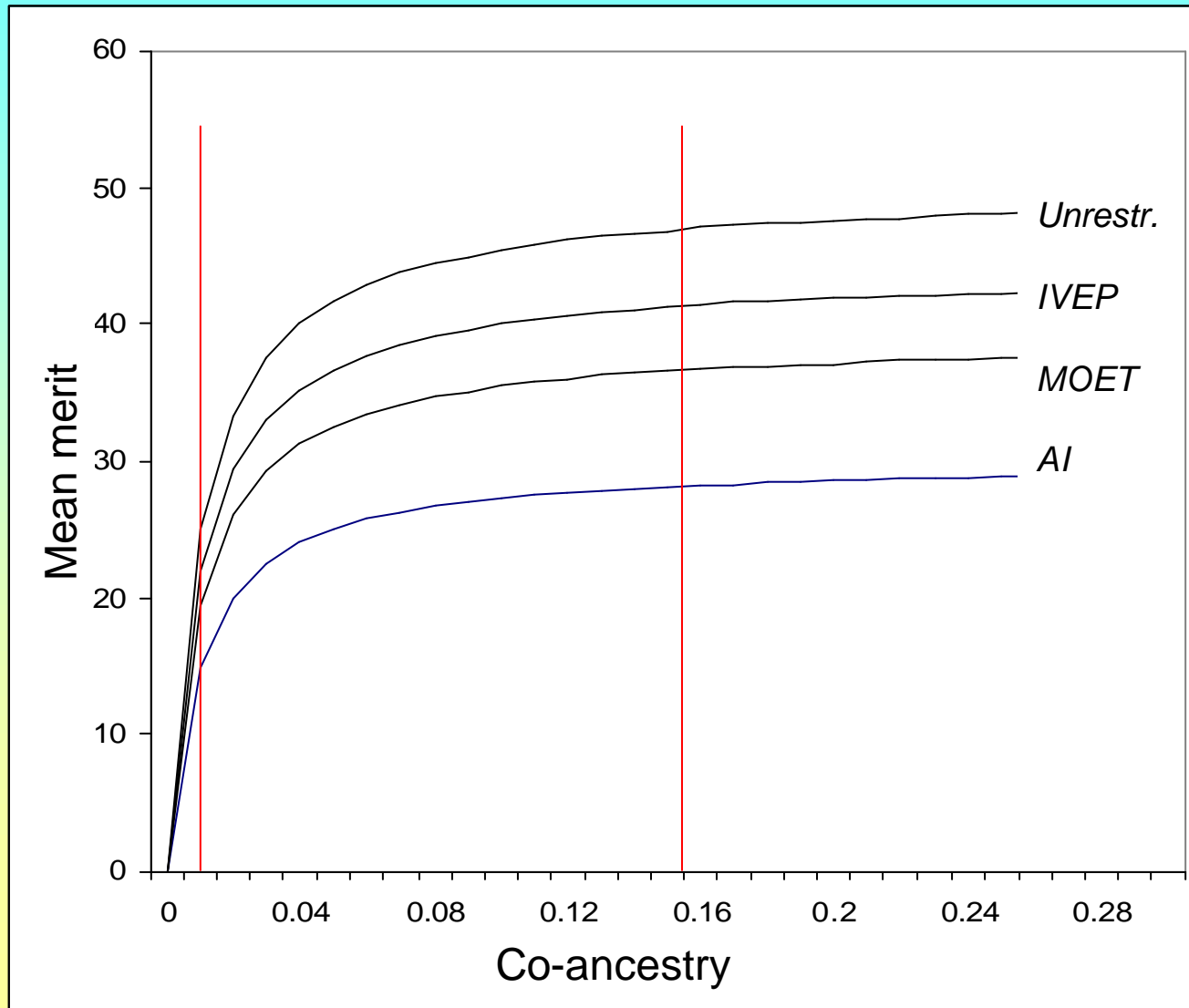


Inbreeding

Genetic gain versus genetic diversity

- Sustainable breeding programs require optimal selection balancing genetic gain and genetic diversity
- Potential short term benefits from reproductive technologies are inhibited by the need to maintain diversity

