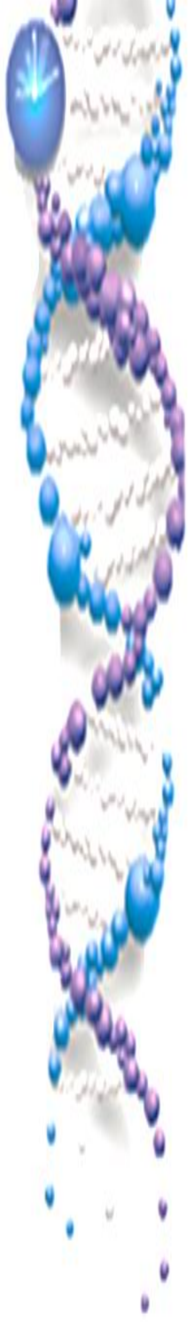
EAAP 2018
69th Annual Meeting of the European Federation of Animal Science



Improving Prediction Accuracy of Meat Tenderness in Nelore Cattle using Artificial Neural Networks

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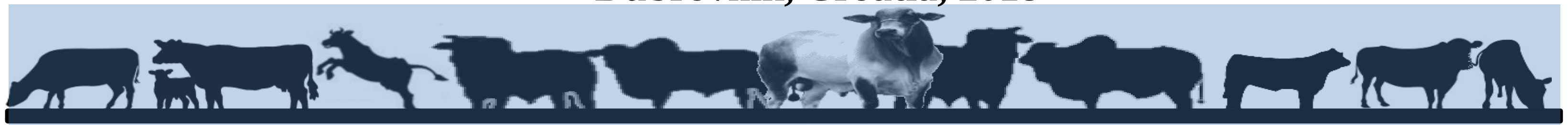
Dubrovnik, Croatia, 2018



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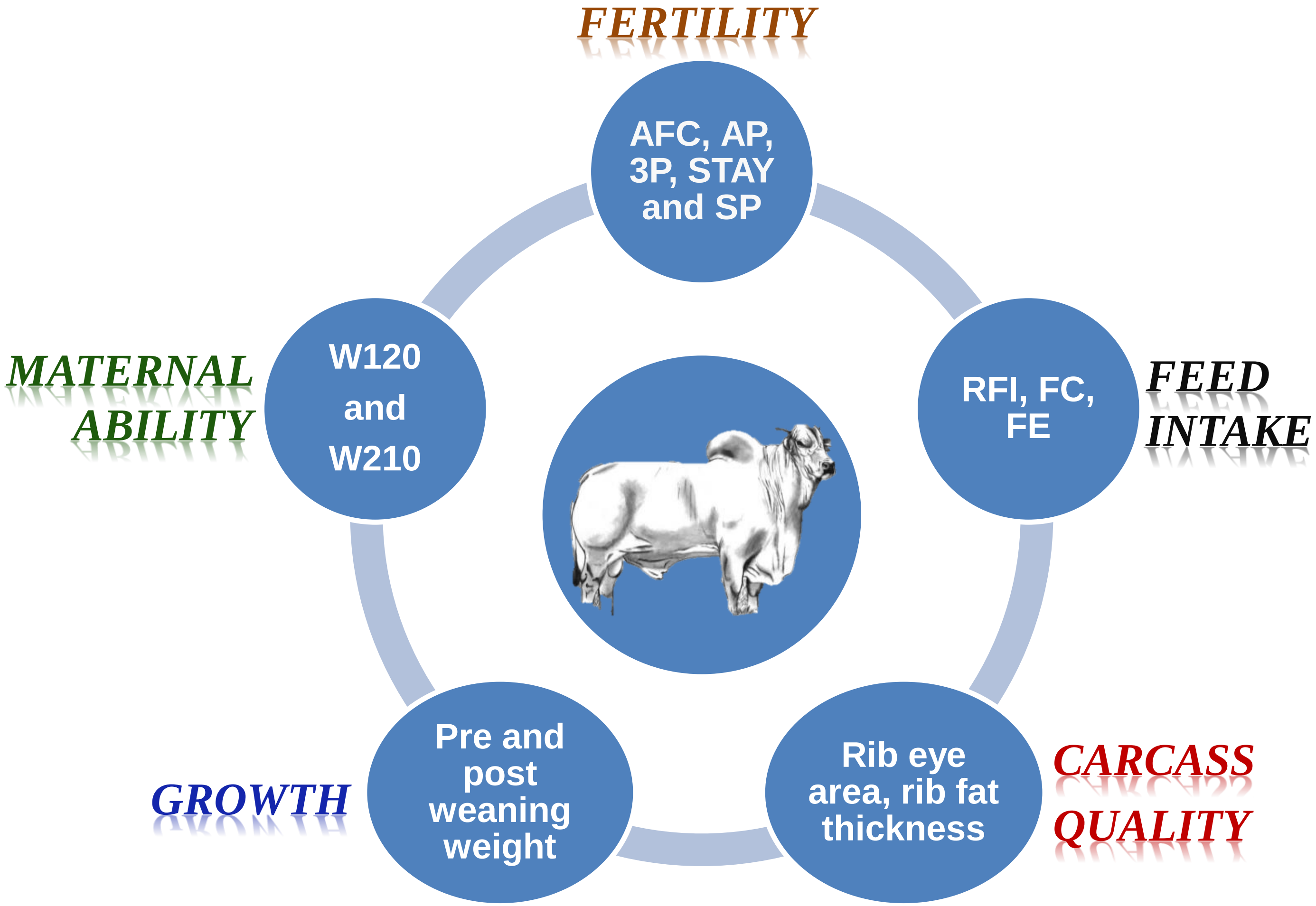
Selection Criteria in Brazilian Beef Cattle



