

# Tightening the Screws on BOLT

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# Stayability

- Implemented with the Spring 2017 genetic evaluation
- Based on a Canadian Simmental research project (Jamrozik et al, 2013)
- Uses a technique called random regression
- Incorporates genomic data using a super hybrid model



# Stayability

- Introduced a lot of changes with the Fall 2017 evaluation:
  - Increased the number of genotyped animals from 65,129 to 82,373
  - Changed the way we filter genotyped animals
  - Increased the number of iterations because of the higher number of genotypes
  - Fine-tuned several input variables



# Stayability

- Result:
  - EPD changes primarily on young genotyped animals
  - Subsequent changes to API

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- Result:
  - EPD changes primarily on young genotyped animals
  - Subsequent changes to API
- Note to Self:
  - Software development is never complete.



# Growth

- Biggest challenge was how to account for differences among breeds
  - Were using a combination of breed by birth year effects obtained from the Cornell software and breed comparisons from MARC
  - Now applying additive genetic groups (Westell et al, 1988) to account for genetic merit of animals of different breeds entering the population at different times



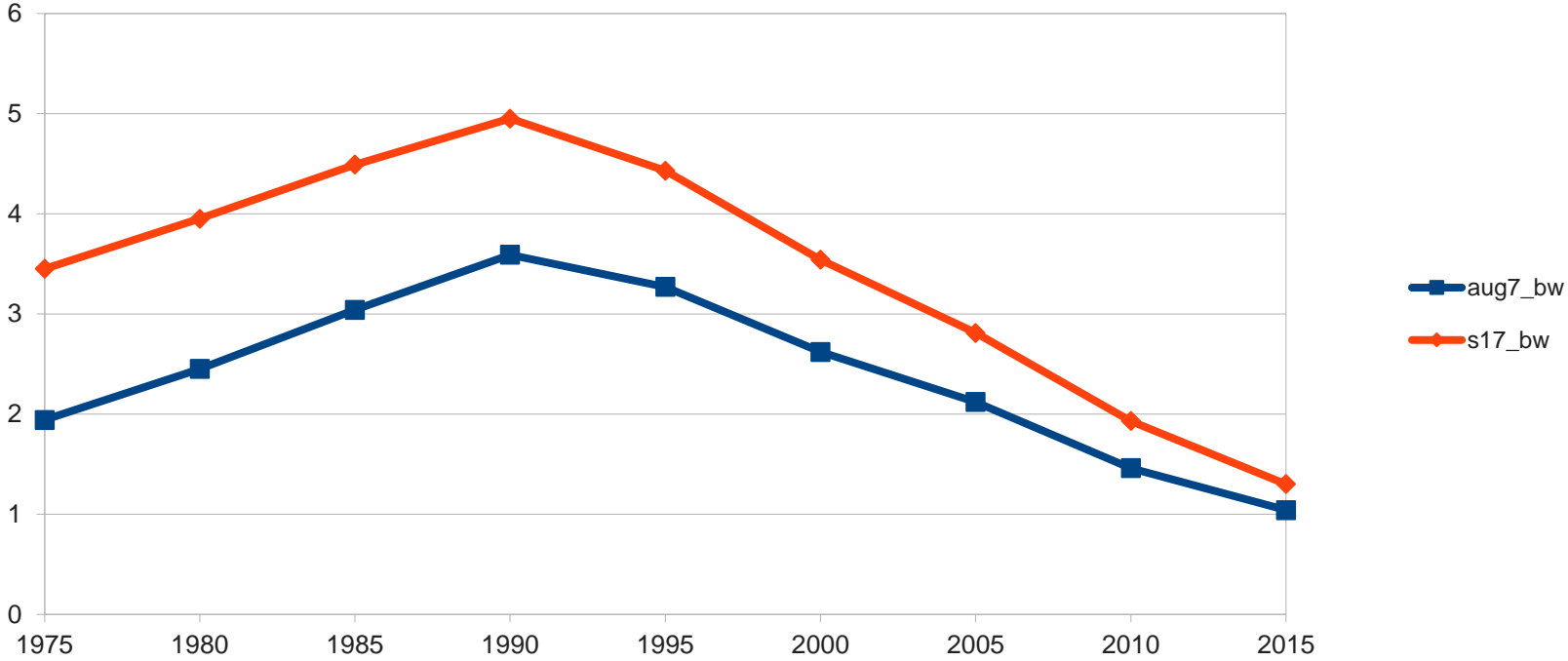
# Growth

	All Animals	SIMUSA	SIMCAN
BW	.96	.95	.96
WW	.88	.89	.88
YW	.87	.88	.90
MILK	.84	.83	.85



