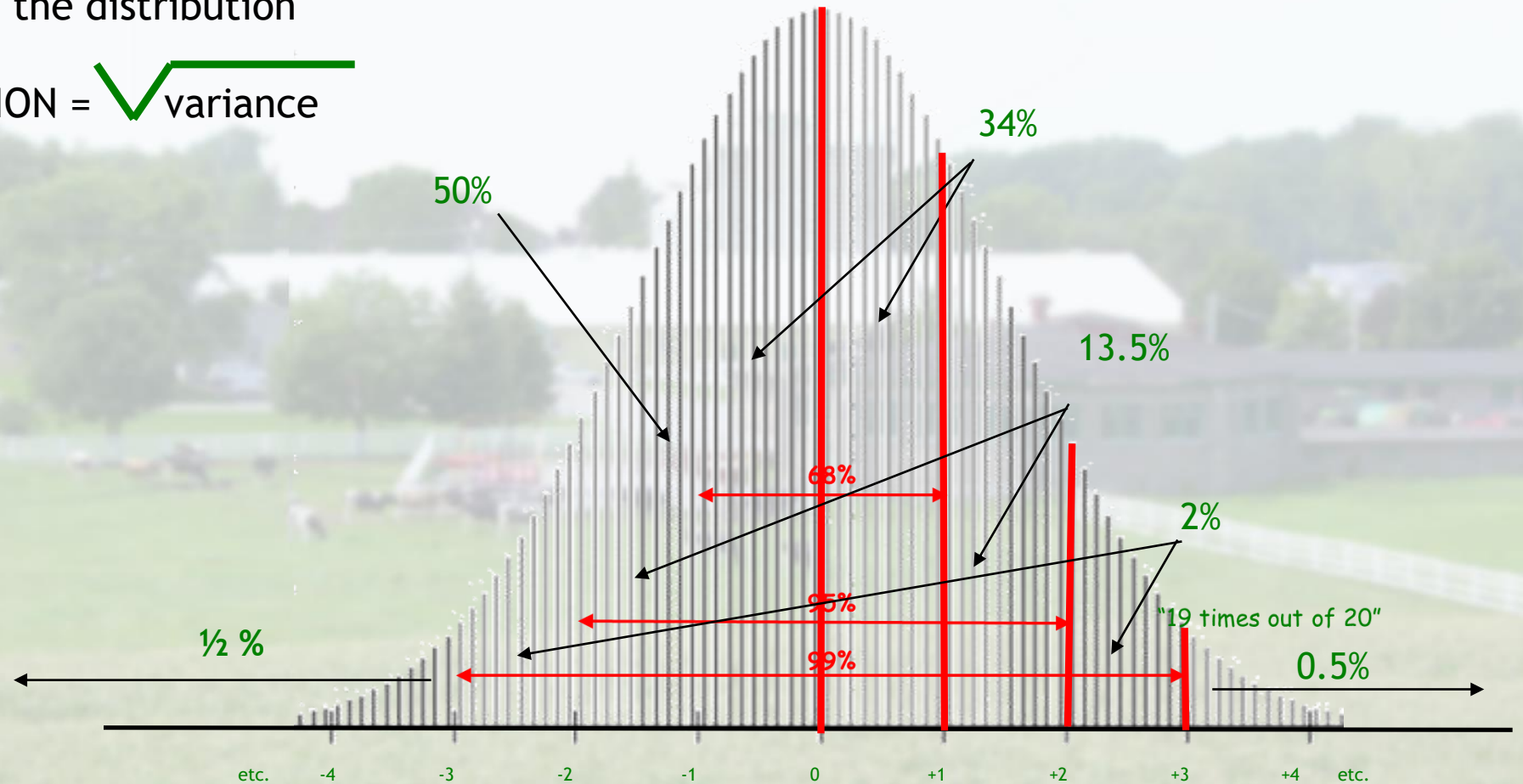


How to make use of the Normal Distribution...

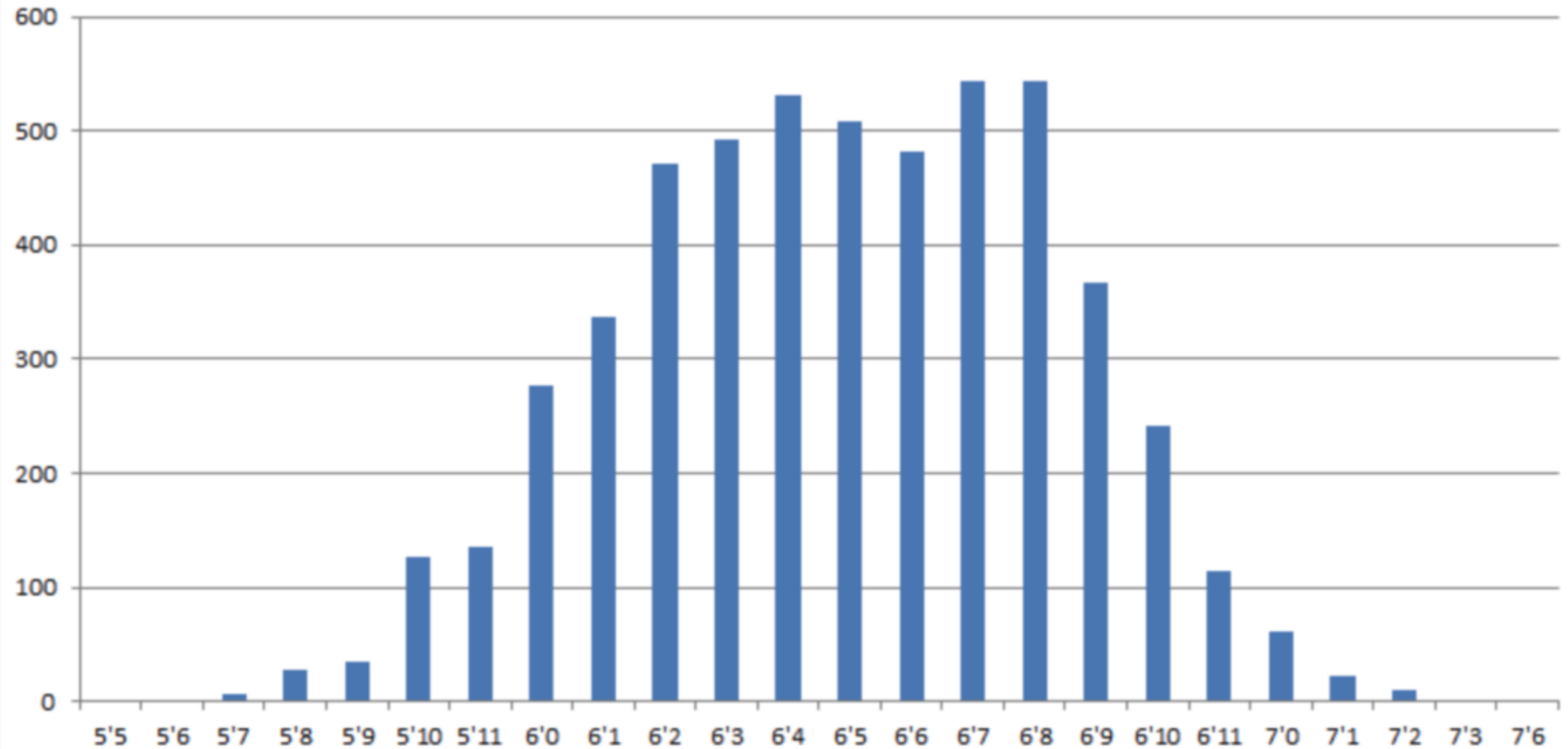
1. MEAN (or AVERAGE) = centre of the distribution

2. VARIANCE = “spread” of the distribution

2a. The STANDARD DEVIATION = $\sqrt{\text{variance}}$



NCAA I Basketball Players by Height 2016-17



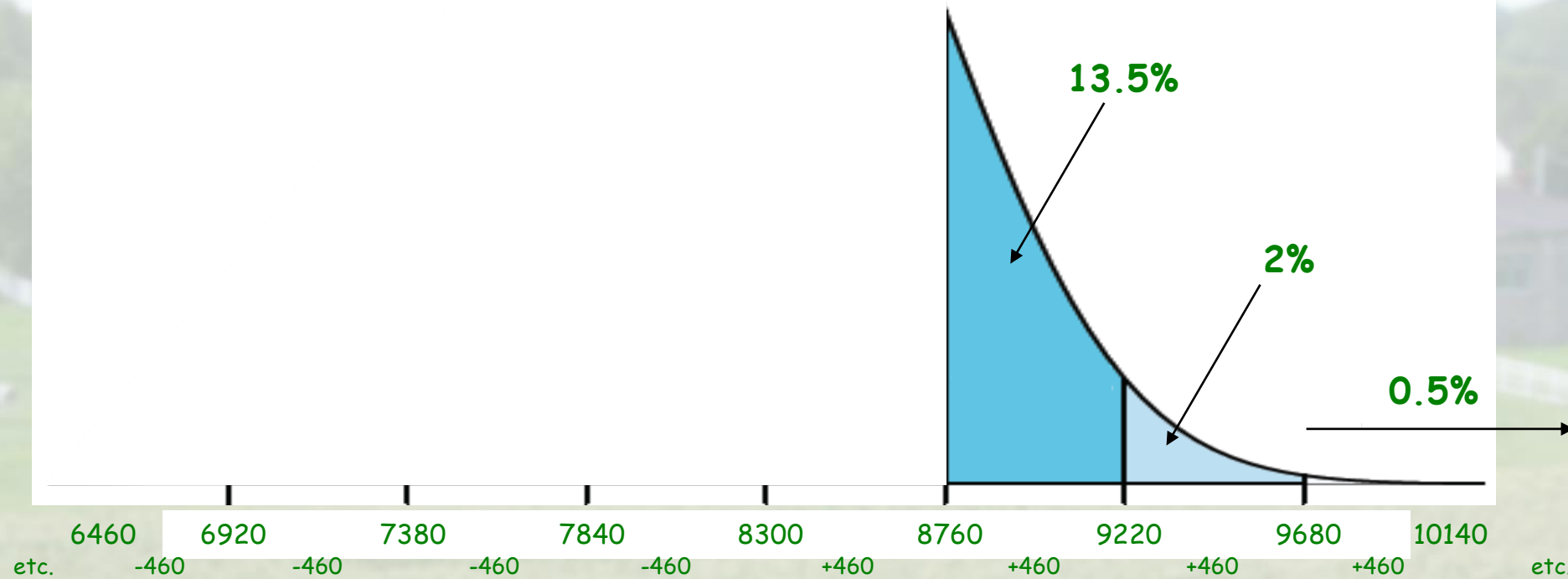


- The average milk production for a herd of jersey cows is 8300kg
- The variance for the herd is 211,600kg
- What proportion of the animals is expected to be greater than 8760kg?
- What proportion of the animals is expected to be between 7840kg and 9220kg?

Average = 8300kg
Variance = 211600
 $SD = \sqrt{211600}$
= 460kg

> 8760kg = ?

