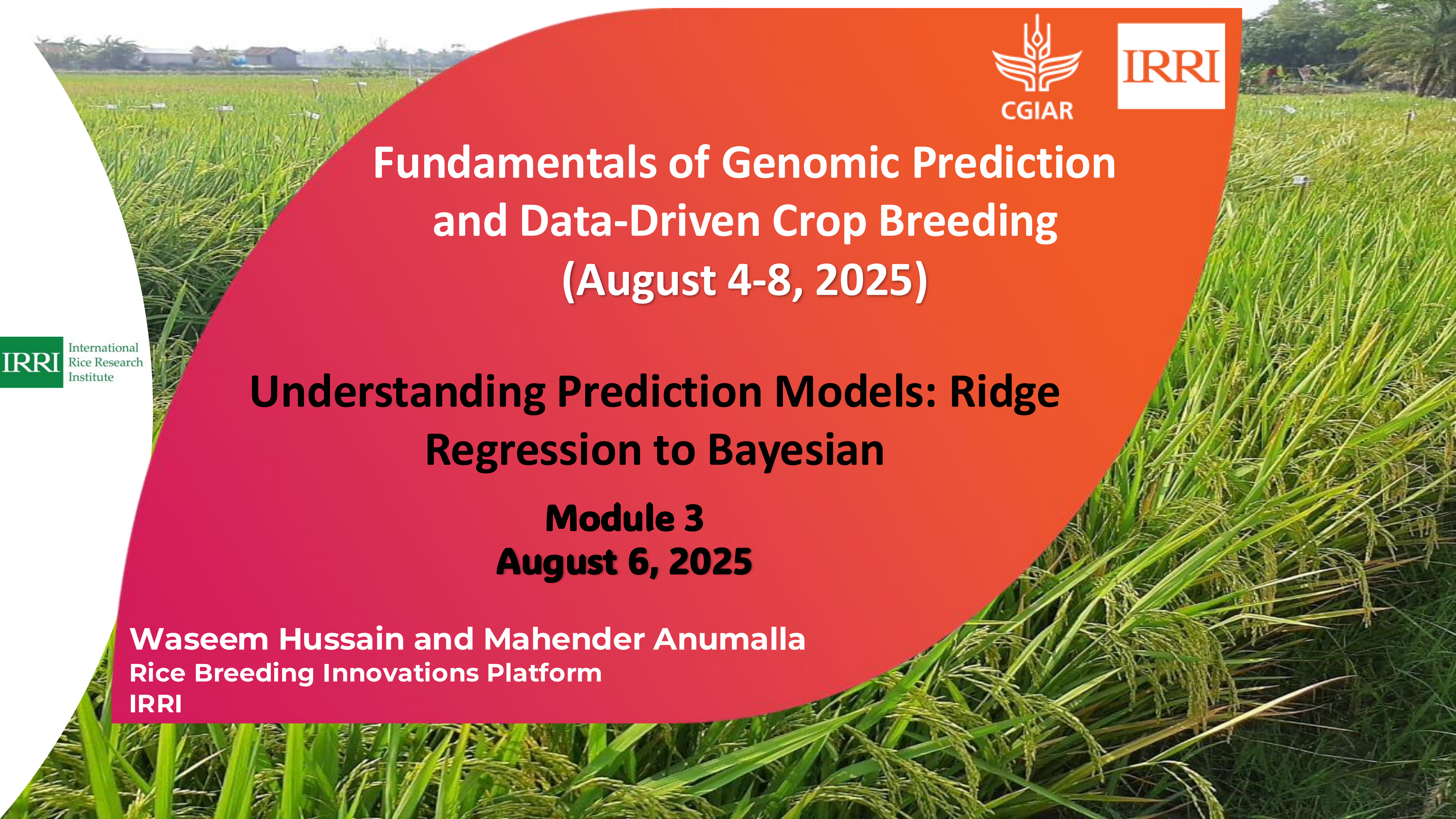


Fundamentals of Genomic Prediction and Data-Driven Crop Breeding (August 4-8, 2025)

Understanding Prediction Models: Ridge Regression to Bayesian

Module 3
August 6, 2025

Waseem Hussain and Mahender Anumalla
Rice Breeding Innovations Platform
IRRI

Genomic Prediction Models

$$\underbrace{y}_{\text{Trait}} = \underbrace{\mu}_{\text{mean}} + \sum_{k} \underbrace{x_k}_{\text{Design matrix}} \underbrace{\beta_k}_{\text{Effect of } k\text{th marker}} + \underbrace{\varepsilon}_{\text{Error}}$$

