



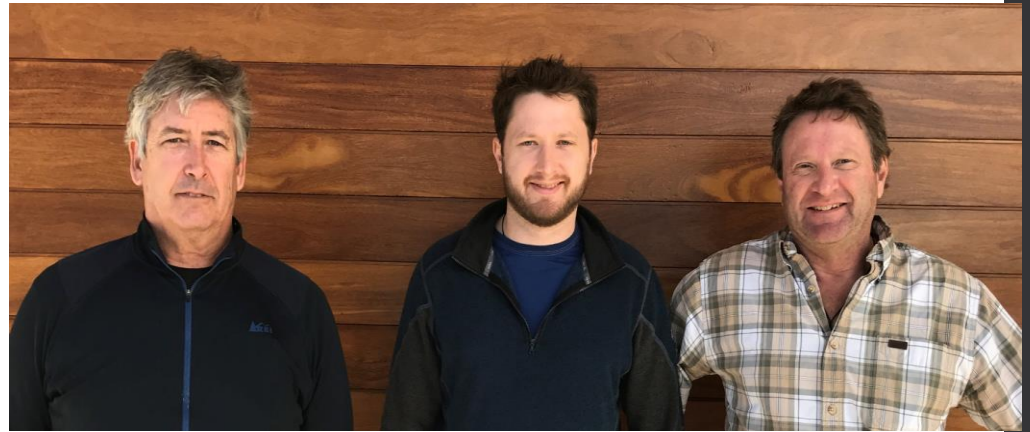
Single Step Implementation Using Marker Effects Modes

Stayability and Sustained Cow Fertility

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Our team



- Bruce Golden, PhD (Colorado State - Animal Breeding & Genetics)
 - Co-founder - CEO and President
 - Bruce is the principal developer and writer of the command-line tools (in C)
- Dorian Garrick, PhD (Cornell University - Animal Breeding & Genetics)
 - Co-founder - CSO and CFO
 - Dorian focuses on alternative efficient algorithms and approaches
- Daniel Garrick, PhD (Iowa State - Aerospace Engineering)
 - Junior Partner, Software and Product Support Engineer since January 2017
 - Daniel brings expertise in Computational Fluid Dynamics (CFD) including non-linear and linear computing strategies, numerical methods, data processing and visualization



Topics

.Using Genomic Data

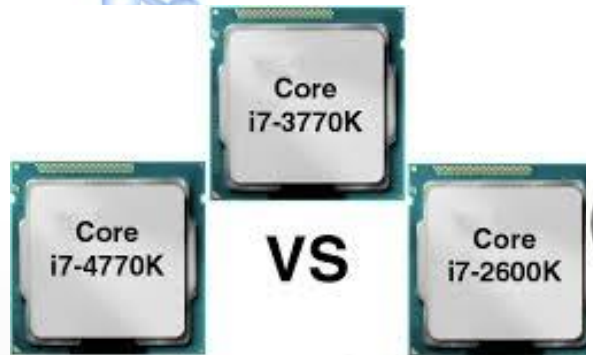
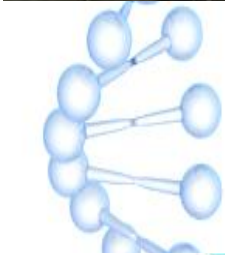
.Marker Effects Model