FERTILITY

AFC, AP, 3P, STAY and SP

FEED INTAKE

RFI, FC, FE

CARCASS QUALITY

Rib eye area, rib fat thickness

GROWTH

Pre and post weaning weight

MATERNAL ABILITY

W120 and W210

Animal Model

Breeding Value

Fixed Effects

Maternal Effect

$$y = X\boxed{\beta} + Z_1\boxed{a} + Z_2\boxed{m} + Z_3\boxed{mpe} + \varepsilon$$

$$y = X\boxed{\beta} + Z_1\boxed{a} + \varepsilon$$

Additive Genetic Effect

Maternal Permanent Environment effect

Animal Model

Breeding Value for Meat Tenderness

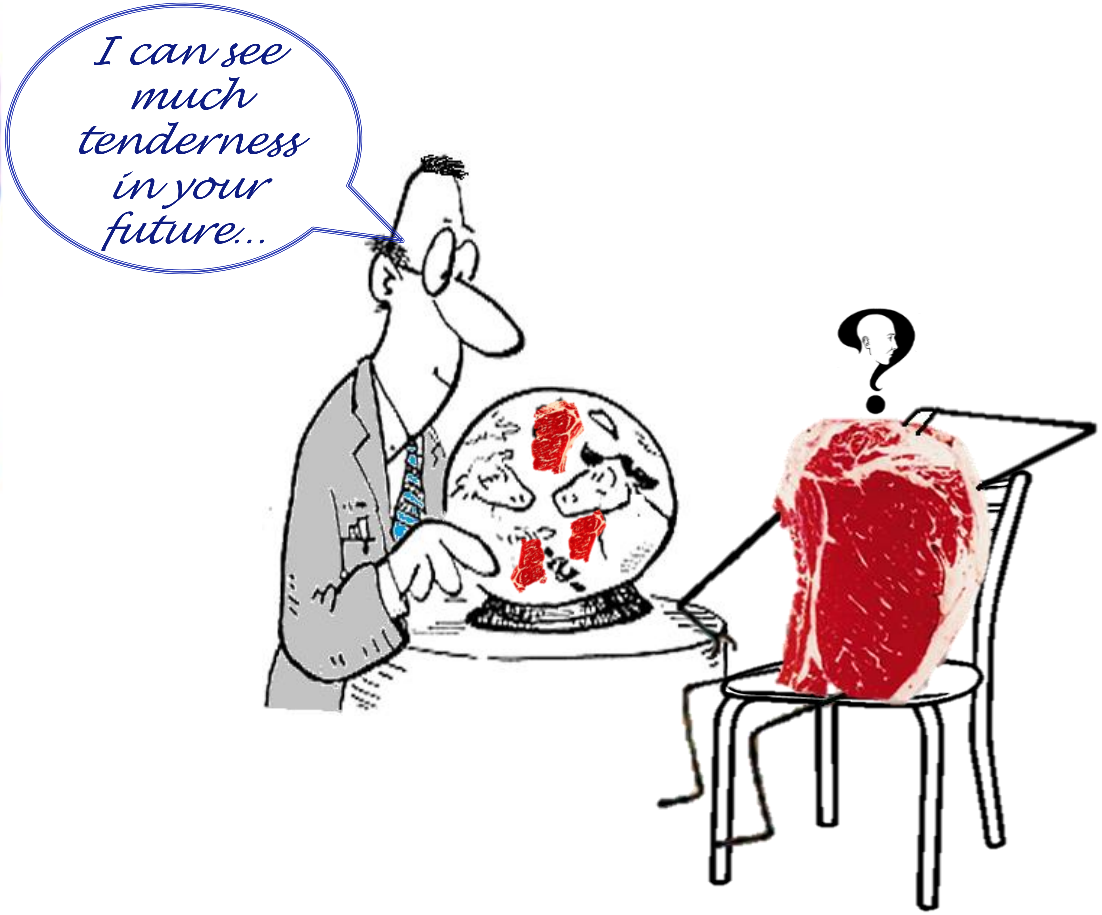
Contemporary Group

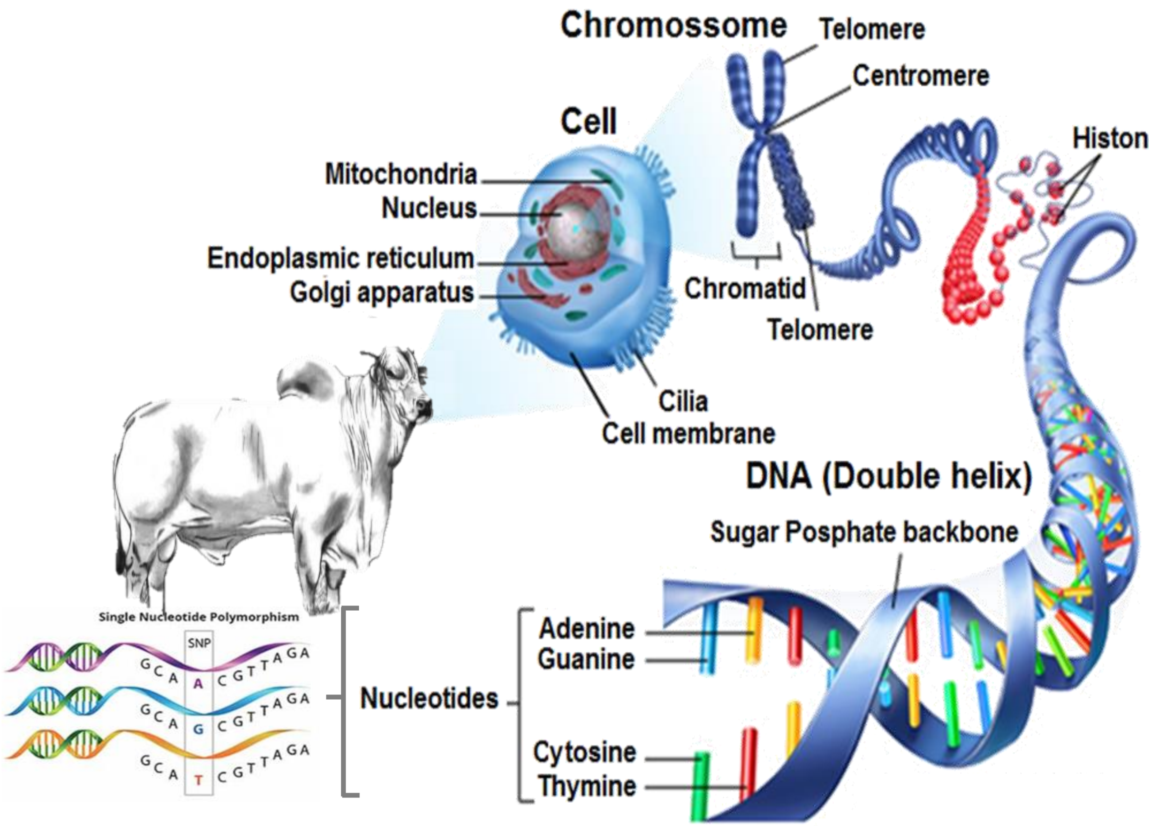
Sex

$$y = X\boxed{\beta} + Z_1\boxed{a} + \varepsilon$$