13.5 + 2.0 + 0.5 = 16%

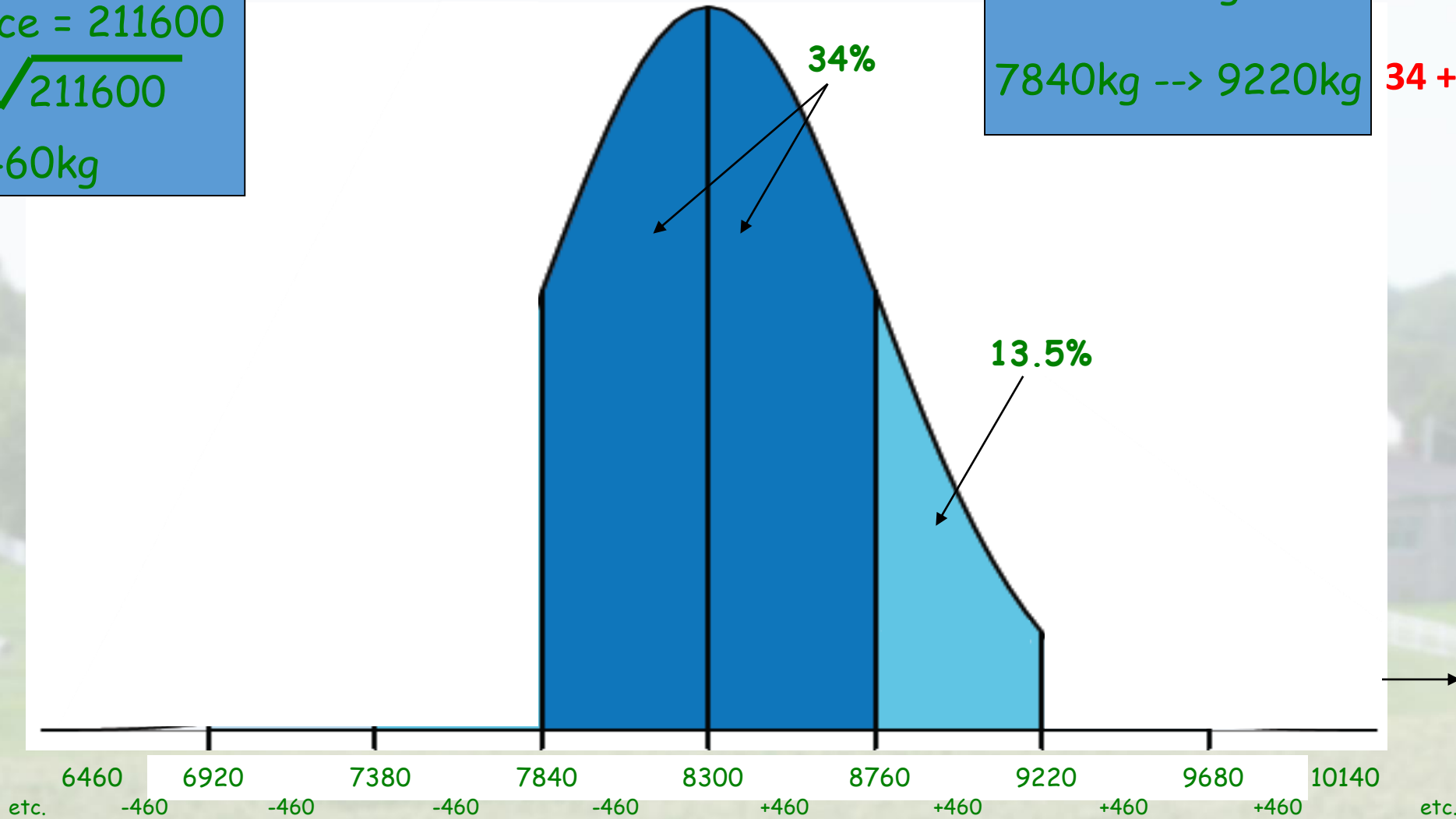


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= 460kg

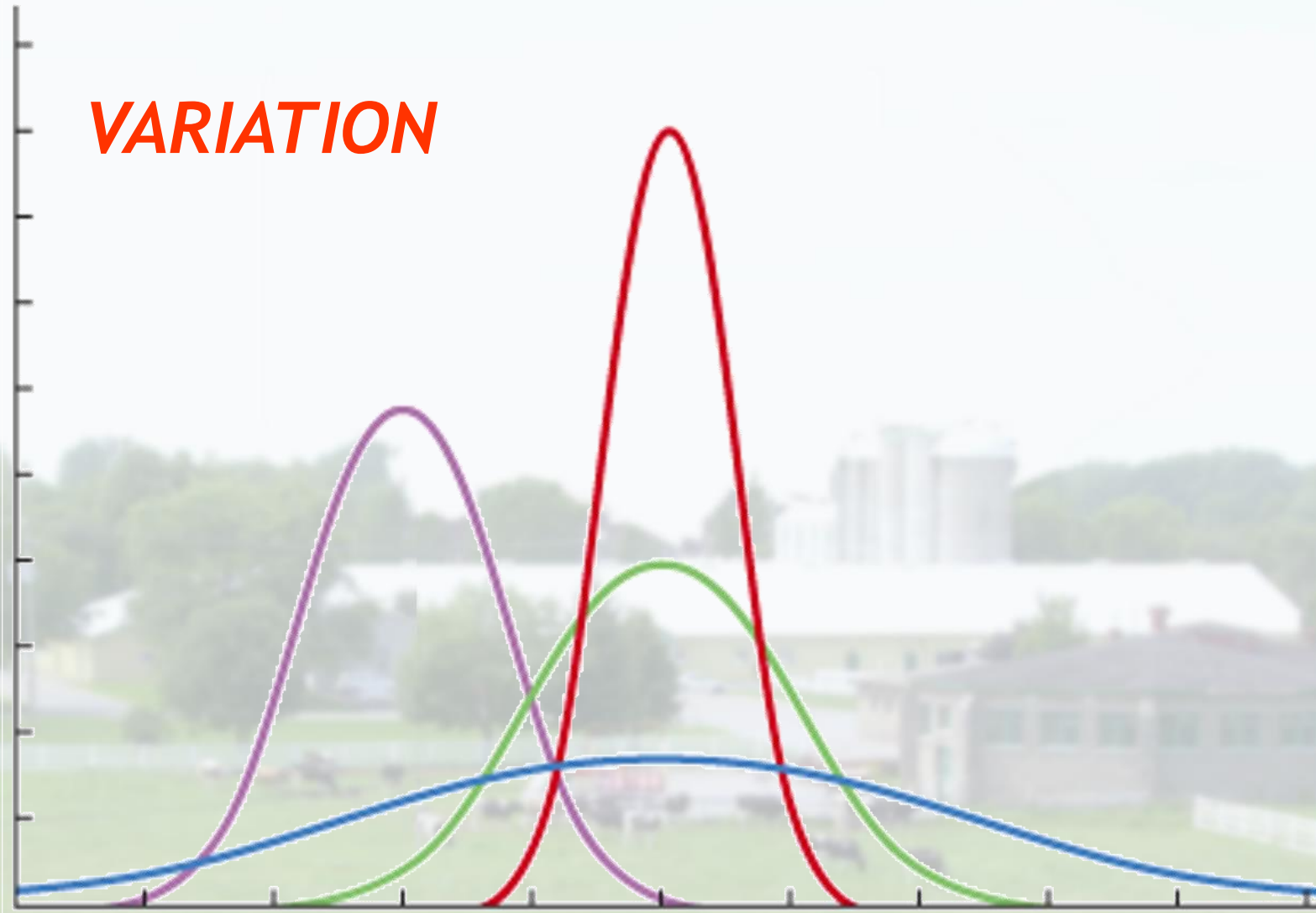
> 8760kg = ?
7840kg --> 9220kg

13.5 + 2.0 + 0.5 = 16%

34 + 34 + 13.5 = 81.5%



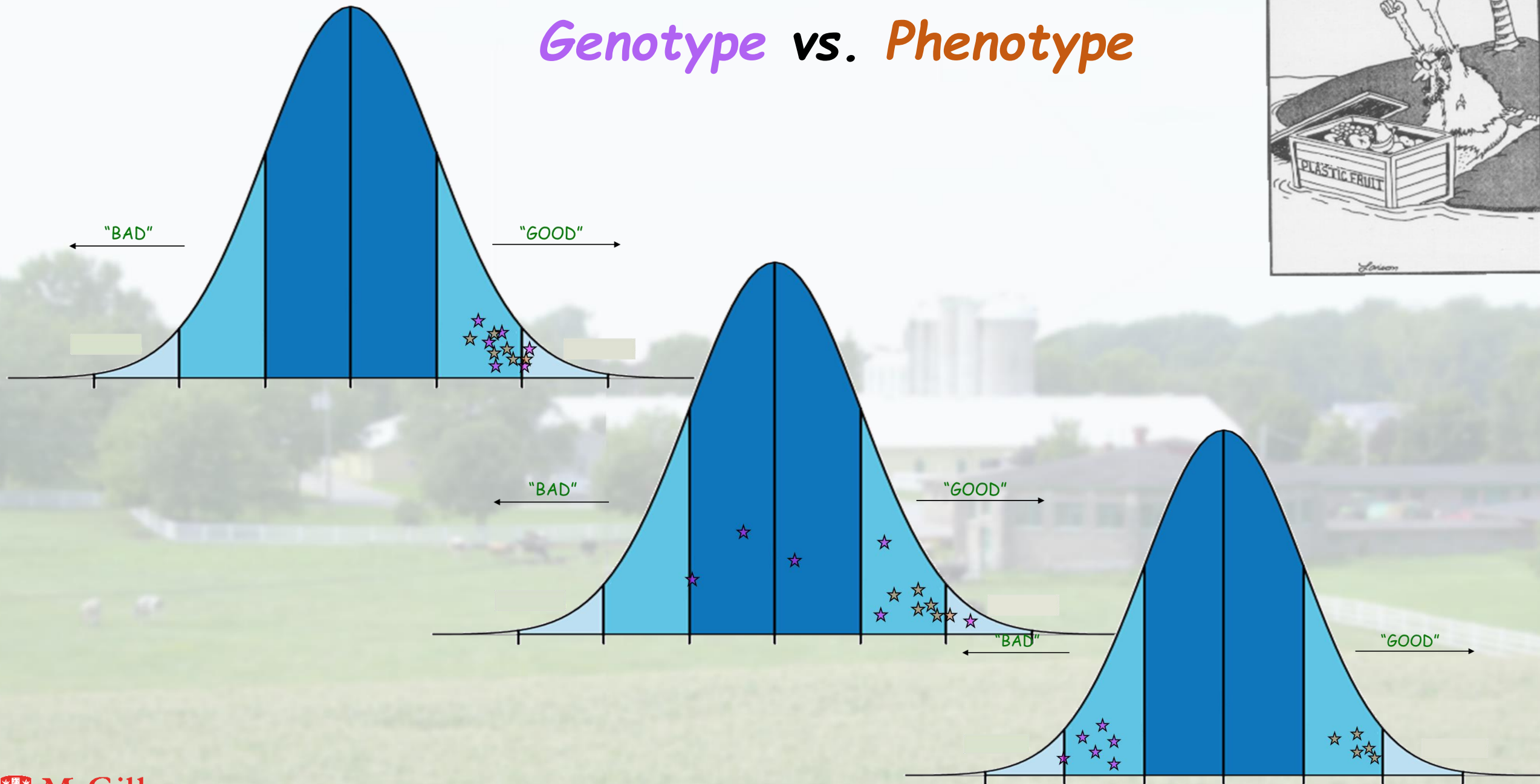
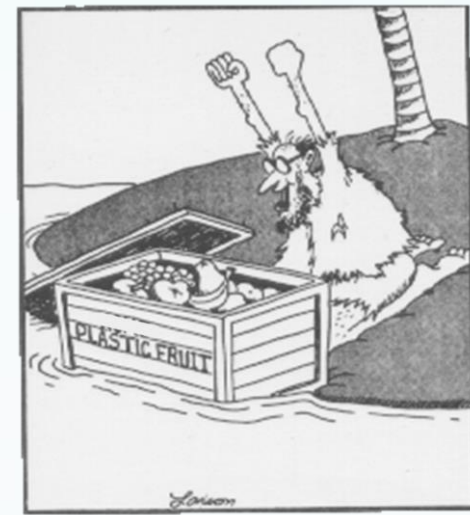
VARIATION