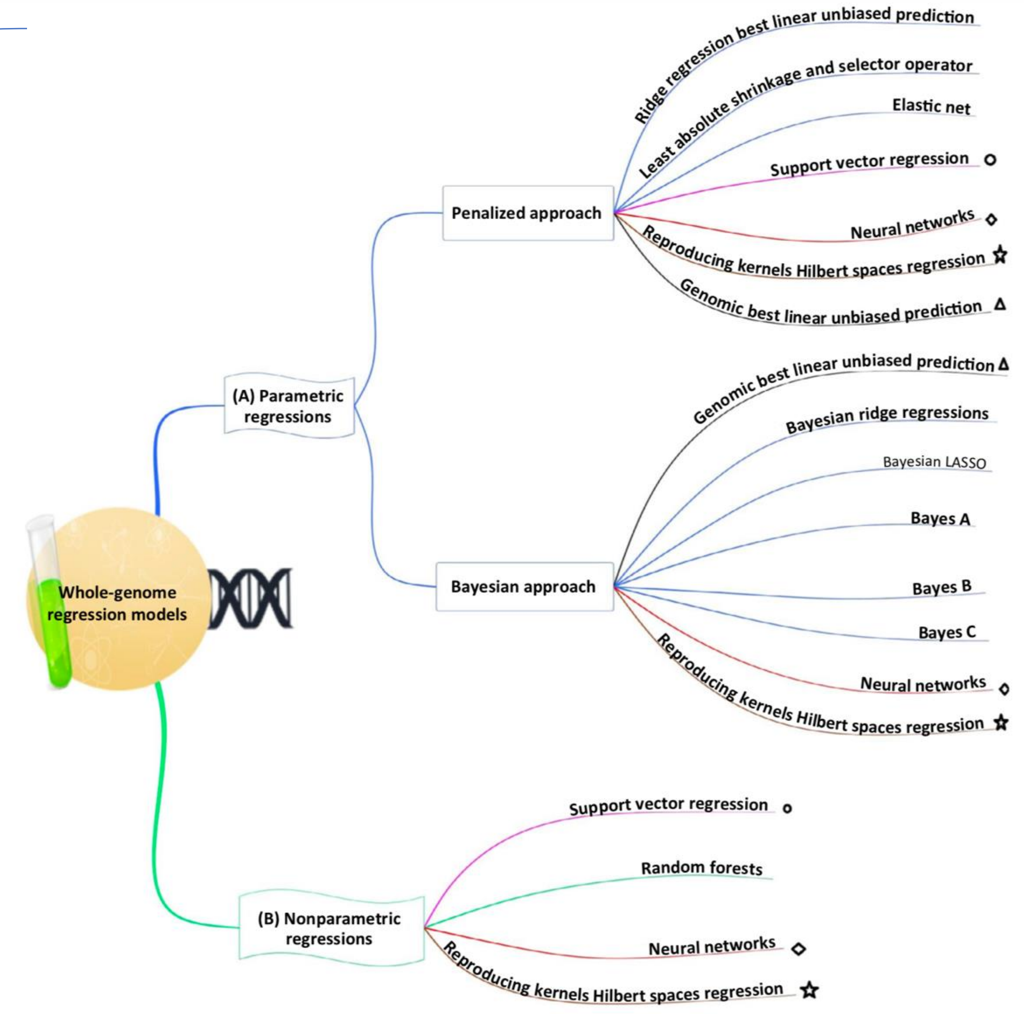
Key: How we estimate and Assume Marker Variances.

a. **Shrinkage Models**: RR BLUP and GBLUP

b. **Dimension Reduction Methods: Partial Least Squares (PLS) and Singular Value Decomposition (SDV)**

c. **Bayesian Approach: Variable Selection Models (priors)**

d. **Kernel and Machine Learning Methods**


Whole-genome regression models
(A) Parametric regressions
Penalized approach
Ridge regression best linear unbiased prediction
Least absolute shrinkage and selector operator
Elastic net
Support vector regression ○
Neural networks ◇
Reproducing kernels Hilbert spaces regression ☆
Genomic best linear unbiased prediction △
Bayesian approach
Genomic best linear unbiased prediction △
Bayesian ridge regressions
Bayesian LASSO
Bayes A
Bayes B
Bayes C
Neural networks ◇
Reproducing kernels Hilbert spaces regression ☆
(B) Nonparametric regressions
Support vector regression ○
Random forests
Neural networks ◇
Reproducing kernels Hilbert spaces regression ☆

Adapted from manuscript Desta and Ortiz, 2014

Ordinary Least squares (OLS)

Simple linear regression:

$$\hat{Y}_i = \alpha + \beta x_i + \varepsilon_i$$

dependent variable

intercept

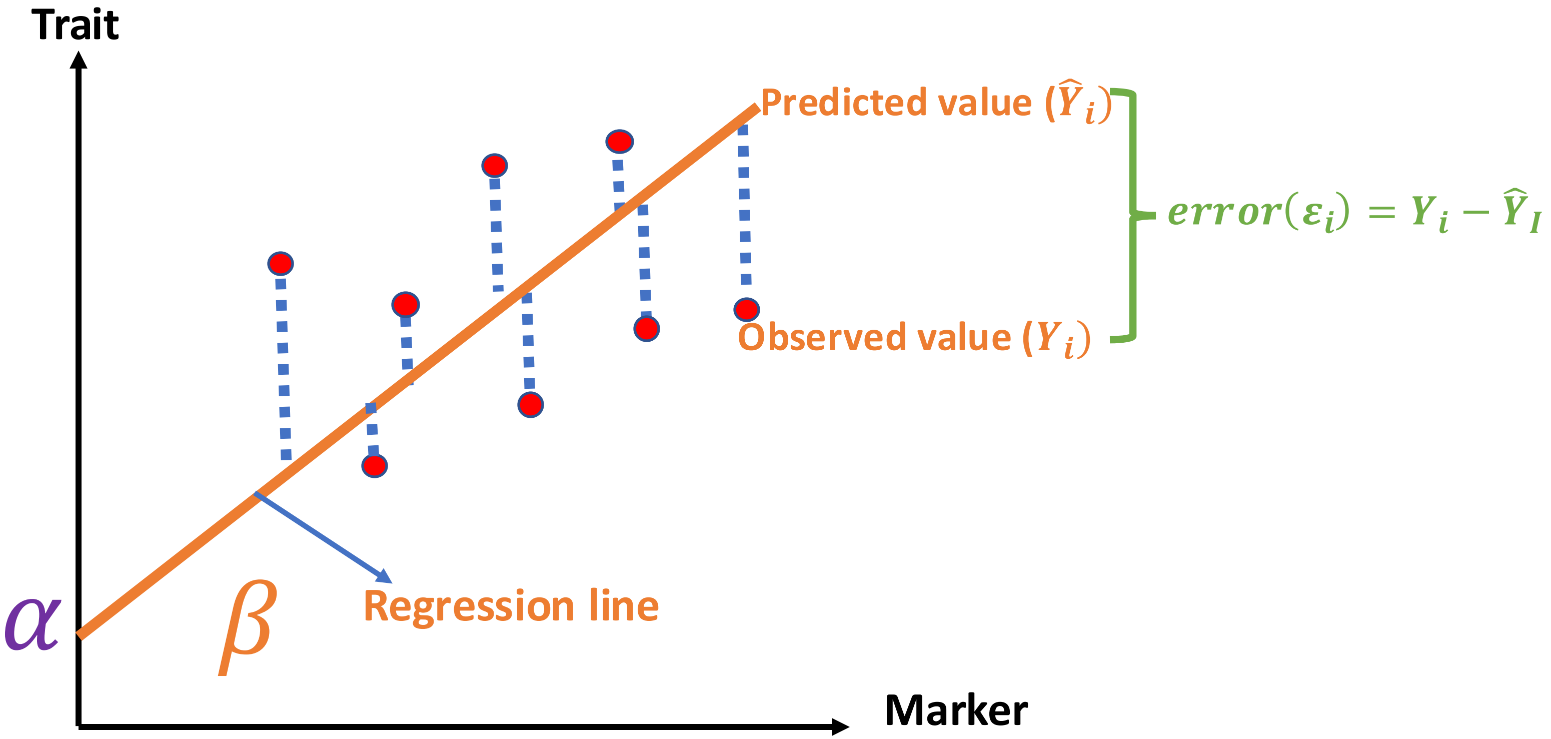
coefficient

Independent variable

error

Parameters (un-observed)

Aim is to estimate α and β parameters by minimize the squared errors

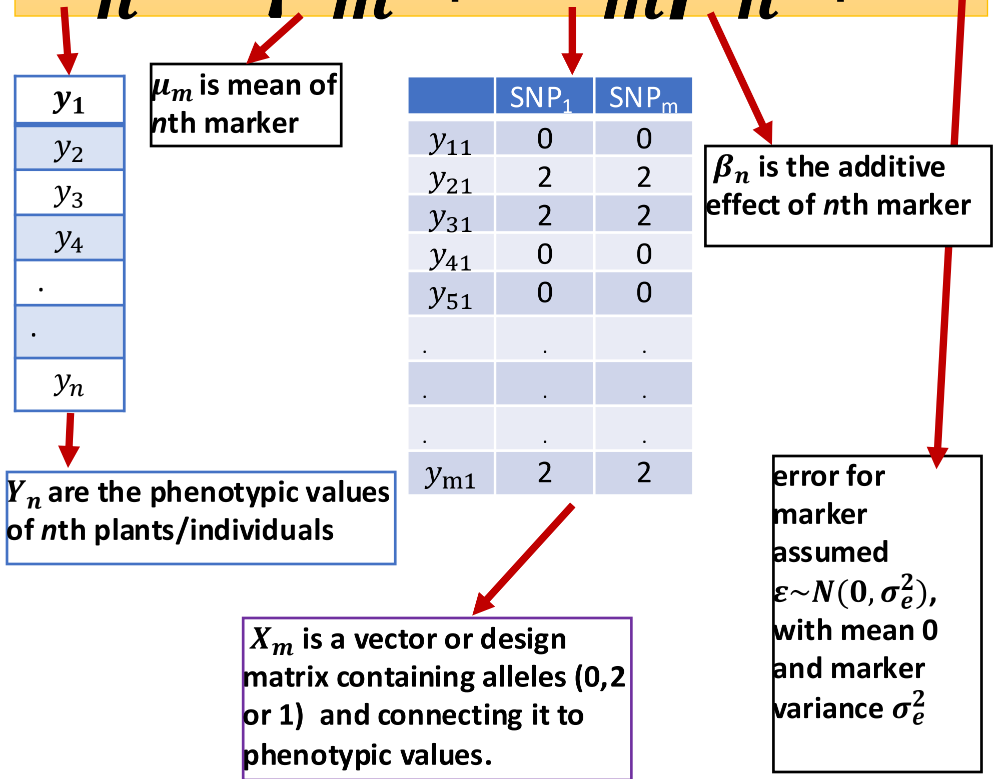


Trait
Predicted value ($\hat{Y}_i$)
$error(\varepsilon_i) = Y_i - \hat{Y}_I$
Observed value (Y_i)
α
β
Regression line
Marker

OLS in Relevance to Genomic Predictions

Simple marker regression model

$$Y_n = \mu_m + X_m\beta_n + \varepsilon$$



y_1
y_2
y_3
y_4
.
.
y_n

μ_m is mean of nth marker

	SNP$_1$	SNP$_m$
y_{11}	0	0
y_{21}	2	2
y_{31}	2	2
y_{41}	0	0
y_{51}	0	0
.	.	.
.	.	.
.	.	.
y_{m1}	2	2

β_n is the additive effect of *n*th marker

Y_n are the phenotypic values of *n*th plants/individuals

X_m is a vector or design matrix containing alleles (0,2 or 1) and connecting it to phenotypic values.

error for marker assumed $\varepsilon \sim N(0, \sigma_e^2)$, with mean 0 and marker variance σ_e^2

Aim is to minimize residual squares

$$argmin(\varepsilon`\varepsilon) = \mathrm{argmin}(\mathrm{y} - X\beta)`(y - x\beta)$$

…

$$\beta = (\acute{X}X)^{-1}\,\acute{X}Y$$

Limitations

1. m>>n, we cannot fit OLS (curse on dimensionality)

$\acute{X}X$ is a singular, and determinate of $\acute{X}X$ is 0 so cannot take inverse, $\acute{X}X$ is not invertible