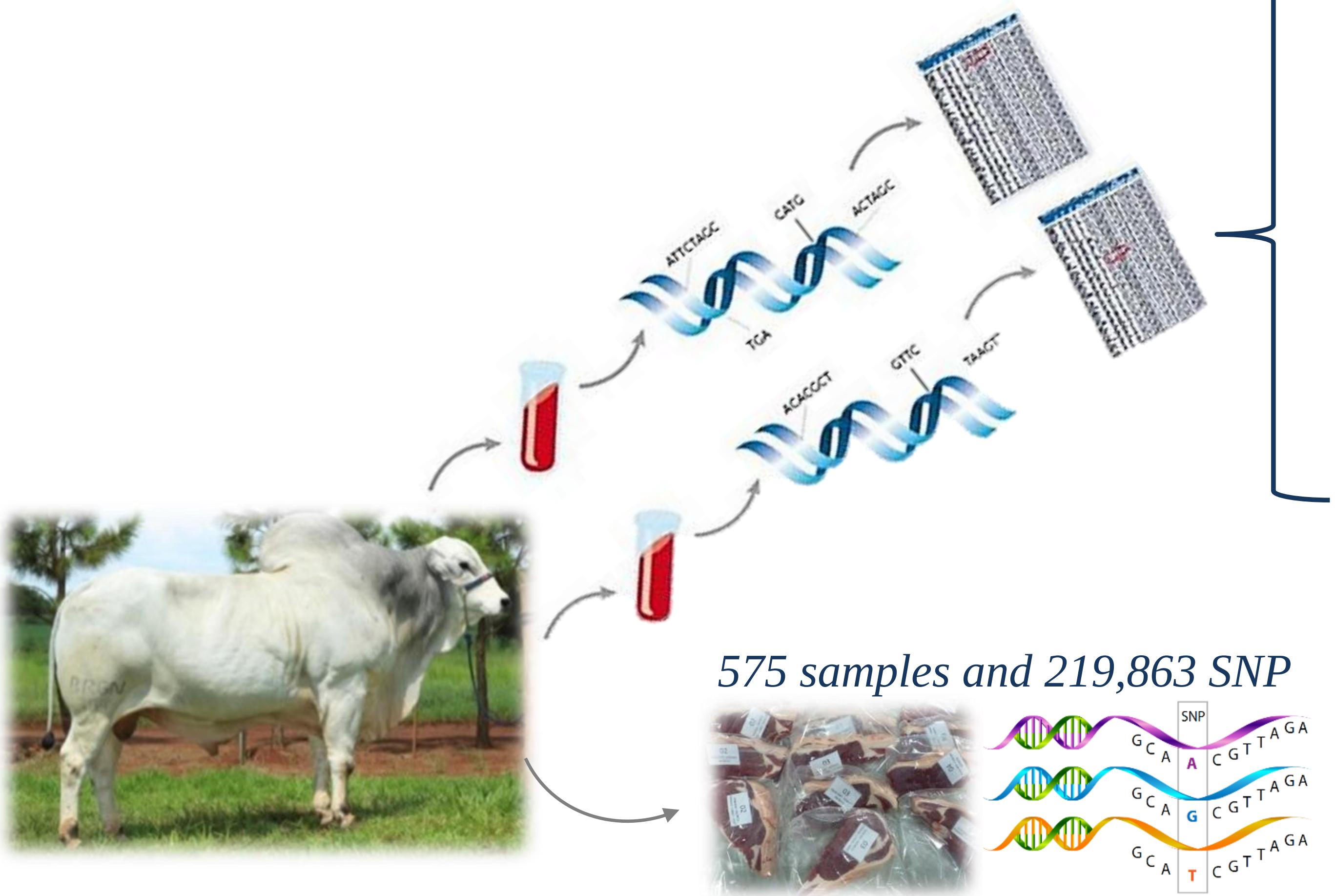
Additive Genetic Effect

Genomic Analyses





Quality Control

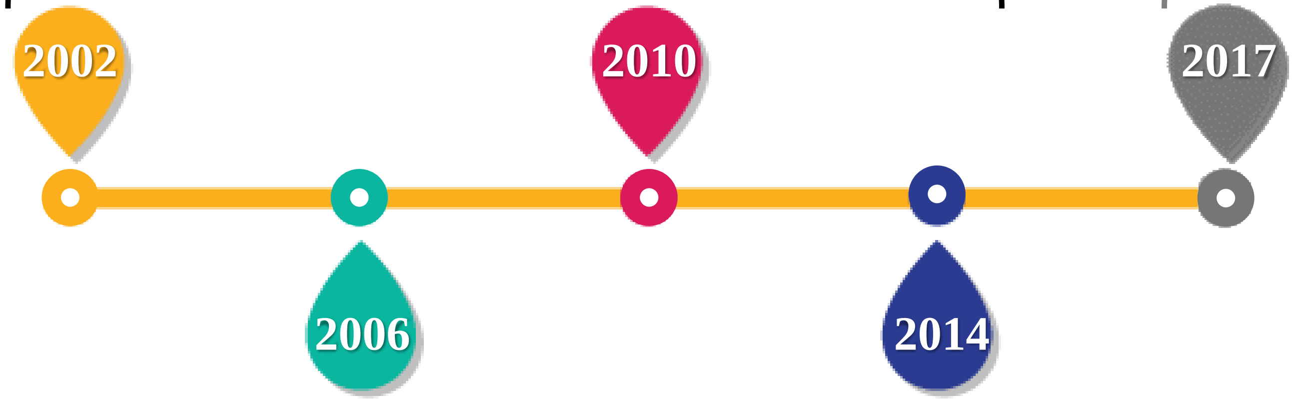


575 samples and 219,863 SNP

- ✓ *Redundant position*
- ✓ *X, Y and MT Chromosome*
- ✓ *Minor Allele Frequency < 5%*
- ✓ *Deviation from HWE ($p<10^{-6}$)*
- ✓ *Linkage Disequilibrium > 0.8*