# Growth

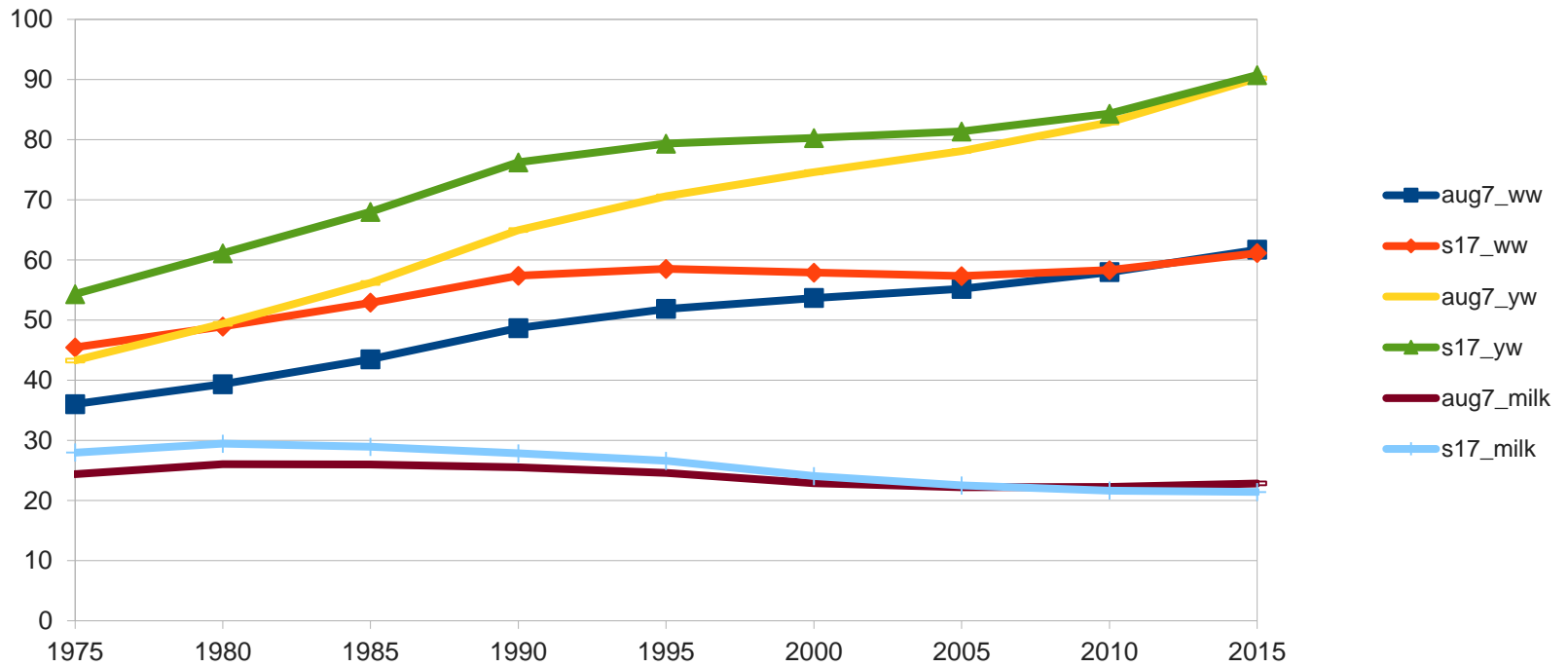
Birth Wt





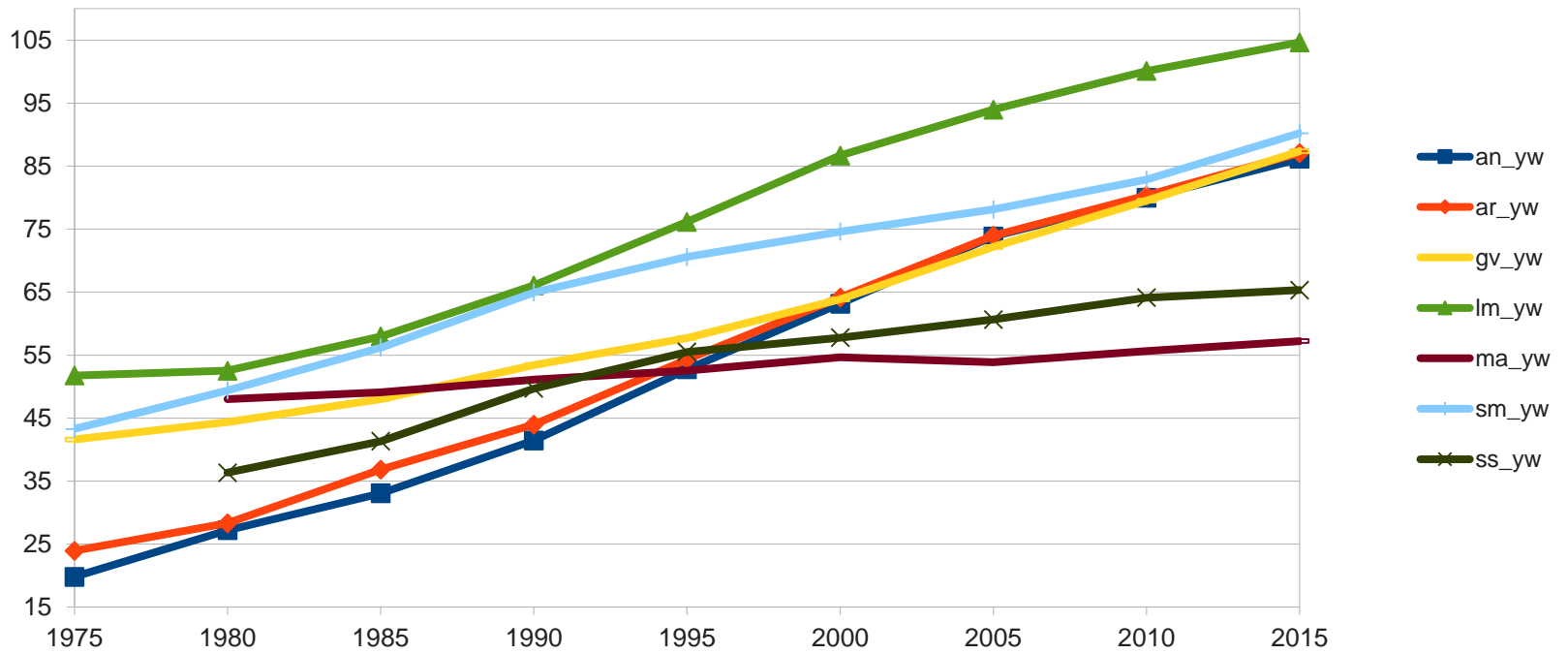
# Growth

Wean,Year,Milk



# Growth

Yearling



# Carcass

- Initial runs for CWT, REA and UREA have been very promising
- Correlations with and without MARC breed effects
  - CWT: .64 and .70
  - REA: .62 and .56
- Adding genetic groups to see if correlations improve
- If so, will run MARB, UIMF, FAT and UFAT

# Calving Ease

- Was based on a random regression marker effects model
- Now using a classic marker effects model
- Eliminated shifting on animals with external EPDs (primarily Angus)
- Waiting for results...



# Docility

- Last, but not least
- Data preparation procedures are in place
- Should not be difficult because there is only one trait