2. m>>n, multi-collinearity produces singular matrix

3. m>>n, not perfect multi-collinearity, but predictors are highly correlated

OLS estimates are not stable and have high variance

Need alternative strategy

Ridge Regression

Provides solution and overcomes problems of OLS

Aim is to minimize residual squares

$$argmin(\varepsilon`\varepsilon) = \mathrm{argmin}(\mathrm{y} - X\mathrm{\beta})`(y - x\beta)$$

...

$$\beta = (\acute{X}X + \lambda I)^{-1} \; \acute{X}Y$$

Add constant, Penalty/Shrinkage Factor

$$E\left(\hat{\beta}_{ridge}\right) = (\acute{X}X + \lambda I)^{-1} \; X\acute{E}(Y)$$

$$E\left(\hat{\beta}_{ridge}\right) = \beta - \lambda(\acute{X}X + \lambda I)^{-1}$$

Biased, but with minimum variance

adding λ, we take inverse but we have biased estimates

$$when, \lambda = 0, E(\widehat{\beta) =} \beta, i.e, OLS$$

Ridge-Regression BLUP (RRBLUP)

$$y=\mu+\sum_k x_k\beta_k+\varepsilon$$

estimate β by adding positive constraint

$$\beta_{ridge}=(X^TX)^{-1}+\lambda I)\,X^T\,y$$

$$\lambda=\frac{\sigma_e^2}{\sigma_\beta^2}$$

$$\beta_k \sim N(0,\sigma_e^2)$$

❖ **Ridge regression induces homogeneous shrinkage and it depends upon allele frequency**

❖ **Assumes all markers have same variance with small but non-zero effect.**

- We add constant to diagonal, thus it is invertible
- Degree of shrinkage depends upon λ, larger the λ larger is the shrinkage

$$\frac{\beta_{OLS}}{1+\lambda}$$

- We basically shrink OLS estimates towards 0
- λ**I** term reduces collinearity and prevents the matrix **X**^{T}**X** from becoming singular.

Things to Know (RRBLUP)

$$y=\mu+ \sum_k z_k \beta_k + \varepsilon$$

$$\beta_{ridge} = (Z^T Z)^{-1} + \lambda I)\ Z^T \mathrm{y}$$

- We add constant to diagonal, thus it is invertible
- Degree of shrinkage depends upon λ, larger the λ larger is the shrinkage

$$\frac{\beta_{OLS}}{1+\lambda} \qquad \lambda = \frac{\sigma_\beta^2}{\sigma_\epsilon^2}$$

- We basically shrink β (OLS) estimates towards 0
- λ**I** term reduces collinearity and prevents the matrix **X**$^{\mathrm{T}}$**X** from becoming singular.

❖ **Ridge regression induces homogeneous shrinkage, same for all markers**

❖ **Assumes all markers have the same variance with small but non-zero effect.**

❖ **Shrinkage depends upon allele frequency**

$$\hat{\beta}_{ridge} = \frac{2p_j(1-p_j)_n}{2p_j(1-p_j)_n+\lambda} * \hat{\beta}_{OLS}$$

❖ **Markers with extreme frequency are shrunk more.**

RR BLUP Model

$$\mathbf{y} = \mathbf{Z}g + \boldsymbol{\varepsilon}$$

$$\begin{bmatrix} y_1\\ y_2\\ y_3\\ y_4\\ .\\ y_n \end{bmatrix} = \left(\begin{array}{ccc} \text{SNP1} & \text{SNP2} & \text{SNP3} \\ 1 & 2 & 0 \\ 0 & 1 & 1 \\ 1 & 0 & 2 \end{array}\right) \begin{bmatrix} a_1\\ a_2\\ a_3\\ a_4\\ a_5\\ a_p \end{bmatrix} + \begin{bmatrix} \boldsymbol{\varepsilon} \end{bmatrix}$$

n x 1 *n x m* *p x 1* *n x 1*

n is # of individuals

P is # of markers

$$\begin{bmatrix} \boldsymbol{a}\\ \boldsymbol{\varepsilon} \end{bmatrix} \sim \left(N\left(0, \begin{matrix} \sigma_a^2 & 0 \\ 0 & \sigma_\varepsilon^2 \end{matrix}\right) \right)$$

Solve mixed model equation (Henderson, 1989)

$$\begin{bmatrix} \acute{X}X & \acute{X}Z \\ \acute{Z}X & \acute{Z}Z + \lambda I^{-1} \end{bmatrix} \begin{bmatrix} b \\ a \end{bmatrix} = \begin{bmatrix} \acute{X}\,y \\ \acute{Z}y \end{bmatrix}$$

$$\begin{pmatrix} \hat{a}_1 \\ \hat{a}_2 \\ \hat{a}_3 \\ \hat{a}_4 \\ \hat{a}_5 \\ \hat{a}_6 \end{pmatrix} = \begin{pmatrix} -0.35 \\ -0.25 \\ 1.35 \\ -1.15 \\ 1.45 \\ 0.45 \end{pmatrix}$$