Training and Validation Population

Training



510 samples and 219,863 SNP

Validation

65 samples and 219,863 SNP

Bayesian Regression Models

Bayes B

$$g_j \mid \sigma_j^2 \sim N\left(0, \sigma_j^2\right)$$

$$\begin{cases} \sigma_j^2 = 0 \\ \sigma_j^2 \sim \chi^{-2}(df, S) \end{cases}$$

$$\sigma_e^2 \sim \chi^{-2}(-2{,}0)$$

Bayes Cπ

$$\begin{cases} g_j = 0 \\ g_j \mid \sigma_g^2 \sim N\left(0, \sigma_g^2\right) \end{cases}$$

$$\pi \sim Uniform(0{,}1)$$

$$\sigma_g^2 \sim \chi^{-2}(df, S)$$

$$\sigma_e^2 \sim \chi^{-2}(-2{,}0)$$

Bayes A

$$g_j \mid \sigma_j^2 \sim N\left(0, \sigma_j^2\right)$$

$$\sigma_j^2 \sim \chi^{-2}(df, S)$$

$$\sigma_e^2 \sim \chi^{-2}(-2{,}0)$$

Bayesian Lasso

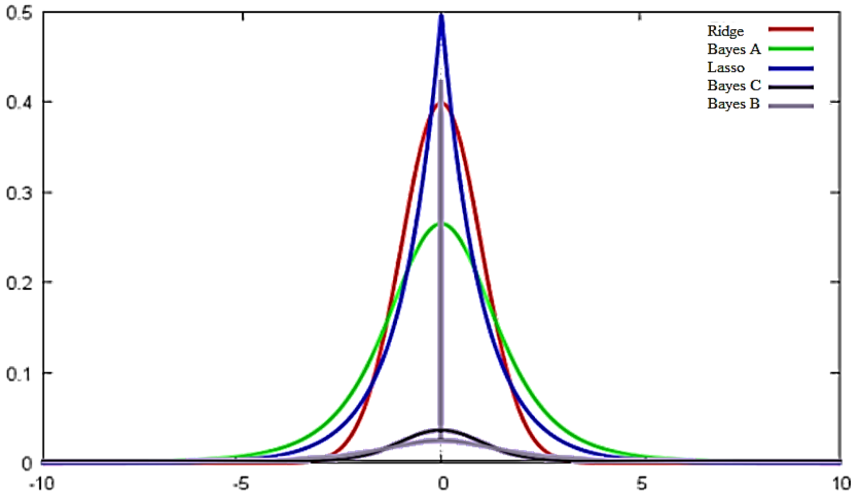
$$g_j \mid \sigma_j^2 \sim N\left(0, \sigma_j^2\right)$$

$$\sigma_j^2 \sim DE(\lambda)$$

$$\sigma_e^2 \sim \chi^{-2}(-2{,}0)$$

Genome-Wide Regression and Prediction with the BGLR Statistical Package

Paulino Pérez*,1 and Gustavo de los Campos†
*Socio Economía Estadística e Informática, Colegio de Postgraduados 56230, México and †Department of Biostatistics, Section on Statistical Genetics, University of Alabama, Birmingham, Alabama 35294



Bayesian Ridge Regression

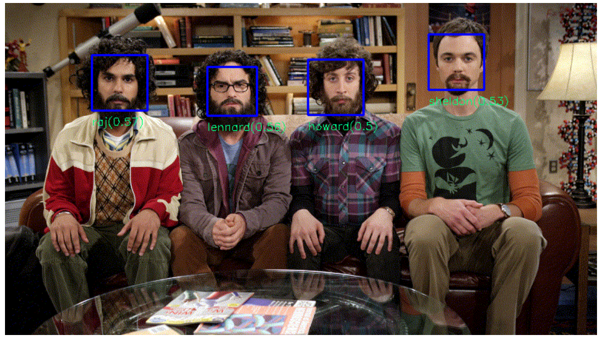
$$g_j \mid \sigma_j^2 \sim N\left(0, \sigma_j^2\right)$$