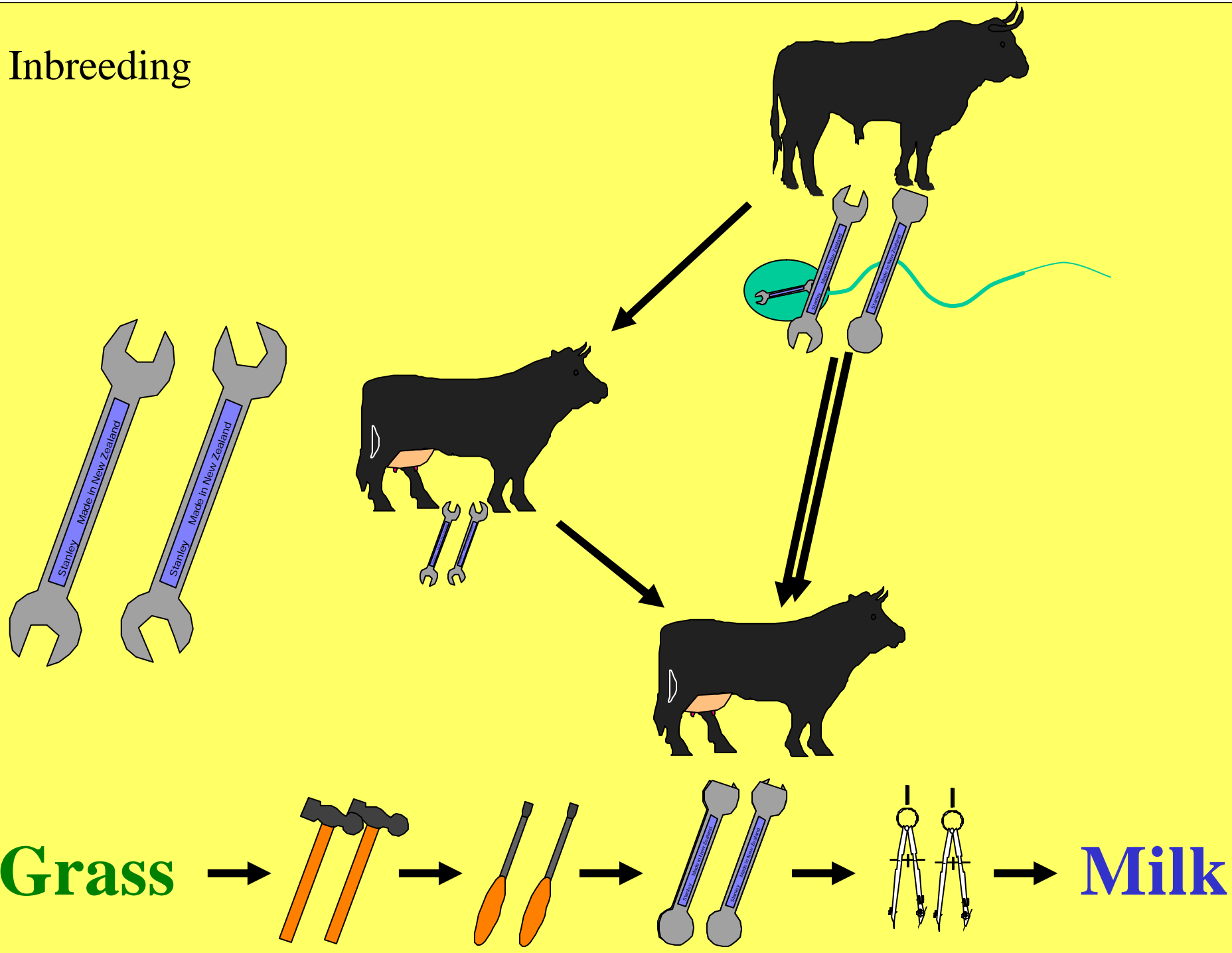
The balance between increased merit and inbreeding



Optimum Selection Strategies

- Maintain effective size of population
- Optimized selection (BLUP ~ co-ancestry)
 - Can be done tactically
 - Hard to implement in deterministic modeling
- Can predict inbreeding from genetic contributions theory

Inbreeding



So, previous slide illustrates

- Inbreeding coefficient

Animals that have related parents have more chance to carry two alleles that are identical by descend

- Genetic defects

Inbred individuals have more chance to express genetic defects

- Inbreeding depression:

Heterozygosity has often positive effects on phenotypes (and therefore inbreeding/homozygosity a negative effect >>