Phenotypic Variation = Genetic Variation + Environmental Variation

$$V_p = V_g + V_e$$

Genotype vs. Phenotype



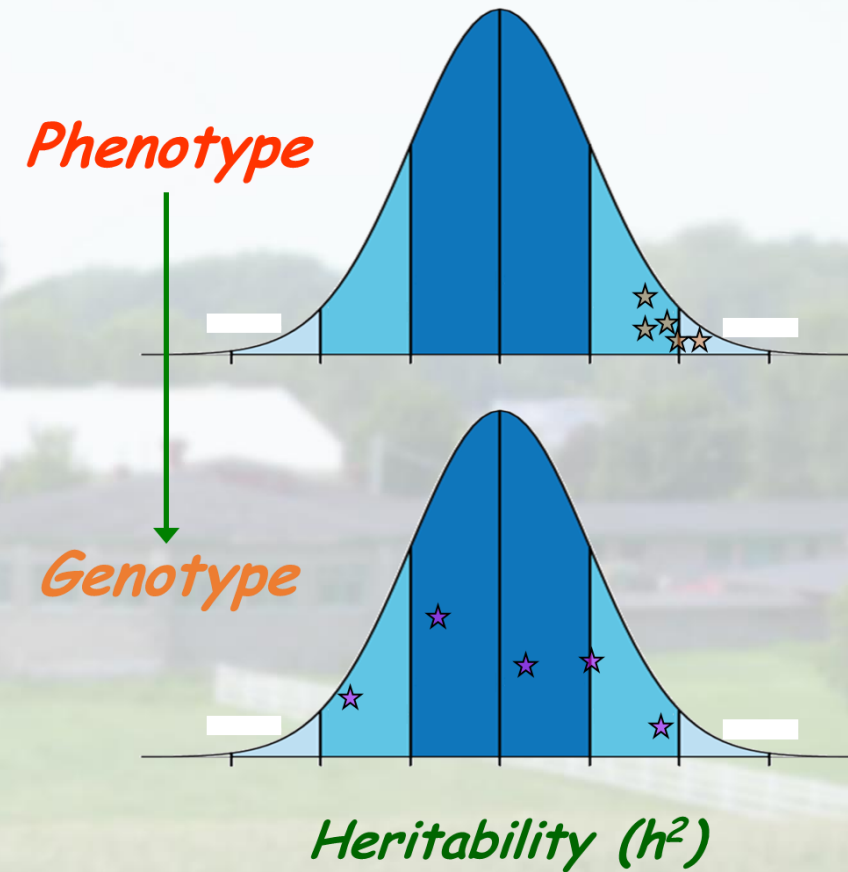
Heritability

- The “link” between **Genotype** and **Phenotype**
- The “agreement” between **Genotype** and **Phenotype**
- The proportion of observable (phenotypic) variability that is due to genetic sources

LOW agreement means it's difficult to make improvement in the desired trait through selection (must use other methods)

MEDIUM agreement means that genetic improvement is possible

HIGH agreement means there is a good relationship between genotype and phenotype, therefore selection based on phenotype is likely to be quite successful



Heritability Definition

- The symbol for heritability = h^2
- h^2 is defined as V_g/V_p or $V_g/(V_g + V_e)$ (because $V_p = V_g + V_e$)
- The value for h^2 ranges between 0 and 1 (100%)
- If $h^2 = 0$ then $V_e = 1$ (no genetic influence)
- If $h^2 = 1$ then $V_e = 0$ (no environmental influence)

Examples of Heritability Estimates for some Quantitative Traits

(Low < 15; 15 < Medium < 40; High > 40)



As a rule of thumb...

- **Carcass** traits *generally* have a HIGH heritability
- **Growth** traits *generally* have a MEDIUM to HIGH heritability
- **Fertility** traits *generally* have a LOW heritability

Genetic Progress for Quantitative Traits

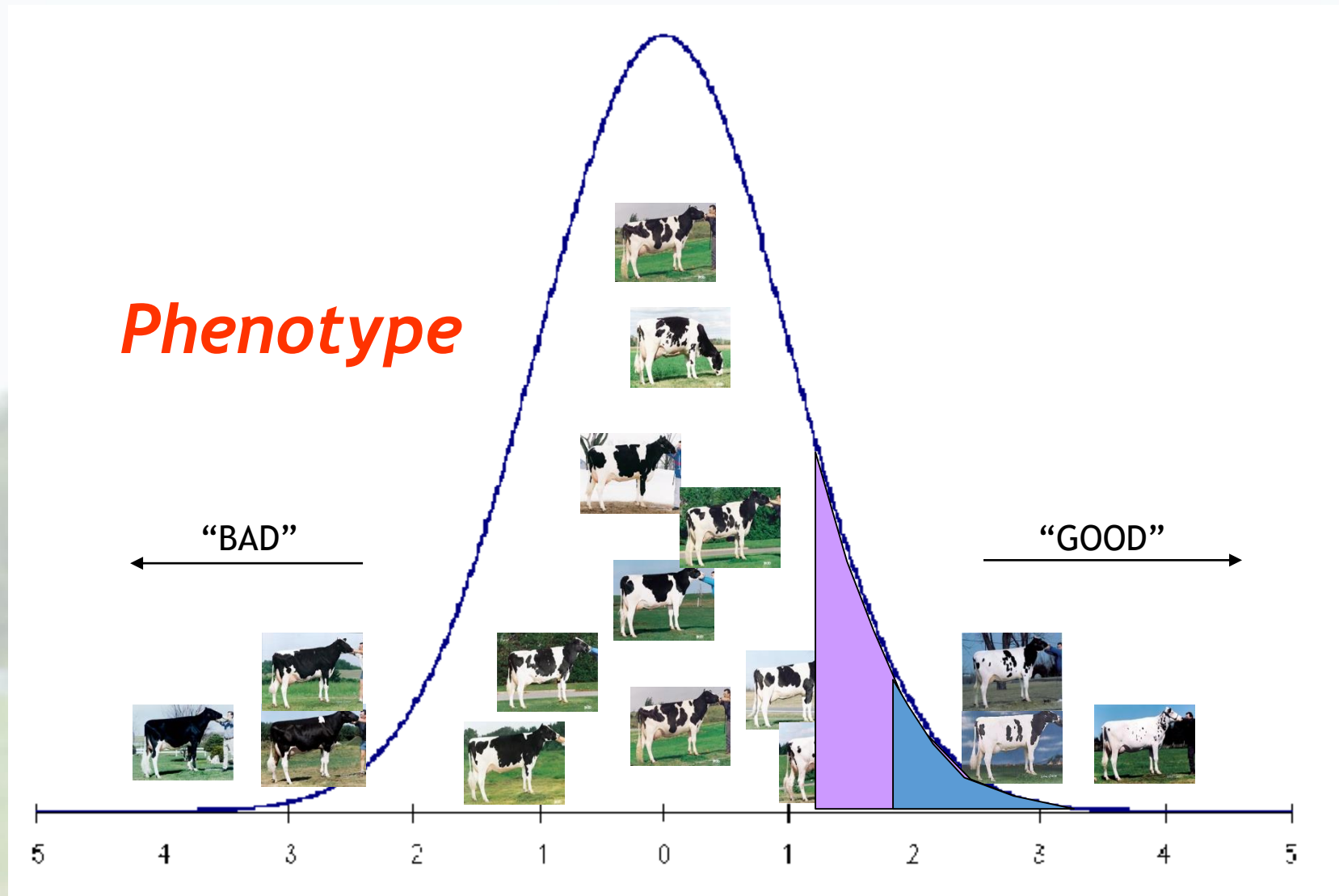
Genetic Progress = ΔG (“delta G” or “change in G”)