$$\sigma_j^2 \sim N(\lambda)$$

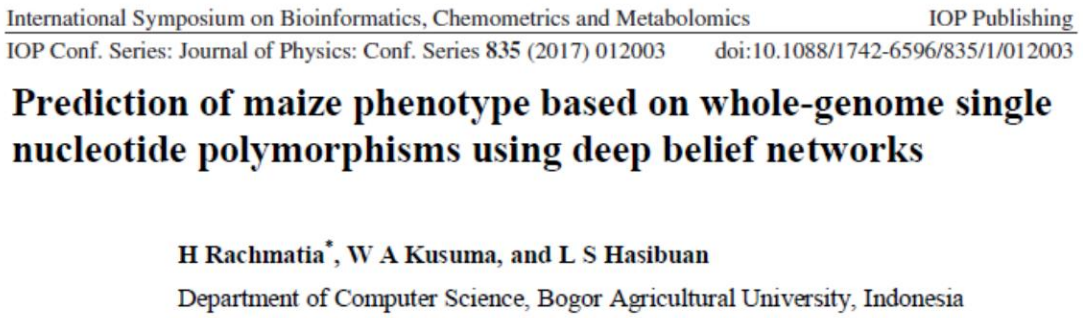
$$\sigma_e^2 \sim \chi^{-2}(-2{,}0)$$

Artificial Neural Network

- Successful examples



- Genomic prediction



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Prediction of maize phenotype based on whole-genome single nucleotide polymorphisms using deep belief networks

H Rachmatia*, W A Kusuma, and L S Hasibuan

Department of Computer Science, Bogor Agricultural University, Indonesia

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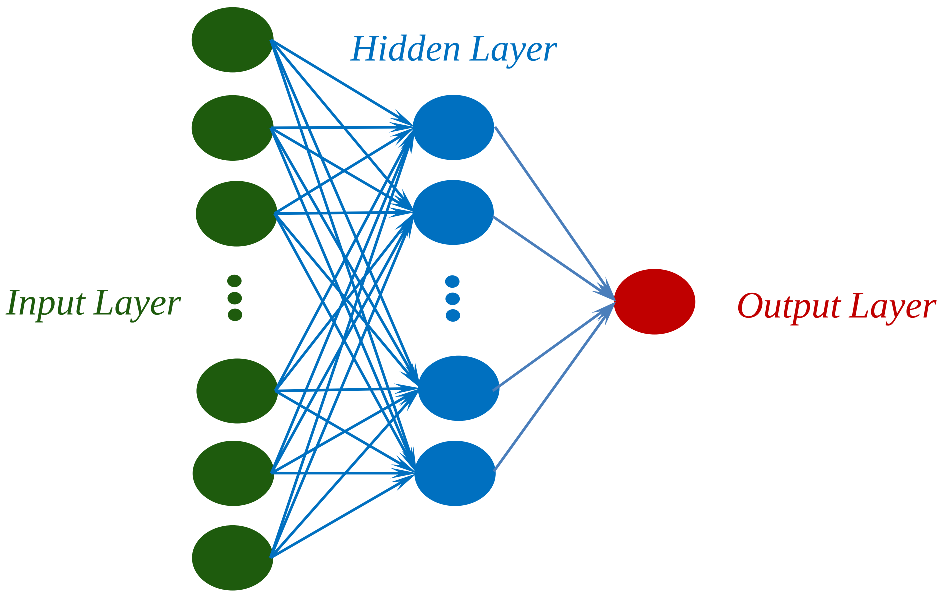
Genomic Selection with Deep Neural Networks