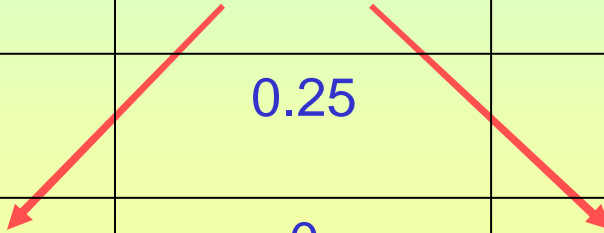
Further

Inbred populations have less genetic variance

Change in genotype frequencies in response to inbreeding

- For example, $p=q=0.5$

Genotype	aa	Aa	AA
Frequency	q^2+pqF	$2pq-2pqF$	p^2+pqF
At F=0	0.25	0.50	0.25
At F=0.5	0.375	0.25	0.375
At F=1.0	0.5	0	0.5



Note that allele frequencies do not change

Consequences of inbreeding

Increased frequency of 'genetic defects'

Let q be equal to 1%. We have then

F of individual	Frequency of aa	Probability of being affected
0 (normal)	q^2	1 in 10,000
0.125	$q^2 + pqF$	13.4 in 10,000
0.25	$q^2 + pqF$	25.8 in 10,000

Inbreeding depression reduces productivity & viability

- Inbreeding depression
 - Due to increased homozygosity, in relation to traits that show dominance
 - Most notable effect is on reproductive fitness
- Inbreeding depression is typically greater in the wild than in captivity
 - Trait depression variable, often 2-20% per 10% F

Inbreeding reduces genetic variance

- As individuals become more alike, the *within* population genetic variance decreases
- V_A is additive genetic variance
- V_A (with inbreeding) = $(1-F) V_A$ (without inbreeding)

Predicting rate of inbreeding from population size and structure

- Predict population mean F after some generations
- Inbreeding occurs more frequently in small populations as there is a larger chance for an individual to mate with a related individual.

