



AGIL UPDATE 2023

Milking Speed, Factors Project, & a lot of other interesting stuff

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100 years ago Tracy was set to become dairy central

Sam Matthews Feb 25, 2023 0

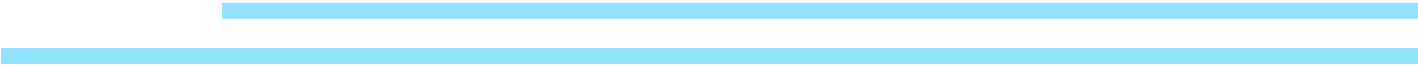
1923 - 1947

The General Milk Co.

Capacity of 100,000 lbs of milk daily

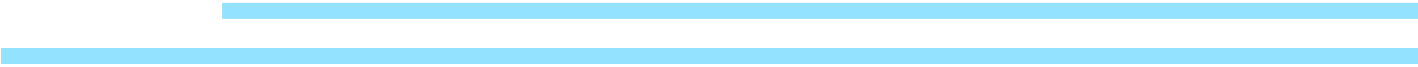


TOPICS FOR DISCUSSION

- Staffing Changes
 - Embryo Transfer
 - Milking Speed
 - A New Evaluation Model
 - Gene Tests
 - Lactation Yield Adjustment Factors
- 
- Two horizontal blue lines of different lengths, with the longer one on top, positioned at the bottom right of the slide.



“It’s not rocket science...”

Two horizontal light blue lines of different lengths are positioned at the bottom right of the slide, with the longer line in front of the shorter one.

Courtesy of
<https://xkcd.com/1133/>

(PLANS COURTESY NASA-MFC 101.04574 VIA UP-SHIP.COM)

US SPACE TEAM'S UP GOER FIVE

THE ONLY FLYING SPACE CAR THAT'S
TAKEN ANYONE TO ANOTHER WORLD

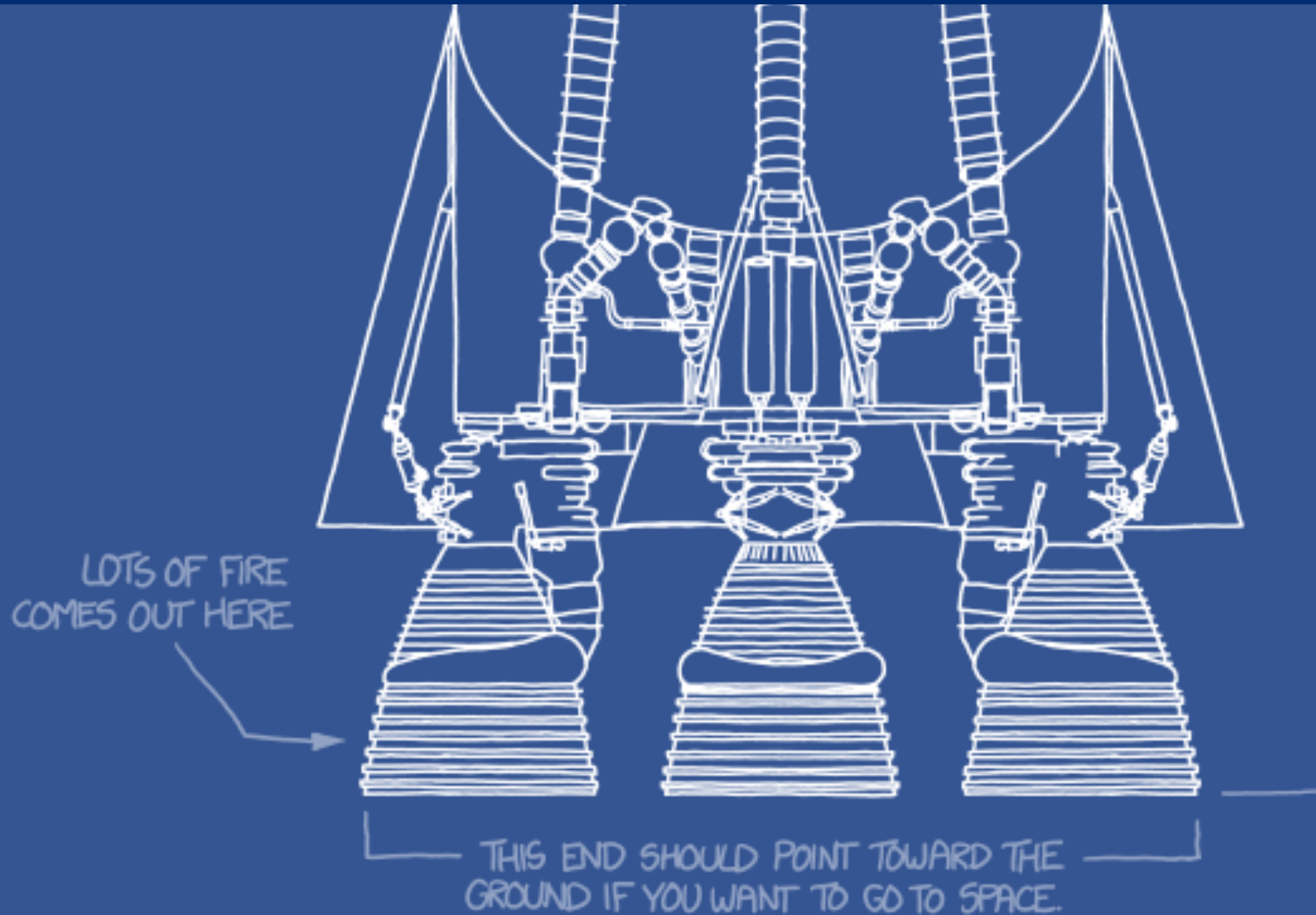
(EXPLAINED USING ONLY THE TEN HUNDRED
WORDS PEOPLE USE THE MOST OFTEN)

THING TO HELP PEOPLE ESCAPE REALLY FAST
IF THERE'S A PROBLEM AND EVERYTHING IS ON
FIRE SO THEY DECIDE NOT TO GO TO SPACE

STUFF TO BURN TO MAKE THE BOX WITH
THE PEOPLE IN IT ESCAPE REALLY FAST



THING TO CONTROL WHICH DIRECTION
THE ESCAPING PEOPLE GO





WELCOME DR. JOHN ODHIAMBO



JOHN ODHIAMBO

Animal Scientist
Animal Genomics and Improvement
Laboratory, Beltsville, Maryland

Est. start April 2023

PhD 2008 Reproductive Physiology, West Virginia University

-Conception Rate
-Transition Cow Health

-Multigenerational Effects
-Epigenetics



EMBRYO TRANSFER:

Popularity, Reporting, Implications for Fertility Evaluations,
and Data Needs

Asha Miles, Jana Hutchison, and Paul VanRaden

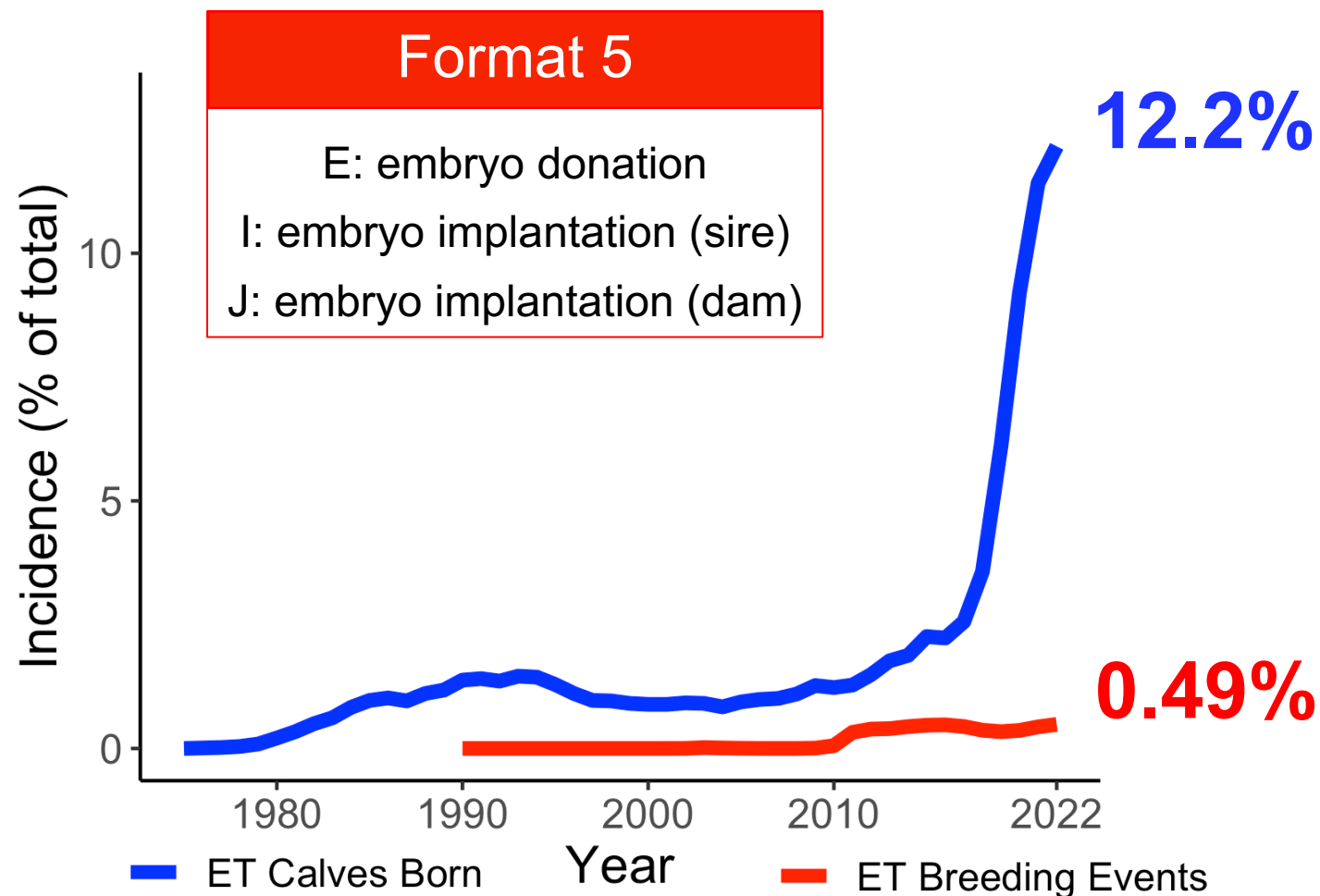
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ET CONTINUES TO RISE



ET reporting error rates:

- 1% of recipients correctly reported as ET
- 2% incorrectly reported as AI
- 97% no breeding event reported at all