Riley Mitchell Mcdowell
Iowa State University

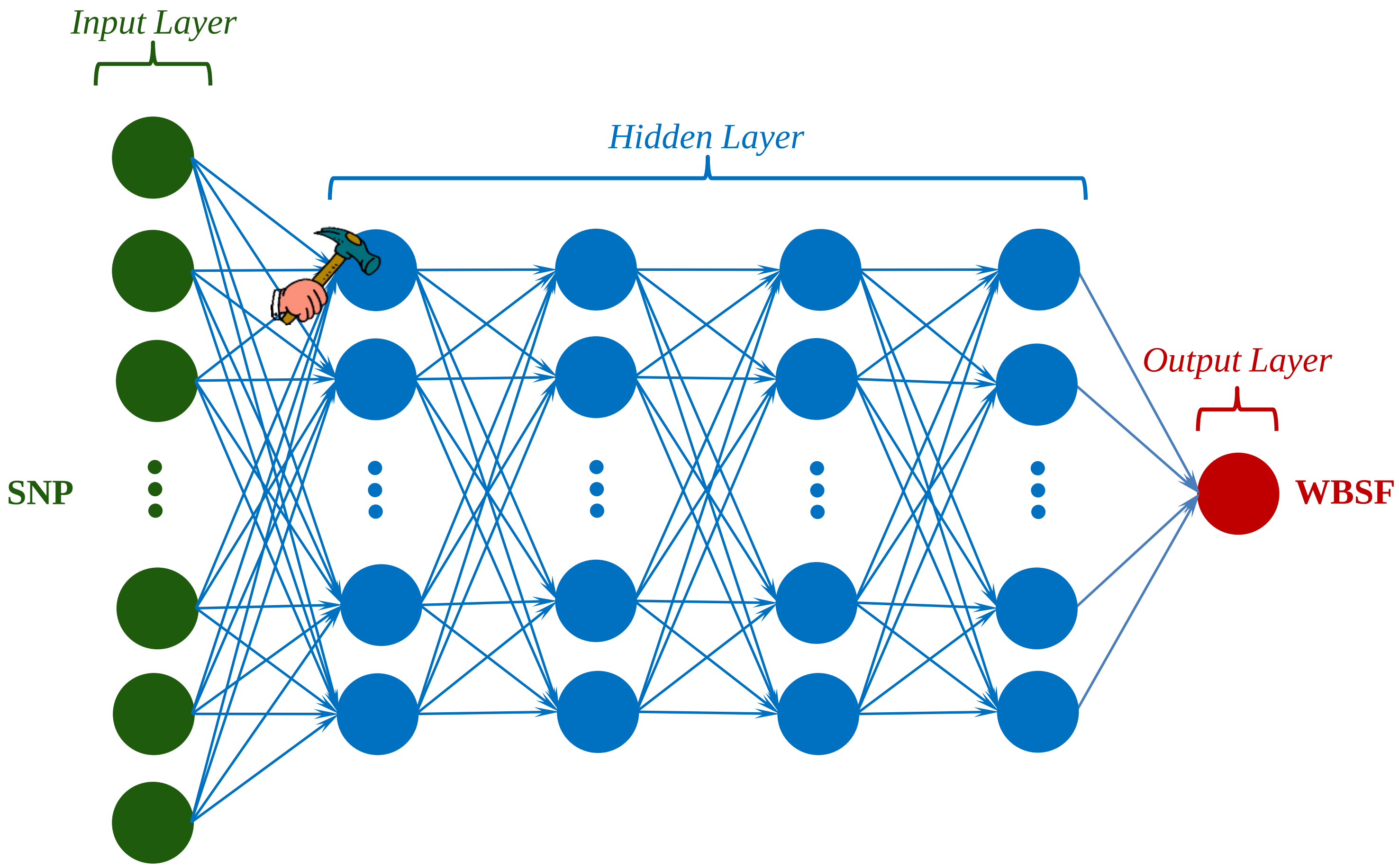
Artificial Neural Network

- Delivery high prediction accuracy
- Can handle large number of variables
- Can capture non-linear relationship between predictors and outcome variable
- No assumption about the distribution of predictors and output variable

