Week 1 – Genetics of Breeding Populations

Quick review: Definitions, Mendel laws and linkage

Forces that contribute to changes in allele frequency

Evolutionary forces: mutation, random genetic drift and natural selection
Breeding forces: artificial selection and inbreeding

Inbreeding

Consequences of inbreeding
The inbreeding coefficient *F*
Calculating the inbreeding coefficient from pedigrees (take-home exercise)
Accumulated effect of inbreeding – population size
Accumulated effect of inbreeding – regular mating systems
Calculating the inbreeding coefficient from molecular data (in-class demo)

Inbreeding – causes and consequences (fitness)

- Negative consequences in outcrossing species
- Inbreeding depression
- Associated with increased homozygosity of rare recessive alleles
- Reduction in fitness – reduced viability and fertility

Inbreeding reduces reproductive fitness – Darwin (1876)

Characters	# Sp.	# Exp.	O>I	O<I	Similar	Difference (O-I)
Height	54	83	57	8	18	13%
Weight	8	11	8	1	2	
Flowering	32	58	44	9	5	
Seed Set	23	33	26	2	5	41%

What about crops that are outcrossing but where inbreds are used?

Inbreeding – causes and consequences (productivity)

Table 3. Percent oil per generation for the different populations averaged over replicates (C – population, N_b – size, % – selection pressure)

Generation	C	1	2	3	4	5	6
	N_b	6	10	50	6	10	50
	%	17%	17%	17%	5%	5%	5%
1963		4.66 ± 0.09	4.80 ± 0.04	4.70 ± 0.00	4.75 ± 0.03	4.85 ± 0.13	4.75 ± 0.05
1964		4.56 ± 0.10	4.47 ± 0.10	4.50 ± 0.00	4.80 ± 0.19	4.80 ± 0.04	4.75 ± 0.05
1965		5.18 ± 0.17	5.12 ± 0.15	5.30 ± 0.00	5.58 ± 0.16	5.80 ± 0.12	5.80 ± 0.00
1966		5.38 ± 0.12	5.42 ± 0.22	5.50 ± 0.10	6.00 ± 0.13	6.32 ± 0.22	6.30 ± 0.20
1967		5.49 ± 0.32	5.45 ± 0.37	5.44 ± 0.26	6.09 ± 0.36	6.43 ± 0.23	6.41 ± 0.32
1968		5.48 ± 0.49	6.02 ± 0.37	5.75 ± 0.08	6.25 ± 0.27	6.82 ± 0.35	6.94 ± 0.18
1969		5.67 ± 0.30	6.06 ± 0.26	6.05 ± 0.13	6.55 ± 0.23	7.03 ± 0.31	7.34 ± 0.16
1970		6.03 ± 0.34	6.55 ± 0.27	6.53 ± 0.11	6.86 ± 0.19	7.43 ± 0.25	8.00 ± 0.32
1971		5.51 ± 0.54	6.36 ± 0.35	6.34 ± 0.14	7.12 ± 0.30	7.01 ± 0.26	7.69 ± 0.37
1972		5.75 ± 0.20	6.14 ± 0.28	6.51 ± 0.15	7.67 ± 0.44	7.40 ± 0.69	8.37 ± 0.40
1973		6.00 ± 0.31	5.81 ± 0.23	6.66 ± 0.06	7.29 ± 0.20	8.68 ± 0.42	8.43 ± 0.32

Silvela et al. Theor Appl Genet (1989) 78:298-304

Table 4. Overall selection responses calculated as the regression of percent oil on generation number (generation intervals 0–10, 0–5, 5–10) and realized heritabilities (Rh^2) for the different populations (C – population, N_b – size, % – selection pressure)

Population			Response			Rh^2
C	N_b	%	0–10	0–5	5–10	
1	6	17	0.13±0.02	0.20±0.05	0.07±0.05	0.27±0.08
2	10	17	0.17±0.04	0.27±0.06	−0.03±0.07	0.29±0.03
3	50	17	0.22±0.02	0.24±0.05	0.17±0.04	0.31±0.01
4	6	5	0.28±0.02	0.34±0.05	0.25±0.05	0.25±0.02
5	10	5	0.33±0.04	0.44±0.06	0.29±0.11	0.27±0.04
6	50	5	0.39±0.03	0.47±0.06	0.29±0.06	0.34±0.03

Silvela et al. Theor Appl Genet (1989) 78:298-304

The Inbreeding Coefficient (*F*)

- Probability that two alleles at a locus in an individual are identical by descent (IBD ~ share a common ancestor).
- Assume the most extreme case of inbreeding (selfing)

Aa

×

- What is the probability in the progeny of this selfed individual, that that two alleles at a locus are identical by descent?