.Models Re-imagined

.Effects of the New Accuracy Calculation

.New and Improved Stayability/Sustained
Cow Fertility

Using technology built for computer gaming

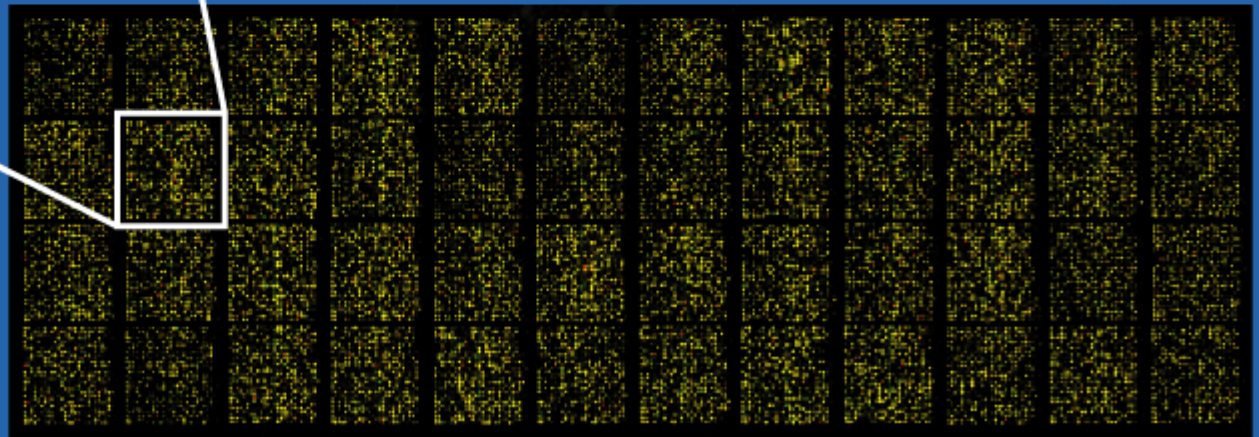
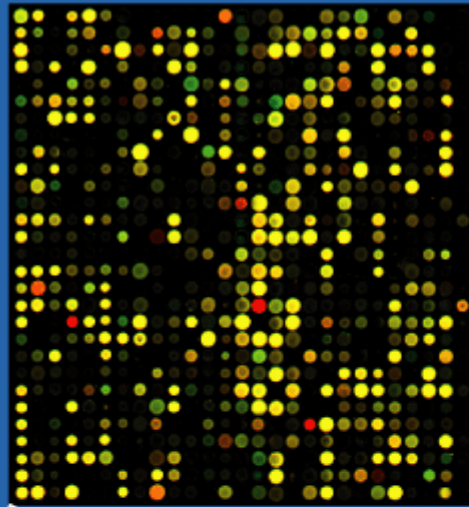
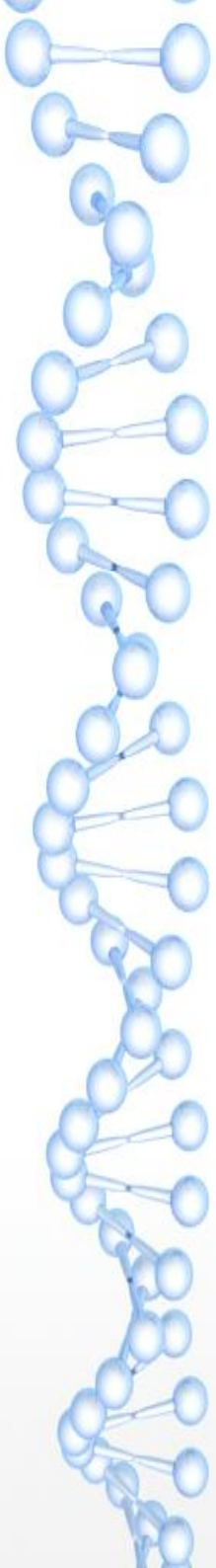