- Biological interpretation
- Overfitting



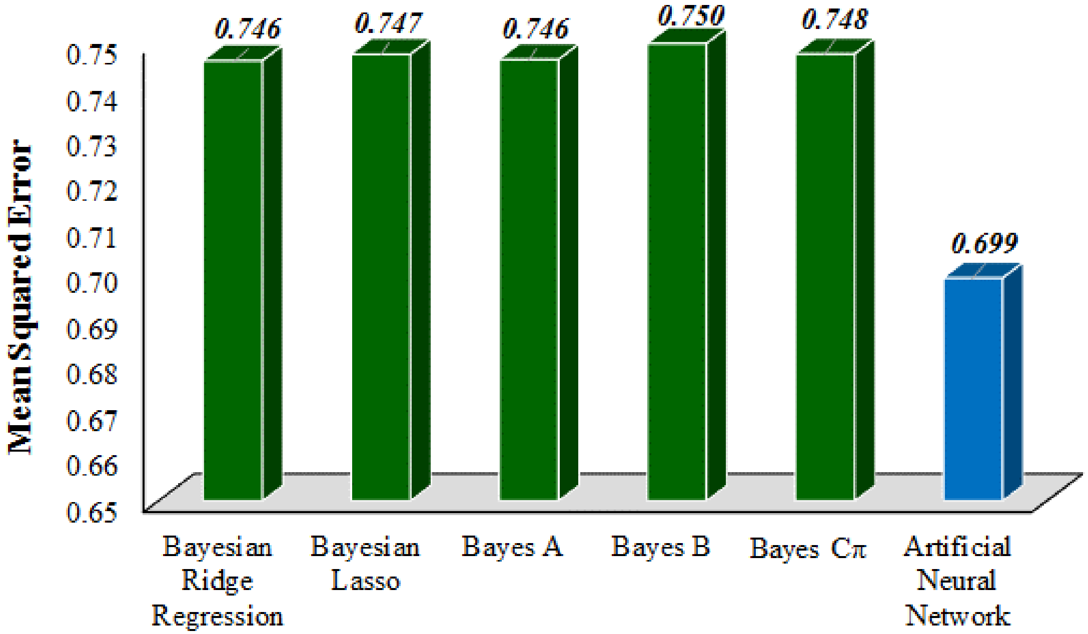
Deep Neural Network

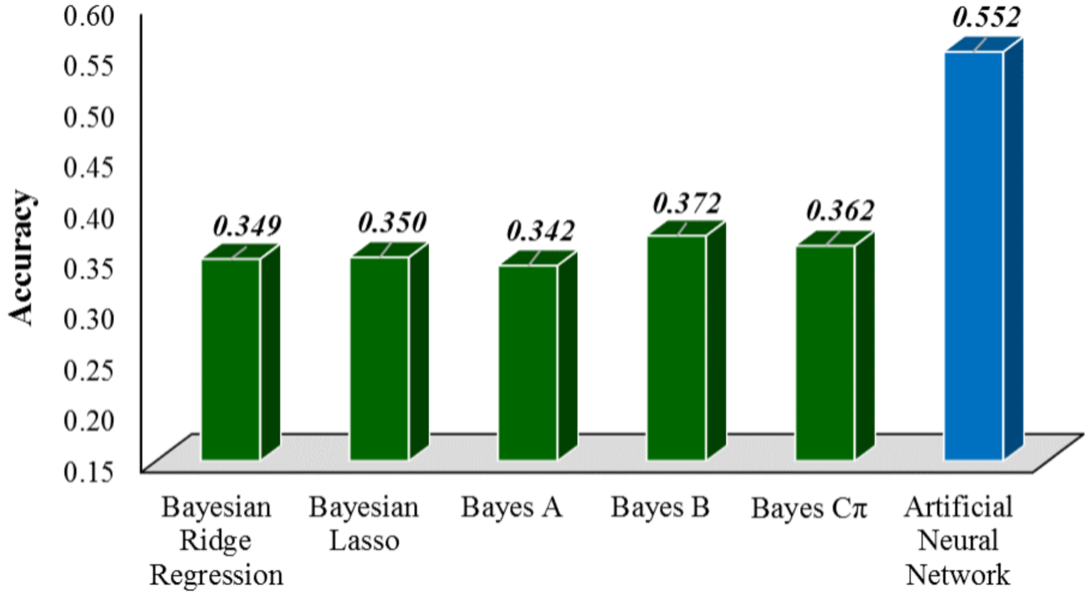


Topology

- ✓ *1 to 4 hidden layers*
  - ➢ *10, 35, 75, 105 and 250 neurons*
- ✓ ***Rectifier and Maxout activation***
- ✓ ***Dropout (50%)***
- ✓ ***Quadratic loss function***
- ✓ ***10K Epochs***
- ✓ ***ADADELTA adaptive learning rate algorithm***
  - ➢ *Rho: 0.99*
  - ➢ *Epsilon: 1e-08*
- ✓ **Stopping criterion: 1e-06**

Genomic Prediction Ability





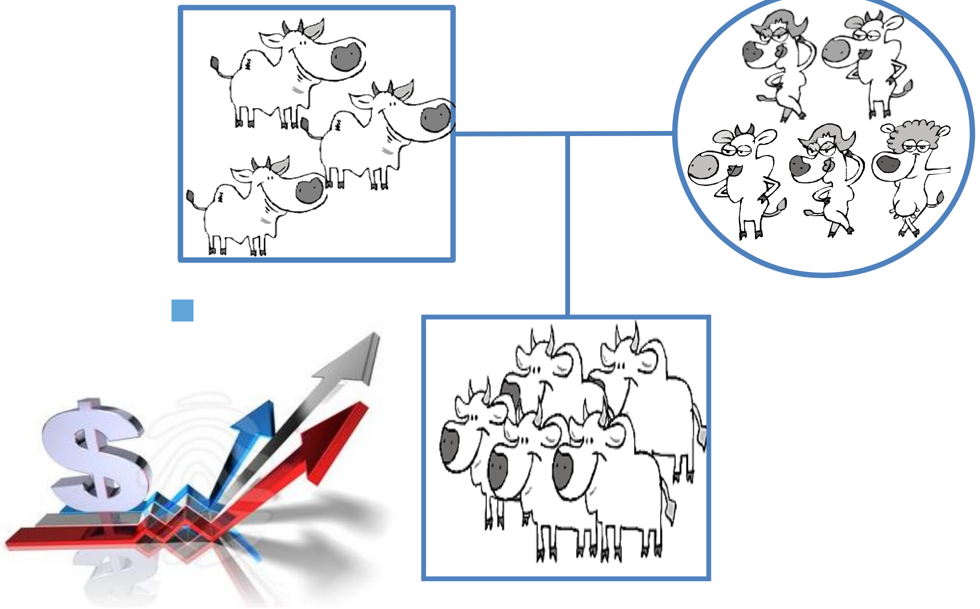
Animal Breeding Framework

GEBV

Pedigree / Genomic Information

Mating

Optimum Contribution Selection



Thank you!

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DO ESTADO DE SÃO PAULO

Marca OB

CV NELORE MOCHO

DEPARTMENT OF ANIMAL SCIENCES
University of Wisconsin-Madison

ANCP