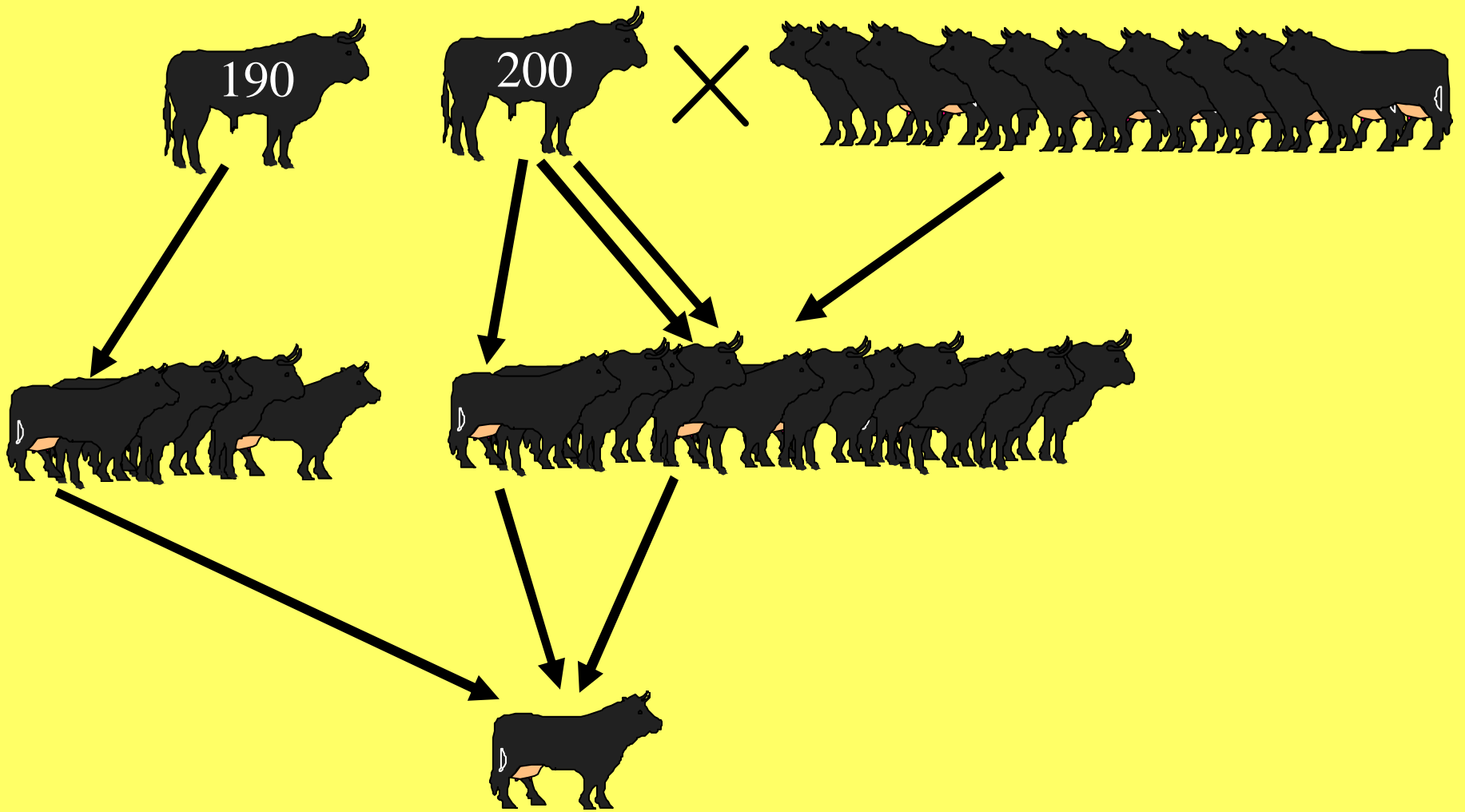
Calculating N_e

Accounting for unequal sex ratio

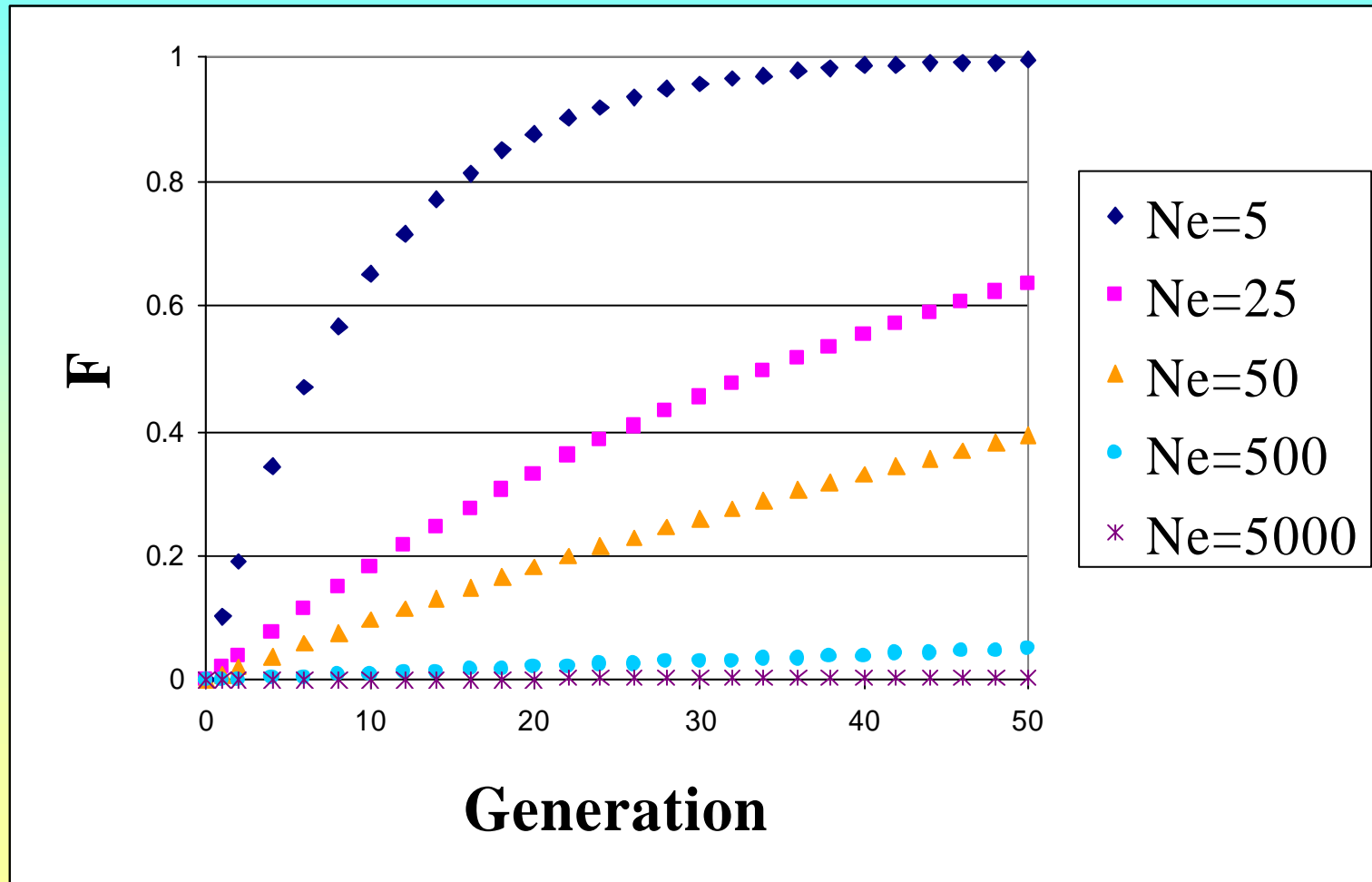
- Effective pop'n size (N_e) reduces towards sex with fewer breeding individuals