Gaming Performance



Genomic Evaluation

Improves prediction accuracy by predicting SNP marker effects



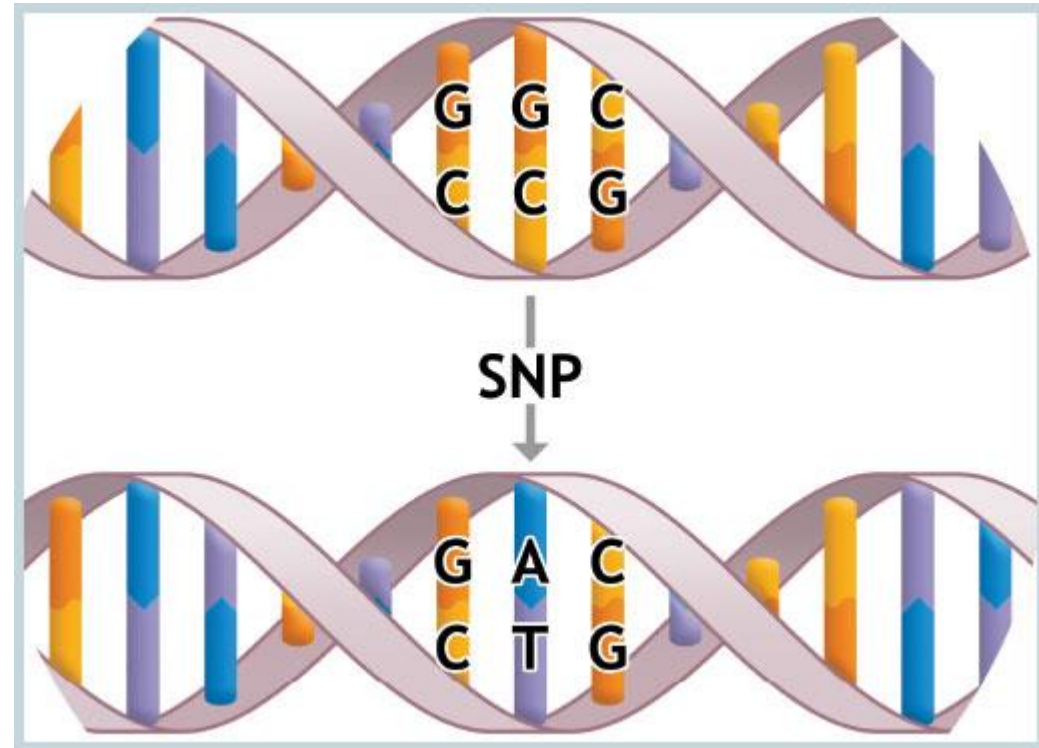
Genomic Data

3 Billion Base Pairs

~22,000 Genes

~98% Non-coding

~6,000,000 SNPs





Single Step Super Hybrid Marker Effects Model

.Both Genotyped and Non-genotyped
Animals

– IGS

- 12,699,644 animals (082118)
- 139,757 genotyped (082118)

– AHA

- 2,317,144 animals (100118)
- 46,847 genotyped (100118)

.Multiple Traits

.Multiple Components

Super Hybrid Marker Effects Model

$$\begin{bmatrix} y_n \\ y_g \end{bmatrix} = \begin{bmatrix} X_n \\ X_g \end{bmatrix} \beta + Z u_{1-c} + \begin{bmatrix} Z_n^* & 0 \\ 0 & Z_g^* M_g \end{bmatrix} \begin{bmatrix} u_c \\ \alpha \end{bmatrix} + e$$

$$\begin{bmatrix} X'X & X'Z & X'R^{-1}Z_n & Z'R^{-1}Z_gM_g \\ S & Z'Z + A^{-1}\frac{\sigma_e^2}{(c-1)\sigma_g^2} & Z'Z_n & Z'Z_gM_g \\ S & S & Z'_nZ_n + A^{nn}\frac{\sigma_e^2}{c\sigma_g^2} & A^{ng}M_g\frac{\sigma_e^2}{c\sigma_g^2} \\ S & S & S & Q \end{bmatrix} \begin{bmatrix} \hat{\beta} \\ \hat{u}_{1-c} \\ \hat{u}_n \\ \hat{\alpha} \end{bmatrix} = \begin{bmatrix} X'y \\ Z'y \\ Z'_ny \\ M'_gZ'_gy \end{bmatrix}$$

$$Q = M'_gZ'_gZ_gM_g + I\frac{\sigma_e^2}{\sigma_\alpha^2} + M'_nA^{nn}M_n\frac{\sigma_e^2}{c\sigma_g^2}$$