The Inbreeding Coefficient (*F*)

- The consequence of inbreeding to a population in HWE can be calculated by adding a "correction" to genotypes based on the inbreeding coefficient.

Genotype	Frequency
AA	$p^2 (1-F) + pF$
Aa	$2pq (1-F)$
aa	$q^2 (1-F) + qF$

The Inbreeding Coefficient (*F*)

- If complete outbreeding (F = 0)

Genotype	Frequency	Frequency
AA	$p^2 (1-F) + pF$	p^2
Aa	$2pq (1-F)$	$2pq$
aa	$q^2 (1-F) + qF$	q^2

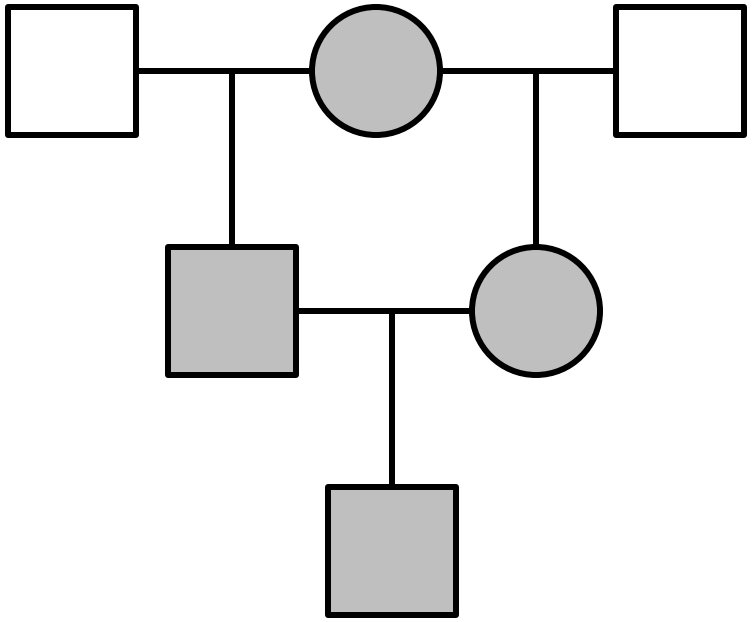
The Inbreeding Coefficient (*F*)

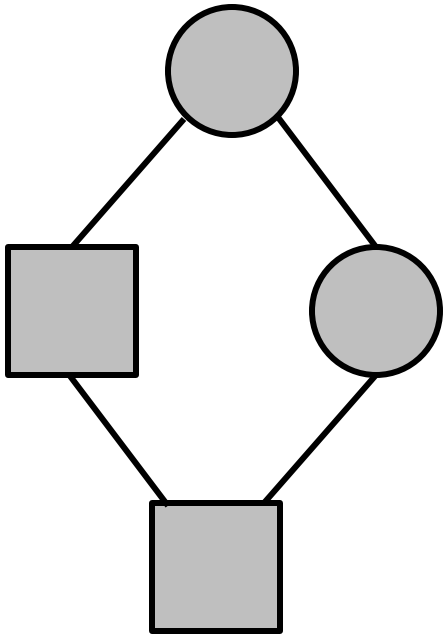
- If complete inbreeding (F = 1)

Genotype	Frequency	Frequency
AA	$p^2 (1-F) + pF$	p
Aa	$2pq (1-F)$	0
aa	$q^2 (1-F) + qF$	q

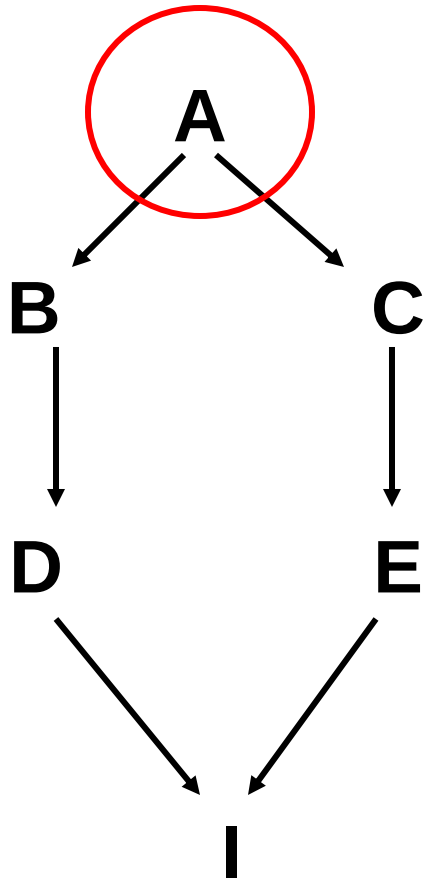
Calculating the Inbreeding Coefficient from Pedigrees