Marker effects (BLUP)

$$\text{GEBVs}(\widehat{u}) = Z\hat{a}$$

	a_1	a_2	a_3	a_4
y_1	0	0	0	2
y_2	2	1	0	2
y_3	2	2	2	2
y_4	2	2	0	0

$$GEBV(y_1) = [0 * (-0.35) + [0 * (-0.25)] + \cdots. + [2 * (-1.15)$$

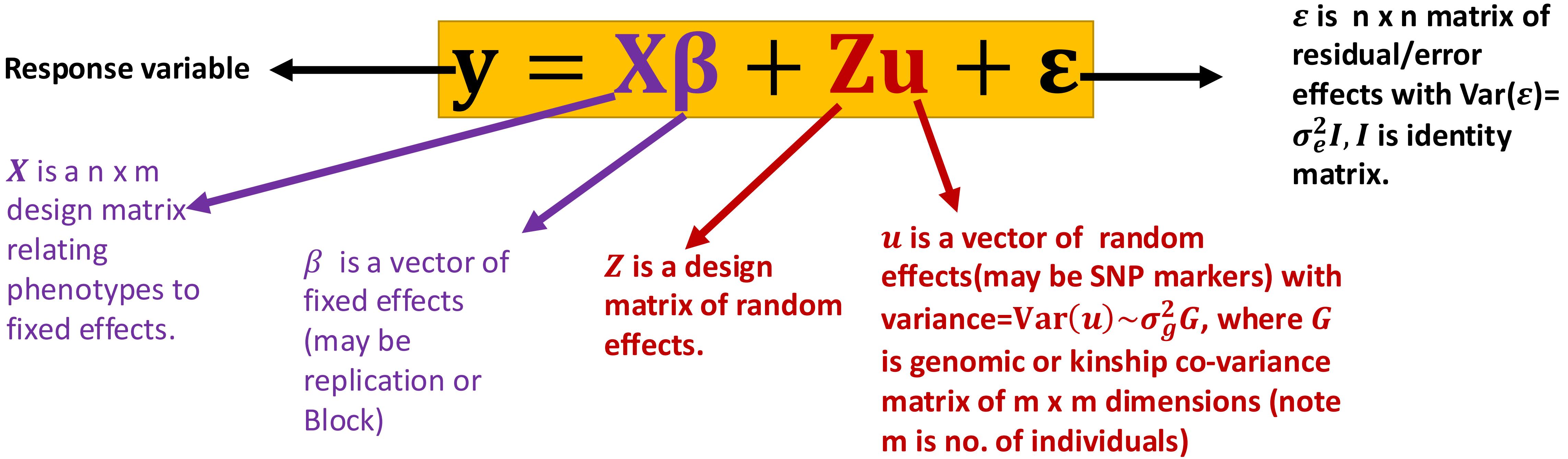
What if LD exists between markers?

RRBLUP or Ordinary least squares (OLS) do not consider:

LD Between Markers and account for the relationship between the genotypes

Better to compute and Integrate the Relationship matrix in the model

Mixed Effect Model



$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{u} + \boldsymbol{\varepsilon}$$

Response variable

$\boldsymbol{\varepsilon}$ is n x n matrix of residual/error effects with Var(ε)= $\sigma_e^2 \boldsymbol{I}$, $\boldsymbol{I}$ is identity matrix.

X is a n x m design matrix relating phenotypes to fixed effects.

β is a vector of fixed effects (may be replication or Block)

Z is a design matrix of random effects.

u is a vector of random effects(may be SNP markers) with variance=$\mathrm{Var}(u) \sim \sigma_g^2 G$, where G is genomic or kinship co-variance matrix of m x m dimensions (note m is no. of individuals)

$$\begin{bmatrix} \mathbf{u} \\ \boldsymbol{\varepsilon} \end{bmatrix} \sim \left[N\left(0, \begin{matrix} \sigma_{\mathbf{u}}^2 K & 0 \\ 0 & \sigma_{\boldsymbol{\varepsilon}}^2 R \end{matrix}\right) \right]$$

Note: cov($\mathbf{u}$, $\boldsymbol{\varepsilon}$)=0

Solving Mixed model Equation

$$\tilde{\boldsymbol{\beta}} = (\mathbf{X}'\mathbf{V}^{-1}\mathbf{X})^{-}\mathbf{X}'\mathbf{V}^{-1}\mathbf{y}, \quad \text{with} \quad \mathrm{BLUE}(\mathbf{X}\boldsymbol{\beta}) = \mathbf{X}\tilde{\boldsymbol{\beta}}$$

BLUE

$$\underbrace{\begin{bmatrix}\acute{X}X & \acute{X}Z\\ \acute{Z}X & \acute{Z}Z+\lambda G^{-1}\end{bmatrix}}_{\textbf{LHS}}\begin{bmatrix}\beta\\ u\end{bmatrix}=\underbrace{\begin{bmatrix}\acute{X}\,y\\ \acute{Z}y\end{bmatrix}}_{\textbf{RHS}}$$

$$\tilde{\mathbf{u}} = \mathbf{D}\mathbf{Z}'\mathbf{V}^{-1}(\mathbf{y} - \mathbf{X}\boldsymbol{\beta}) = \mathrm{BLUP}(\mathbf{u})$$

BLUP

$$\begin{bmatrix}\hat{\beta}\\ \hat{u}\end{bmatrix}=\begin{bmatrix}\acute{X}X & \acute{X}Z\\ \acute{Z}X & \acute{Z}Z+\lambda G^{-1}\end{bmatrix}^{-1}\cdot\begin{bmatrix}\acute{X}\,y\\ \acute{Z}y\end{bmatrix}$$

We decompose the matrices and get solutions through iterative methods

Genomic BLUP (gBLUP)

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z}\mathbf{u} + \boldsymbol{\varepsilon}$$

$$\hat{u} = \left[\mathbf{I} + \mathbf{G}^{-1}\frac{\sigma_e^2}{\sigma_u^2}\right]\mathbf{y}$$