$$-M'_gA^{gn}M_n = M'_nA^{nn}M_n$$


$$EBV =$$

Genomic Effect + Extra Polygenic Effect

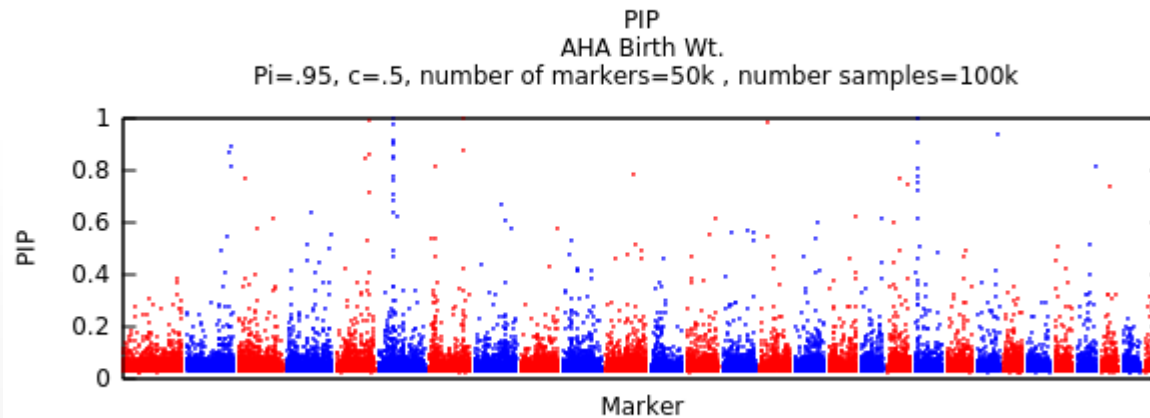
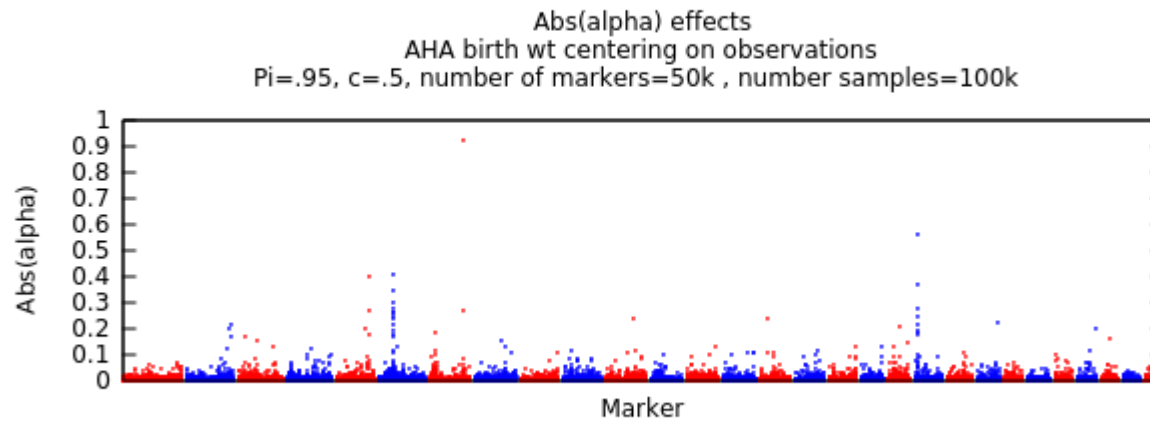
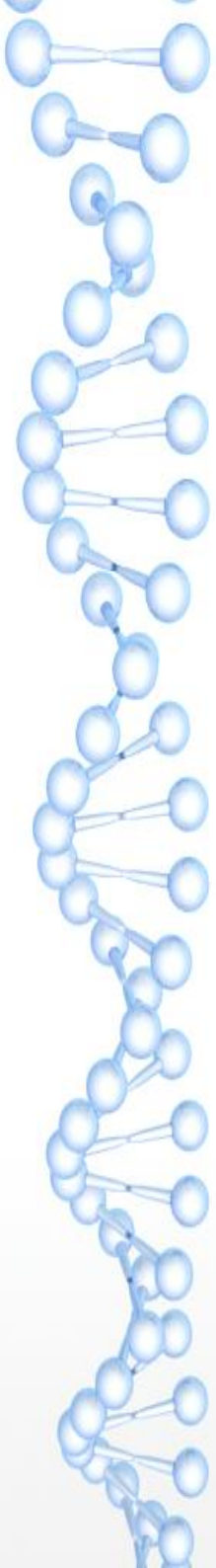
$$= M\alpha + EPE_g$$