- Many breeding programs have reasonably good records of parents involved in crosses that were made, and selected individuals in the progeny.
- Based on these records, one can estimate the inbreeding coefficient (assuming ancestor of the pedigree is not inbred).





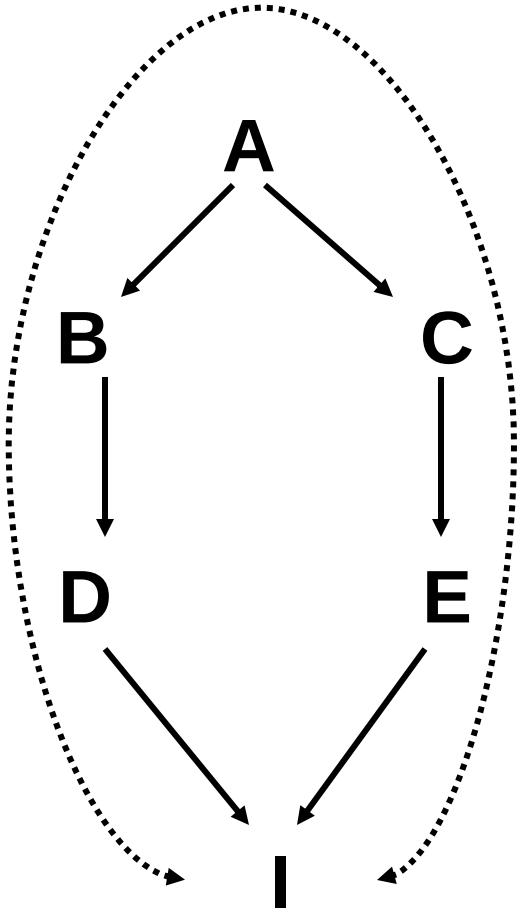
Exact estimate of *F*



To compute *F*:

1. Find all common ancestors in a pedigree. Alleles in individual I can only be IBD if they were inherited through both its parents via a common ancestor.
2. Trace all genetic paths up through one parent and down another – where individual A is the common ancestor of both parents.
3. Trace the probabilities of passing an allele down between individuals.

Exact estimate of *F*

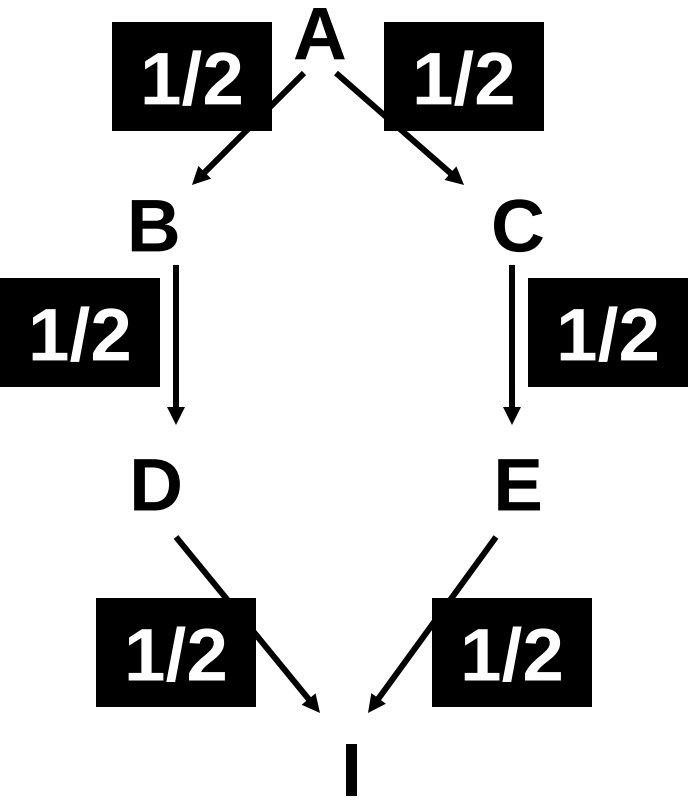


D B A C E

To compute *F*:

1. Find all common ancestors in a pedigree. Alleles in individual I can only be IBD if they were inherited through both its parents via a common ancestor.
2. Trace all genetic paths up through one parent and down another – where individual A is the common ancestor of both parents.
3. Trace the probabilities of passing an allele down between individuals.