GRM to account for mendelian sampling

Equivalence between rrBLUP and gBLUP

For gBLUP the $Var(y) = \mathbf{ZGZ}'\sigma_u^2 + \mathbf{I}\sigma_e^2$

For rrBLUP the $Var(y) = \mathbf{XX}'\sigma_\beta^2 + \mathbf{I}\sigma_e^2$

Genomic BLUP (gBLUP Model)

$$\mathbf{y} = Za + \varepsilon$$

$$\begin{bmatrix} y_1 \\ y_2 \\ y_3 \\ y_4 \\ . \\ y_n \end{bmatrix} = \begin{pmatrix} 1 & 0.5 & 0.3 & 0.9 \\ 0.5 & 1 & -0.2 & 0.8 \\ 0.3 & -0.2 & 1 & 0.4 \\ 0.9 & 0.8 & .4 & 1 \end{pmatrix} \begin{bmatrix} a_1 \\ a_2 \\ a_3 \\ a_4 \\ a_5 \\ a_p \end{bmatrix} + \begin{bmatrix} \varepsilon \end{bmatrix}$$

n x 1 *n x g* *g x 1* *n x 1*

n is # of individuals

g is # of breeding values

$$\begin{bmatrix} g \\ \varepsilon \end{bmatrix} \sim \left\{ MNV\left(0, \begin{matrix} G\sigma_a^2 & 0 \\ 0 & \sigma_\varepsilon^2 \end{matrix}\right) \right\}$$

GRM accounts for Mendelian sampling

Solve mixed model equation (Henderson, 1989)

$$\begin{bmatrix} \acute{X}X & \acute{X}Z \\ \acute{Z}X & \acute{Z}Z + \lambda G^{-1} \end{bmatrix} \begin{bmatrix} b \\ g \end{bmatrix} = \begin{bmatrix} \acute{X}\,y \\ \acute{Z}y \end{bmatrix}$$

$$\begin{pmatrix} \hat{g}_1 \\ \hat{g}_2 \\ \hat{g}_3 \\ \hat{g}_4 \\ g \\ \hat{g}_6 \end{pmatrix} = \begin{pmatrix} -0.35 \\ -0.25 \\ 1.35 \\ -1.15 \\ 1.45 \\ 0.45 \end{pmatrix}$$

(BLUP of Breeding values)

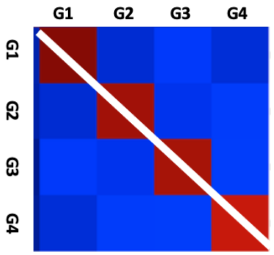
GEBVs($\widehat{g}$)

Construction of G matrix

3 steps

1. Create a centered Z matrix
2. Create the cross product
3. Divide it by $\sum_{i=1}^{m} 2p_j(1\text{-}p_j)$

$$\mathbf{G} = \frac{\mathbf{ZZ^T}}{\sum_{i=1}^{m} 2p_j\,(1-p_j)}$$



First G matrix, VanRanden (2008)

$\sigma^2 a$ is additive variance = $\sum_{i=1}^{m} 2p_j\,(1-p_j$

Difference Between RRBLUP and gBLUP

RR BLUP	gBLUP
Marker as Predictors (BLUPs)	Predict Additive breeding Values directly
Markers are directly used	Markers are used to compute covariance matrix (Relationship Matrix)
Dimension of genetic effects is p x p	Dimension of effects is n x n, computationally easy
Does not account for the relationships between genotypes. Assuming genotypes are independent	Accounts relationship between genotypes, thus more appropriate for predictions or dissecting G x E (WHY?)
$var(y) = Z\acute{Z}\ \sigma_u^2 + I\sigma_e^2$	$var(y) = ZG\acute{Z}\ \sigma_u^2 + I\sigma_e^2$
$blup(\hat{u}) = (Z\acute{Z} + I\lambda)^{-1}Z(Y' - \hat{\mu})$	$blup(\hat{u}) = (Z\acute{Z} + G^{-1}\lambda)^{-1}Z(Y' - \hat{\mu})$

Pedigree BLUP (pBLUP Model)

$$\mathbf{y} = Za + \boldsymbol{\varepsilon}$$

$$\begin{bmatrix} y_1 \\ y_2 \\ y_3 \\ y_4 \\ . \\ y_n \end{bmatrix} = \begin{pmatrix} 1 & 0.5 & 0.3 & 0.9 \\ 0.5 & 1 & -0.2 & 0.8 \\ 0.3 & -0.2 & 1 & 0.4 \\ 0.9 & 0.8 & .4 & 1 \end{pmatrix} \begin{bmatrix} a_1 \\ a_2 \\ a_3 \\ a_4 \\ a_5 \\ a_p \end{bmatrix} + \begin{bmatrix} \boldsymbol{\varepsilon} \end{bmatrix}$$

n x 1 *n x g* *g x 1* *n x 1*

n is # of individuals

g is # of breeding values

$$\begin{bmatrix} g \\ \boldsymbol{\varepsilon} \end{bmatrix} \sim \left[MNV \left(0, \begin{matrix} A\sigma_a^2 & 0 \\ 0 & \sigma_{\varepsilon}^2 \end{matrix} \right) \right]$$

Accounts for relationships (Coefficient of co-ancestry , $r = 2\theta_{xy}$)

Solve mixed model equation (Henderson, 1989)

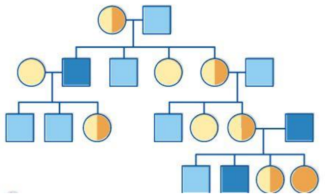
$$\begin{bmatrix} \acute{X}X & \acute{X}Z \\ \acute{Z}X & \acute{Z}Z + \lambda A^{-1} \end{bmatrix} \begin{bmatrix} b \\ g \end{bmatrix} = \begin{bmatrix} \acute{X}\,y \\ \acute{Z}y \end{bmatrix}$$