HANDLING UNREPORTED ET



With embryo transfer, conception is not actually occurring



The US excludes all known ET donors & recipients in evaluations



Unreported ET may bias fertility evaluations in the population



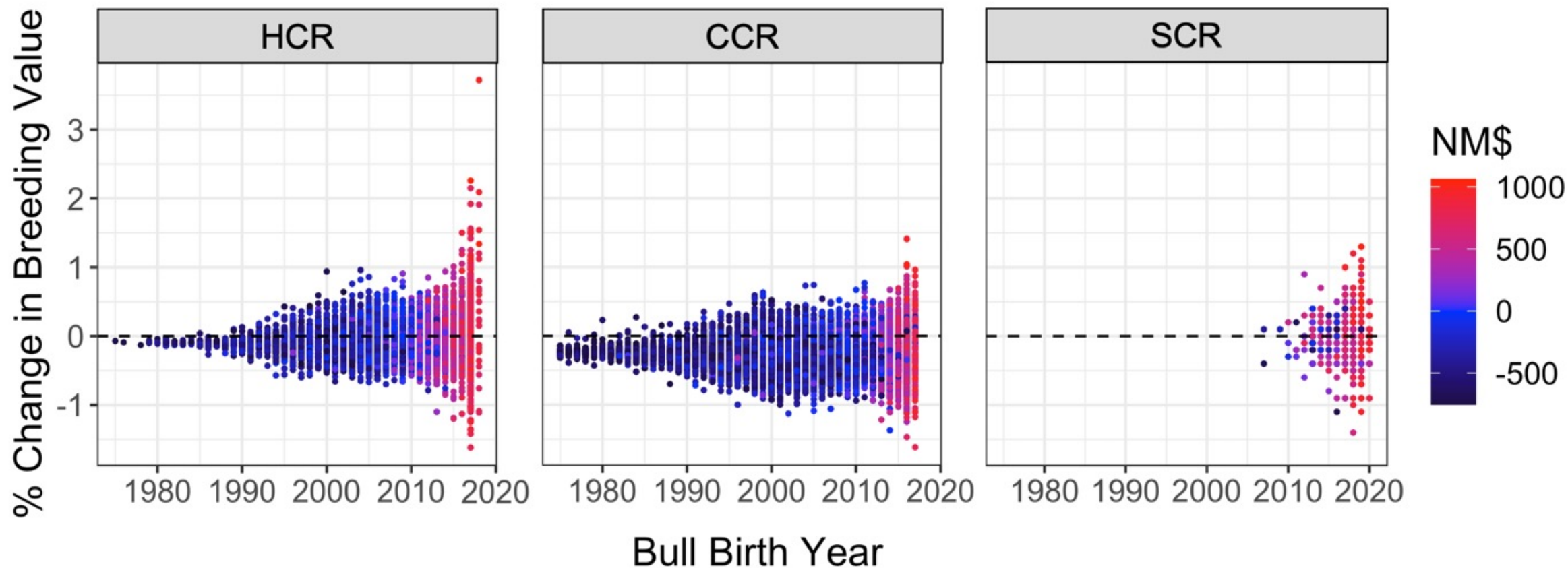
Censor herdyears reporting

>10 % calves born by ET, but

< 1/2 the expected number of ET breeding events

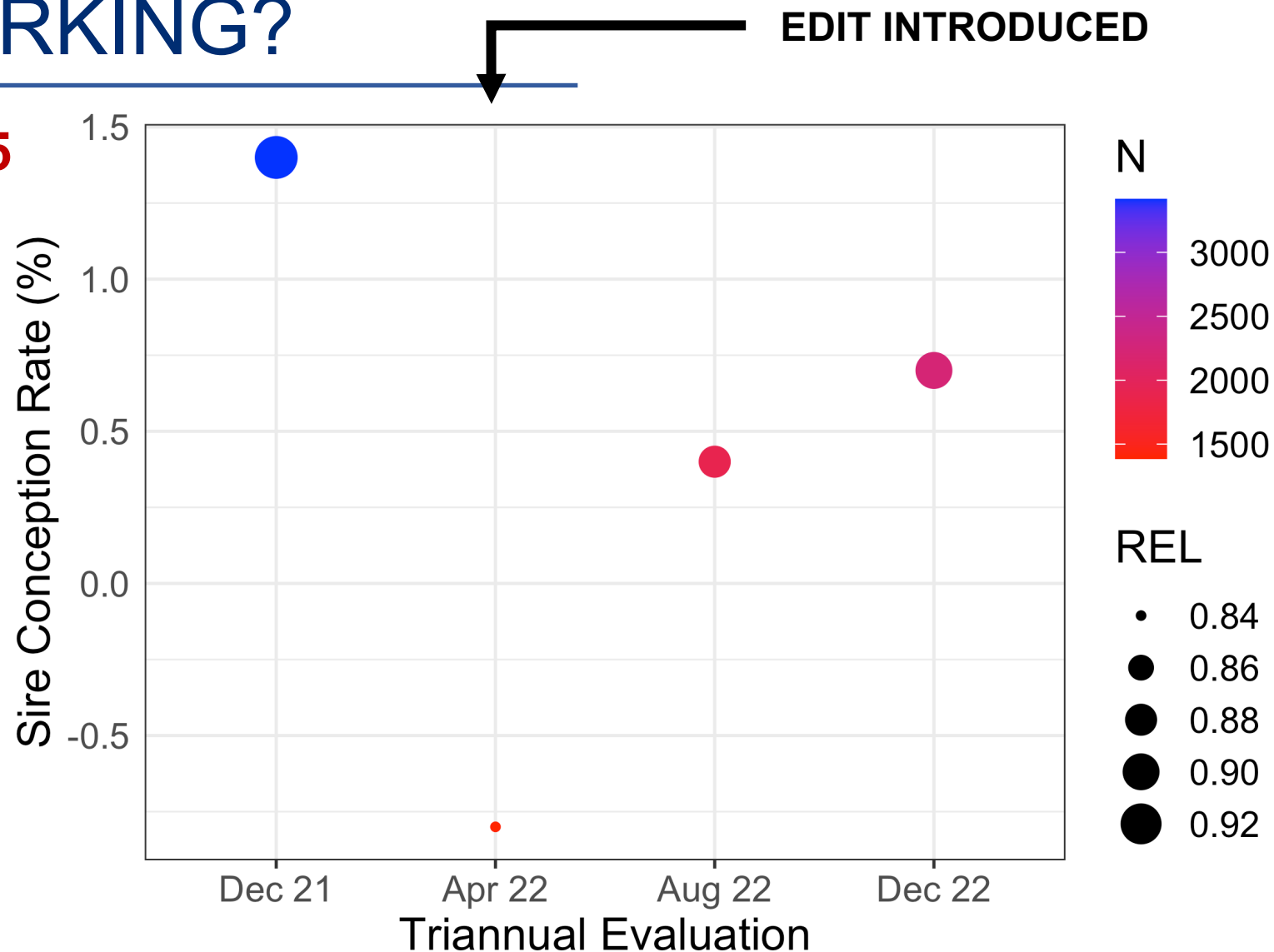
ELITE YOUNG BULLS MOST AFFECTED

Applied to Conception Rate



ARE THE EDITS WORKING?

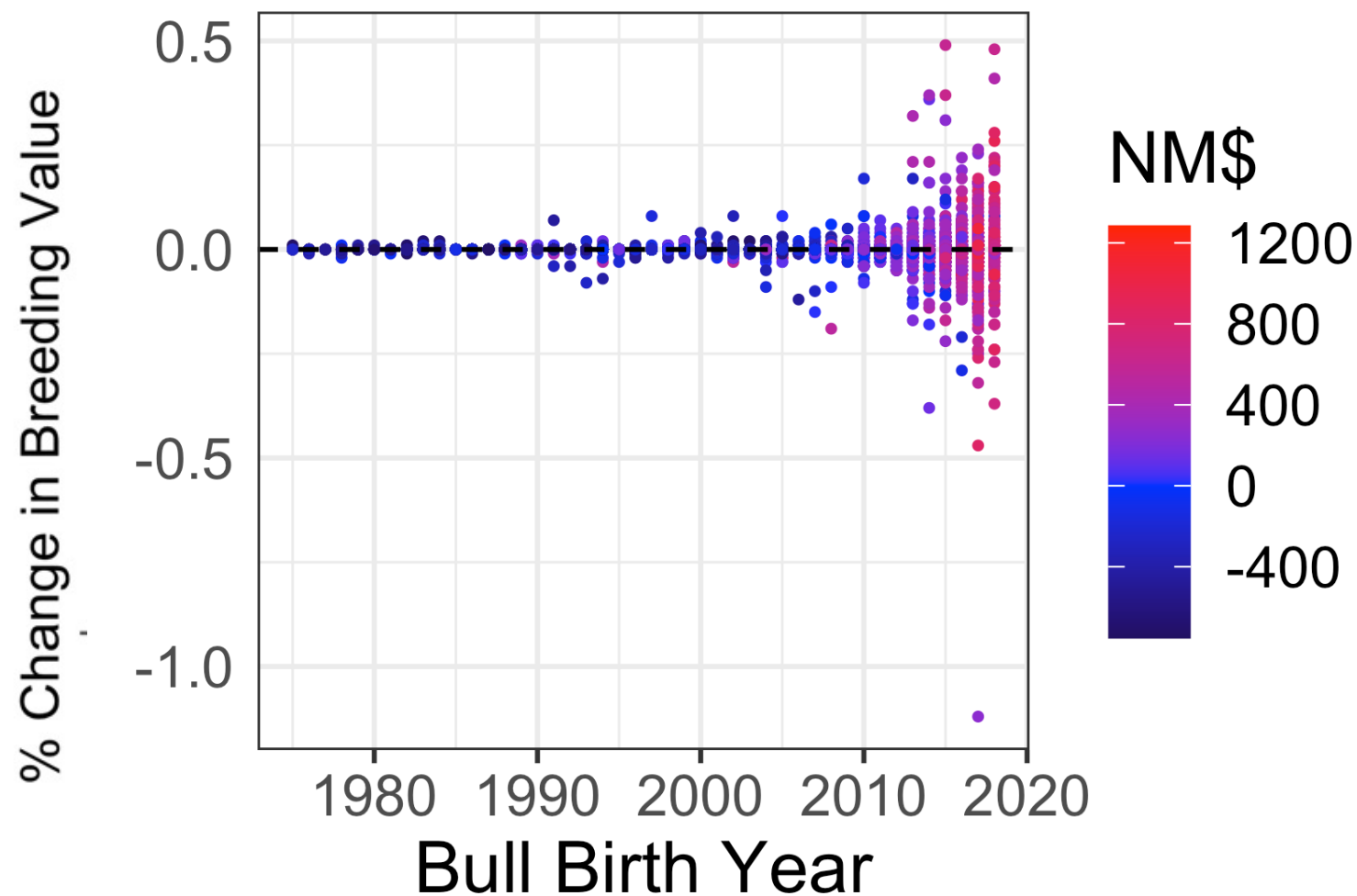
Example: HO840003146121925

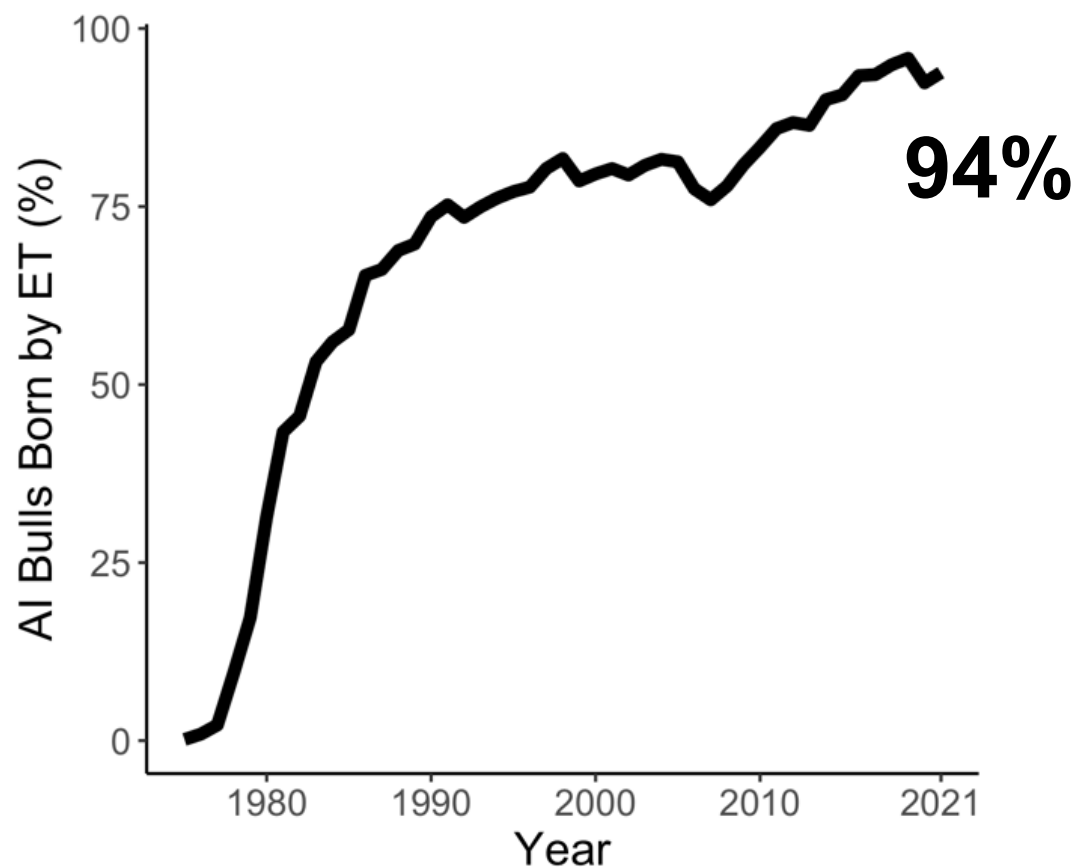


RUN	PTA	REL	N
DEC 21	1.4	0.93	3416
APR 22	-0.8	0.84	1386
AUG 22	0.4	0.88	1886
DEC 22	0.7	0.90	2226

ELITE YOUNG BULLS MOST AFFECTED

Applied to Gestation Length





ET for cows may continue to increase, as it has for AI bulls

Key Messages

- Effects of edits are overall small, except for elite new bulls popular for ET usage
- Bulls with biggest initial changes appear to stabilize over time as more daughter records are added
- Acquiring high quality ET records will be essential to providing accurate fertility evaluations in the future
- Beginning to apply this edit to DPR