Increasing the frequencies of desired alleles for a specific trait

Decreasing the frequencies of *undesired* alleles for a specific trait

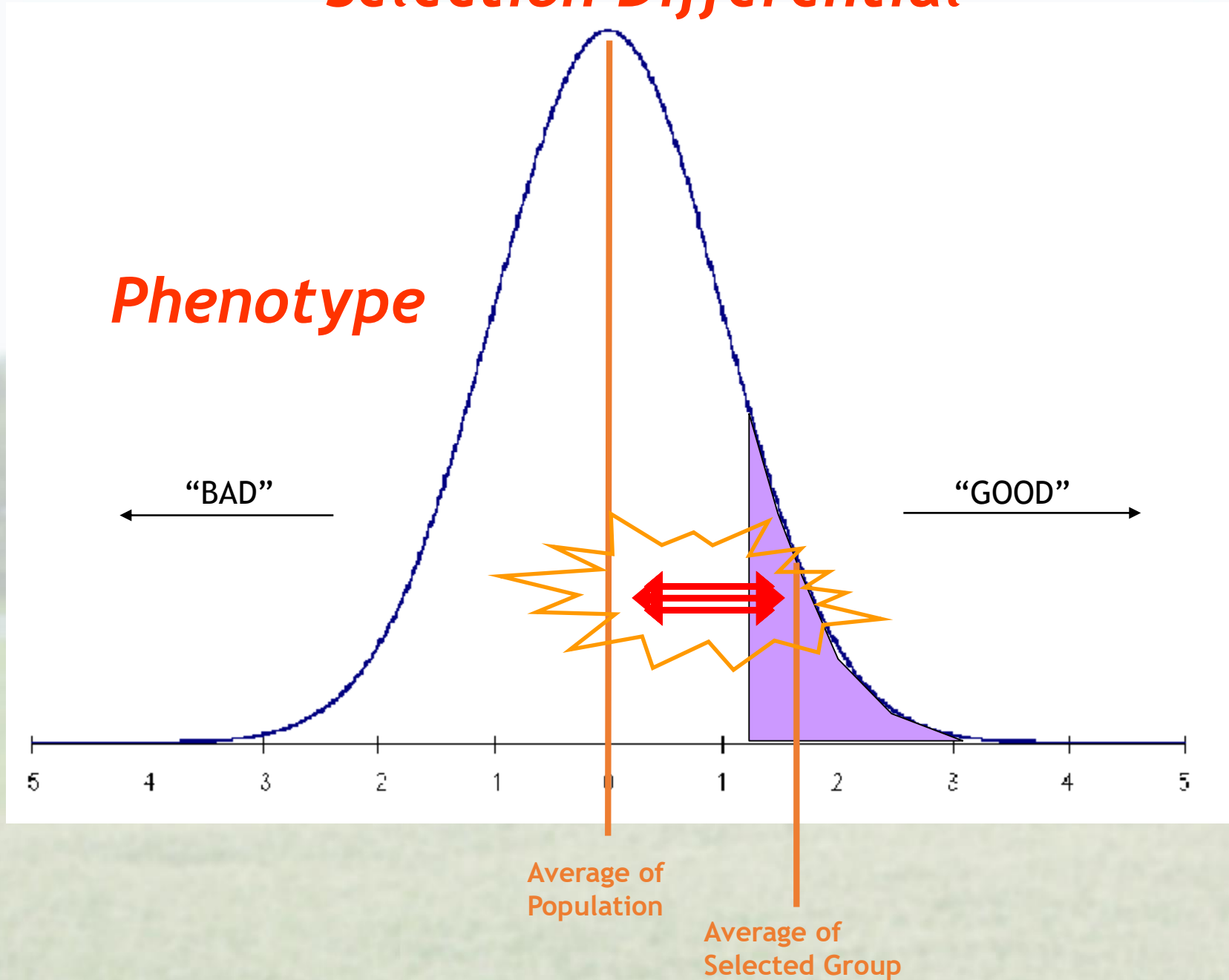
It is “influenced” by 4 main factors

- ΔG {
1. Heritability (h^2)
(amount of phenotypic variation due to genetic variation)
 2. Selection Differential (S)
(how big a “risk” are we are willing to take in choosing the parents)
 3. Generation Interval (L)
(the “waiting period”)
 4. Accuracy of Prediction (A)
(our confidence in our ability to choose better animals *precisely*)



Selection Differential = “Risk”

Selection Differential



Selection Differential

- The difference between the average of the **Selected** group and the average of the **Population**
- $\text{AVERAGE}_{\text{Selected}} - \text{AVERAGE}_{\text{Population}}$
- The **sign** is important !

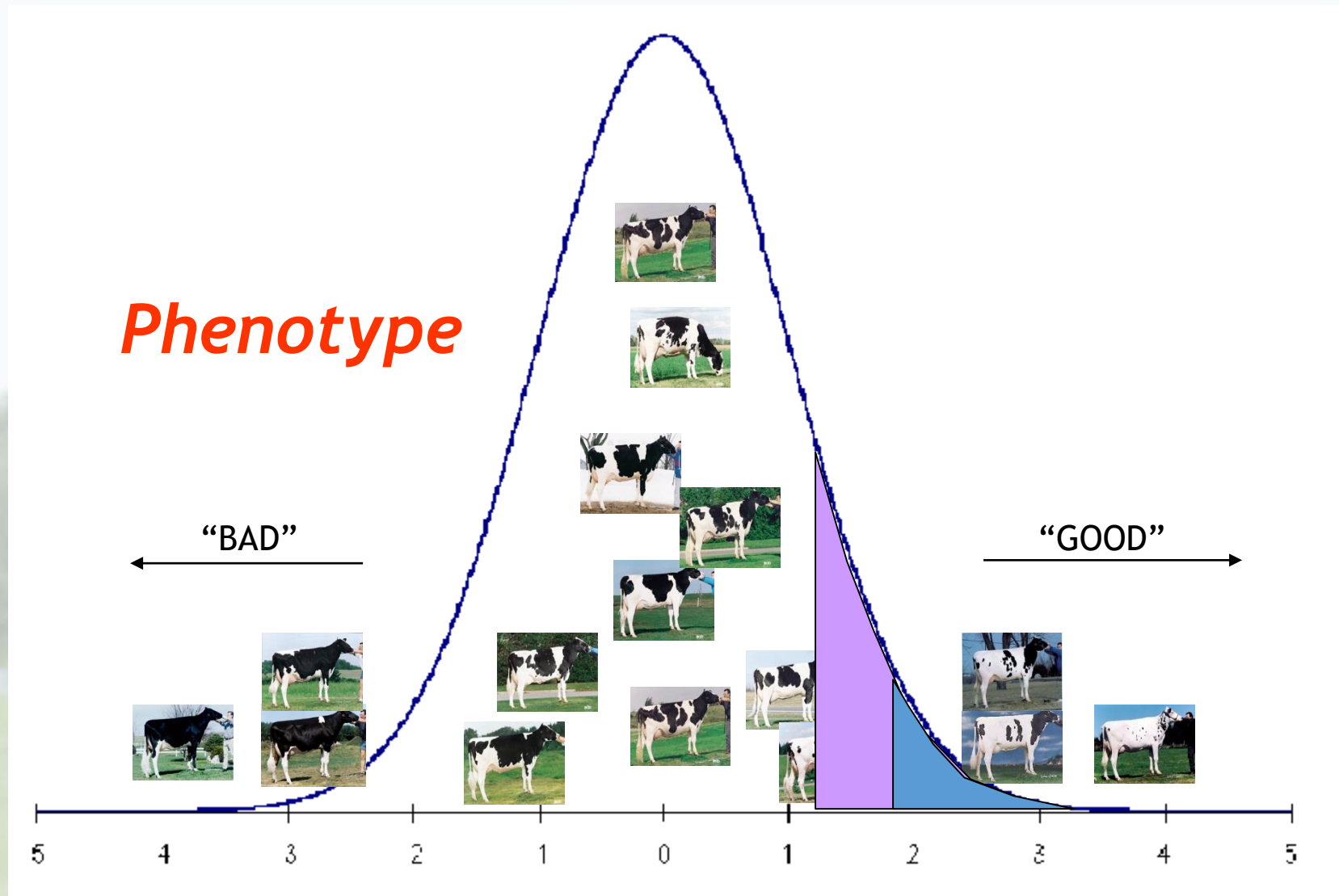
Sire Breed Group Averages for Birth, Weaning and Feedlot Performance Traits¹

Breed Group	% Unassisted Births	% Survival to Weaning	Birth Weight (lbs)	200 day Wean. Weight (lbs)	Average Daily Gain (lbs)	Final Weight (lbs)
Orig. Hereford-Angus	94.8	95.7	75.2	432	2.51	1068
Curr. Hereford-Angus	92.7	91.5	80.4	458	2.74	1152
Orig. Charolais	83.5	85.8	86.4	461	2.77	1160
Curr. Charolais	86.8	89.5	86.5	479	2.89	1219
Chianina	88.4	89.3	86.9	459	2.63	1124
Gelbvieh	94.1	91.0	83.8	456	2.66	1129
Limousin	91.8	90.8	80.6	443	2.49	1080
Maine Anjou	79.4	88.9	88.0	456	2.72	1147
Salers	95.2	91.7	80.9	464	2.70	1148
Shorthorn	97.6	91.9	82.4	460	2.73	1156
Simmental	89.2	88.8	84.9	458	2.73	1148

¹Adapted from Cundiff et al., 1993.

Example

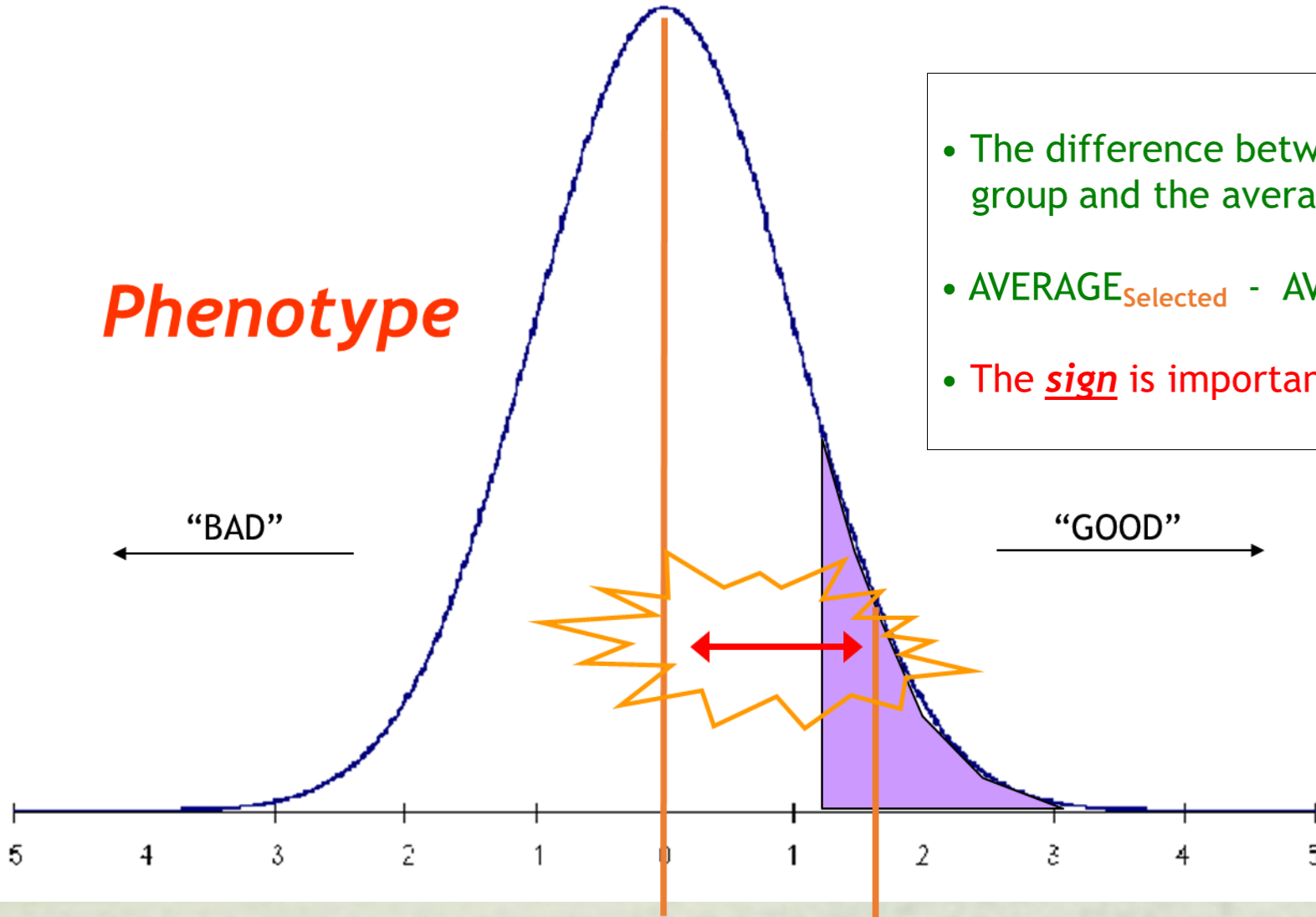
- The average growth rate for a herd of beef cattle is 1.2kg/day
- Animals with an average growth rate of **1.25kg/day** are selected as parents for the next generation
- What is the selection differential (superiority of the selected group)?
- How much of this superiority will be passed on to the next generation?



Selection Differential = “Risk”

Selection Differential

Phenotype



- The difference between the average of the **Selected** group and the average of the **Population**
- $AVERAGE_{Selected} - AVERAGE_{Population}$
- The sign is important !