$$N_e = \frac{4 \cdot N_m \cdot N_f}{N_m + N_f}$$

Males / generation	2	2	2	5	20	1
Females / generation	2	20	200	200	200	99999
N	4	22	202	205	220	100,000
N_e	4	7.3	7.9	19.5	72.7	4



Inbreeding rate & Effective Size (Ne)



More sophistication in predicting inbreeding rate

- variation in family size -

$$N_e = \frac{8N}{V_{km} + V_{kf} + 4}$$

With selection → makes dF a few times higher

- genetic contributions theory

Avoiding inbreeding

- Mating strategies ?
- Manage effective populations size
 - Nr of parents selected (.....males)
 - Relatedness of selected animals
 - Nr. of Offspring per sire (think of V_{km})

Balancing Selection and Inbreeding

- Higher selection intensities make bigger gain
- Fewer animals are selected, so also more inbreeding
- This trend is more evident with higher rates of fecundity
- Effect of new reproductive technologies
- Genetic evaluation (BLUP) favors selection of related animals
- rationalization of selection make inbreeding restriction methods a necessity

Why restrict inbreeding

- Avoid loss of genetic variation/genetic diversity
- Inbreeding depression
- Increase of homozygotes with deleterious recessives
- Inbreeding is closely associated with risk (and genetic drift)