MILKING SPEED:

Summary of Knowledge, Key Questions, & Proposed Research

Asha Miles, Robert Fourdraine, Steven Sievert, Kristen Parker Gaddis, Jeffrey Bewley, Sophie Eaglen, Jay Weiker, Jana Hutchison, and Joao Dürr



Agricultural Research Service
U.S. DEPARTMENT OF AGRICULTURE



EVALUATIONS FOR MILKING SPEED

- Interbull-participating countries (N = 14) include milking speed in their “workability” evaluations
 - Australia, Canada, Denmark/Sweden/Finland, France, Germany/Austria/Luxembourg, Great Britain, Italy, Japan, the Netherlands, New Zealand, Norway, Poland, Slovenia, and Switzerland
- Nearly all phenotypes collected during first parity only and sometimes from a single classification
- If milk flow rates were available, classification data were discarded

REGARDING QUANTITATIVE MS

- Heritabilities range from 0.02 – 0.42 depending on the trait definition
- Repeatabilities range from 0.40 – 0.54
- Conflicting evidence of variation in MS across lactations
- Favorable correlations between MS and milk yield
- Unclear relationship between udder health and MS

PROPOSED RESEARCH



- Obj. 1:** Assemble a high-resolution dataset pertinent to MS representing different dairy breeds, equipment manufacturers, parlor types, and milking management strategies
- Obj. 2:** Characterize MS for herds grouped by equipment manufacturer and parlor type and assess the impact of additional system effects on the phenotype
- Obj. 3:** Characterize any biological effects that impact MS, especially concerning udder health
- Obj. 4:** Standardize MS trait definition and estimate heritability to determine its suitability for selection

OBJ 1: ASSEMBLE DATA

Demographics

~300 herds
~220,000 cows

31 States
6+ Breeds
11 OEMs

DeLaval	80
GEA	75
Lely	47
Boumatic	46
AfiMilk	45
SCR	13
DairyMaster	10
AIC Waikato	5
AMS Galaxy	3
Jantec	2
Universal	2



OBJ 1: ASSEMBLE DATA

Data Cleaning

Summary stats on data											
		N	Minimum	Q1	Median	Mean	Q3	Maximum	StDev		
Milking Duration										0 or missing	greater than 15
	M1time	38877488	0	3.6	4.4	5.425	5.4	1440	30.1	3254587	85677
	M2time	38611378	0	3.5	4.3	5.772	5.2	1440	39.791	3493311	89253
	M3time	29804057	-1435.5	3.5	4.2	6.17	5.1	-1435.5	46.83	12223012	61510

OBJ 1: ASSEMBLE DATA

Data Cleaning

	AY		BS		GU		HO		JE		MS	
	2X	3X	2X	3X	2X	3X	2X	3X	2X	3X	2X	3X
Initial Records	28,412	1,632	67,850	93,193	20,233	495	6,154,246	21,772,400	633,289	599,840	2,119	5,334
After 1/1/2022	28,412	1,597	62,282	92,829	17,604	495	5,852,454	21,224,965	527,501	521,253	2,119	5,334
0 < duration < 15	25,374	994	45,509	57,621	12,130	398	5,138,997	15,803,428	475,668	392,451	1,354	3,661
0 < milk < 60	25,223	993	45,177	57,349	12,126	398	4,778,714	15,665,401	474,852	392,130	1,348	3,659
1 < MSPD < 15	24,646	956	39,324	56,806	10,972	389	4,611,960	15,422,775	463,138	378,765	1,333	3,613
>10 obs per cow	24,621	953	39,193	56,603	10,939	389	4,606,970	15,407,922	461,910	377,735	1,333	3,585
% reduction in data	13.3%	41.6%	42.2%	39.3%	45.9%	21.4%	25.1%	29.2%	27.1%	37.0%	37.1%	32.8%

OBJ 2: SYSTEM EFFECTS

- What is the impact (if any) of:
 - OEM
 - Parlor type
 - Age of equipment
 - Pulsation ratios
 - Milking interval/frequency
 - Meter calibration protocols
 - Milker training protocols
 - Incomplete udder evacuation
 - Fault codes

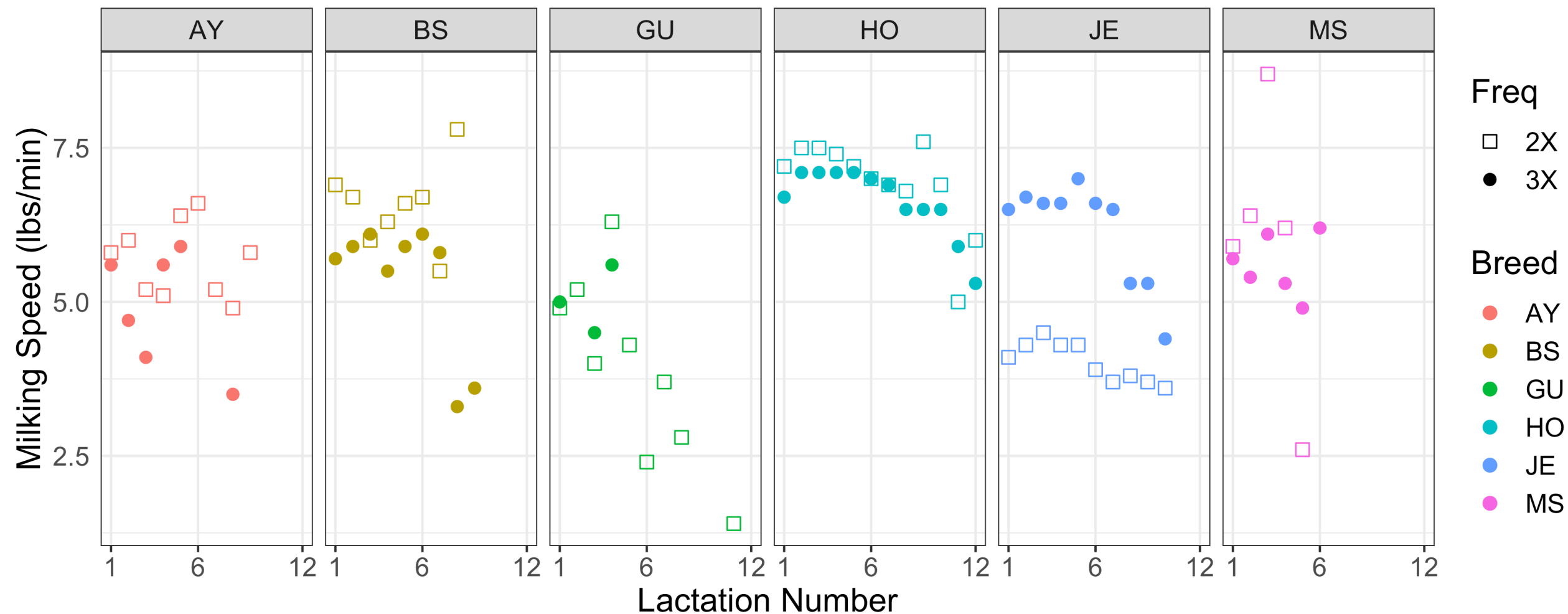
OBJ 3: BIOLOGICAL EFFECTS

- What is the impact (if any) of:
 - Breed
 - Parity
 - Age
 - Stage of lactation
 - Somatic Cell Score
 - Clinical Mastitis
 - Milk components (via Fat & Protein 305-MEs)

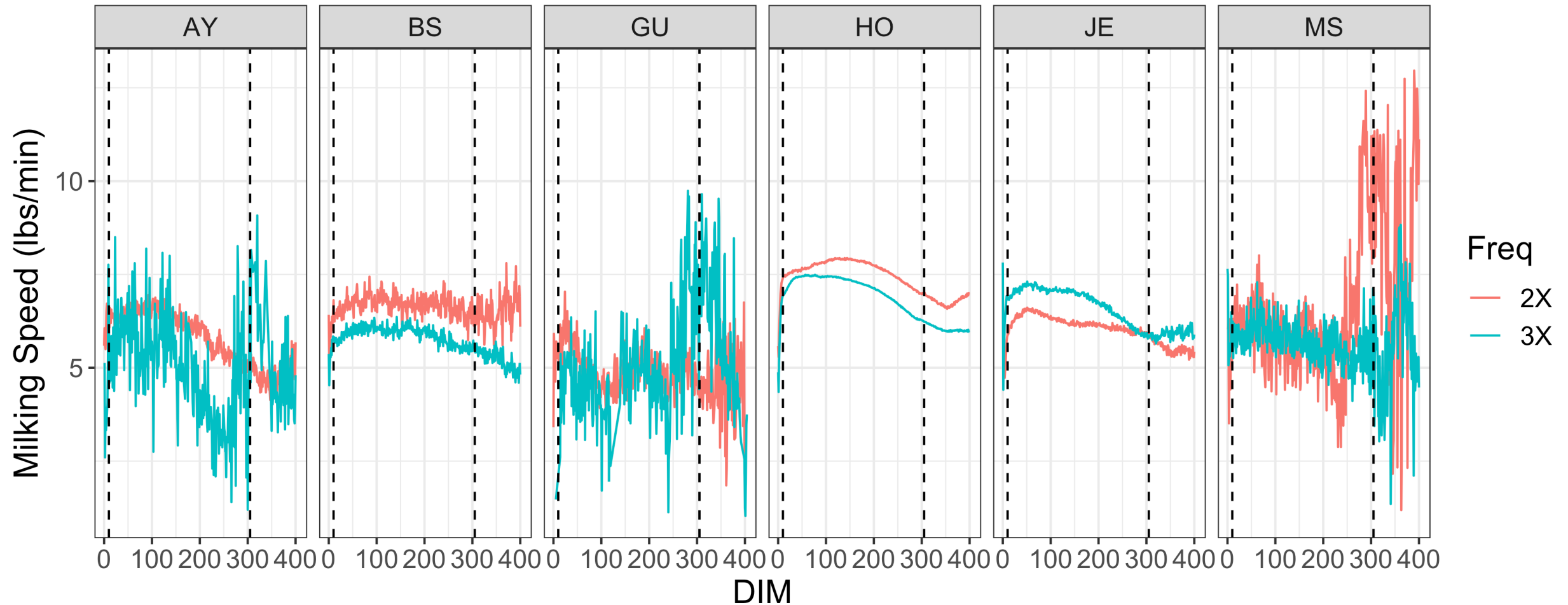
OBJ 4: STANDARDIZE

- Can MS measures from different systems be considered the same trait?
- Do they require pre-adjustments to harmonize data?
- Is a single measurement enough to accurately characterize MS?
- Does a cow's MS change over her lifetime?
- What is the heritability of this standardized MS?