Average of
Population

Average of
Selected Group

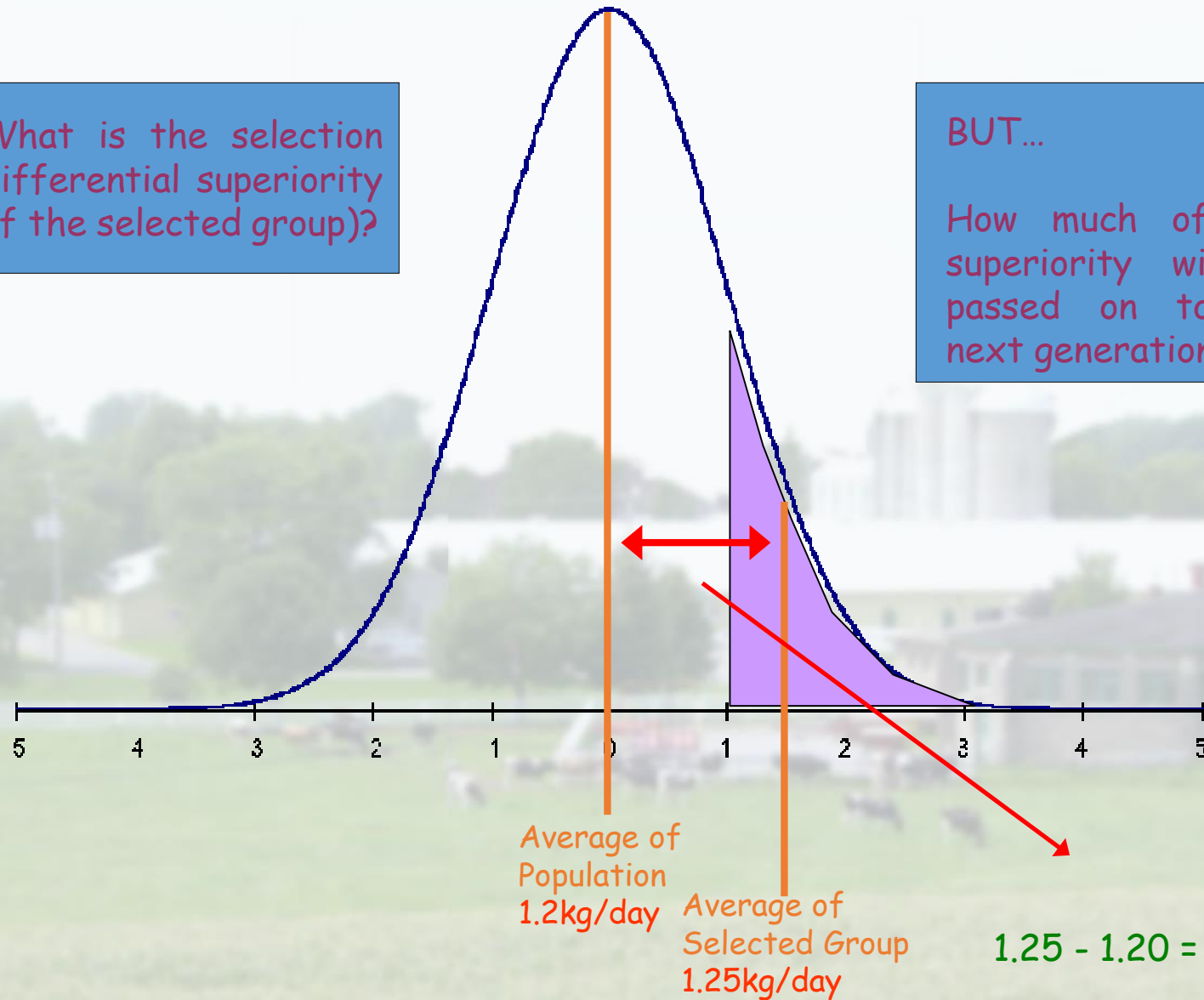
Example

- The average growth rate for a herd of beef cattle is 1.2kg/day
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- How much of this superiority will be passed on to the next generation?

What is the selection differential superiority of the selected group)?

BUT...

How much of this superiority will be passed on to the next generation?



Genetic Progress (ΔG) can be calculated by...

Heritability \times Selection Differential

$h^2 \times S$

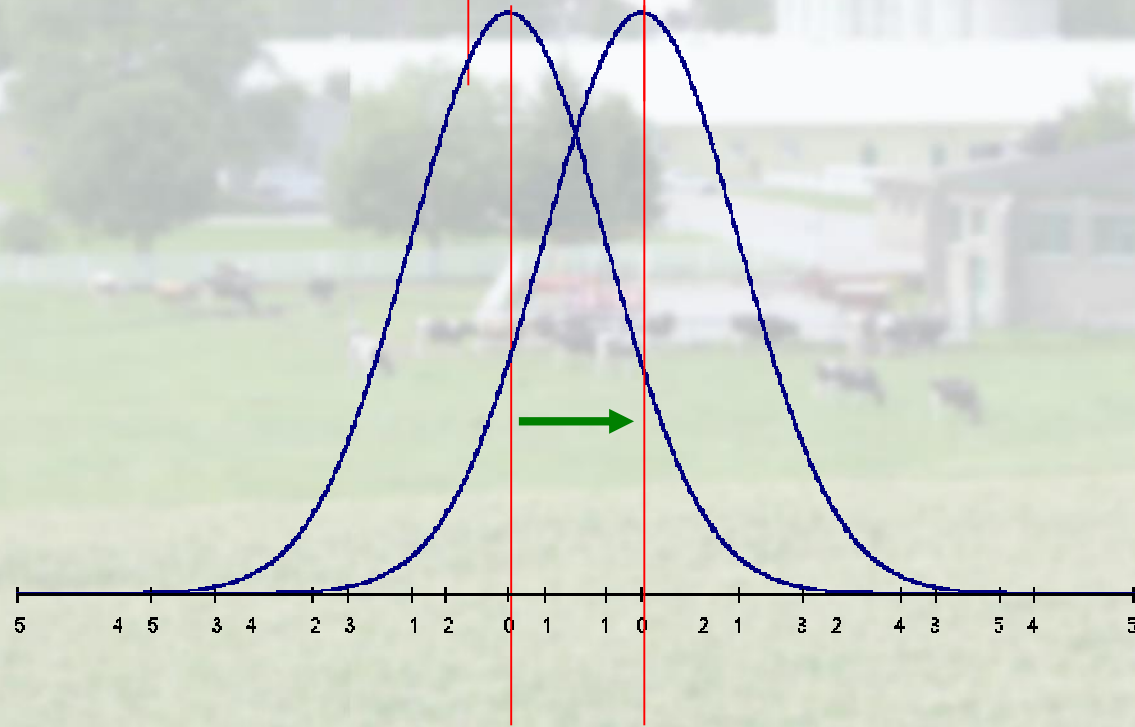
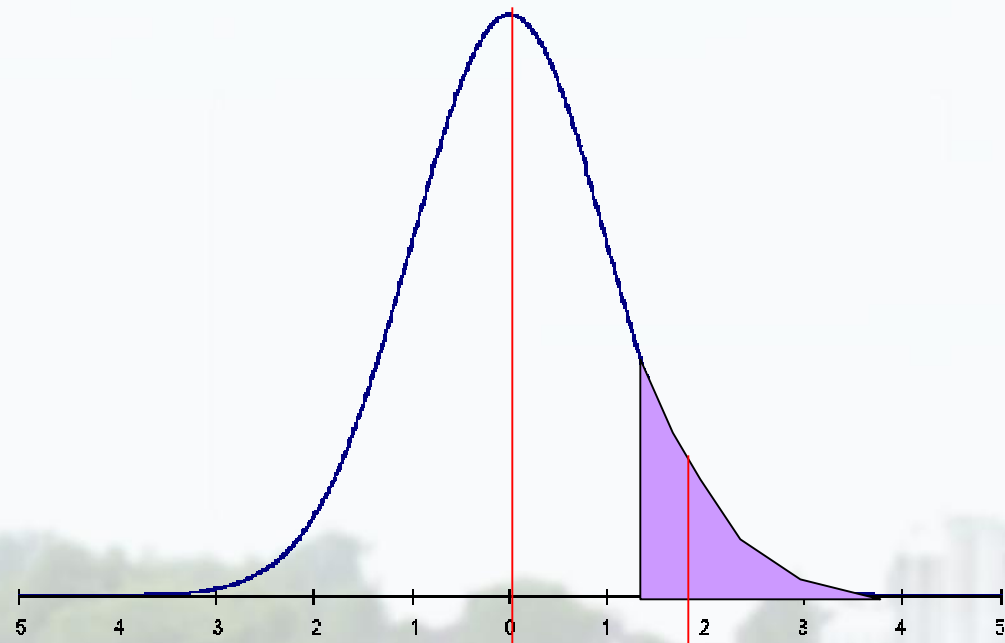
?

Beef Cattle
Calving Interval = Low
Birth Weight = Medium
Carcass Traits = High
Growth Rate = High



$$\Delta G = \overset{S}{0.05} \times \overset{h^2}{0.40} = \overset{\Delta G / \text{generation}}{0.02 \text{kg/} \underline{\text{Generation}}}$$

- The average growth rate for the *previous* generation was 1.20kg/day
- The average growth rate for the *new* generation of selected animals would be “*more than*” 1.20kg/day (i.e., this assumes that the older animals are not included)



Genetic Progress for Quantitative Traits

Genetic Progress = ΔG (“delta G”)

Increasing the frequencies of desired genes for a specific trait

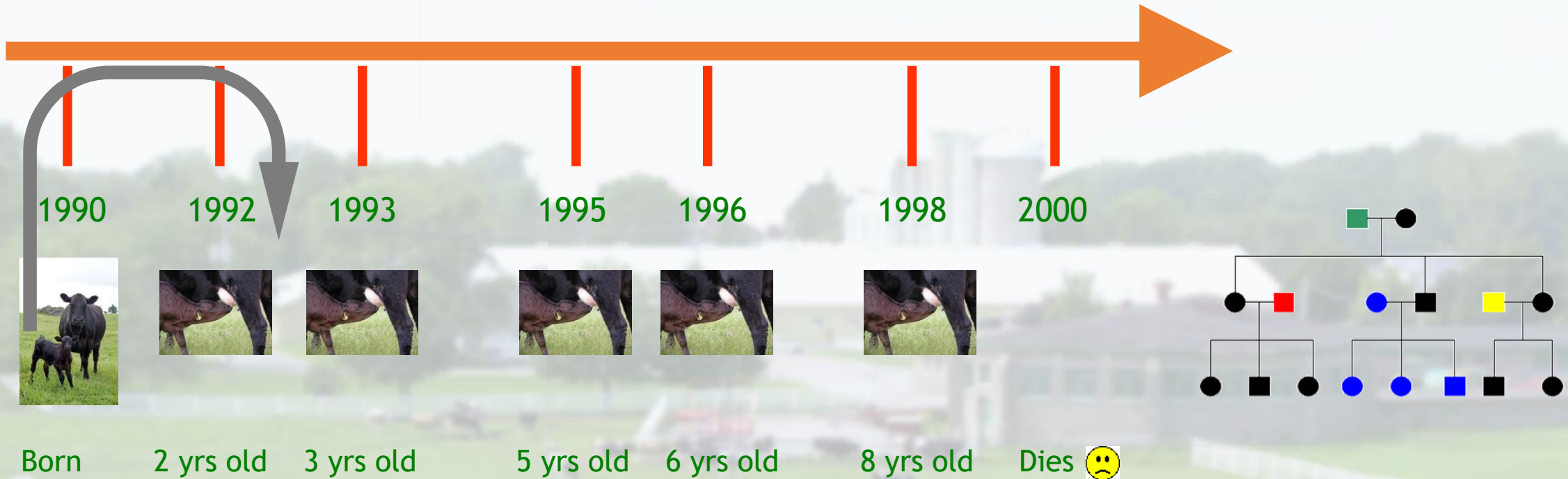
It is “influenced” by 4 main factors

- ΔG {
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(our confidence in our ability to choose better animals *precisely*)