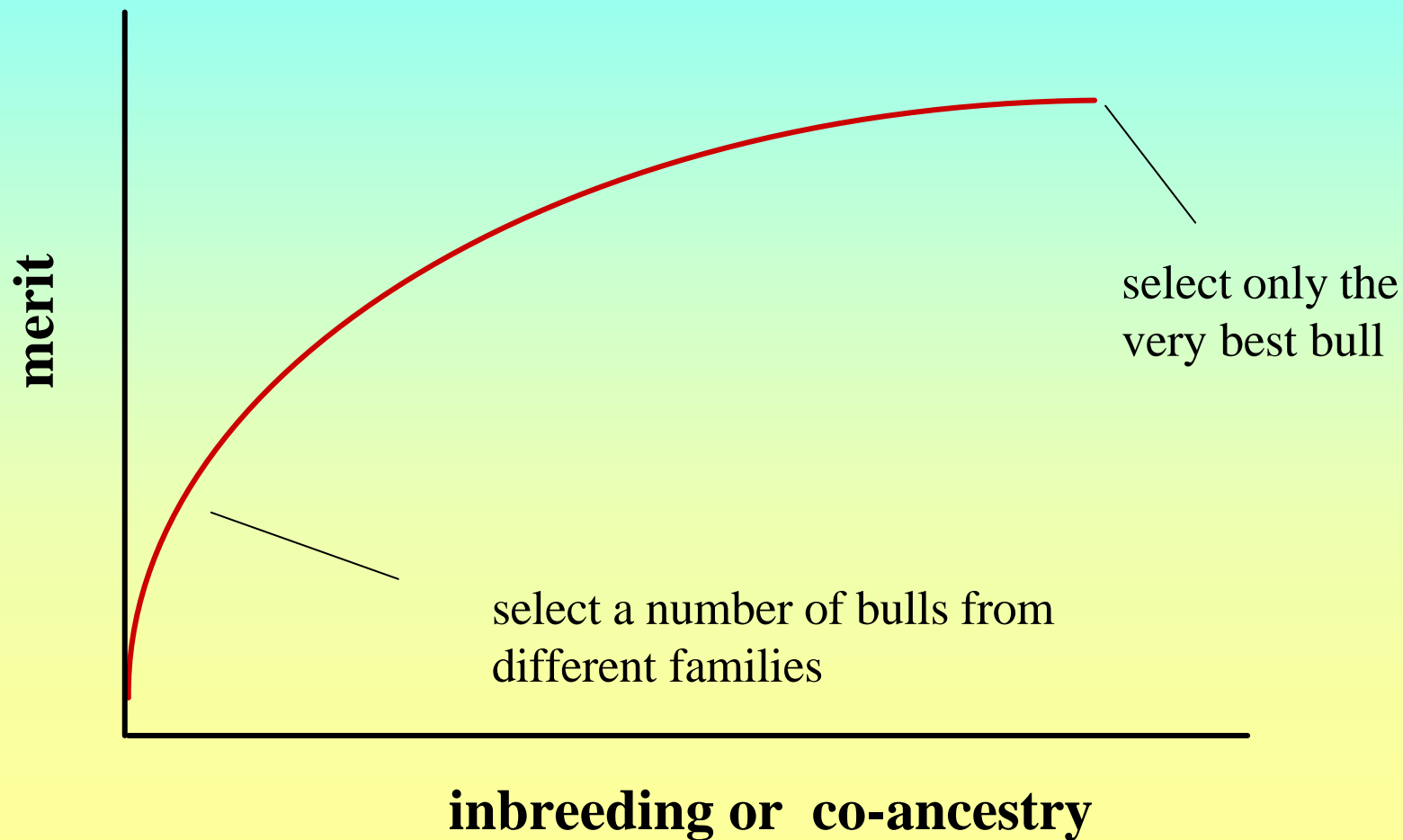
How to restrict inbreeding?

- Mating policies mostly affect
 - progeny inbreeding (*short term*)
 - but not *long term* rate of inbreeding ΔF
 - The long term inbreeding rate depends on *effective population size*
- Long term inbreeding is restricted by restricting the average co-ancestry among selected parents
 - Manage effective populations size
 - Nr of parents selected (.....males)
 - Relatedness of selected animals
 - Nr. of Offspring per sire (think of V_{km})

Balancing inbreeding and merit

- Restricting co-ancestry but this slows genetic (short term) progress
- How much inbreeding can we afford?
- Often inbreeding is restricted by limiting ΔF to a certain preset value
- This optimal value may depend on your situation (how open is your nucleus)

Balancing inbreeding and merit



Jointly optimizing merit and inbreeding

In notes this x is a “c” p186

- merit: $x'G$
 - x = vector with each animal's contribution to progeny
 - G = the vector with merit (EBV's) for each animal
- Co-ancestry: $x'Ax$
 - x = vector with each animal's contribution to progeny
 - A = Numerator Relationships Matrix

Remember: $\Delta F = x'Ax/2$

$$F_i = 0.5 a_{ij}$$

Vector x of animal contributions

Source of animals	Animal#	$x =$ Contribution	
Male candidates	1	0	} $\Sigma = 0.5$
	2	.1	
	3	.05	
	4	0	
	5	.01	
	6	0	
	7	0	
	8	0	
	
Female candidates	101	0	} $\Sigma = 0.5$
	102	.01	
	103	.01	
	104	.01	
	105	0	
	106	0	
	107	0	
	108	.08	
	

