OsPPKL3

Thank you for your attention!

World class scenery, Research & Education