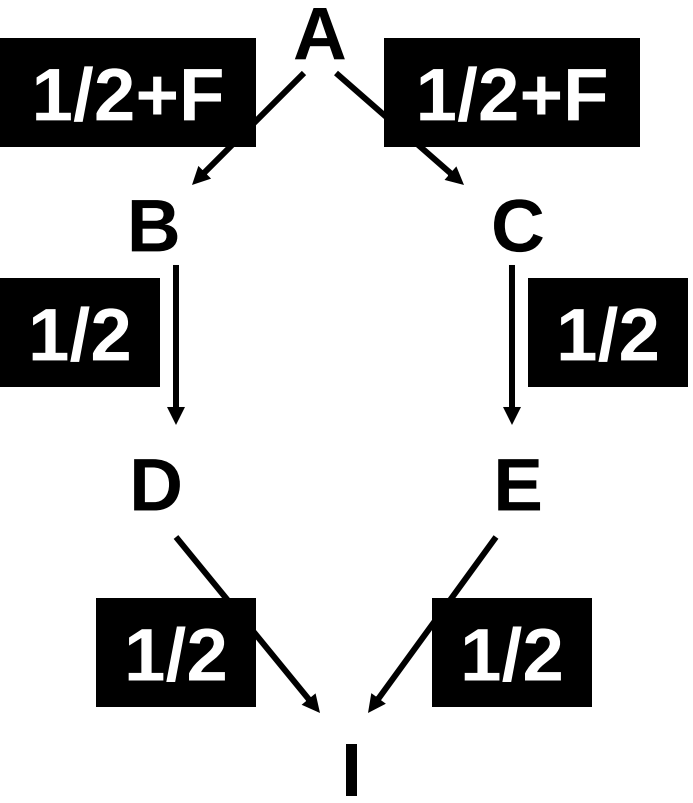
Exact estimate of *F*



To compute *F*:

1. Find all common ancestors in a pedigree. Alleles in individual I can only be IBD if they were inherited through both its parents via a common ancestor.
2. Trace all genetic paths up through one parent and down another – where individual A is the common ancestor of both parents.
3. Trace the probabilities of passing an allele down between individuals.

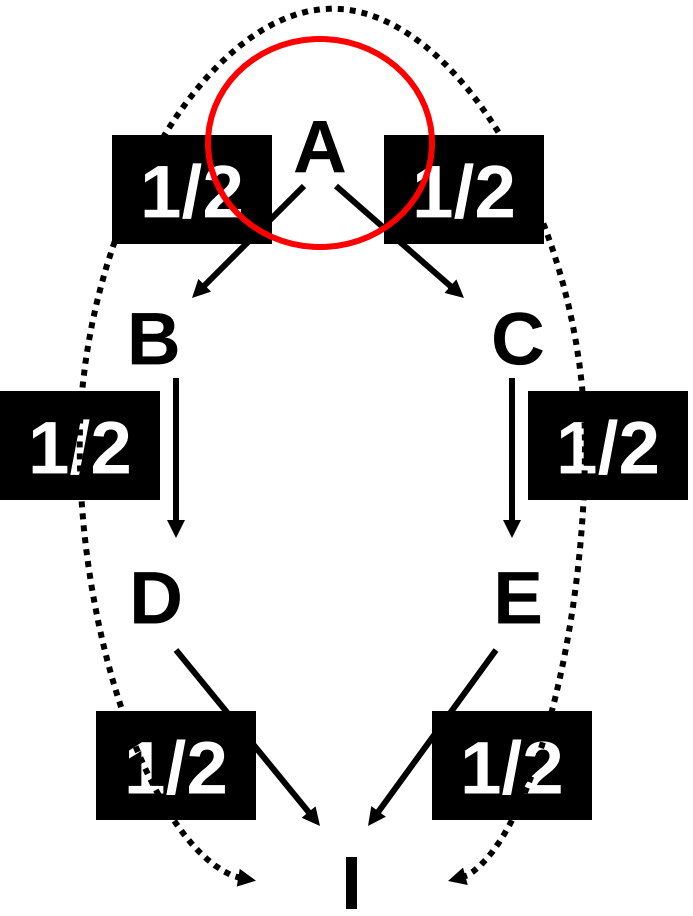
Exact estimate of *F*



To compute *F*:

1. Find all common ancestors in a pedigree. Alleles in individual I can only be IBD if they were inherited through both its parents via a common ancestor.
2. Trace all genetic paths up through one parent and down another – where individual A is the common ancestor of both parents.
3. Trace the probabilities of passing an allele down between individuals.
4. BUT IF THE ANCESTORS HAD ANY INBREEDING THEMSELVES…

Exact estimate of *F*



D B A C E

The exact value of F can be estimated by using the following formula:

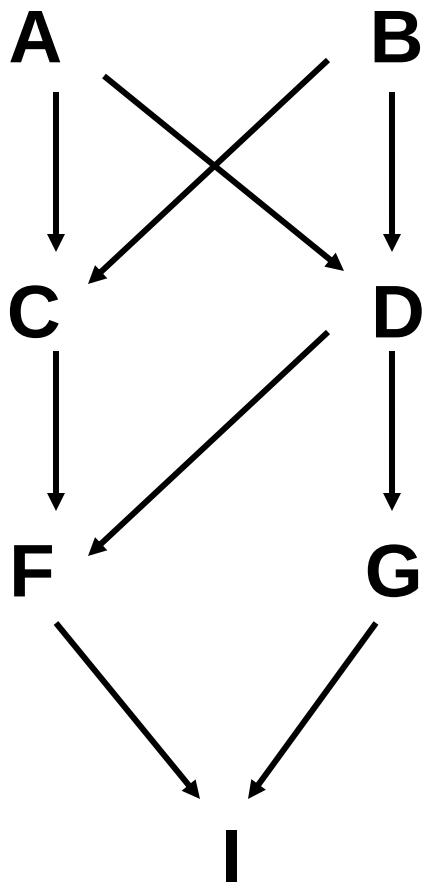
$$F = (1/2)^i + (1 + F_A)$$

Where "i" is the number of individuals in the genetic path. The genetic path in this example is DBACE (5).

This calculation also allows for inbreeding to be present in the common ancestor. If the ancestor in this example is not inbred, then $F_A = 0$.

$$F = (1/2)^5 + (1 + 0)$$
$$= 0.03125$$

Exact estimate for F – more complex pedigree:



For more complex pedigrees, *F* can be estimated by calculating all the possible paths and summing them:

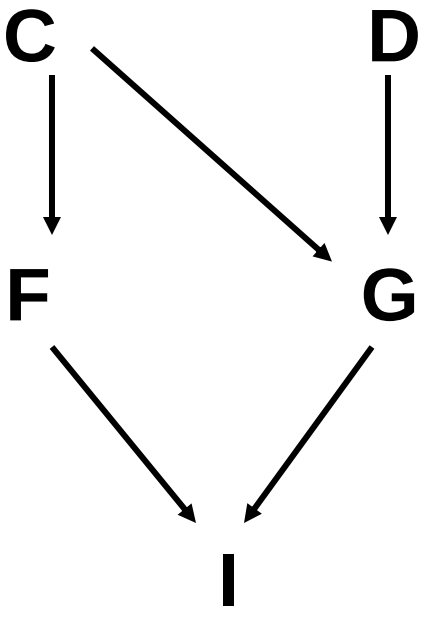
F C A D G $F_I = (1/2)^5 + (1 + F)$

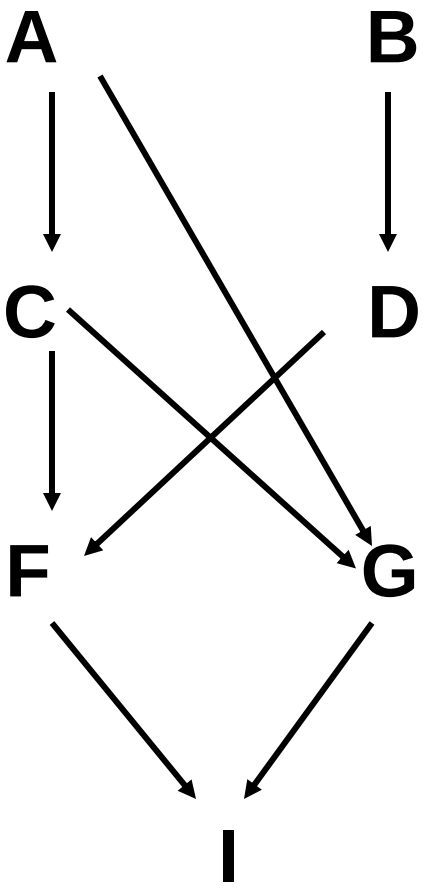
F C B D G $F_I = (1/2)^5 + (1 + F)$

F D G $F_I = (1/2)^3 + (1 + F)$

Assuming that all common ancestors were not inbred:

$$F_I = (1/2)^5 + (1/2)^5 + (1/2)^3 = 0.1875$$

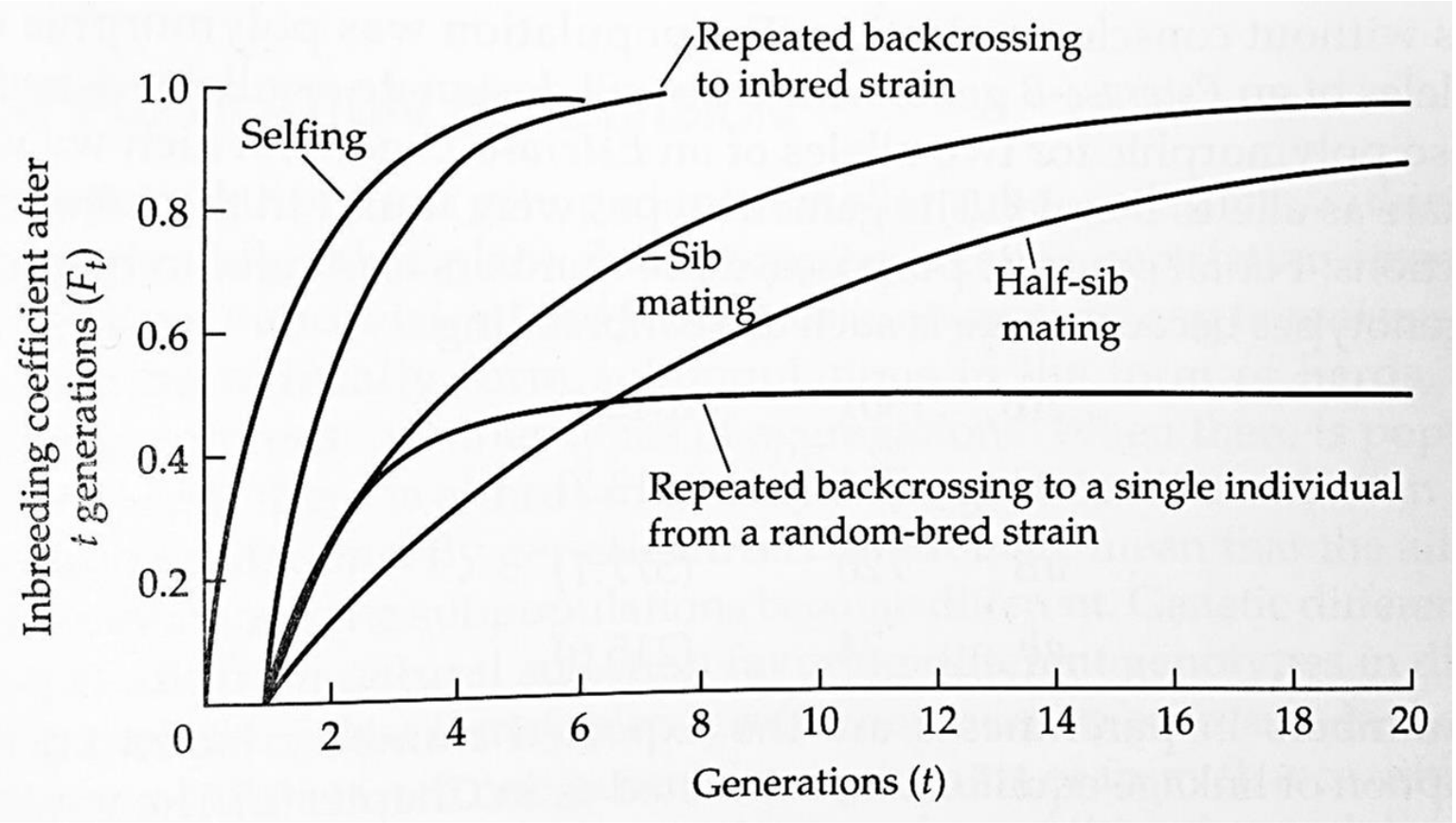

C
D
F
G
I



Estimate *F*

Accumulated effects of inbreeding – Mating system

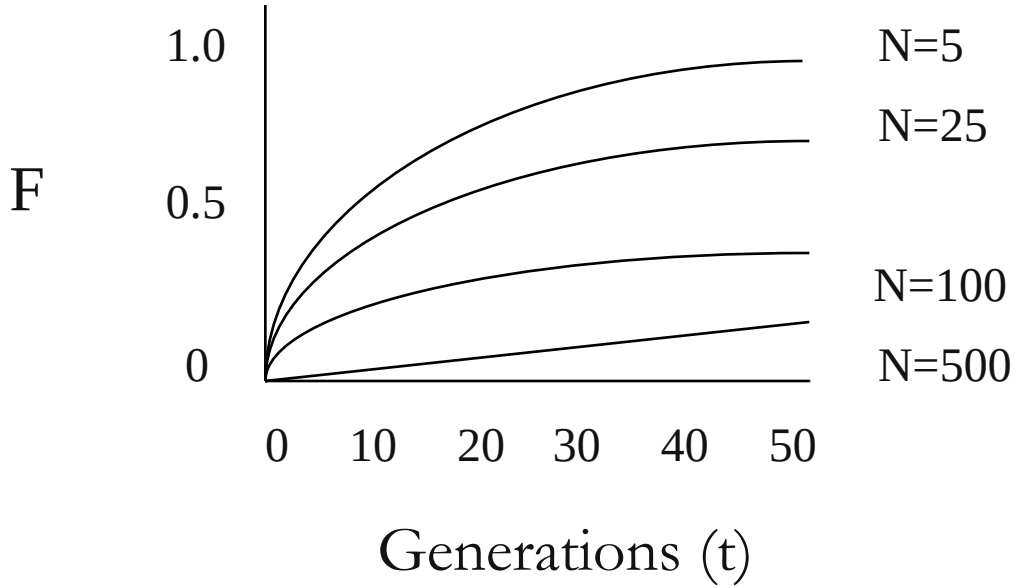
Expectedly, the inbreeding coefficient increases at a rate that is dependent on the system of mating.



Hartl and Clark, Principles of Population Genetics (4th ed.)

Accumulated effects of inbreeding – Population size

In addition of accumulating along generations, inbreeding also increases at a rate that is dependent on the population size. Inbreeding accumulates faster in smaller than larger populations.



For instance:
F (N=5) after 50 generations = 1.00
F (N=500) after 50 generations = 0.049

But what about if there are no pedigree records?

(or even more common, I think they are wrong!!!)

Molecular markers can be used to estimate the inbreeding coefficient of each individual in the population.

Several estimators exist – all are based on the principle that homozygous loci are more frequent among inbred individuals.

To calculate F, the observed frequency of homozygous loci at each individual is essentially compared to the expected frequency of homozygous loci if random mating occurred.

The observed frequency of homozygous loci is obtained by molecular marker data. The expected frequency of homozygous loci is obtained by the overall population allele frequencies.

Estimators of the inbreeding coefficient are implemented in publically available software such as COANCESTRY.

Wang, J. 2011. Molecular Ecology Resources, 11: 141–145.

COANCESTRY (http://www.zsl.org/science/software/coancestry)

Click on File→New Project

Enter project name (less than 40 characters), and set to Empirical Data→OK

Click on Load Genotype Data

select file containing genotype data in following format:

```
AA_n006aripo 169 169 190 278 125 131 ...
AA_n007aripo 169 173 184 184 125 131 ...
AB_n008aripo 169 209 150 196 131 141 ...
```

Click on Check Genotype Data

Click on Allele Frequency

select if known or unknown, if unknown it will calculate if from the data

Click on Check Allele Frequency

Click on Parameters and select the estimates, then Check and Save

Click on File→Run→Start Running

Click on File→View Results

Wang, J. 2011. Molecular Ecology Resources, 11: 141–145.