BREED, FREQUENCY, & PARITY

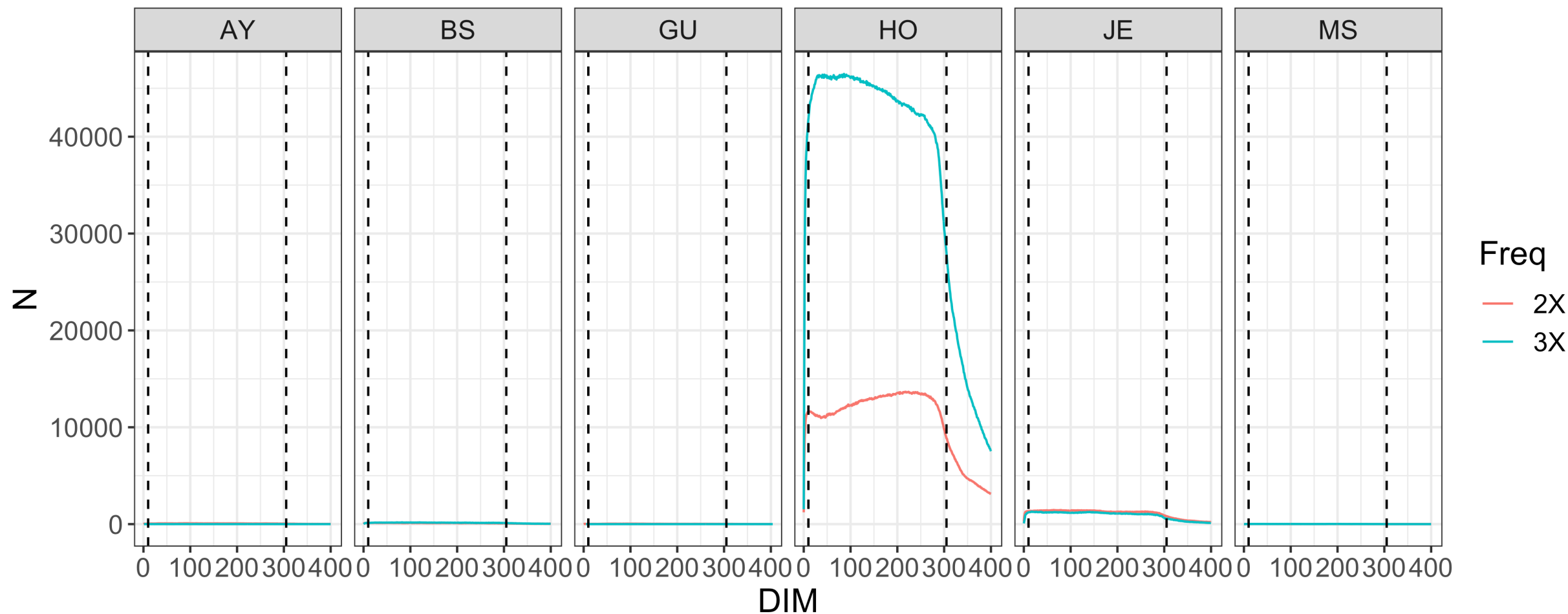


BREED, FREQUENCY, & DIM

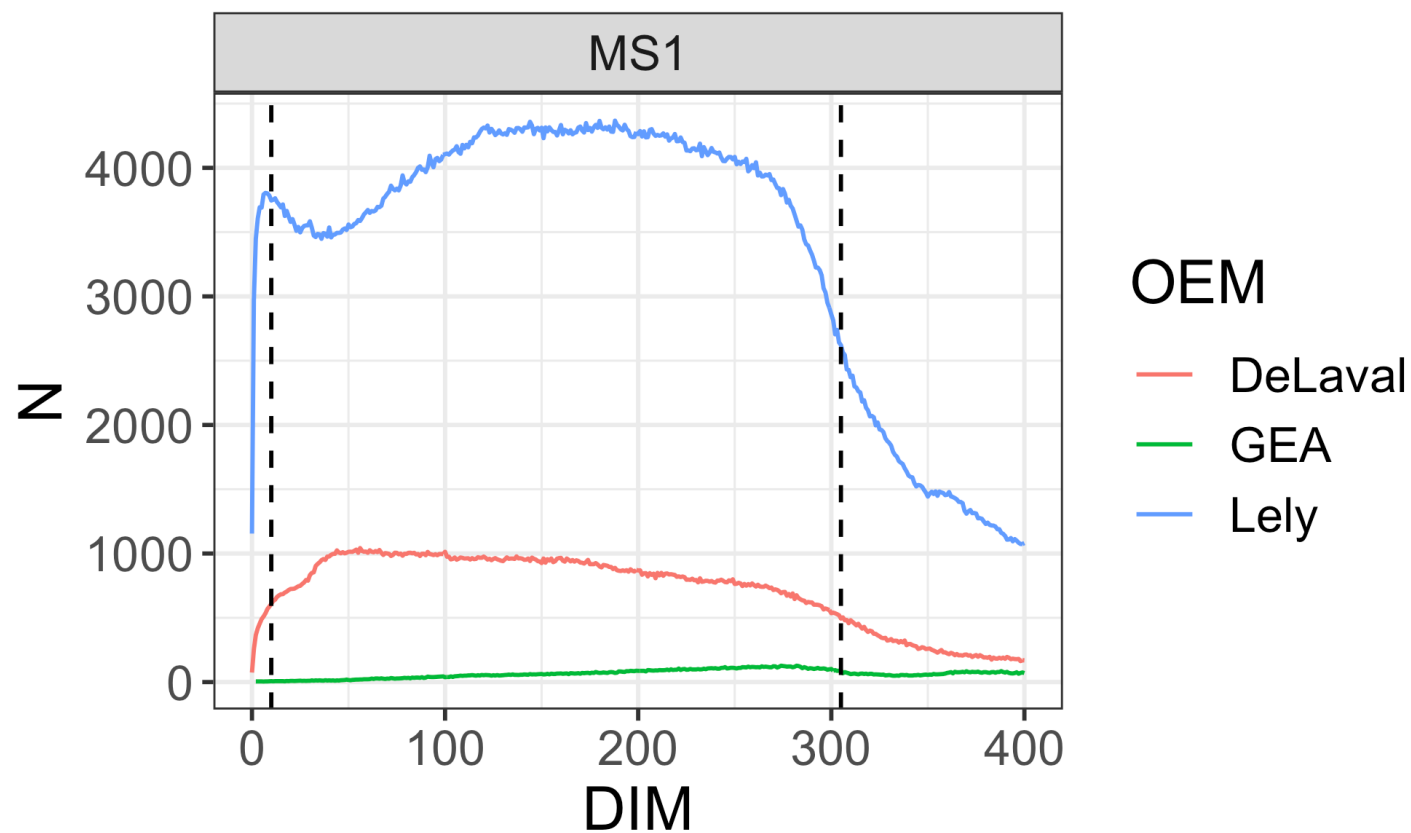
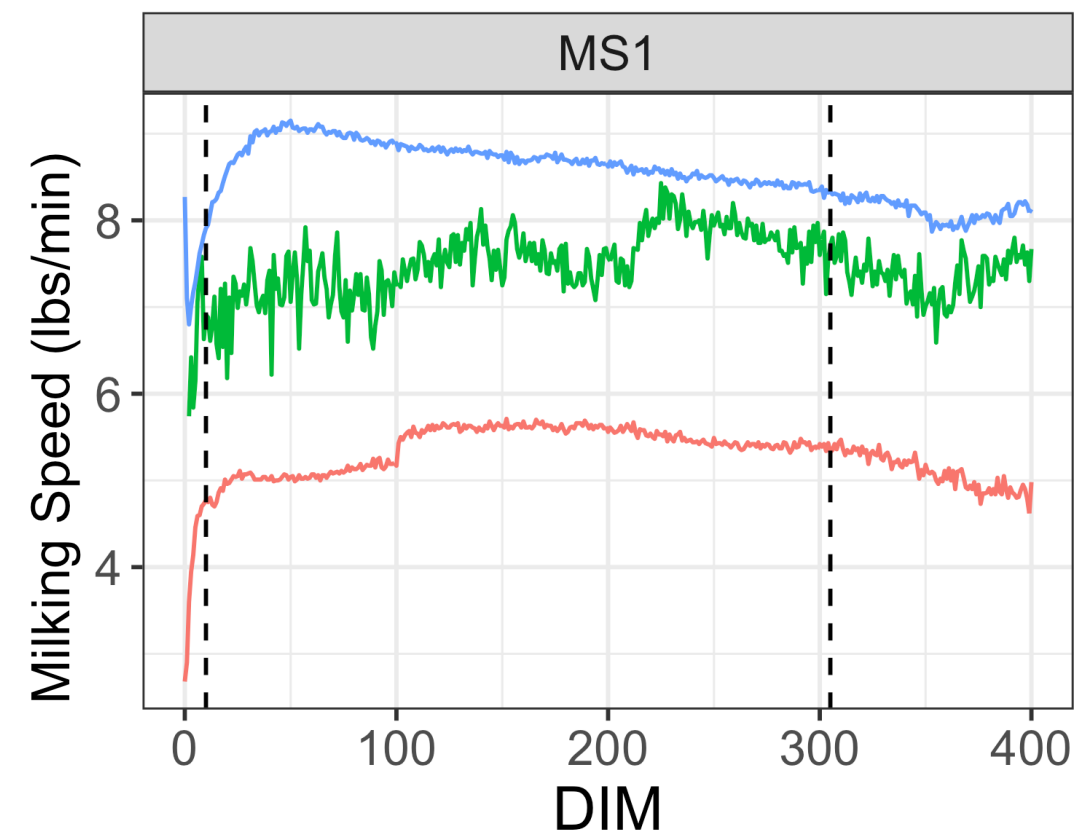


BREED, FREQUENCY, & DIM

Sparsity is a challenge



AMS & OEM, HOLSTEIN ONLY





Surveys indicate high producer enthusiasm for MS evaluations

Key Messages

- MS is actively used by both conventional and AMS herds
- MS evaluations could be of significant economic value
- We need to first understand system & biological effects on MS to standardize a phenotype definition and determine its suitability for selection

HYBRID MODEL

A new method of genomic prediction that prioritizes influential SNPs based on population differentiation



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HIGH COMPUTATIONAL COSTS



Over 7 million dairy animals are now genotyped



The number of SNPs potentially contributing to phenotypes has dramatically increased