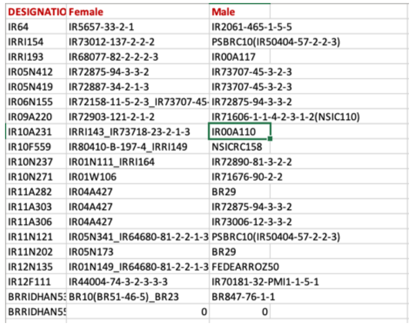
$$\begin{pmatrix} \hat{g}_1 \\ \hat{g}_2 \\ \hat{g}_3 \\ \hat{g}_4 \\ g \\ \hat{g}_6 \end{pmatrix} = \begin{pmatrix} -0.35 \\ -0.25 \\ 1.35 \\ -1.15 \\ 1.45 \\ 0.45 \end{pmatrix}$$

(BLUP of Breeding values)

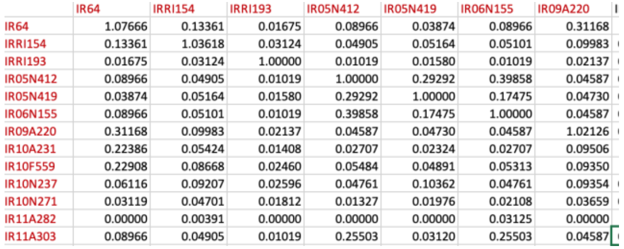
GEBVs($\widehat{g}$)

Construction of A matrix





DESIGNATIO	Female	Male
IR64	IR5657-33-2-1	IR2061-465-1-5-5
IRRI154	IR73012-137-2-2-2	PSBRC10(IR50404-57-2-2-3)
IRRI193	IR68077-82-2-2-2-3	IR00A117
IR05N412	IR72875-94-3-3-2	IR73707-45-3-2-3
IR05N419	IR72887-34-2-1-3	IR73707-45-3-2-3
IR06N155	IR72158-11-5-2-3_IR73707-45-	IR72875-94-3-3-2
IR09A220	IR72903-121-2-1-2	IR71606-1-1-4-2-3-1-2(NSIC110)
IR10A231	IRRI143_IR73718-23-2-1-3	IR00A110
IR10F559	IR80410-B-197-4_IRRI149	NSICRC158
IR10N237	IR01N111_IRRI164	IR72890-81-3-2-2
IR10N271	IR01W106	IR71676-90-2-2
IR11A282	IR04A427	BR29
IR11A303	IR04A427	IR72875-94-3-3-2
IR11A306	IR04A427	IR73006-12-3-3-2
IR11N121	IR05N341_IR64680-81-2-2-1-3	PSBRC10(IR50404-57-2-2-3)
IR11N202	IR05N173	BR29
IR12N135	IR01N149_IR64680-81-2-2-1-3	FEDEARROZ50
IR12F111	IR44004-74-3-2-3-3-3	IR70181-32-PMI1-1-5-1
BRRIDHAN5:	BR10(BR51-46-5)_BR23	BR847-76-1-1
BRRIDHAN5!	0	0



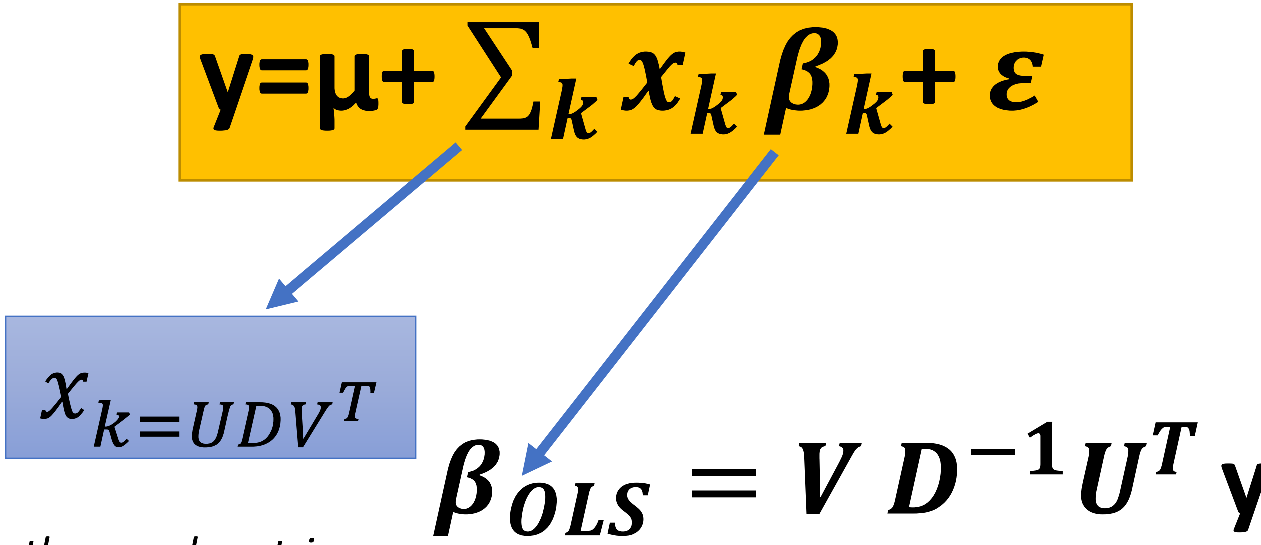
	IR64	IRRI154	IRRI193	IR05N412	IR05N419	IR06N155	IR09A220
IR64	1.07666	0.13361	0.01675	0.08966	0.03874	0.08966	0.31168
IRRI154	0.13361	1.03618	0.03124	0.04905	0.05164	0.05101	0.09983
IRRI193	0.01675	0.03124	1.00000	0.01019	0.01580	0.01019	0.02137
IR05N412	0.08966	0.04905	0.01019	1.00000	0.29292	0.39858	0.04587
IR05N419	0.03874	0.05164	0.01580	0.29292	1.00000	0.17475	0.04730
IR06N155	0.08966	0.05101	0.01019	0.39858	0.17475	1.00000	0.04587
IR09A220	0.31168	0.09983	0.02137	0.04587	0.04730	0.04587	1.02126
IR10A231	0.22386	0.05424	0.01408	0.02707	0.02324	0.02707	0.09506
IR10F559	0.22908	0.08668	0.02460	0.05484	0.04891	0.05313	0.09350
IR10N237	0.06116	0.09207	0.02596	0.04761	0.10362	0.04761	0.09354
IR10N271	0.03119	0.04701	0.01812	0.01327	0.01976	0.02108	0.03659
IR11A282	0.00000	0.00391	0.00000	0.00000	0.00000	0.03125	0.00000
IR11A303	0.08966	0.04905	0.01019	0.25503	0.03120	0.25503	0.04587

