2.2) WF : covariance in offspring number

Let C_i be the number of offsprings of i

$$\mathbb{P}(C_i=n, C_j=m) = \mathbb{P}(C_i=n \mid C_j=m)\,\mathbb{P}(C_j=m)$$
$$= \binom{N-m}{n}\left(\frac{1}{N-1}\right)^{n}\left(1-\frac{1}{N-1}\right)^{N-m-n} \cdot \binom{N}{m}\left(\frac{1}{N}\right)^{m}\left(1-\frac{1}{N}\right)^{N-m}$$

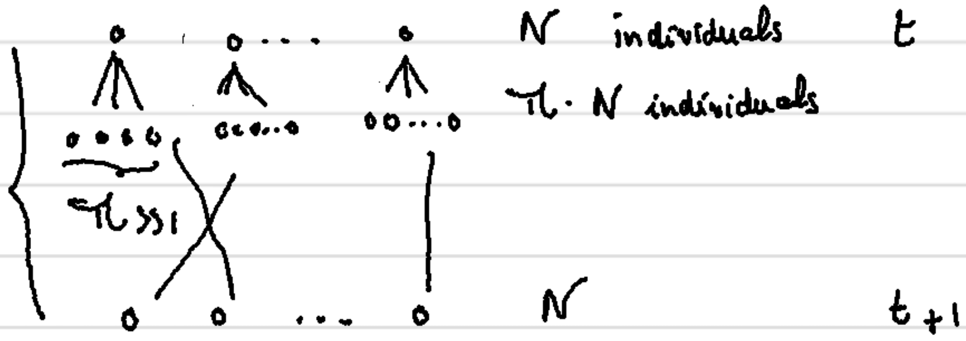
$$\sum_{m=0}^{N}\sum_{n=0}^{N-m} n \cdot m\, \mathbb{P}(n,m)$$
$$= \sum_{m} m \binom{N}{m}\left(\frac{1}{N}\right)^{m}\left(1-\frac{1}{N}\right)^{N-m} \underbrace{\sum_{n=0}^{N-m} n \binom{N-m}{n}\left(\frac{1}{N-1}\right)^{n}\left(1-\frac{1}{N-1}\right)^{N-m-n}}_{\text{mean of } Bi\left(N-m, \frac{1}{N-1}\right)}$$

$$= \sum_{m=0}^{N-m} m\,\mathbb{P}(m)\,\frac{N-m}{N-1}$$

$$= \frac{N}{N-1}\langle m\rangle - \frac{1}{N-1}\langle m^2\rangle, \quad \langle m^2\rangle = Var(m) + \langle m\rangle^2 = 1 + 1 - \frac{1}{N} = 2 - \frac{1}{N}$$
$$= \frac{1}{N-1}\left(N - 2 + \frac{1}{N}\right) = \frac{1}{N-1}\left(N-1-\frac{N-1}{N}\right)$$
$$= 1 - \frac{1}{N}$$

$$\Rightarrow \quad \langle C_i C_j\rangle - \langle C_i\rangle\langle C_j\rangle = -\frac{1}{N} \xrightarrow[N\infty]{} 0$$

2.1) WF : independent pick of ancestor



1) $\mathbb{P}(1 \to i) = \frac{\pi}{\pi N} = \frac{1}{N}$

2) $\mathbb{P}(2 \to i \mid 1 \to i) = \frac{\pi - 1}{\pi N - 1}$

3) $\mathbb{P}(2 \to i \mid 1 \to i) \simeq \frac{1}{N}$?

$$\frac{\mathbb{P}(2 \to i \mid 1 \to i)}{1/N} = \frac{N\pi - N}{N\pi - 1} = \frac{N\pi - 1 + 1 - N}{\cdots} = 1 - \frac{N-1}{N\pi - 1} \sim 1 - \frac{1}{\pi}$$

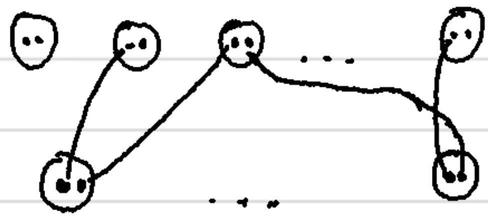
si $\pi \gg 1$, $N \cdot \pi \gg N \Rightarrow N \cdot \pi - 1 \gg N - 1$ if $N \gg 1$

$\to$ il faut $\pi \gg 1$

2.3) Heterozygosity and inbreeding

Note: given the hypothesis, WF model is a good description

t :



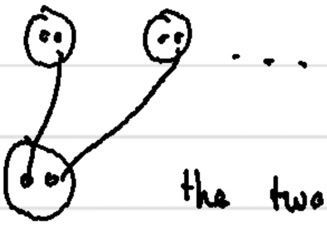
N individuals, $2N$ alleles

$t+1$:

each allele picked randomly among ancestral alleles!

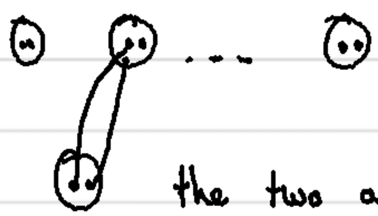
1) H: prob. of heterozygosity.
$\Rightarrow$ prob. that two different random alleles are different!
(It does matter whether they are in the same individual)

Two cases: (i) t



$t+1$ the two alleles have $\neq$ ancestors
$\Rightarrow$ they are different if the two ancestors are $\neq$
$\Rightarrow$ probability $H(t)$

(ii) t



$t+1$ the two alleles have the same ancestor
$\Rightarrow$ they cannot be different.

Prob. of (i): $1 - \frac{1}{2N}$; prob. of (ii): $\frac{1}{2N}$.

$$\Rightarrow \quad H(t+1) = \left(1-\frac{1}{2N}\right) \cdot H(t) + \frac{1}{2N} \cdot 0 = \left(1-\frac{1}{2N}\right) H(t)$$

2) The exact same logic applies to inbreeding

$$\rightarrow \quad I(t+1) = \left(1-\frac{1}{2N}\right) I(t)$$

3) $H(t) = \left(1-\frac{1}{2N}\right)^t H(t=0) \xrightarrow[t\infty]{} 0$ and $I(t) \rightarrow 0$

Timescale: if $N \gg 1$, $\left(1-\frac{1}{2N}\right)^t \simeq \exp\left(-\frac{t}{2N}\right)$

is $\underline{2N}$

Over time $\sim 2N$, heterozygotes disappear

and all alleles are identical by descent