

Ne based on linkage disequilibrium

N_e : the number of breeding individuals in an idealised population that would show the same amount of dispersion of allele frequencies under random genetic drift

$E(\hat{r}^2)$: average correlation of allele frequencies between loci (SNPs) ~ LD [Linkage disequilibrium]

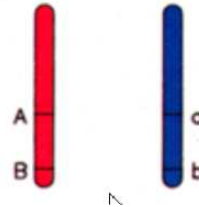
S : sample size (number of individuals)

$$E(\hat{r}_{\Delta}^2) \approx \frac{1}{3N_e} + \frac{1}{S}$$

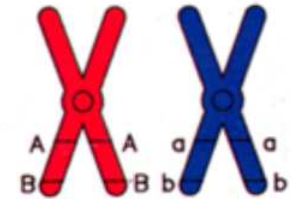
Ne using genomics

$$E(\hat{r}_{\Delta}^2) \approx \frac{1}{3N_e} + \frac{1}{S}$$

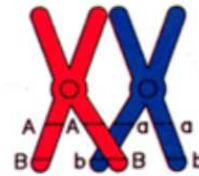
Linked genes on a pair of homologous chromosomes:



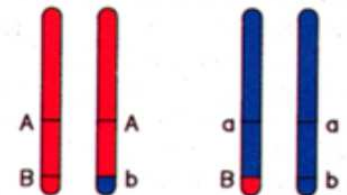
Replication takes place at the beginning of meiosis:



The homologous chromosomes undergo synapsis and crossover occurs between adjacent chromatids:



The chromatids separate:



Now four different kinds of gametes form

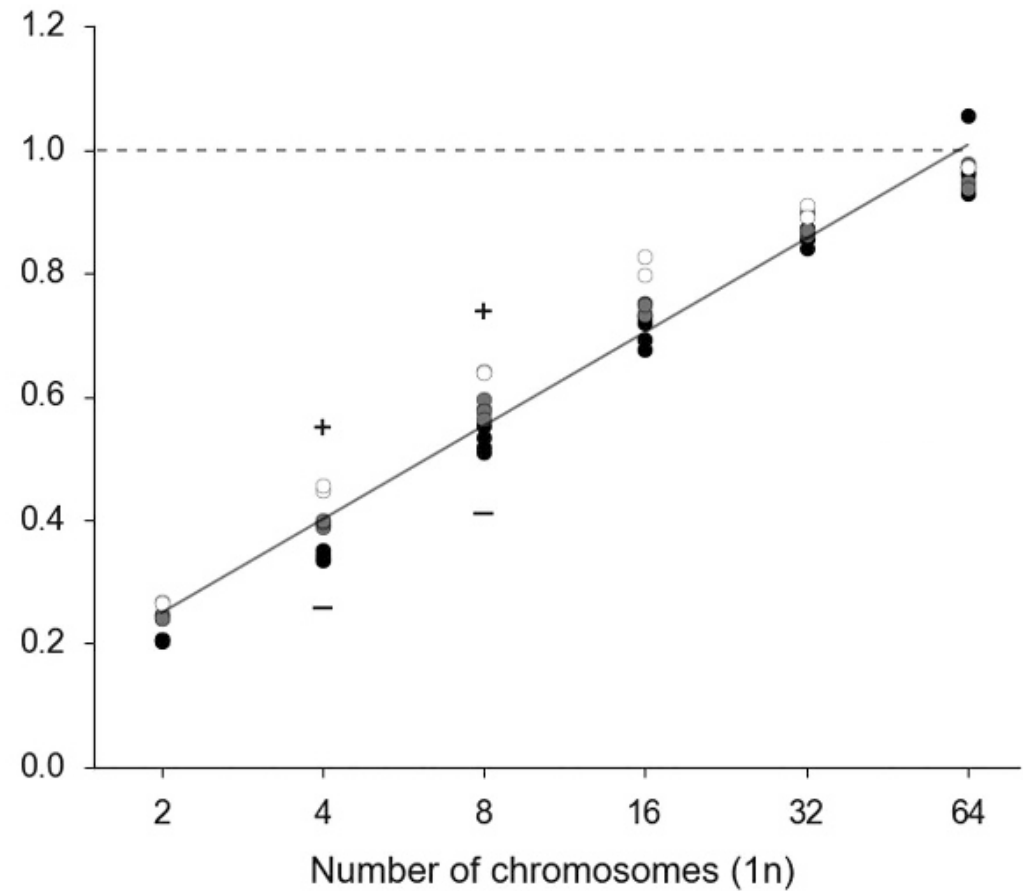
Ne using genomics

$$E(\hat{r}_{\Delta}^2) \approx \frac{1}{3N_e} + \frac{1}{S}$$

Only true for non-linked SNPs!!!

$$\text{Bias} = \frac{\hat{N}_e}{N}$$

Bias depends on number of chromosomes



Waples et al. 2016

Ne using genomics

$$E(\hat{r}_{\Delta}^2) \approx \frac{1}{3N_e} + \frac{1}{S}$$

Only true for non-linked SNPs!!!

