



# Variability in response

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Nov. 5th, 2018

# Announcements

- **Exam II:** Nov. 12th, (M) 7:30am
- **Office hour:**
  - Friday 3-5pm
  - Keim Hall 363
- HW key posted on Canvas

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## Classes this week

- Finish Chapter 11 and 12
- For Ch12: empirical results and interpretation
  - [Illinois long-term selection experiment for oil and protein in corn:](#) > **100 generations since 1896**
  - [E coli long-term selection by Richard Lenski](#) > **50,000 generations since 1988**

# Breeder's equation

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- $R$ : response
- $i$ : selection intensity
- $h^2$ : heritability
- $\sigma_P$ : standard deviation of the phenotypic value
- $L$ : generation interval

# Improvement of response

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- selection during the off-season in plants
- **genomic selection**



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- maximizing the repeatability of trait evaluation.
- sound measurement methods and proper experimental design

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  - **Be cautious:** increase the inbreeding coefficient and hence loss of alleles through genetic drift.
  - **Increase  $i$  is likely not the most efficient path!** i.e.  $p$  from 10% to 5% =>  $i$  from 1.755 to 2.063.

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- increase the population size from which selections are made

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- The breeding population needs to contain adequate additive genetic variation for the trait of interest.
- If no difference in breeding values exist between individuals within the population, genetic gain through selection is not possible.



# Measuring response to selection

Response selection of two chicken populations.

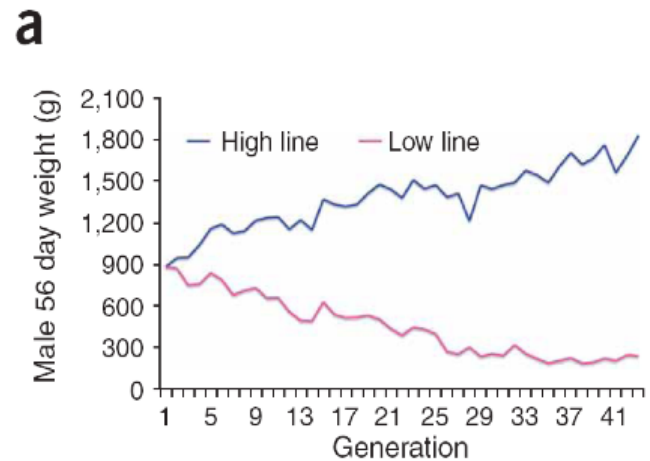
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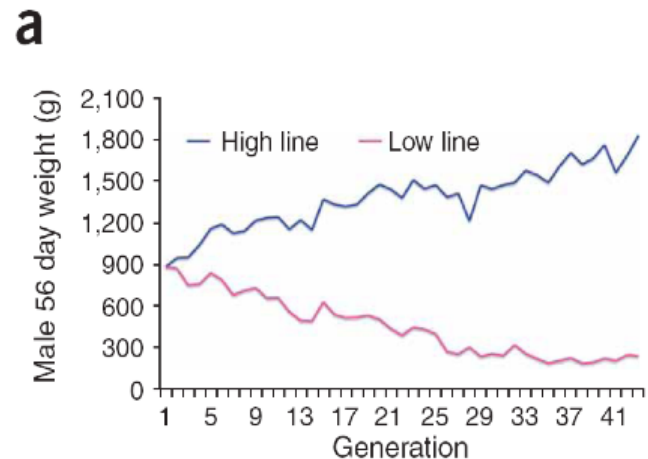
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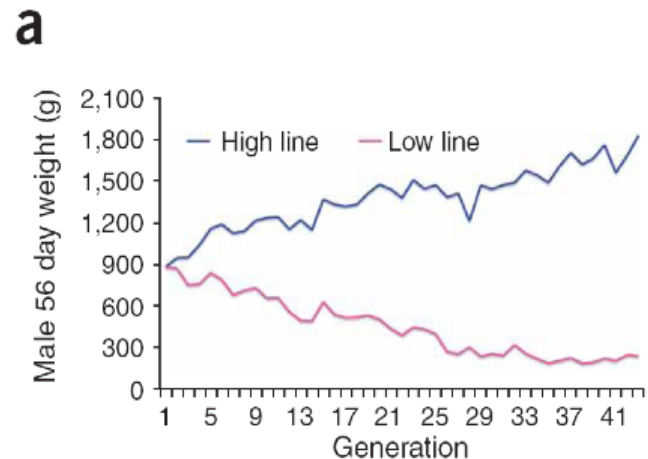