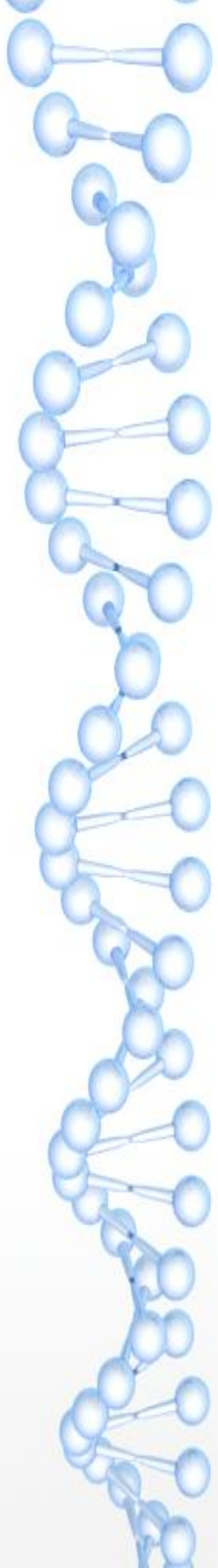
and

$$= u_n + EPE_n$$

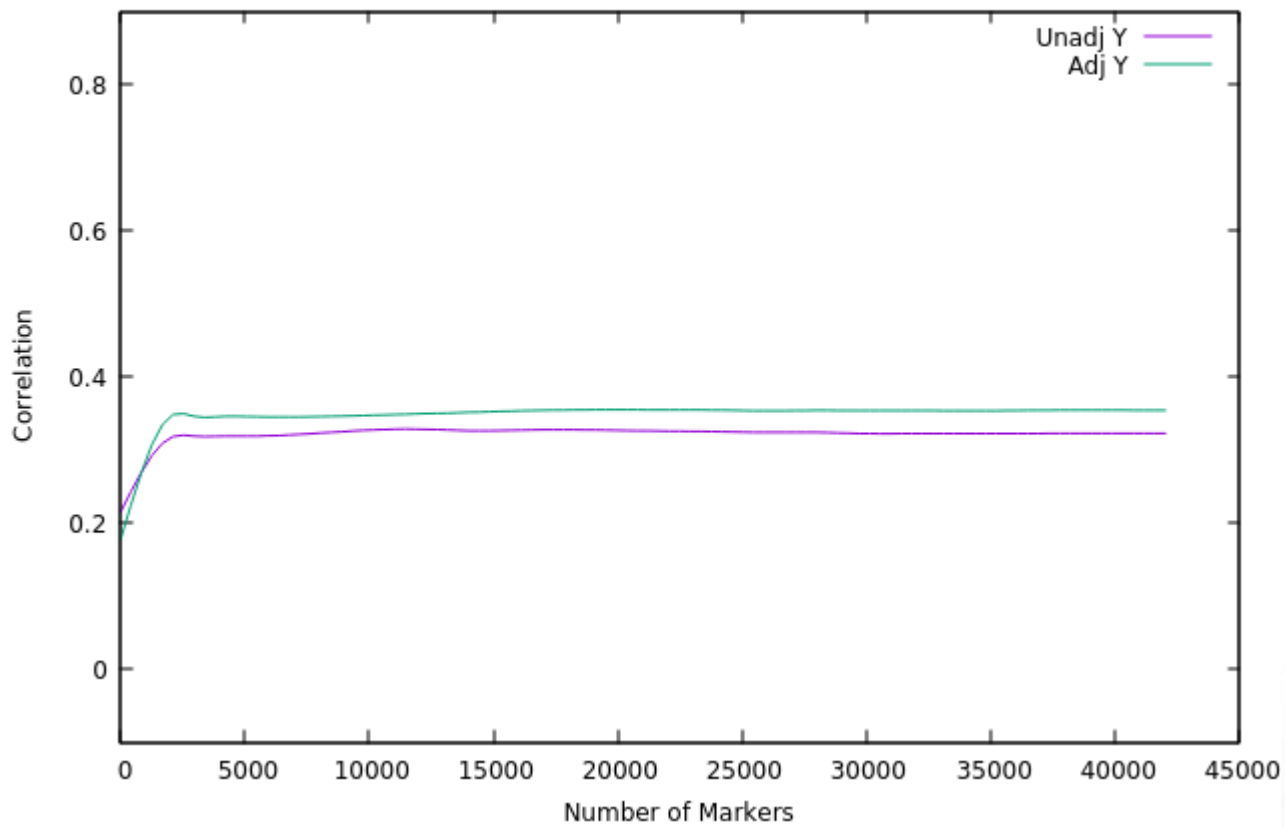
$$EPD = EBV / 2$$

Marker Subsets



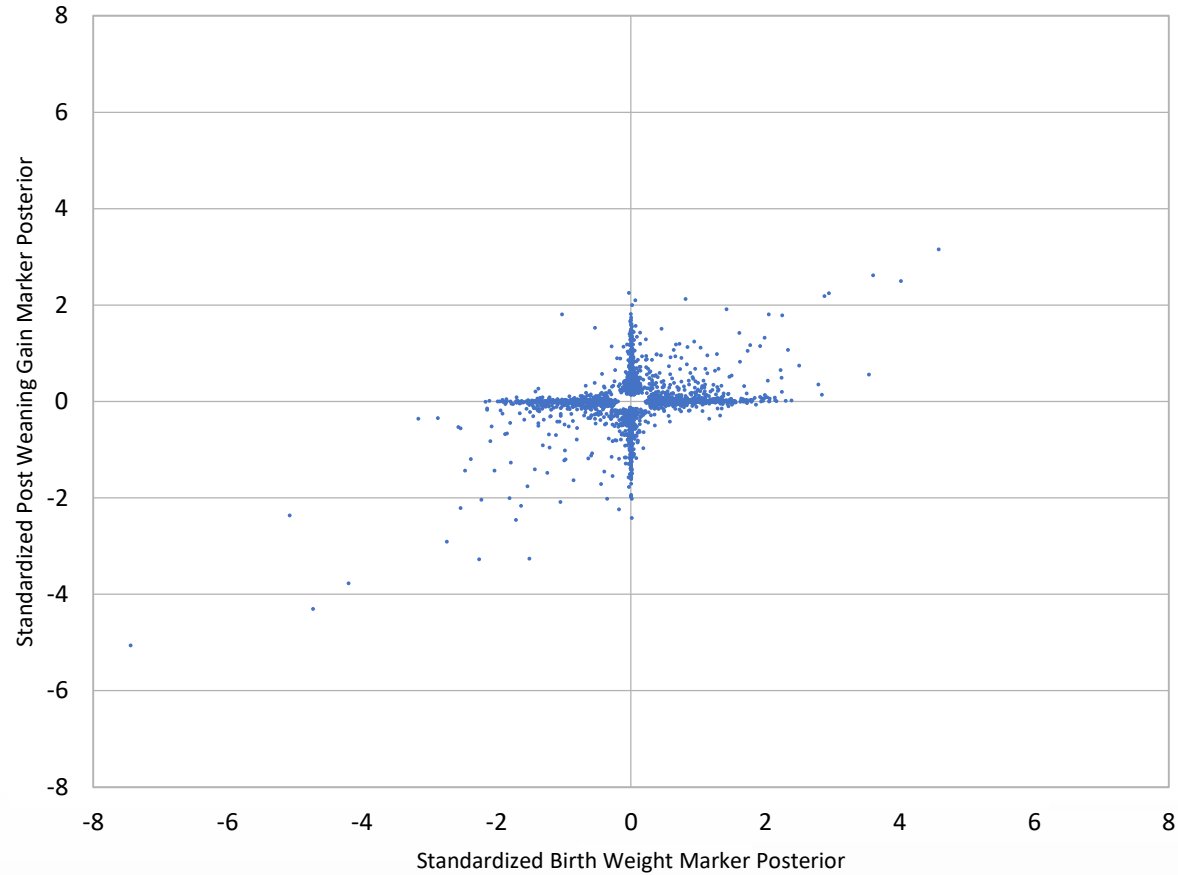