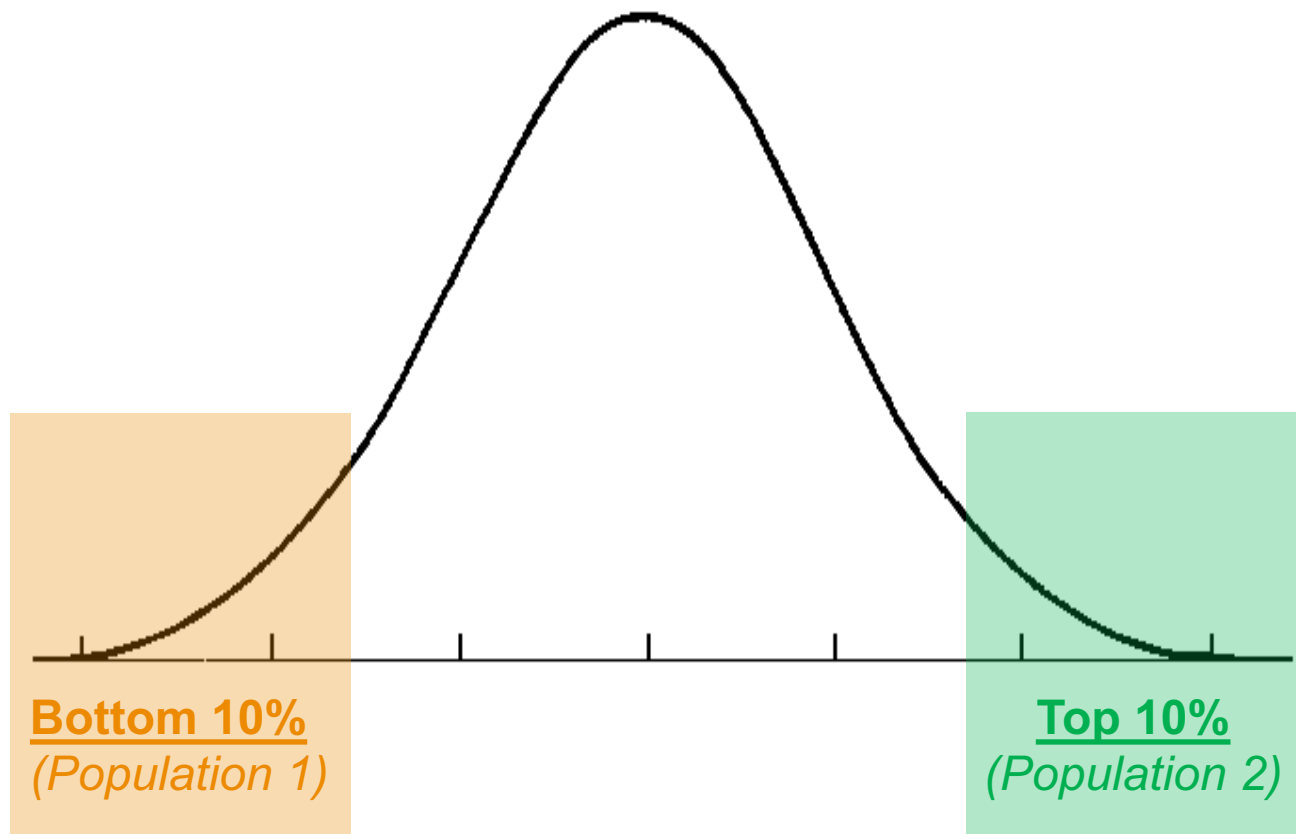
This higher density of genomic data has not automatically increased the accuracy of genomic prediction; but it has increased the computational costs of calculating evaluations



Most SNPs have very small or no effects

PRIORITIZING INFLUENTIAL SNPs

F_{ST} Measures Genetic Variance Between Populations



F_{ST} Interpretation

$$F_{ST} = \frac{H_T - H_S}{H_T}$$

0: No Differentiation

Alleles associated with SNP appear in both populations with equal frequency

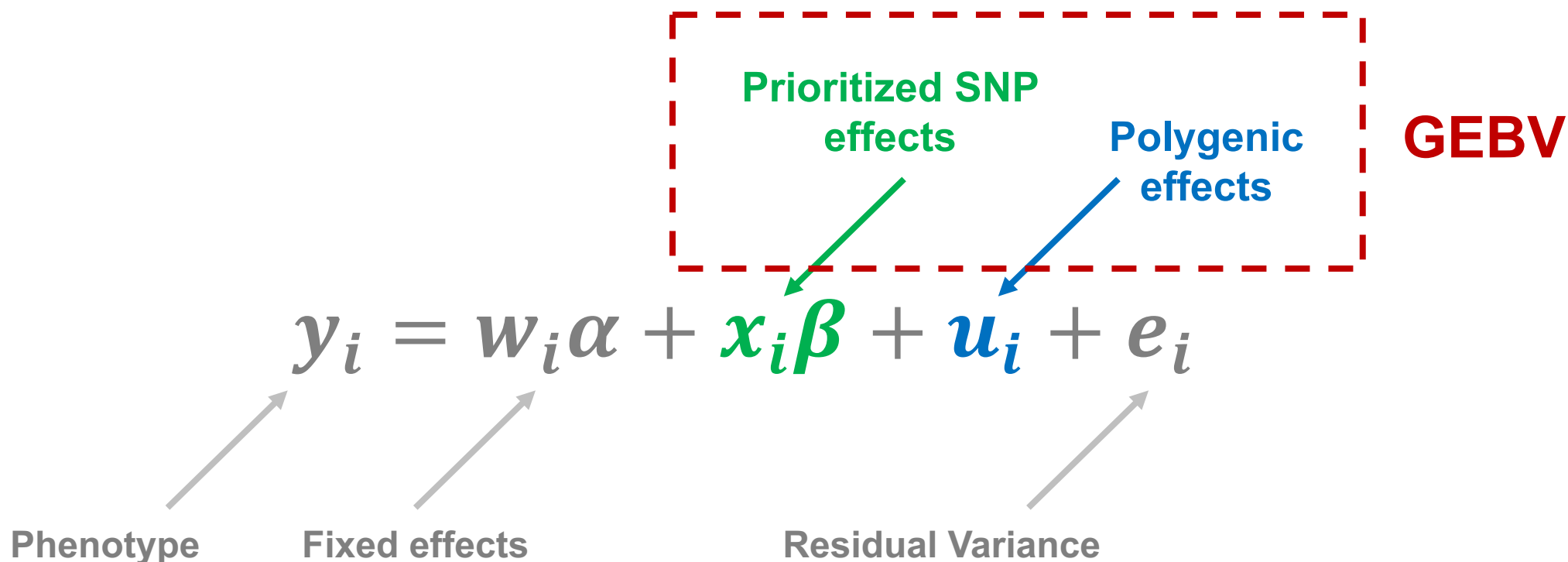
1: Complete Differentiation

No alleles for SNP are shared between populations; genetic variance entirely described by population structure

↑ F_{ST} = ↑ influence on trait

PRIORITIZING INFLUENTIAL SNPs

Hybrid Model to Capture Total Genetic Variance



COMPARING METHODOLOGIES

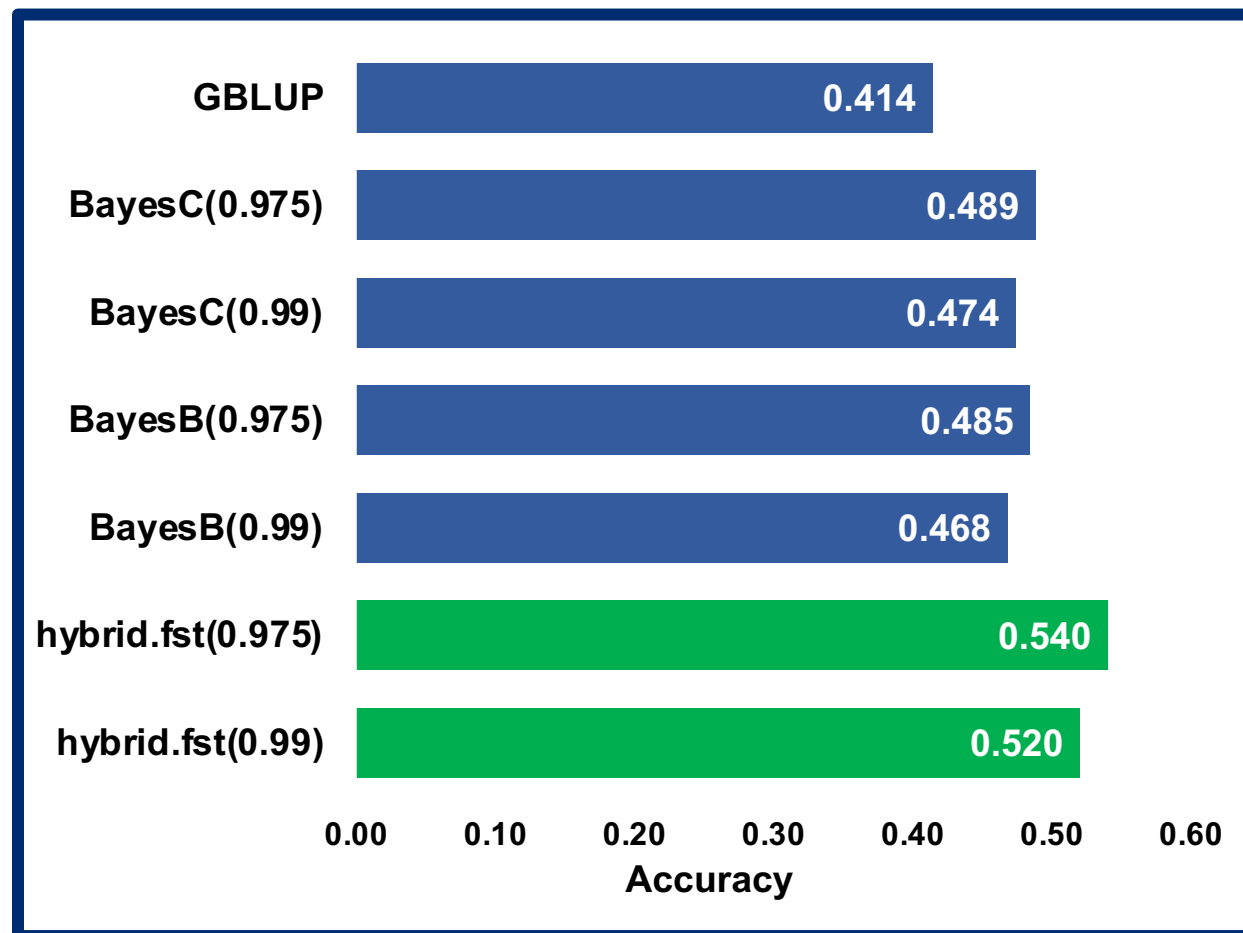
Data for **15,000 animals** randomly generated in QSIM

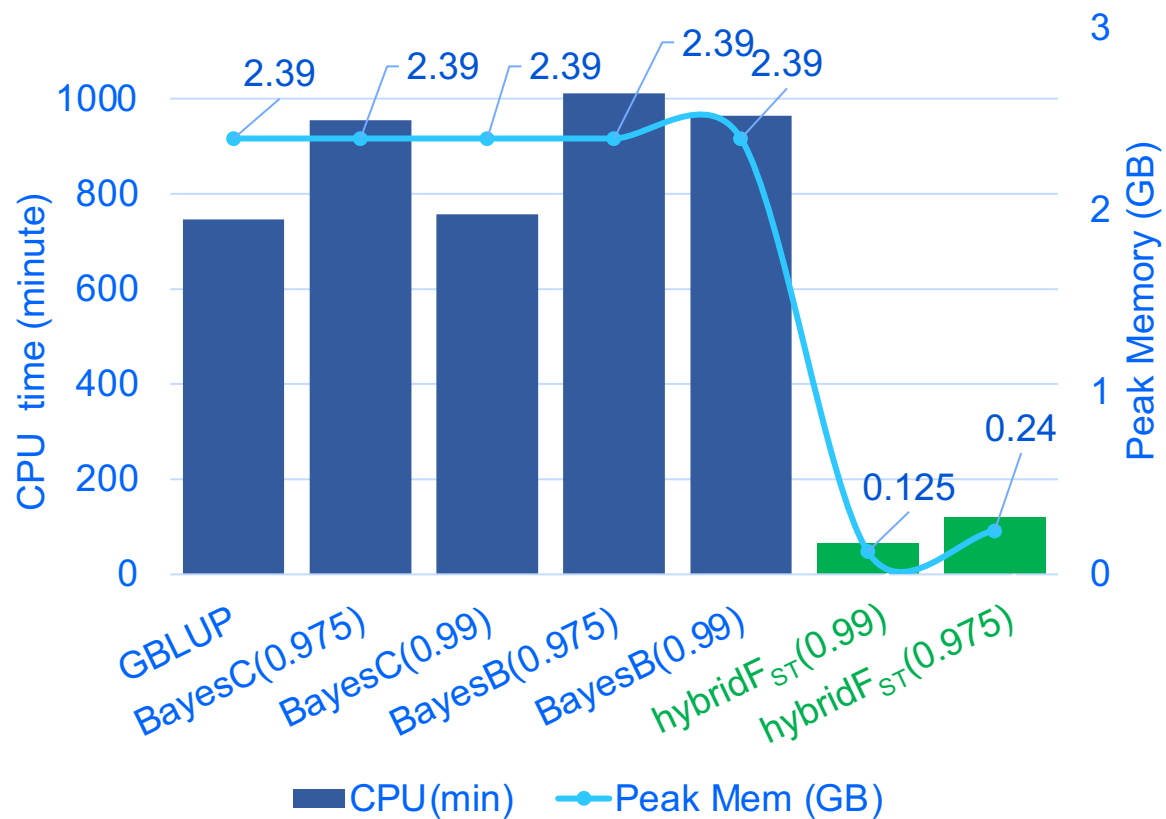
Phenotypes

- Hypothetical trait with $h^2 = 0.4$, normally distributed

Genotypes

- 50K SNP panel
- 200 QTL with predefined effects
 - 40 QTL explaining 1-1.5% genetic variance
 - 160 QTL explaining 0.2-0.5% genetic variance