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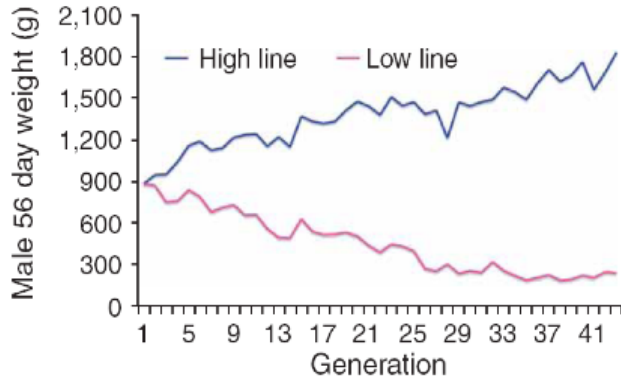


**Causes of response variability to selection?**

1. Genetic drift
2. Sampling error in estimating the generation mean
3. Differences in selection differential
4. Environmental factors

# Measuring response to selection

**a**

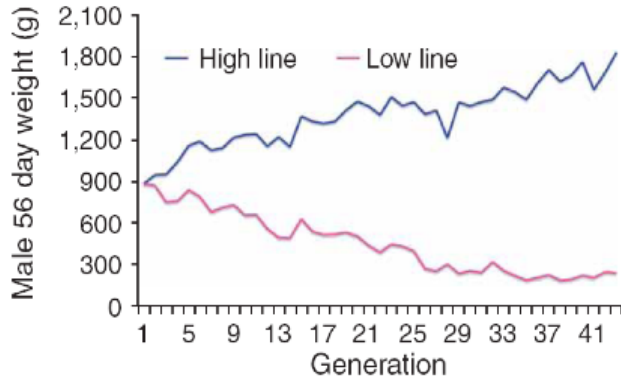


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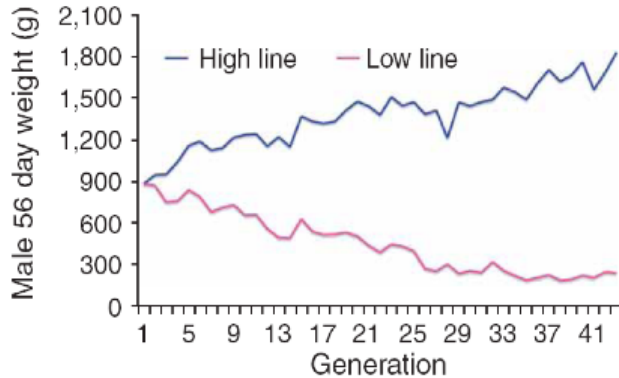
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## Causes of response variability:

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4. Environmental factors

## How to separate these effects?

1. Maintain an unselected control population
2. Practice divergent selection
3. Or carry out replicated, parallel selection programs

# Realized heritability

$$h_R^2 = R/S$$

Shows how the response is related to the selection differential



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```
S <- c(5, 6, 5, 6, 6, 10)
R <- c(3, 2, 1, 3, 2, 3)
df <- data.frame(s=cumsum(S), r=cumsum(R))

library(ggplot2)
ggplot(df, aes(x=s, y=r)) +
  geom_point(color='red', size = 4)
  geom_smooth(method=lm, color='#2C3E50')
```

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Be cautious:

1. Reduces response to selection after first generation for high heritability traits (**Bulmer effect**)
2. Systematic changes in environment or inbreeding depression will affect response.
3. Random drift affects response.

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