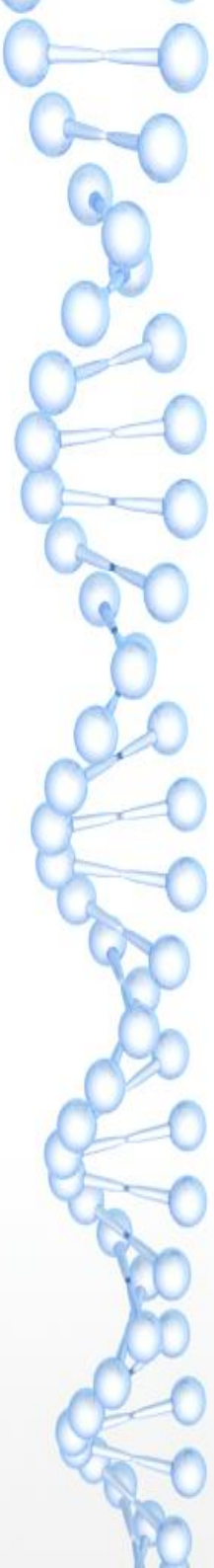
Correlation of Malpha with Test Data Phenotypes by adding markers based on PIP
AHA Birth Wt.
 $P_i = .95$, $c = .5$, number of markers = 50k, number samples = 100k