A matrix

https://github.com/prmunoz/AGHmatrix

Dimension Reduction methods

- Reason is to avoid inverse
- Suitable when predictors are correlated
- And calculations are tedious



$$y=\mu+\sum_k x_k\,\beta_k+\varepsilon$$

$$x_{k=UDV^T}$$

$$\beta_{OLS} = V\,D^{-1}U^{T}\,y$$

U= n x m orthogonal matrix
D= n x m diagonal matrix with singular values
V= n x n orthogonal matrix

Regress phenotypes directly on eigenvectors or principle components

Bayesian Approaches
(Relax the Distribution Assumptions)

Sampling distr.

posterior

prior

$$p(\theta|y) = \frac{p(\theta, y)}{p(y)} = \frac{p(y|\theta)p(\theta)}{p(y)}$$

y is observed data $y \sim p(\theta|y)$
θ is unknown parameter (random)

Bayesian Models differ with respect to the *Prior*

- The even distribution of genetic causation is not satisfactory
- The assumption of common variance does not imply that the effects of all markers
- RR BLUP over shrinkage of large marker effects
- Large effect and small effect QTLs (natural in breeding populations)

Bayesian Ridge-Regression (BRR)

$$\widehat{\boldsymbol{\beta}} = (\boldsymbol{X}\boldsymbol{X}^{T} + \boldsymbol{K}^{-1}\frac{\boldsymbol{\sigma}_{\boldsymbol{e}}^{2}}{\boldsymbol{\sigma}_{\boldsymbol{\beta}}^{2}})^{-1}(\boldsymbol{y}\boldsymbol{X}^{T} + \boldsymbol{K}^{-1}\frac{\boldsymbol{\sigma}_{\boldsymbol{e}}^{2}}{\boldsymbol{\sigma}_{\boldsymbol{\beta}}^{2}})\beta_{o}$$

$$\lambda = \frac{\sigma_e^2}{\sigma_\beta^2}$$

$$\beta \sim N\left(0, \sigma_\beta^2\right)$$

$$\sigma_\beta^2 \sim \mathcal{X}^{-2}(df, s)$$

If we assume prior mean=0, β=0, then $\boldsymbol{K}$=I

$$\boldsymbol{\beta}_{\boldsymbol{ridge}} = (\boldsymbol{X}^{T}\boldsymbol{X})^{-1} + \boldsymbol{\lambda}\boldsymbol{I})\ \boldsymbol{y}\boldsymbol{X}^{T}$$

Prior for markers is given by Gaussian distribution, which differs from LASSO

Scaled inverted chi-square distribution

The only difference in prior information

LASSO (Regularization)

$$\beta_{lasso} = argmin\left[\sum (y_i - \sum_{j=1}^{m} x_{ij}\beta_j)^2 + \lambda \sum_{i=1}^{j} \beta_j^2\right]$$

$$in\ LASSO\ |\beta_j|\ is\ absolute\ value\ (L_1\ Penality)$$
$$however, in\ Rideg\ regression\ value\ is\ \beta_j^2\ (L_2\ Penality)$$

Type equation here.

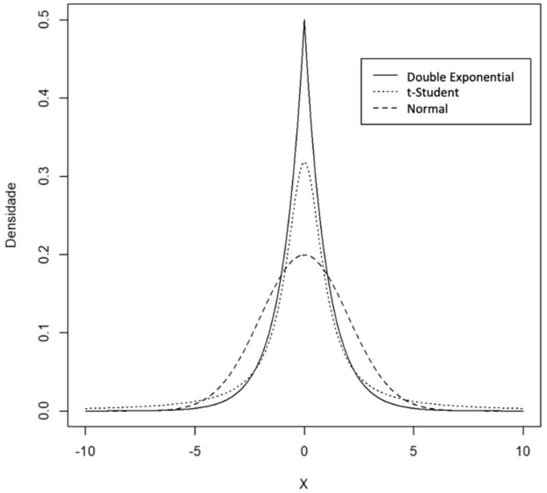
In LASSO, shrinkage is stronger-sets some marker effects equal to 0

Bayesian LASSO

$$\beta_{lasso} = argmin[(y - x\beta)^T(y - x\beta) + \lambda|\beta_j|]$$
$$= \underbrace{exp\left(-\frac{1}{2\sigma_e^2}(y - x\beta)^T(y - x\beta)\right)}_{\text{Gaussian Sampling}} \underbrace{exp(\lambda|\beta_j I|)}_{\text{Double exponential}}$$

In Bayesian Lasso, assumption of marker effects is Double exponential

Double exponential shrink more marker effects close to zero



Higher mass at zero

Bayesian Approaches
(Relax the Distribution Assumptions)

Bayes A

- Assumes marker-specific variance
- Utilizes an inverse chi-square on marker variances
- Shrinks tiny marker effects (variances) towards zero, and larger values survive.

Bayes B

- Fraction of markers with zero effect
- More realistic prior because we expect that some regions of the genome will carry no QTL

Bayes C

- Assumes t-distribution one with large variance for SNP fraction and other with small variance

Genomic Selection is Simply a tool to Supplement the Breeding Pipeline

Thank You

Questions