Linkage depends on #SNPs, length of chromosomes
And #chromosomes

1 chromosome, 6 SNPs



1 chromosome, 24 SNPs



3 chromosome, 24 SNPs

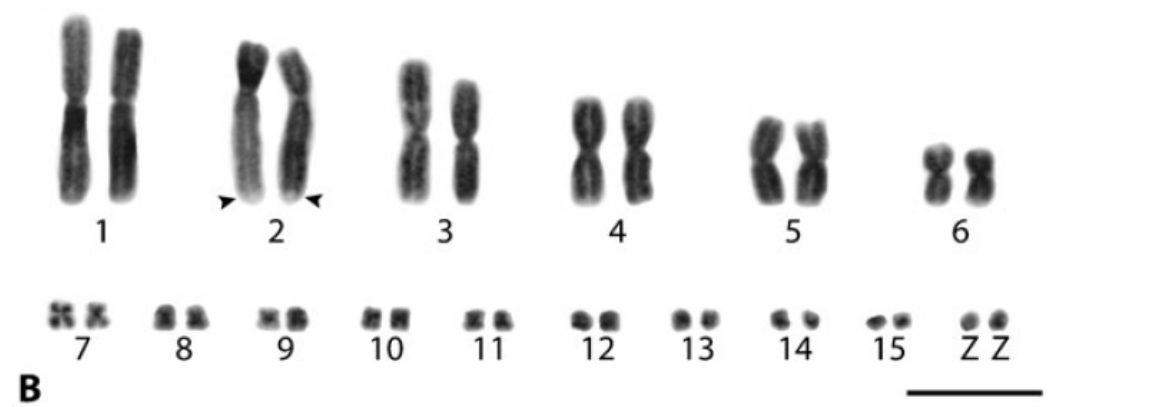


Ne using genomics

$$E(\hat{r}_{\Delta}^2) \approx \frac{1}{3N_e} + \frac{1}{S}$$

Only true for non-linked SNPs!!!

What happens if you have 2000 SNPs and 16 chromosomes of different lengths???

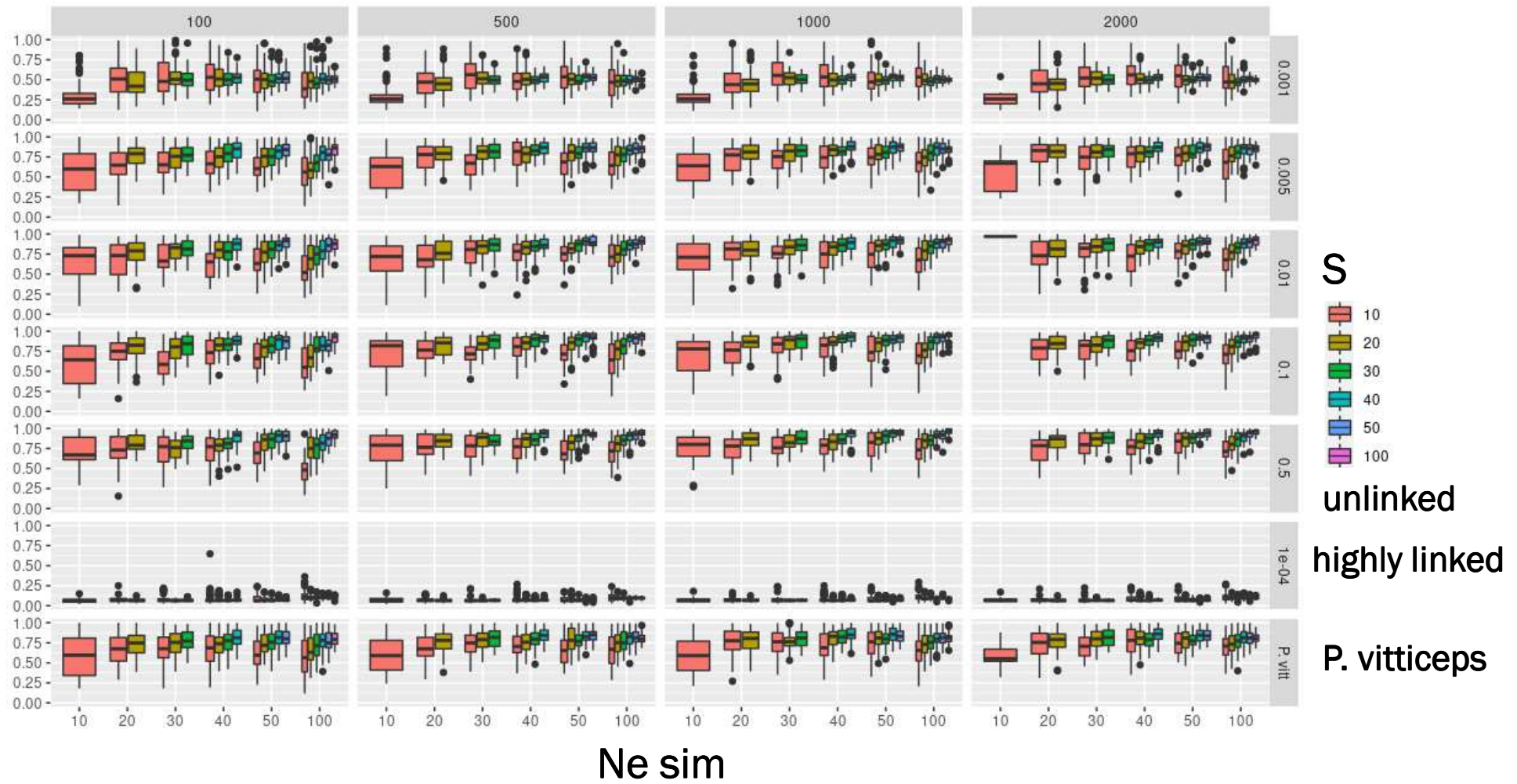


**Molecular cytogenetic map of the central bearded dragon,
Pogona vitticeps (Squamata: Agamidae)**

M. J. Young • D. O'Meally • S. D. Sarre •
A. Georges • T. Ezaz

SNPs

Ne/N



SNPs

Ne/N

