

Sved framework:

Suppose we start with $2N_e$ i.i.d. gametes

$$\left(z_i \right)_{i=1}^{2N_e} = \left(\begin{pmatrix} x_i \\ y_i \end{pmatrix} \right)_{i=1}^{2N_e}$$

where $\begin{pmatrix} x_i \\ y_i \end{pmatrix} \stackrel{\text{i.i.d.}}{\sim} \text{Multinom} (p_{00}, p_{01}, p_{10}, p_{11})$

$$\text{i.e. } \mathbb{P} \left(\begin{pmatrix} x_i \\ y_i \end{pmatrix} = \begin{pmatrix} 0 \\ 0 \end{pmatrix} \right) = p_{00} \quad \text{etc.}$$

Suppose we sample z and \tilde{z} uniformly from

$$\{ z_1, z_2, \dots, z_{2N_e} \}$$

Then because \uparrow are i.i.d.:

$$\text{corr}(z, \tilde{z}) = 1 \quad (\Leftrightarrow) \quad \text{we sampled the same r.v.}$$

$$\text{corr}(z, \tilde{z}) = 0 \quad (\Leftrightarrow) \quad \text{otherwise}$$

Therefore, if we assume $c=0$, at any generation, if we sample z, \tilde{z} uniformly from the gamete pool:

$$\text{corr}(z, \tilde{z}) = \mathbb{P}(\text{IBD})$$

\downarrow
"identity by descent"

Counter example of $r^2 \neq P(1BD)$

~~can be~~ Explanation: r^2 and $P(1BD)$ are conceptually VERY DIFFERENT

• r^2

Let X be the r.v. that indicates whether a randomly picked gamete has allele 1 at the 1st locus

Let Y be the analogous for the 2nd locus

$$\Rightarrow r = \text{corr}(X, Y) = \frac{\sum_{i=1}^n (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_i (x_i - \bar{x})^2 \sum_i (y_i - \bar{y})^2}}$$

where $x_i = \begin{cases} 1 & \text{gamete } i \text{ has allele 1 at locus 1} \end{cases}$

$y_i = \begin{cases} 1 & \text{" " " " locus 2} \end{cases}$

• $P(1BD)$ is explained in the previous page

Suppose we have only 2 gametes, which
 at generation 0 we sample independently
 from this contingency table in equilibrium

	$1/2$	$1/2$
$1/3$	$1/6$	$1/6$
$2/3$	$1/3$	$1/3$

Gen 0 : $E(r^2) = 0$

$P(1BD) = 0$

Gen 1 : Case (1) two children gametes come from
 same parent

$\Rightarrow P(1BD) = 1$

$E(r^2) = 1$

Case (2) two children gametes come from
 different parents

\Rightarrow ~~total~~ $P(1BD) = 0$

$E(r^2) > 0$