Hybrid model uses less memory & has much faster computation

Key Messages

- Proposed hybrid model has superior accuracy compared to competing methods
- Hybrid model reduces the number of SNPs included in calculations and avoids need to invert genomic relationship matrix (a time costly step)
- The effectiveness of this method will depend on the heritability and complexity of the trait in question
- Need external validation with real data

IMPUTED GENE TESTS

Predicting gene content for non-genotyped relatives for the most important QTL on the SNP list



Emmanuella Ogwo, Jeff O'Connell, Paul VanRaden

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GENE TESTS ARE AVAILABLE



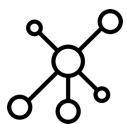
Genotyping laboratories began adding QTL gene tests in 2014



Some have large effects on traits we select for (or should)



Gene tests are already imputed for all genotyped animals, across multiple breeds (AY, BS, GU, HO, JE)



We can estimate gene content for non-genotyped relatives, as in single step GBLUP

8 GENE TESTS EXAMINED

Gene test	Chr:Pos	Function	Effects
Polled	1:2578598	Grow horns	Animal welfare, farm labor
ABCG2	6:36599640	Membrane transport	Yield and NM\$ (biggest effect)
β-casein (a2)	6:84451299	Milk protein	Marketed as more digestible
K-casein (1)	6:85656772	Milk protein	Increased cheese yield
K-casein (2)	6:85656792	Milk protein	Increased cheese yield
β-Lactoglobulin	11:103259232	Milk fat	Allergies – not in human milk
DGAT1	14:611019	Fat and protein %	Fatty acid metabolism, obesity
BGHR	20:31888449	Growth hormone	Protein % (2 nd biggest effect)

IMPUTED GENE TEST RESULTS

Polled

ERROR RATE

AA

AB

BB

A _

B _

_ _

Breed	Tests (N)	Frequency (final, %)	Imputed genotype codes (%)					
			0	1	2	3	4	5
AY	15,110	0.6	92.18	0.58	0.01	7.06	0.02	0.15
BS	65,172	3.5	83.69	8.05	0.43	6.83	0.33	0.67
GU	7,620	1.1	91.48	1.51	0.03	6.67	0.00	0.32
JE	663,366	2.2	94.60	3.94	0.12	1.30	0.02	0.03
HO	5,669,157	1.0	97.00	1.81	0.12	1.04	0.01	0.02



Key Messages

- Some valuable gene tests are sold by genotyping laboratories and not delivered with array genotypes
- Freely imputed QTLs could benefit breeders and progress
- Decreasing costs of WGS data will increase power of QTL discovery
- More available QTL genotypes will increase imputation accuracy, prediction accuracy, and economic gain



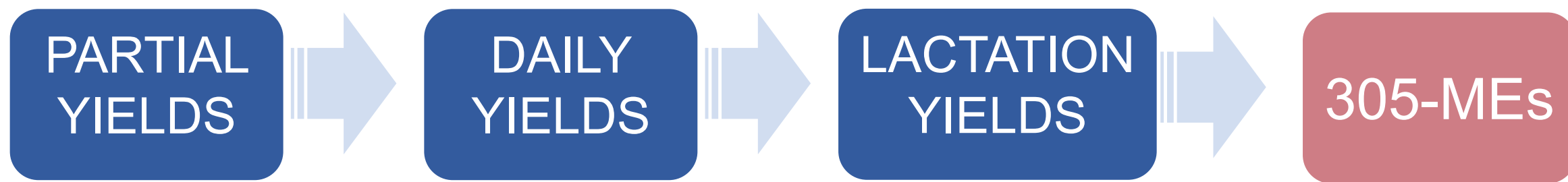
GETTING YIELDS RIGHT:

Evaluating projection factors, updating yield predictions,
revisiting daily & lactation yield standardization

**Asha Miles, Nick Wu, Paul VanRaden, Curt Van Tassell,
Ransom Baldwin, Steven Sievert, Javier Burchard, Jay
Mattison, and Joao Durr**



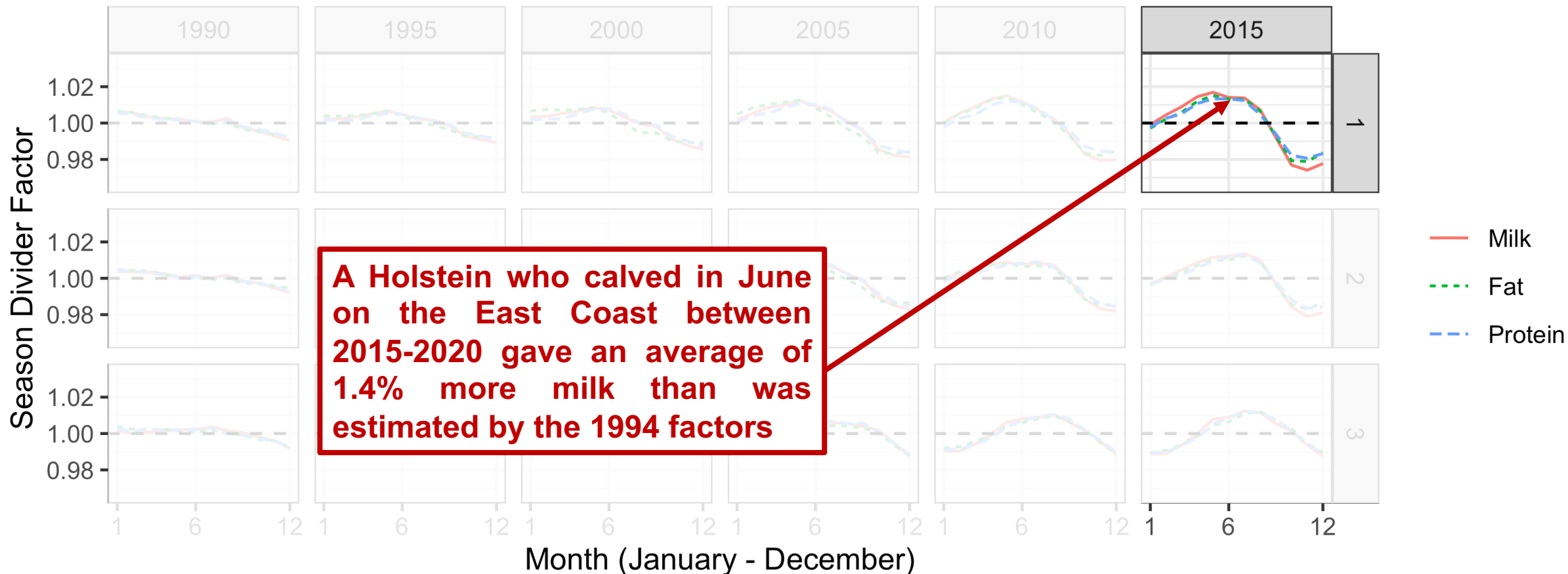
ESTIMATING & COMPARING YIELDS



- **Genetic selection changes maturity patterns** (Norman et al 1995)
- **ME factors last estimated in 1994**
 - **Corrected for parity, age, season of freshening, previous days open, geographical region, and 2X milking**