Generation Interval

- The average age (years) of parents when all their offspring are born
- It varies from species to species
- It is usually different for both sexes
- A longer *gestation* length usually means a longer *generation* interval
- It is influenced by the method of selection (see later lecture)

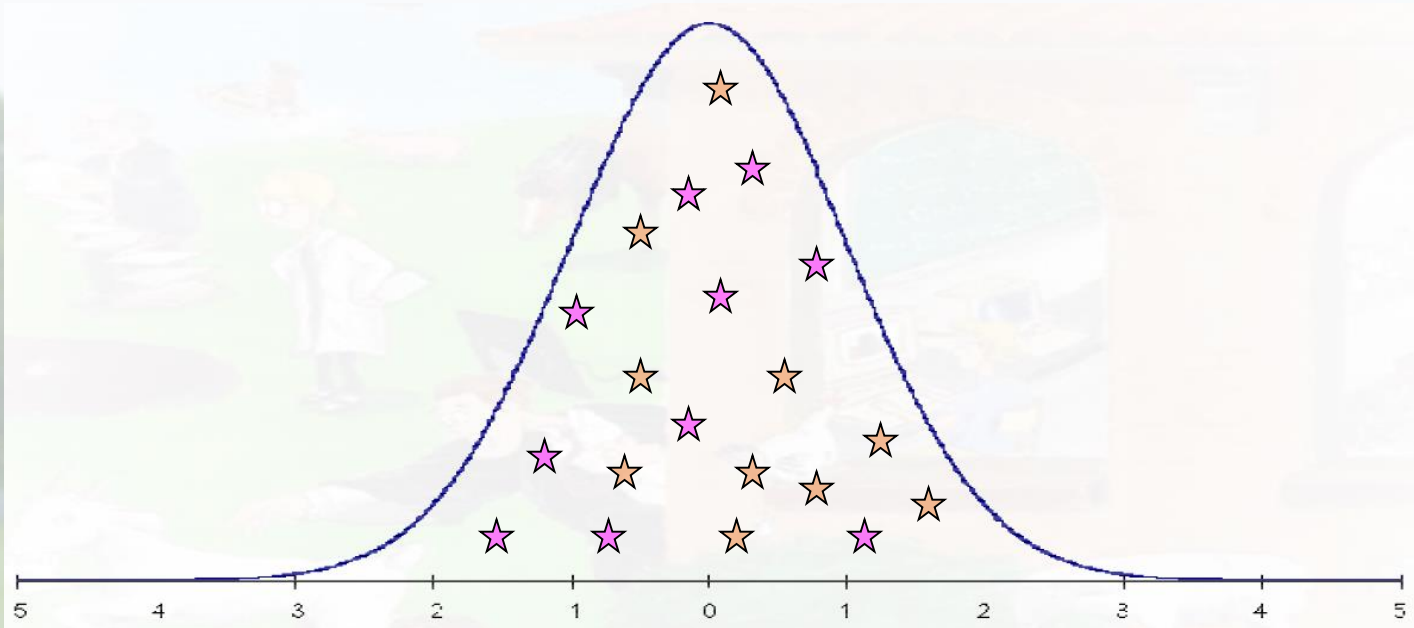
Generation Interval – an example



It's an average!

The Generation Interval is: $(2+3+5+6+8)/5 = 4.8$

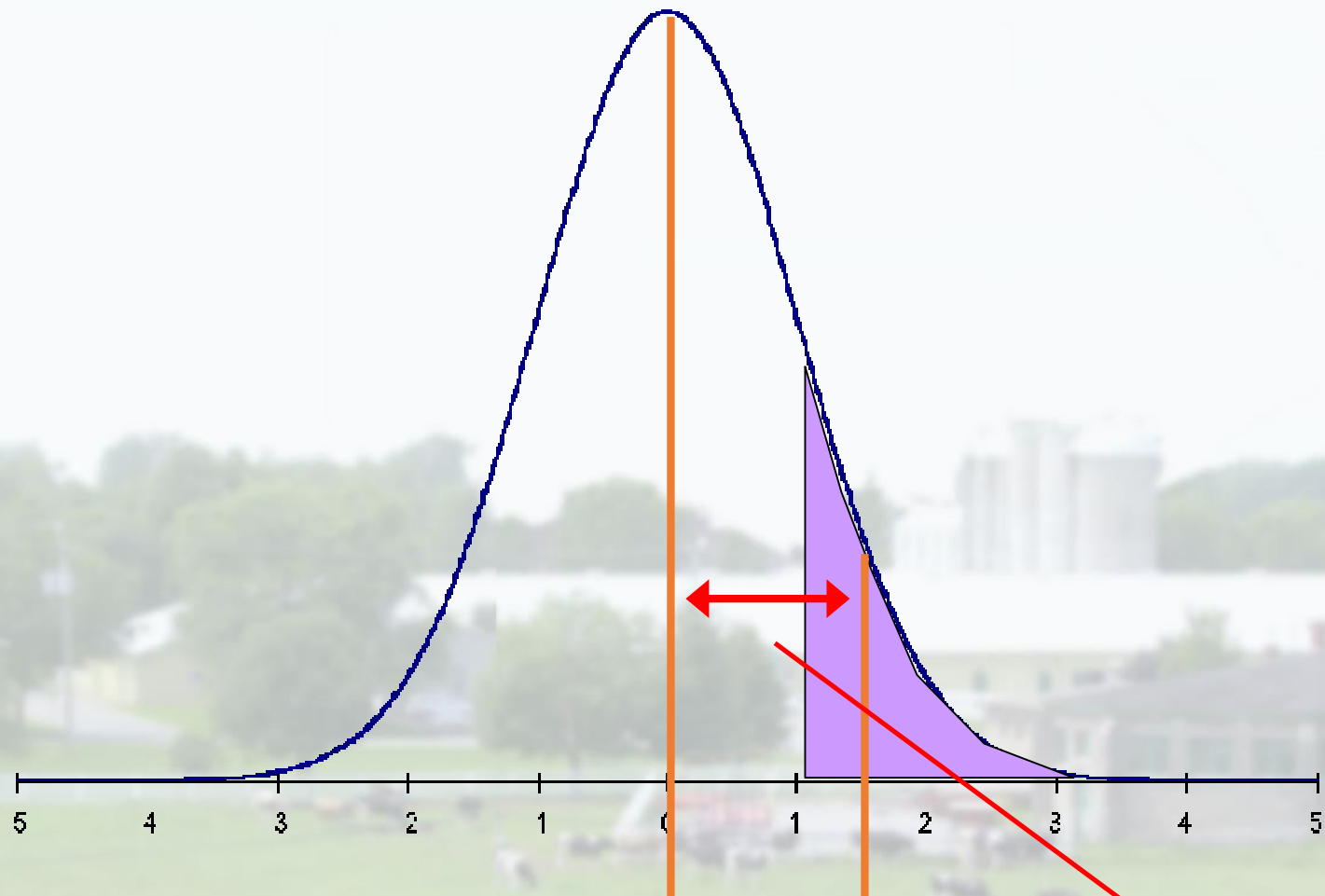
Population Generation Interval



This calculation must be done for each male and each female in the population and averaged to give the Population Generation Interval

Approximate Generation Intervals for Different Species (years)

Beef Cattle 6
Dairy Cattle 7
Sheep 3½
Swine 2½
Poultry 1
...	
Humans 35



Average of
Population
1.2kg/day

Average of
Selected Group
1.25kg/day

$$1.25 - 1.2 = 0.05\text{kg/day}$$

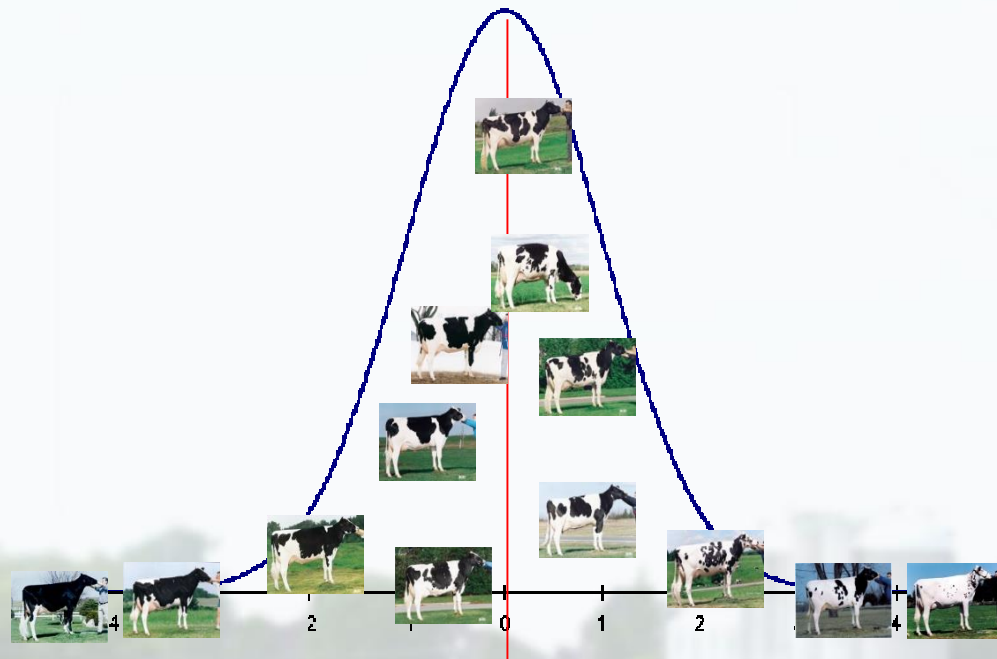
Genetic Progress (ΔG)

Genetic Progress (per Generation)