Optimizing genetic contributions

- Maximize objective function

$$x'G - \underline{\lambda}x'Ax$$

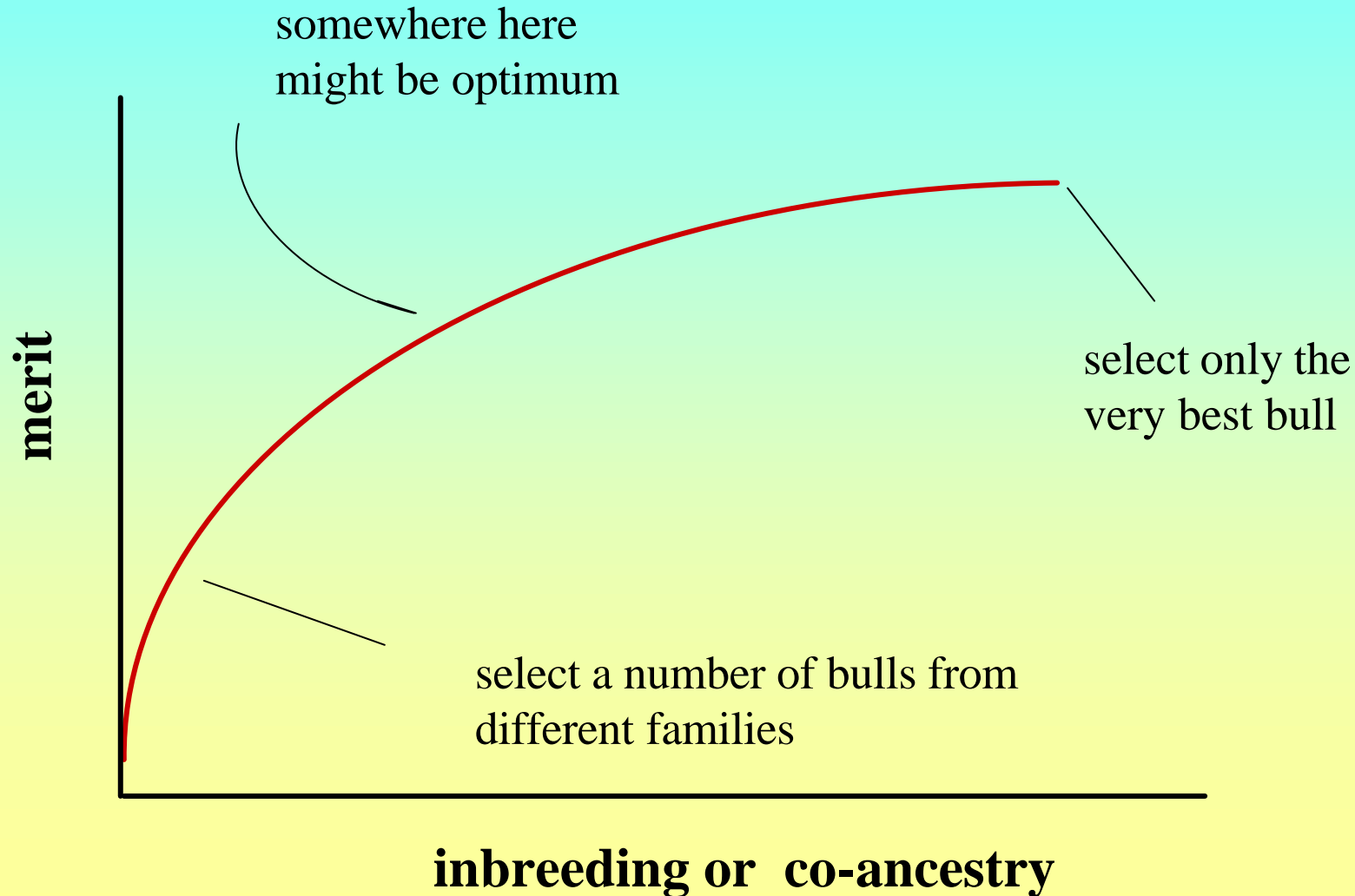
Question: what is best value for λ ?

Could preset rate of inbreeding (e.g. 1%)
and determine λ accordingly (Meuwissen, 1997)

Alternative: look at graph (next slide)

Balancing inbreeding and merit

This graph will look different for each population



Genetic Contributions Theory

- Contribution of an ancestor to future gene pool c_i
- After many generations, all animals within a drop have the same c_i from ancestor i .
- $C_i = a + \beta \cdot u_i$ contribution depends on EBV ($= u_i$)
- Exp. gain depends on sum of $c_i u_i$
- Exp. Inbreeding depends on sum of c_i^2
- Can predict based on selection on phenotype, or BLUP, but not based on optimal selection