

Supplementary material

Title

Effective number of breeders from sibship reconstruction: empirical evaluations using hatchery steelhead

Introduction

Two methods for estimating N_e from sets of sibling assignments (PWOP: Waples 2011, and COLONY: Wang 2009) are compared. Here we discuss how they are conceptually related and show that they are especial cases of each other. The COLONY method can explicitly incorporate deviations from Hardy-Weinberg equilibrium and differences in sex ratio, while the PWOP method relies only on sibling relationships. This difference is not large in practice, as often these values are unknown and assigned default values by researchers.

Using empirical data from the current study, we show that both methods give essentially the same estimates when applied to the same set of sibling assignment inferred from genetic data. Sibling assignments were estimated with COLONY2 (Jones and Wang 2010), assuming either a monogamous or polygamous mating system.

Definitions

N_e = Inbreeding effective population size, a measure of how the average inbreeding coefficient changes from one generation to the next.

N = Census size of the population during the parental generation.

N_p = Number of parents contributing at least one gamete to the next generation.

k_i = The number of offspring produced by the i th parent. This vector can include zeroes when indexed by $1 \rightarrow N$, or exclude zeroes when indexed by $1 \rightarrow N_p$.

\bar{k} = The mean of the vector of k_i values.

$Var(\vec{k})$ = The variance of the vector of k_i values.

S = Number of (observed) offspring. Each offspring has two parents, so $S = \sum k_i/2$.

P_{same} = Chance that two random gametes in the offspring generation come from the same parent. The chance that two random gametes are identical by descent in the previous generation is $P_{same}/2$ if the contribution of alleles by a parent is random and independent.

Equations

Crow and Denniston (1988):

$$N_e = \frac{\bar{k}N - 1}{\bar{k} - 1 + \text{Var}(\bar{k})/\bar{k}} \quad (1)$$

In (1) k_i contains **all** possible parents (N), even those that left zero offspring, not just those that successfully contributed to the next generation.

Waples (2011), equation 2a:

$$N_e = \frac{\sum k_i - 1}{\frac{\sum k_i^2}{\sum k_i} - 1} \quad (2)$$

Waples (2011) noted that (1) holds even when excluding individuals from the parental population that do not contribute offspring. They also note that a sample of offspring can be used to estimate N_e by estimation of k_i .

Wang (2009) addresses a very similar situation: "Equations for the effective size (N_e) of a population were derived in terms of the frequencies of a pair of offspring taken at random from the population being sibs sharing the same one or two parents".

Wang (2009) equation 10:

$$\frac{1}{N_e} = \frac{1 + 3\alpha}{4}(Q_1 + Q_2 + 2Q_3) - \frac{\alpha}{2}\left(\frac{1}{N_1} + \frac{1}{N_2}\right) \quad (3)$$

where α is a measure of departure from Hardy-Weinberg equilibrium, Q_1 , Q_2 , and Q_3 are the probabilities of a pair of offspring being paternal half-siblings, maternal half-siblings, and full-siblings, respectively. N_1 and N_2 are the number of male and female parents.

If we assume Hardy-Weinberg equilibrium ($\alpha = 0$), (3) becomes:

$$\frac{1}{N_e} = \frac{1}{4}(Q_1 + Q_2 + 2Q_3) \quad (4)$$

Note, the expectation of α is $1/(1 - 2N_e)$ in a randomly mating population.

Wang (2009) equation 8 shows that:

$$Q_1 + Q_2 + 2Q_3 = 2p_{same} \quad (5)$$

Substitution into (4) leads to:

$$N_e = \frac{1}{2p_{same}} \quad (6)$$

The chance two gametes that share a parent are identical by decent is 0.5, so we again simplify to:

$$\frac{1}{N_e} = p_{IBD} \quad (7)$$

I.e. Inbreeding N_e is equal to the identity by descent within the the offspring gametes.

For an empirical example of the similarity of these methods, see the notebook at: <http://nbviewer.jupyter.org/github/rwaples/PWOP-vs-SA/blob/master/estimate%20Ne%20COLONY%20vs%20PWOP.html>

Figures

Figure 1: Scatterplot of N_e estimates with the PWOP and COLONY2 methods for sibling assignments assuming a monogamous mating structure. The Pearson correlation coefficient and p-value (as computed by `scipy.stats.pearsonr`) are reported.