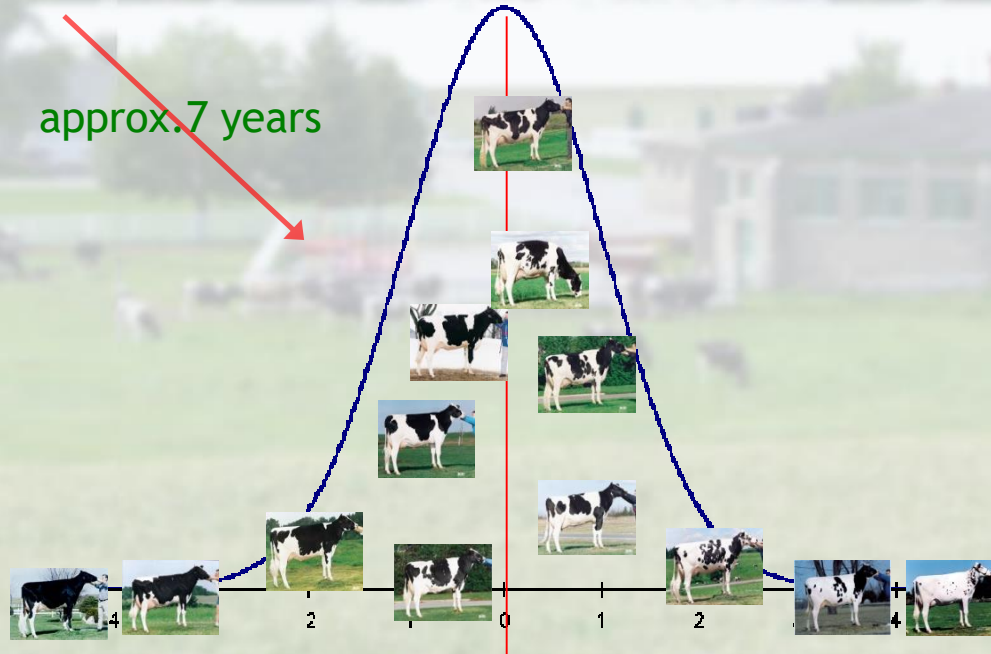
$$\begin{array}{cccc} S & h^2 & \Delta G/\text{generation} & \\ 0.05 & \times 0.4 & = & 0.02\text{kg}/\text{Generation} \end{array}$$

Genetic Progress per Year

$$\begin{array}{cccc} S & h^2 & L & \Delta G/\text{year} \\ (0.05 \times 0.4) \div 6 & = & 0.003\text{kg}/\text{Year} \end{array}$$



approx. 7 years



Genetic Superiority versus How much is passed on (ΔG)...

	Average of selected	Average of herd	Selection Differential (S)	h^2	Total Genetic Superiority	But how much of this is passed on (ΔG)?
3 Bulls	540 kgs	440 kgs	100 kgs	30%	30 kgs	15 kgs
200 Cows	480 kgs		40 kgs		12 kgs	6 kgs

If we're looking at only one animal, these are called → EBV Estimated Breeding Value and ETA Estimated Transmitting Ability

With equal numbers of ♂'s and ♀'s, the average genetic gain in the next generation (ΔG) will be 21kgs

With 3 ♂'s and 200 ♀'s, the average genetic gain in the next generation (ΔG) will still be 21kgs

With equal numbers
of ♂ (540) and ♀ (480)

$$(540 + 480) / 2 = 510$$

$$(510 - 440) * 0.3 =$$

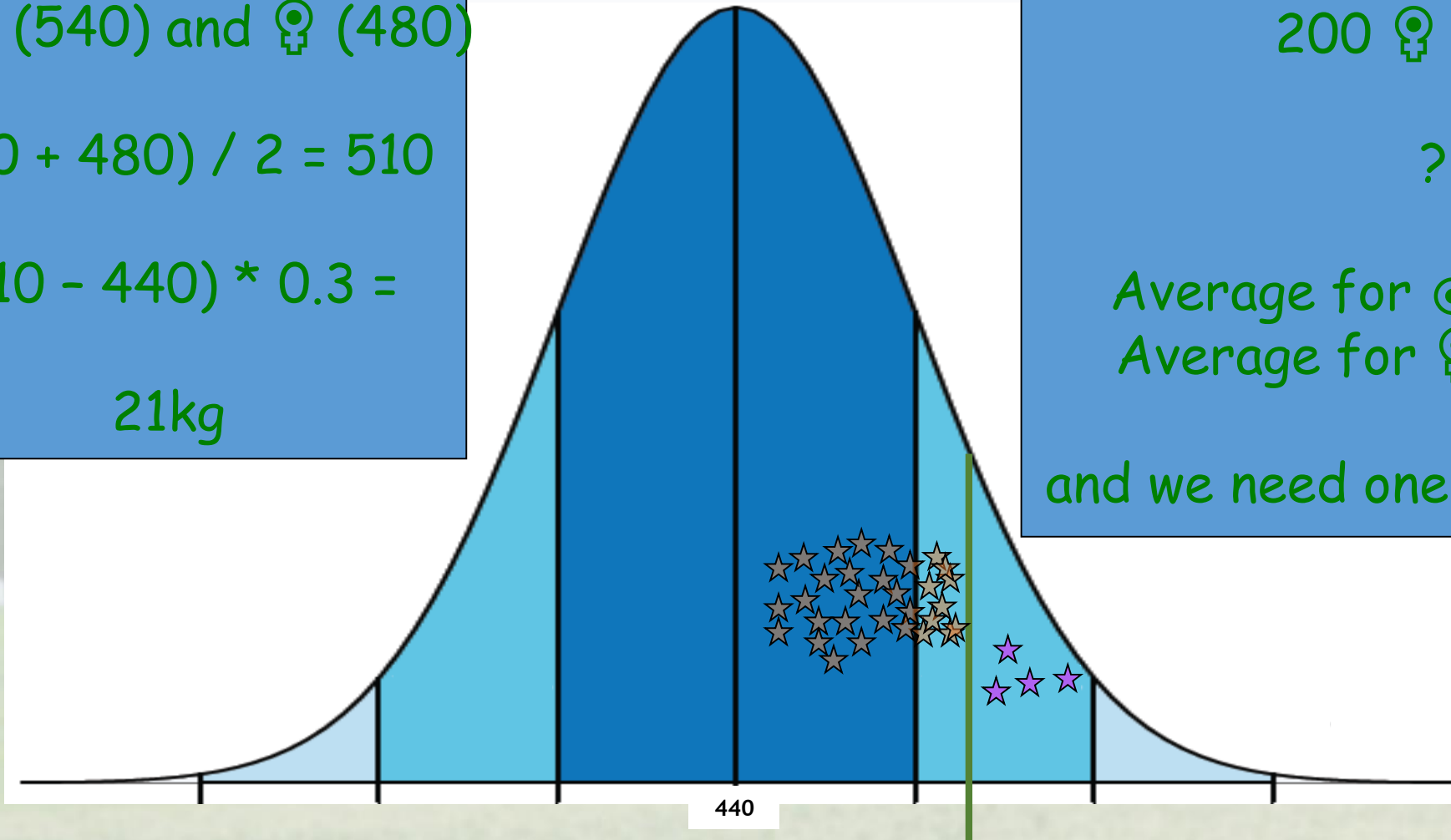
21kg

With 3 ♂ (540) and
200 ♀ (480)

?

Average for ♂ still = 540
Average for ♀ still = 480

and we need one ♂ for each ♀



Average of 540+480 = 510

Genetic Progress for Quantitative Traits

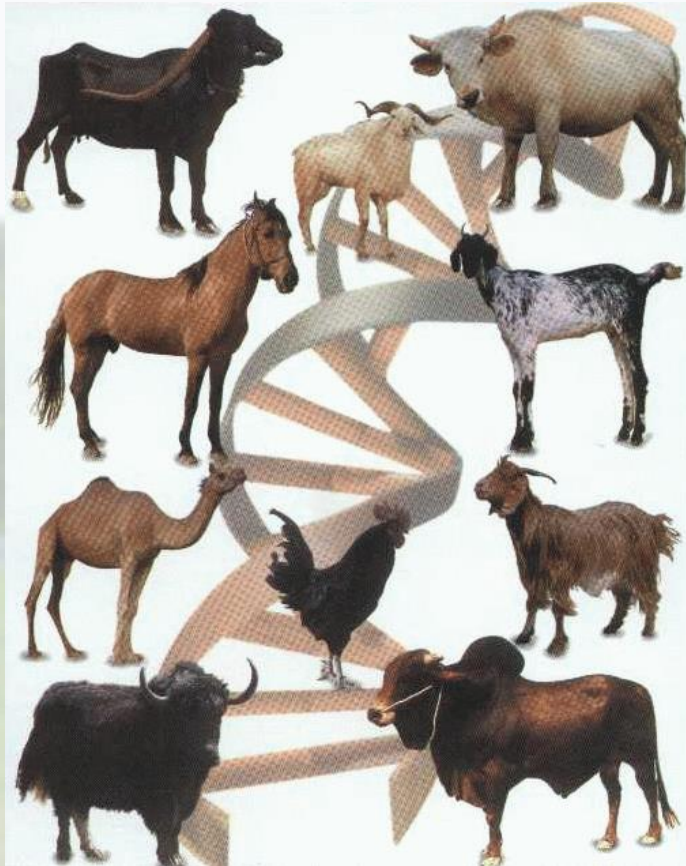
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Animal Genetics



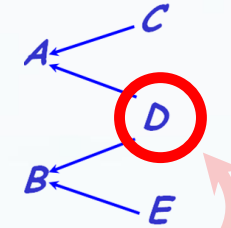
Genetics: "that branch of biology which deals with genes and their transmission from one generation to the next and their effect on external traits and characteristics"

"the science dealing with heredity and variation seeking to discover laws governing similarities and differences in individuals related by descent"

William Bateson, 1906

Relationship

=
the amount of genes that two
individuals have in common *by descent*



- Individuals that have genes in common due to a common ancestor ~~are related~~; the common genes are identical by descent
- Otherwise, genes are identical due to chance; the common genes are identical in state
- Relationship is calculated on the basis of Probability
- The relationship between 2 individuals A and B = R_{AB}

They say everyone has a double...
somewhere!



Not to be confused with Identical Twins...



Kissin' cousins the whole world over

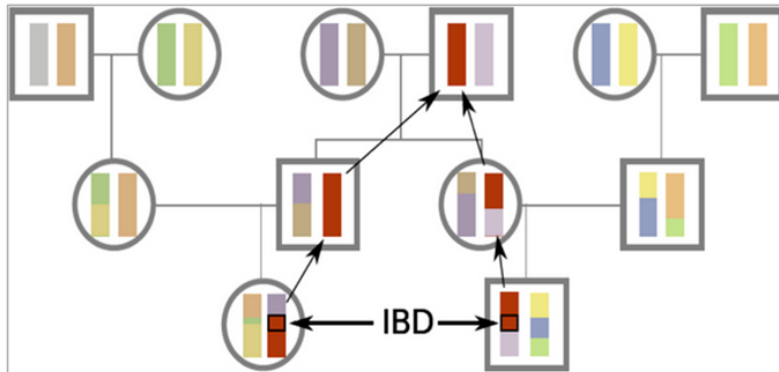
Posted by Kevin Hartnett June 5, 2013 10:00 AM

[Link](#) | [Comments \(0\)](#)

It's one of those fun, intuitive things to wonder: If you go back far enough in time, don't we all turn out to be related?