Marker Selection

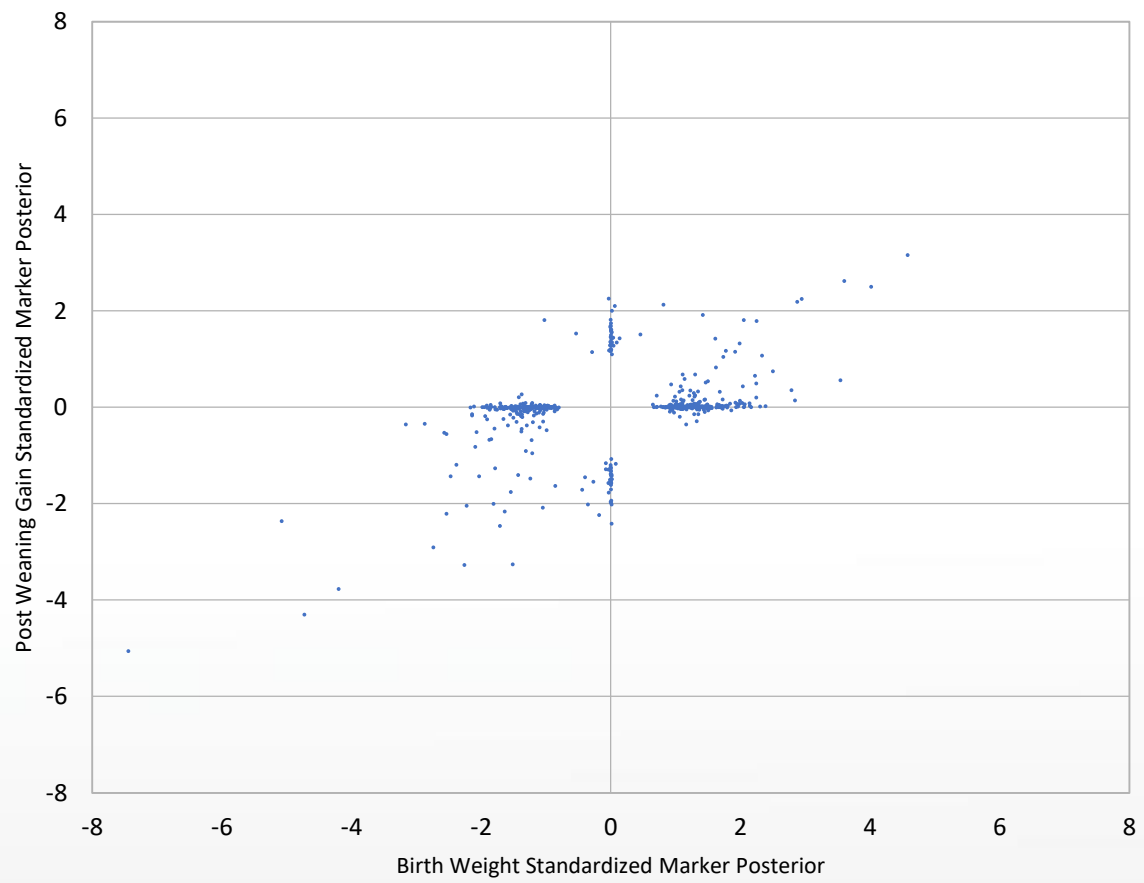
5% of markers entered ($1-\pi$)





Marker Selection

Entered at least 30k times in 40k samples





Progeny Equivalents

Trait	Progeny	Trait	Progeny
CE	15	Stay	25
MCE	3	CW	6
BW	21	MRB	8
WW	22	REA	5
YW	24	FAT	6
Milk	18	DOC	19



Correlations of Bolt and Cornell EPD with progeny performance

Trait	N Sires	BOLT	Cornell
Birth Wt	29,154	0.34	0.27
Weaning Wt	21,571	0.29	0.19
Yearling Wt	10,849	0.26	0.20



Other Effects

- .Breed-Year (cluster) additive genetic groups
- .Heterosis: two-breed type out-crossing equations
- .Contemporary group
- .J equation – genetic merit of genotyped animals
- .K equation – centering across all loci



IGS Traits Produced

.Birth wt.

Carcass wt.

.Weaning wt.

REA

.Yearling wt.

Marbling score

.Milk

Fat thickness

.Total maternal

[Yield grade]