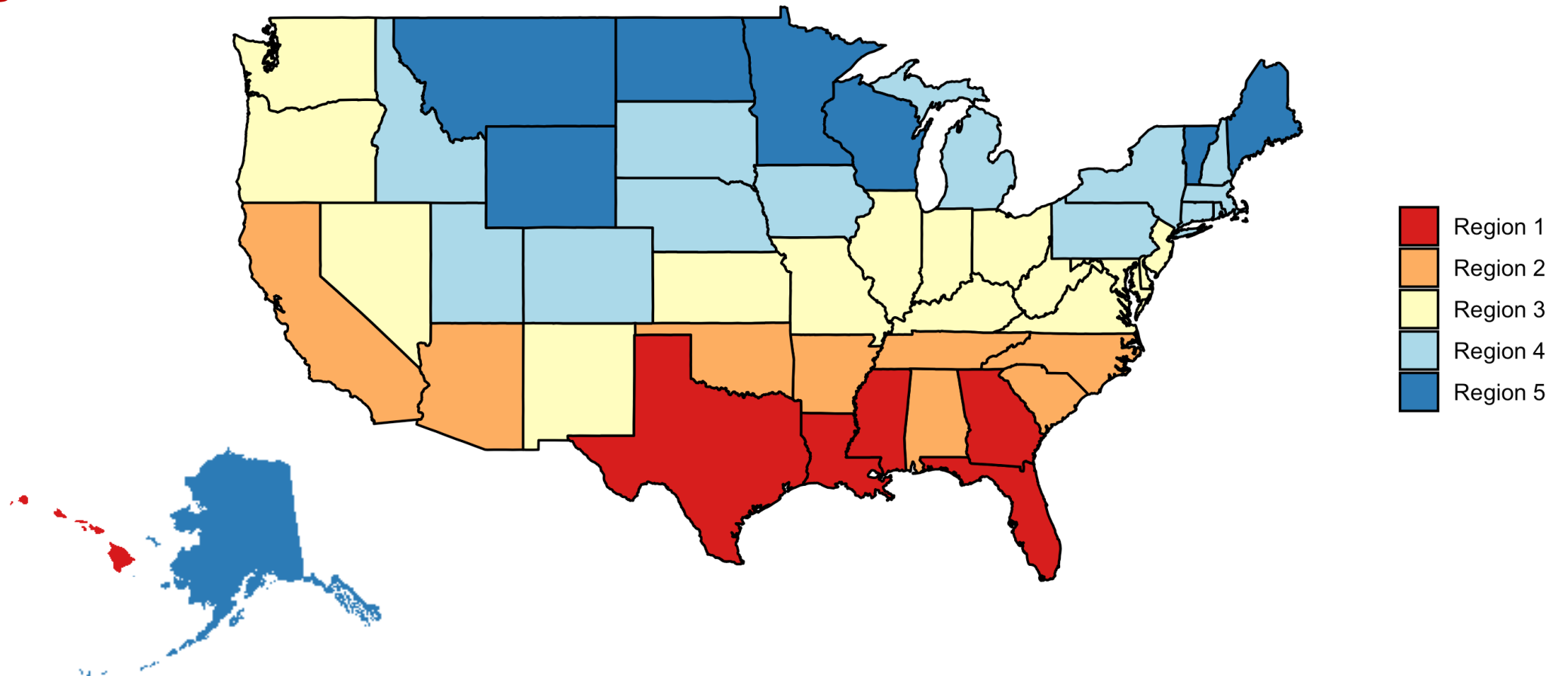
SEASON-REGION CORRECTIONS

Holstein Example



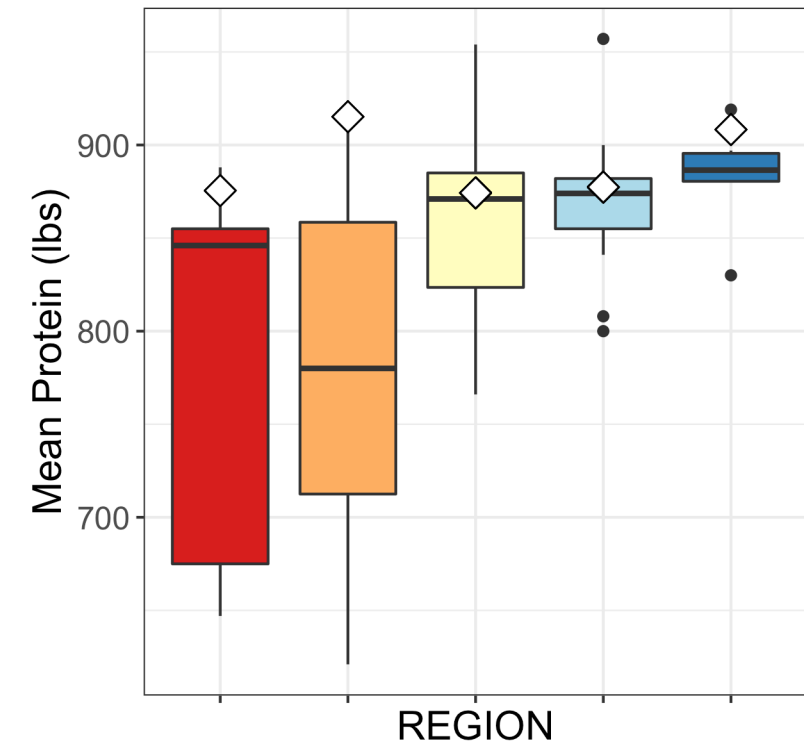
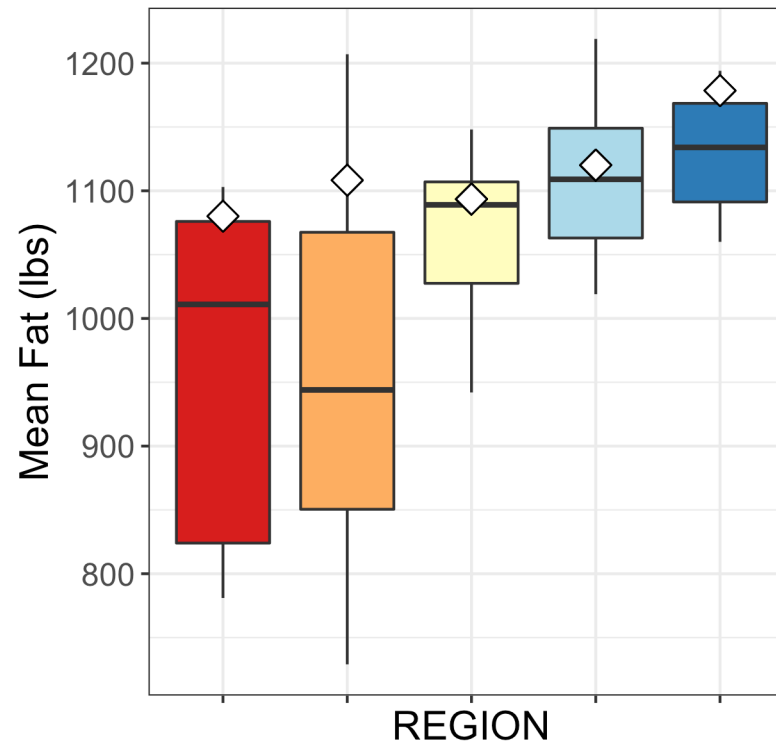
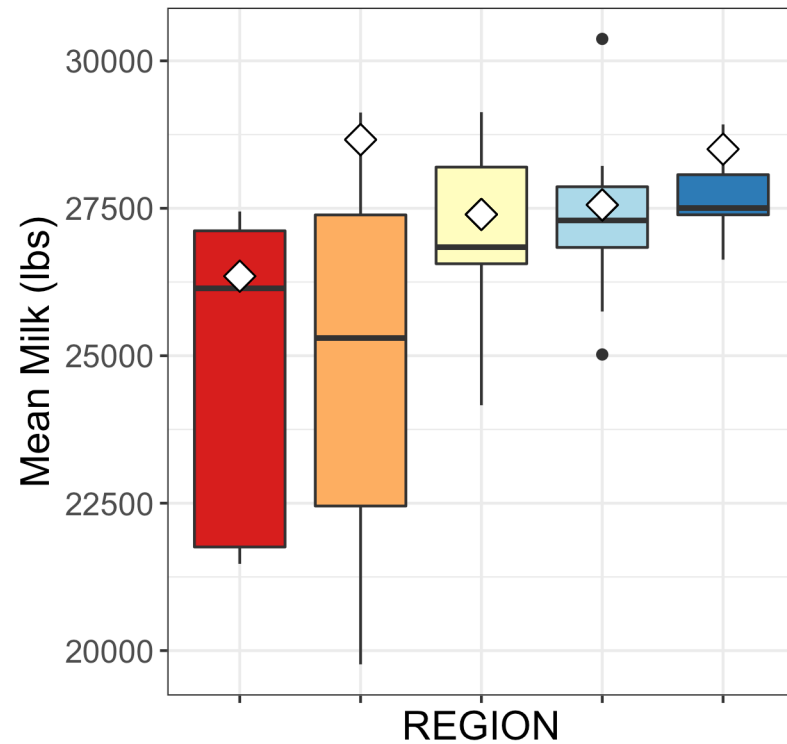
SEASON-REGION CORRECTIONS

New Regions



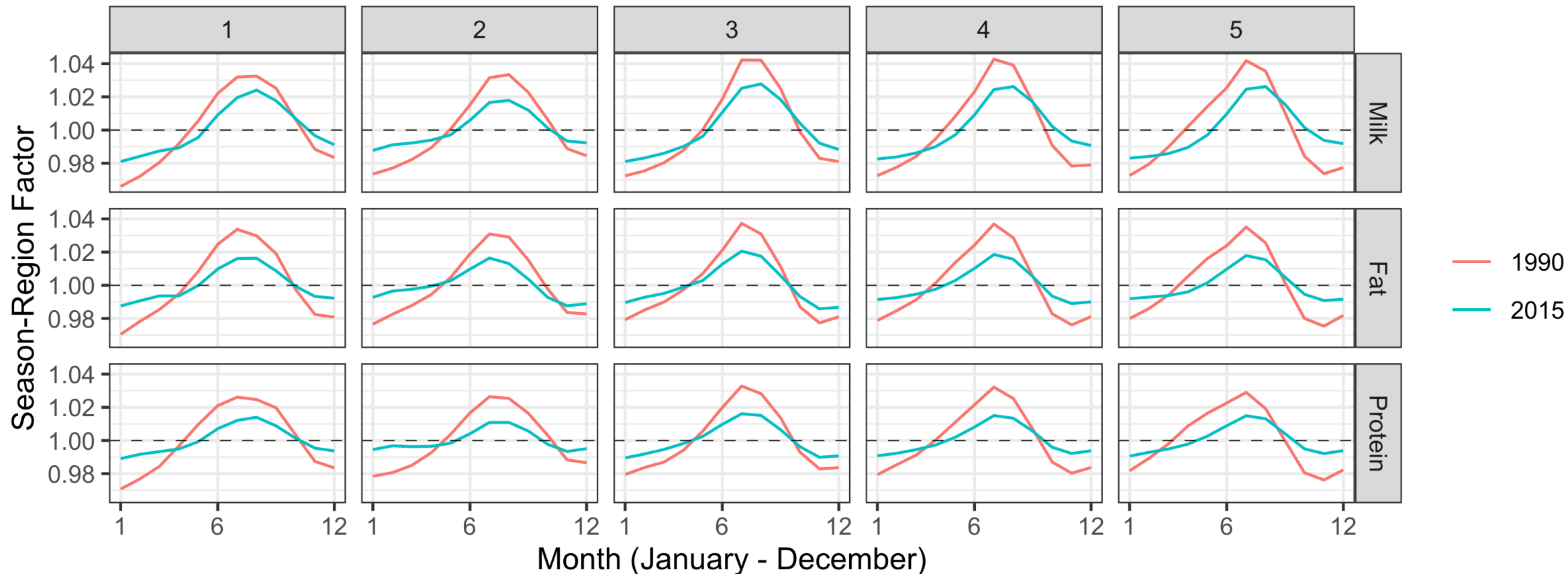
SEASON-REGION CORRECTIONS

Production Levels in 2021

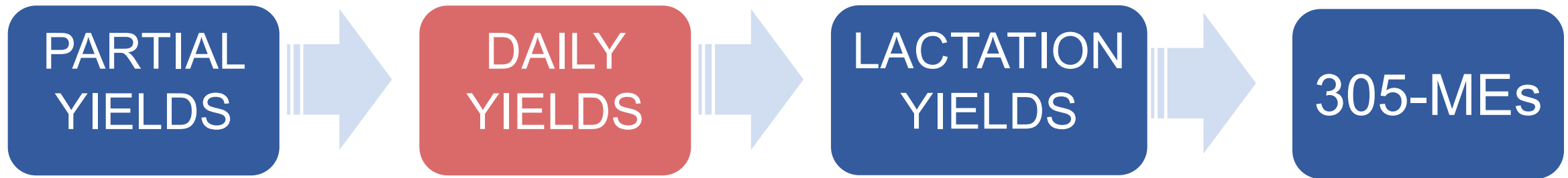


SEASON-REGION CORRECTIONS

New Season-Region Factors



ESTIMATING & COMPARING YIELDS





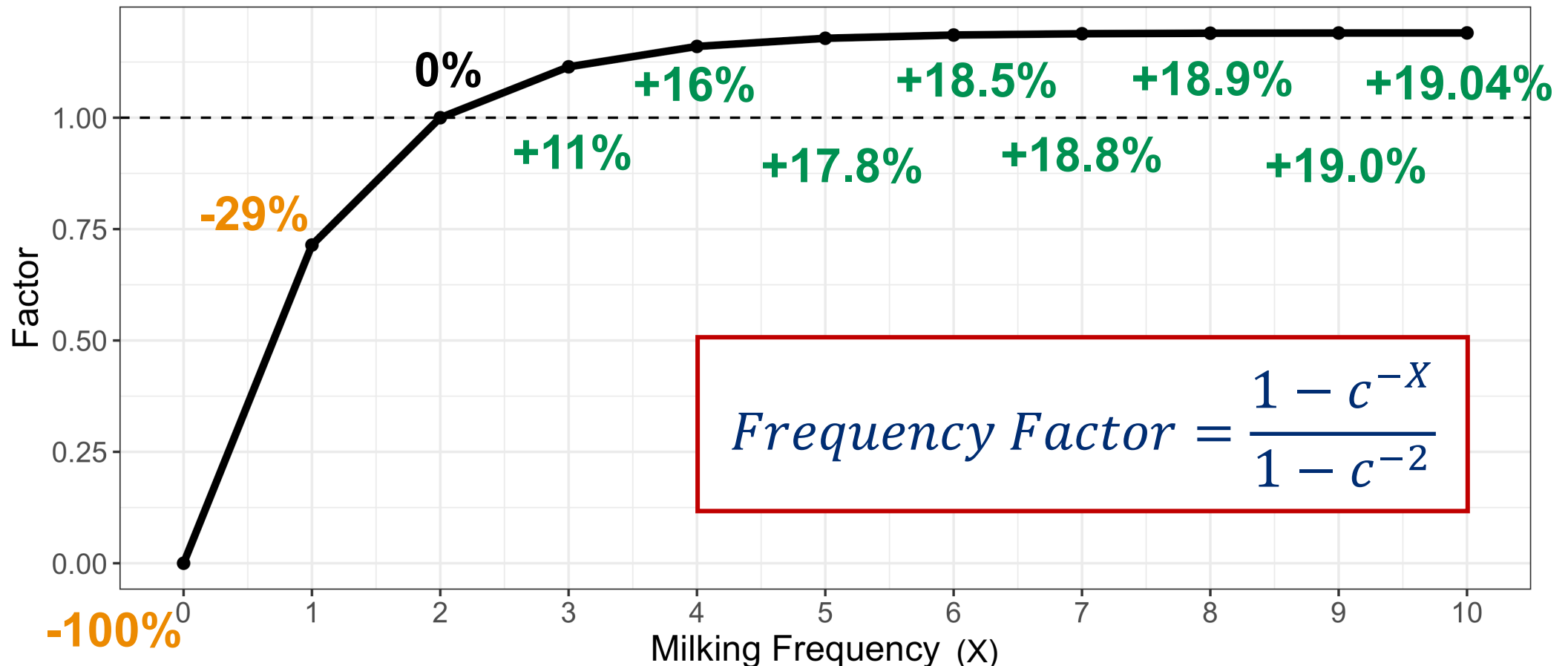
FREQUENCY-INTERVAL CORRECTION

Milk Yield Example

$$\textit{Frequency Factor} = \frac{1 - c^{-X}}{1 - c^{-2}}$$

FREQUENCY-INTERVAL CORRECTION

Milk Yield Example



FREQUENCY-INTERVAL CORRECTION

Milk Yield Example

$$\text{Frequency + Interval Factor} = \sum_i^N w_i \times X_i$$

Sum for all
milking in a
given 24 hrs

$$w_i = \frac{\text{interval (hr)}}{24}$$

(The proportion of time
in a day she had to
make milk)