Recently on NationalGeographic.com, science writer Carl Zimmer [wrote](#) about a [new study](#) out of the University of California, Davis which begins to confirm just that. Geneticists Peter Ralph and Graham Coop looked at genetic samples for 2,257 present-day Europeans and [concluded that you only have to go back about 1,000 years](#) to find common ancestors for all Europeans alive today (with a European defined, for the purpose of this study, as an individual with all four grandparents born in the same country). To reach this conclusion, they looked for segments of DNA that are identical across the 2,257 people in their genetic sample. Two people are more closely (and recently) related when they have longer DNA segments in common, and the shortest lengths of shared DNA in the study's sample suggested common ancestors about a millennium ago. This result confirms the work of Yale statistician Joseph Chang, who in 1999 published a mathematical model showing that everyone alive in Europe 1,000 years ago is either related to every European alive today--or no one alive today (if they or their descendants went childless). Chang further calculated that everyone alive in the world today shares common ancestors if you go back about 3,400 years.

This chart from Ralph and Coop's paper gives a sense of how they performed their calculations. "IBD" stands for "identical by descent," and if you follow the highlighted red chunk of DNA backwards you see that the two cousins share an identical DNA segment inherited from one of their grandparents.



By definition

an individual is normally related to itself by a factor of **1**
and normally...

Parents and Children are related by a factor of $\frac{1}{2}$



Brothers and Sisters are related by a factor of $\frac{1}{2}$



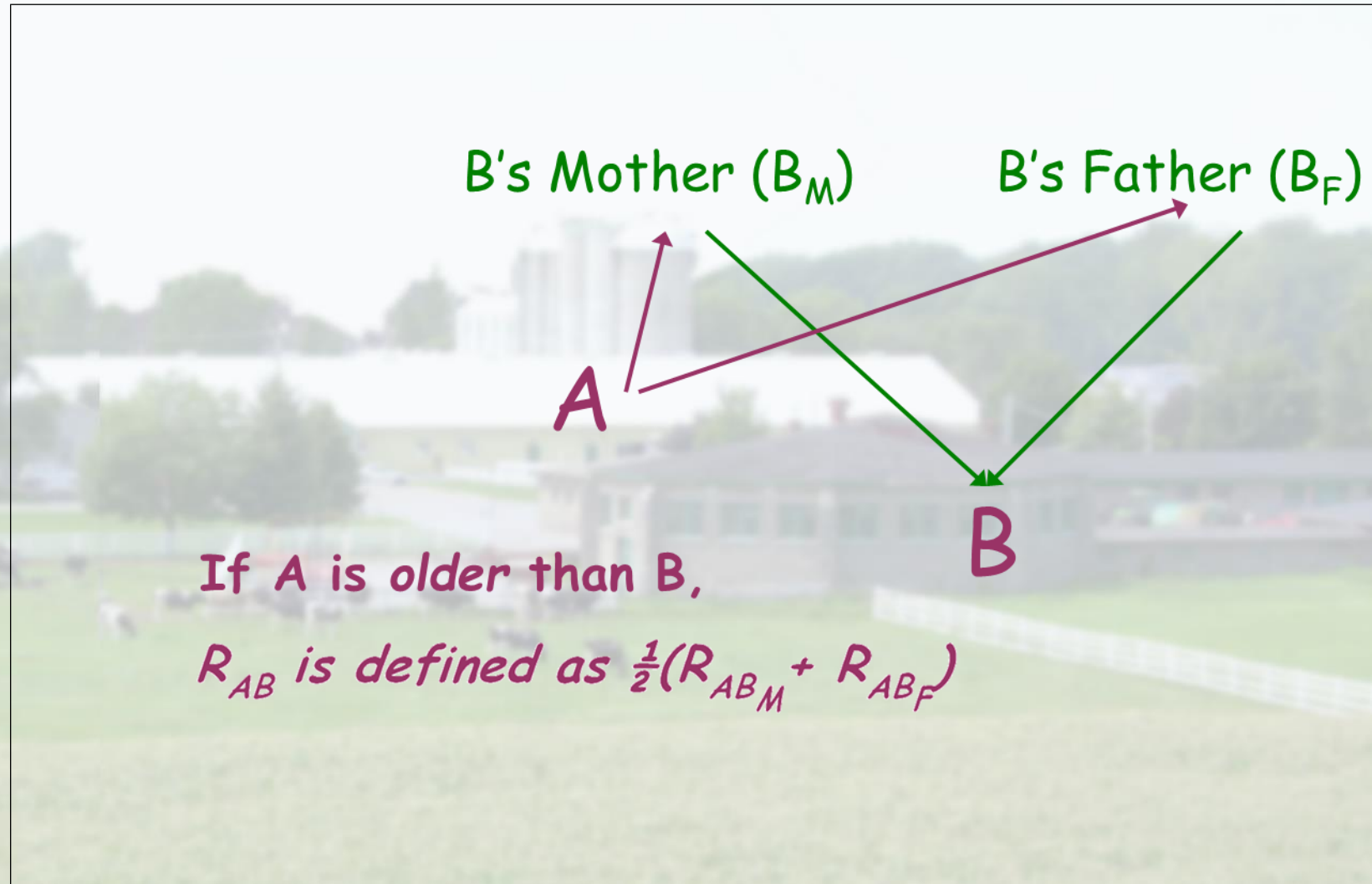
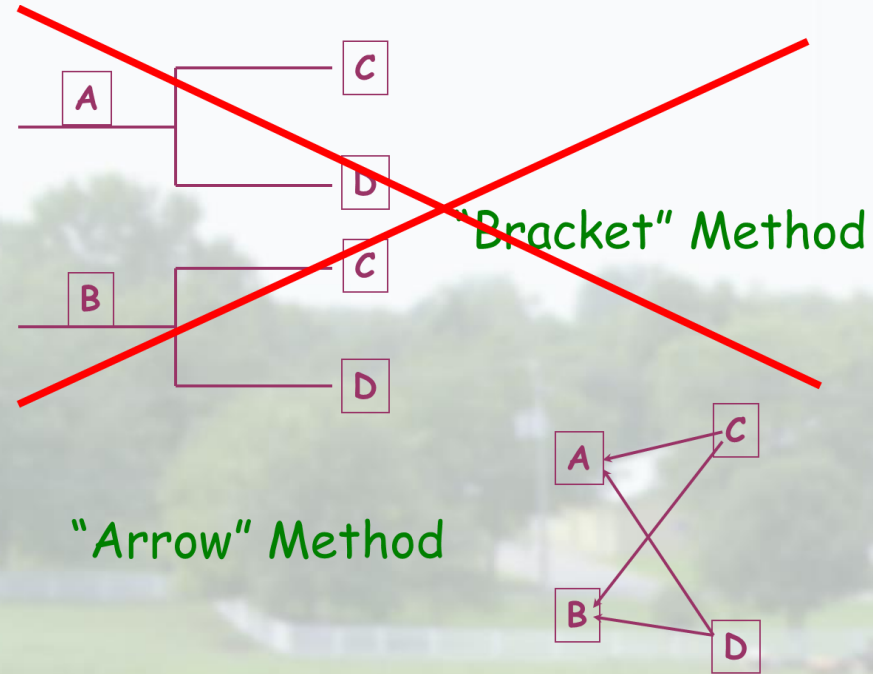
Grandparents and Grandchildren are related by a factor of $\frac{1}{4}$

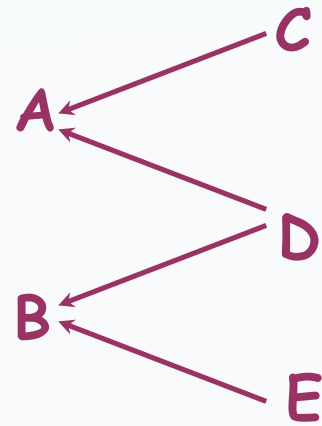


...

And each additional generation gap normally halves the relationship...

Definition of Relationship



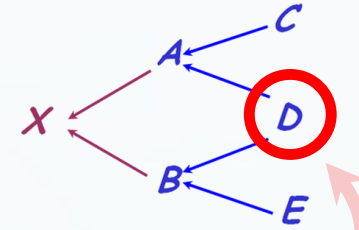


- Draw a box for the number of individuals involved
- Write down the individuals along the top from OLDEST to YOUNGEST as well as down the side
- Write down the parents of each individual on the top row (use 0 for any unknown parents)
- Put 1 in each *diagonal* cell.
- Finish each row by inserting $\frac{1}{2}$ of each of the relationships between the individual and *each* of the other individual's parents
- Copy the value for R_{AB} to R_{BA} since the Table is symmetric

	0 0 E	0 0 D	0 0 C	D E B	C D A
E	1	0	0	$\frac{1}{2}$	0
D	0	1	0	$\frac{1}{2}$	$\frac{1}{2}$
C	0	0	1	0	$\frac{1}{2}$
B	$\frac{1}{2}$	$\frac{1}{2}$	0	1	$\frac{1}{4}$
A	0	$\frac{1}{2}$	$\frac{1}{2}$	$\frac{1}{4}$	1

Inbreeding Coefficient

F



- Normally it is 0 (zero)
- If it is > 0 , that means that an individual's parents have a common ancestor (i.e., they are related to each other!)
- The inbreeding coefficient of an individual is equal to $\frac{1}{2}$ of the relationship between the two parents of the individual
- The Inbreeding Coefficient of "X" is defined as:

$$F_X = \frac{1}{2}(R_{X_M X_F})$$

= $\frac{1}{2}$ of the relationship between X's Mother and X's Father

Rules for using the Tabular Method

to compute relationships

COMPLETE !

- Draw a box for the number of individuals involved
- Write down the individuals along the top from OLDEST to YOUNGEST as well as down the side
- Write down the parents of each individual on the top row (use 0 for any unknown parents)
- Put 1 in each *diagonal cell*. Then add $\frac{1}{2}$ of any relationship that exists between the parents of the individual
- Finish each row by inserting $\frac{1}{2}$ of each of the relationships between the individual and each of the other individual's parents
- Copy the value for R_{AB} to R_{BA} since the Table is symmetric

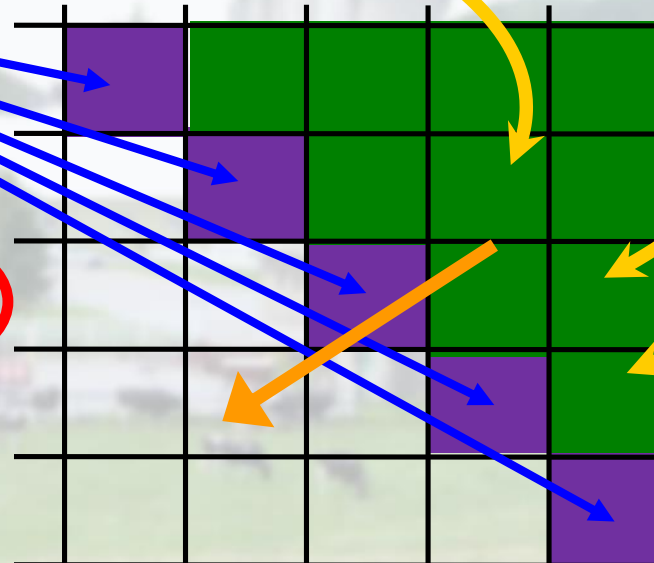
So, the "Three Rules" are...

$$R_{AB} = \frac{1}{2}(R_{AB_M} + R_{AB_F})$$

*A must be older than B
(or, at least, not younger)*

$$R_{AA} = 1 + F_A$$

$$F_A = \frac{1}{2}(R_{A_M A_F})$$



"A" and "B" are two different "Individuals"
"M" = "Mother" and "F" = "Father"