.Calving ease

Stayability

.Calving ease total
maternal

Docility



IGS Traits Under Development

- .Heifer pregnancy
- .Dry matter intake
- .Days/age to finish



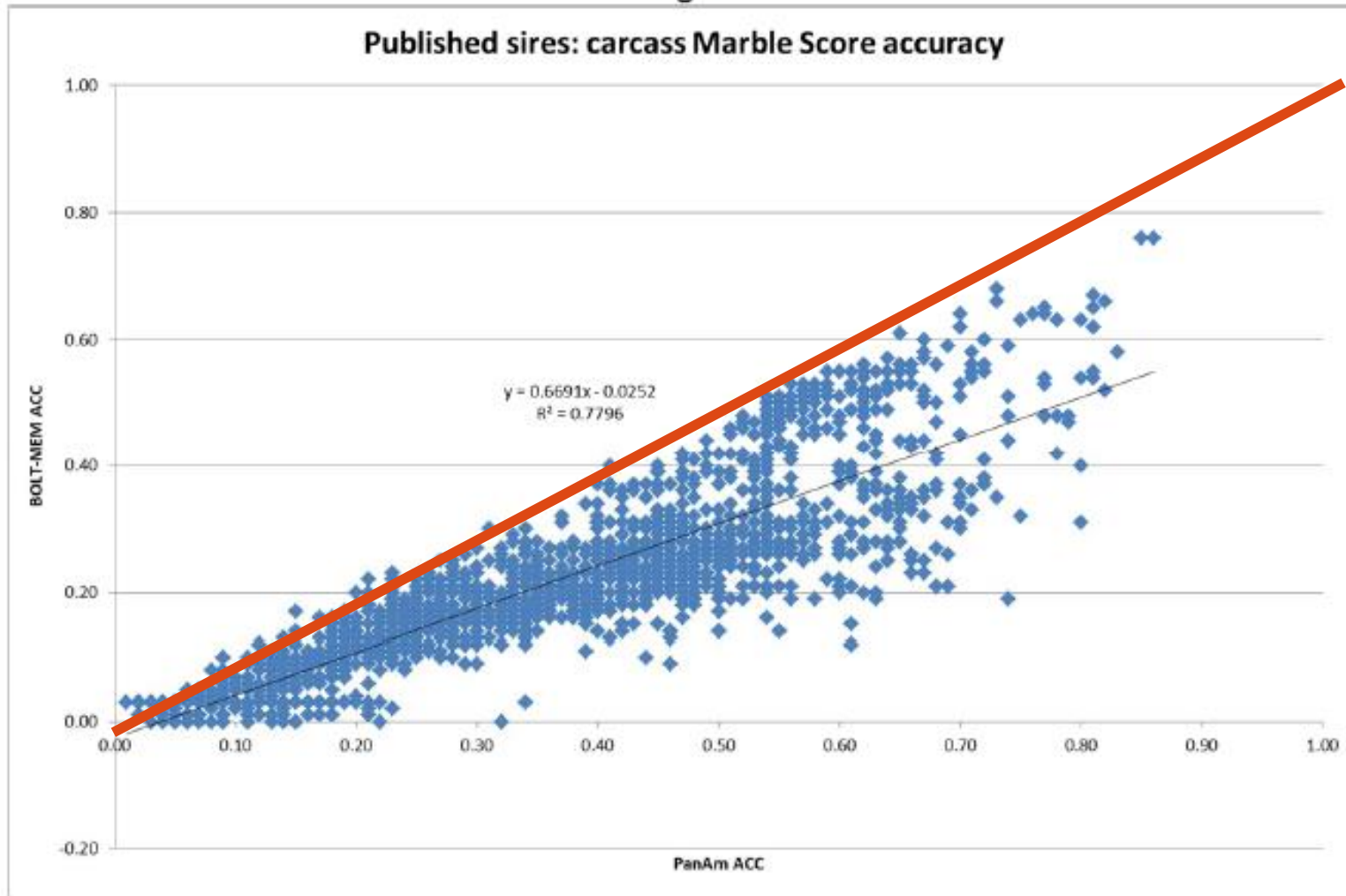
New Accuracy Calculation

- .No “Approximation Bias”
- .“Direct” method to estimate Prediction Error Variance (PEV)

$$BIFAccuracy = \frac{1}{\sqrt{(1+f) * GeneticVariance}}$$

What is the Effect on Accuracy Values?

Fig 6





Completely Reimagined Models for All Traits

.Stayability

.Carcass

.Calving Ease



Predictions of Cow Productivity

.Days to Calving

.Calving Interval

.Cow Longevity – proportional hazard model

.Stayability - MAP

.Snelling, et al., 1995

.Brigham, et al., 2007

.Random Regression

.Jamrozik, et al., 2014



New Stayability Model

- ERT with the most impact in maternal selection index
- .Relatively small changes can make a big difference
- .More calves to sell
- .Fewer replacement females – even more calves to sell
- .Heavier weaning weights of sale calves from older cows
- .Less calving difficulty



Random Regression Stayability

.The random (e.g., genetic) effects are described as a curve (polynomial) on age of cow at record

.Observations:

-0 – Cow did not have calf at a given age

-1 cow had a calf at a given age

-Missing – unknown if the cow had a calf at a given age



Advantages of RR Method

- .Uses observations in a more sensible way
- Simultaneous solution to all ages
- Censoring from culling is “missing” value
- .Handles missing values in a more sensible way
 - e.g., donor cow
- .Easy to implement an animal model
- .Easy to implement genomic information
- Marker Effects Model
- .Faster to obtain answers
- PCG solver



Our Marker Effects Stayability Model

.Year of birth

.Age at first calving

.Random contemporary group (intercept and slope)

.Random permanent environment due to the dam (intercept and slope)

.Genetic marker random effects (intercept and slope)

-Genotyped

-Non-genotyped