$$X_i = \frac{24}{\text{interval (hr)}}$$

(Frequency of milking
based on this particular
interval)

FREQUENCY-INTERVAL CORRECTION

Milk Yield Example

Milked	Even	Uneven	Factor	
2X	12, 12		1.000	+0%
3X	8, 8, 8		1.114	+11.4%
4X	6, 6, 6, 6		1.160	+16.0%

FREQUENCY-INTERVAL CORRECTION

Milk Yield Example

Milked	Even	Uneven	Factor	
2X	12, 12		1.000	+0%
		13, 11	0.998	-0.2%
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FREQUENCY-INTERVAL CORRECTION

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FREQUENCY-INTERVAL CORRECTION

Milk Yield Example

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2X	12, 12		1.000	+0%
		13, 11	0.998	-0.2%
		14, 10	0.991	-0.9%
		16, 8	0.964	-3.6%
3X	8, 8, 8		1.114	+11.4%
4X	6, 6, 6, 6		1.160	+16.0%

FREQUENCY-INTERVAL CORRECTION

Milk Yield Example

Milked	Even	Uneven	Factor
2X	12, 12		1.000
		13, 11	0.998
		14, 10	0.991
		16, 8	0.964
3X	8, 8, 8		1.114
		10, 8, 6	1.102
		12, 6, 6	1.080
4X	6, 6, 6, 6		1.160
		8, 8, 4, 4	1.138

+0%

-0.2%

-0.9%

-3.6%

+11.4%

+10.2%

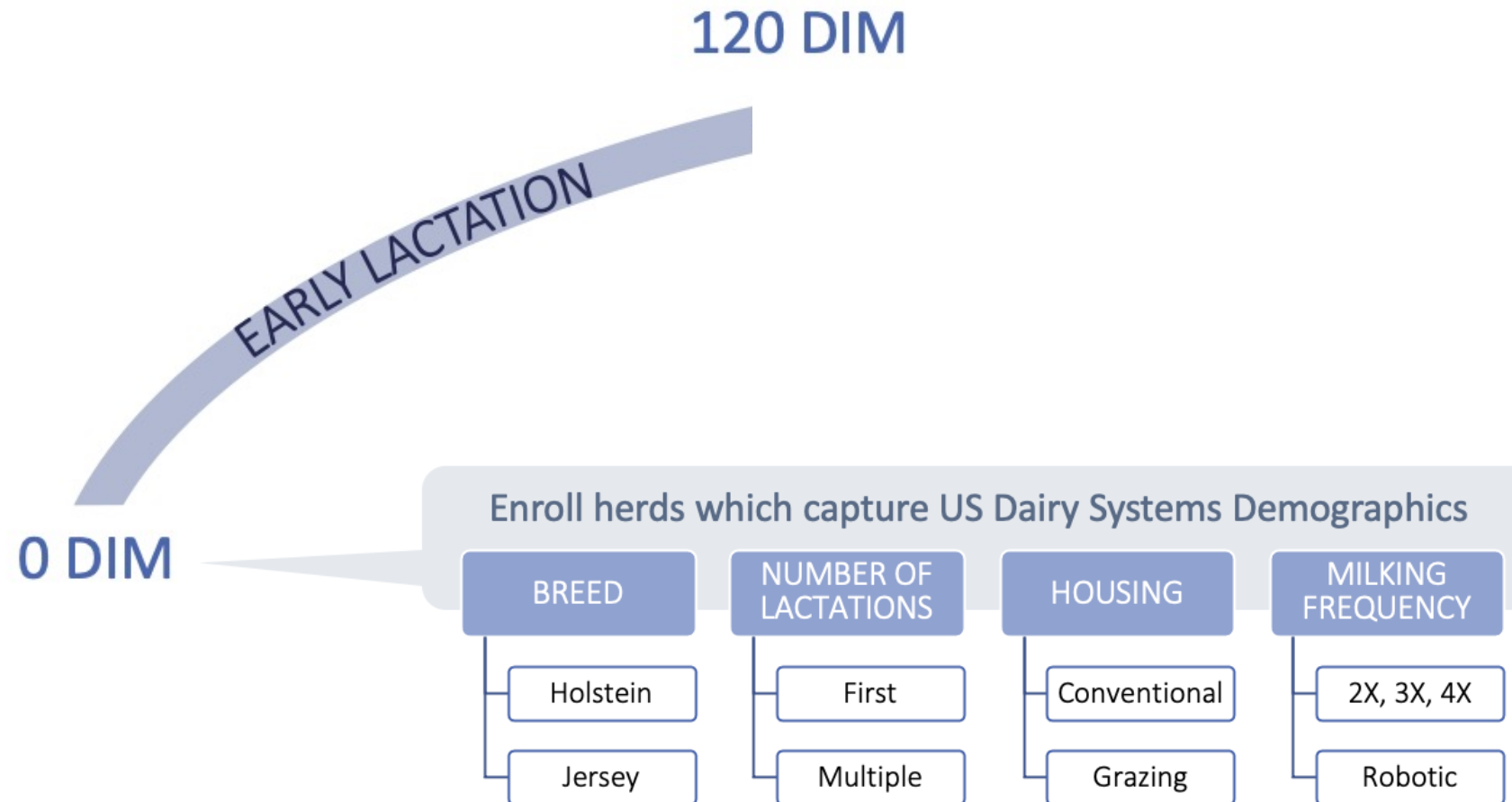
+8.0%

+16.0%

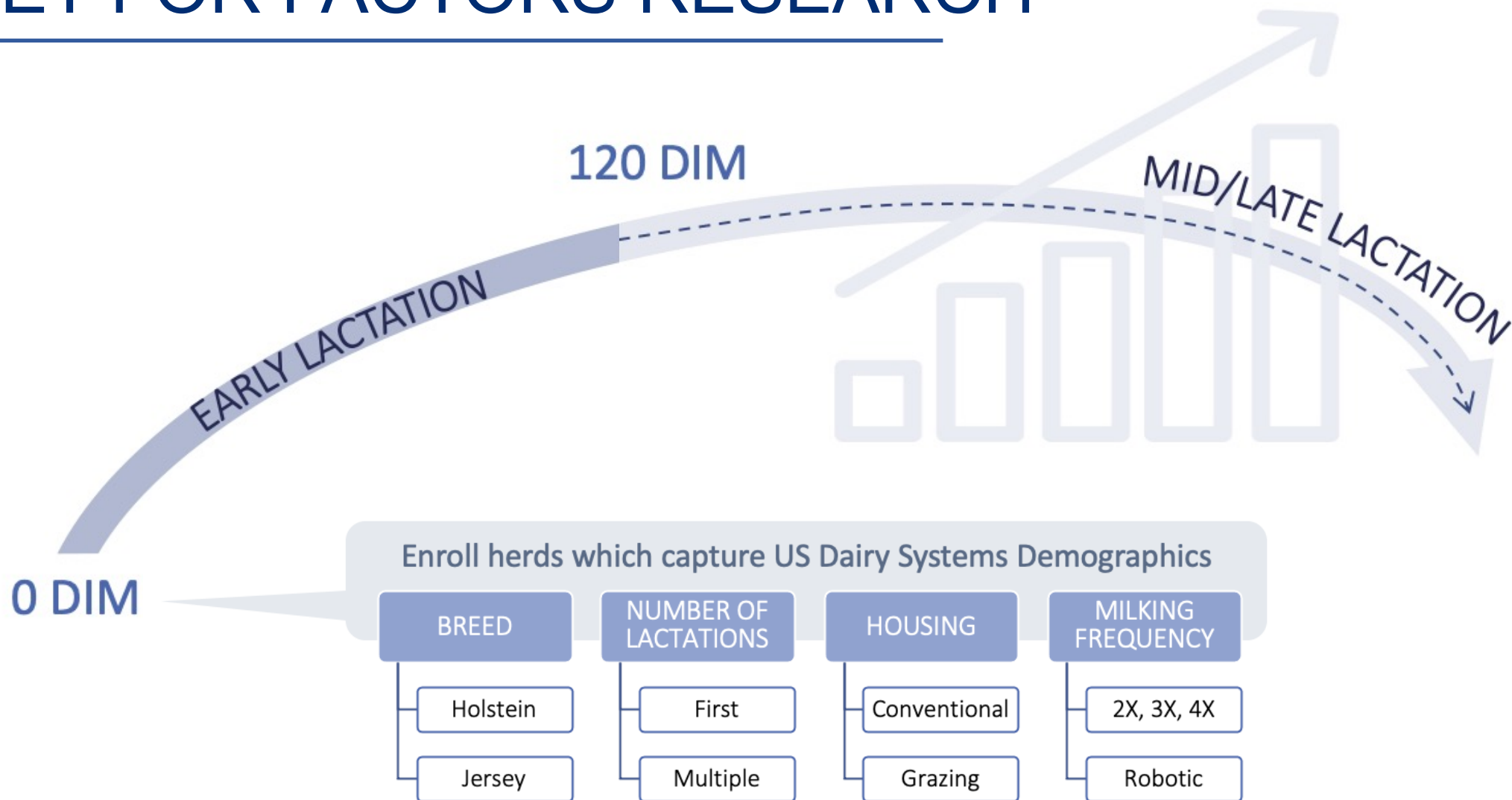
+13.8%

- More milk from more milkings/day
- Less milk from uneven milking intervals
- Can predict milk gain or loss from any set of intervals
- Useful in conventional and AMS herds
- Useful for genetic evaluation & management insights

DATASET FOR FACTORS RESEARCH



DATASET FOR FACTORS RESEARCH





Immediate Impacts

- ↑ **accurate daily yields**
- ↑ **accurate 305-d yields**
- **fairer comparisons**



Long-term Benefits

- **Enhanced genetic selection**

**Updated factors will have
immediate management benefits**

Key Messages

- New standardization factors & methods are under development
- Propose correcting to 36-months, as the PTAs have done since c. 2007
- The new factors dataset generated will be instrumental in validating these new methods & have immense research value for years to come

THANK YOU

Data were available to the authors from CDCB under USDA Agricultural Research Service Material Transfer Research Agreement #58-8042-8-007. While CDCB offers data stewardship, sole ownership and rights pertaining thereto remain with the producer and we thank U.S. dairy producers for sharing their data for research use.

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