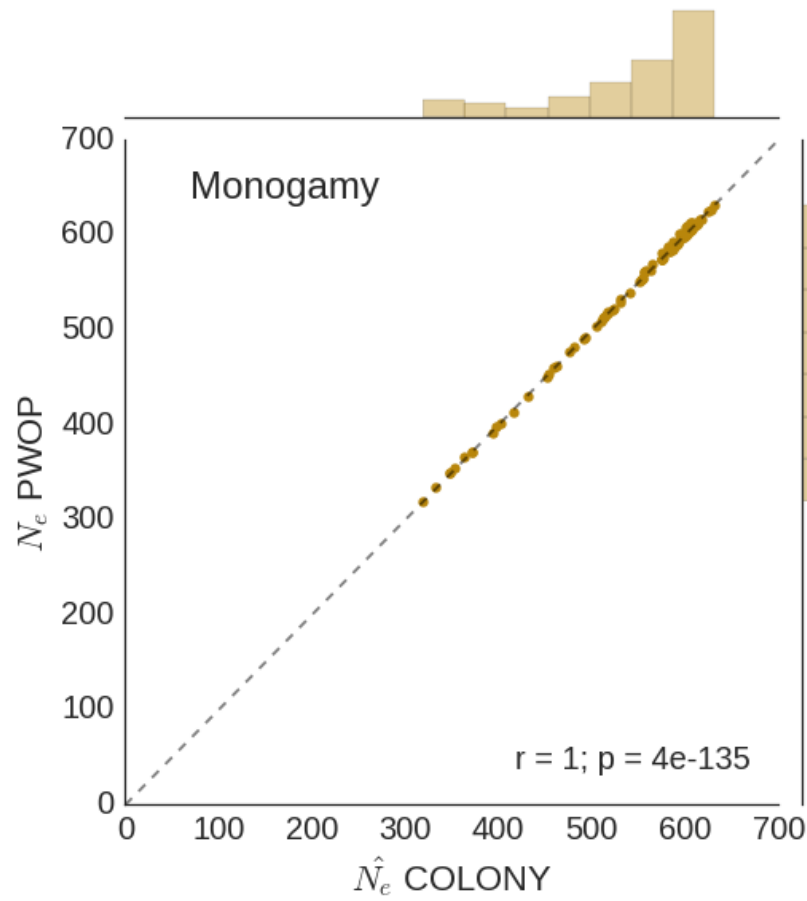
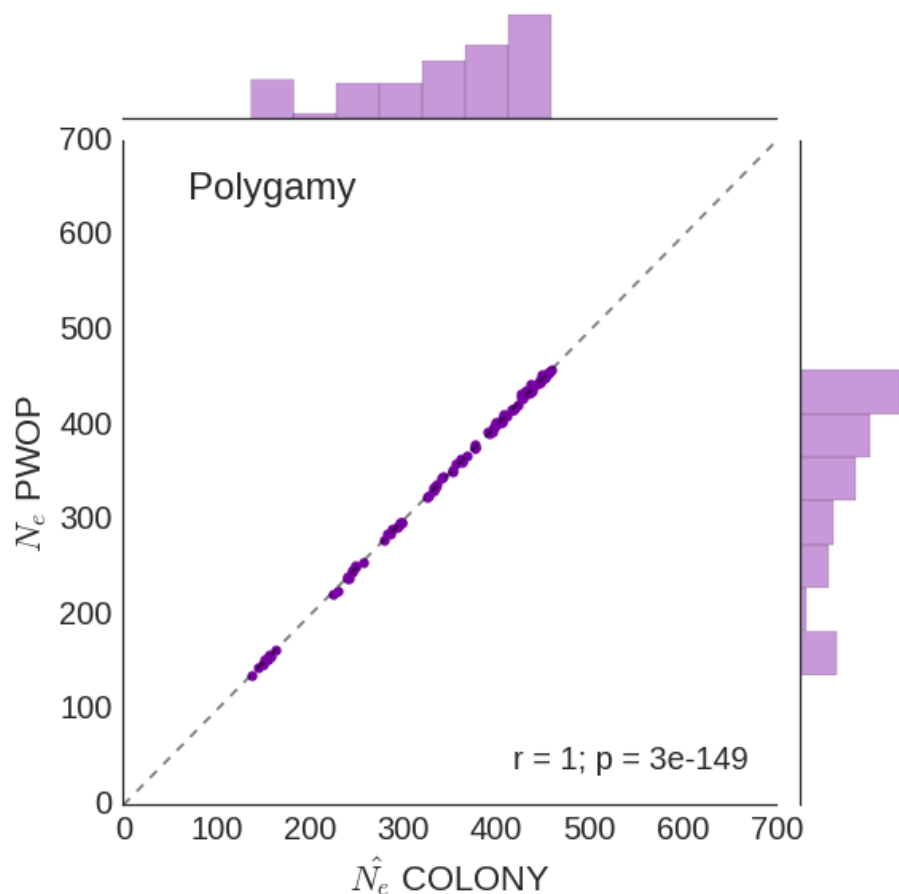


Figure 2: Scatterplot of N_e estimates with the PWOP and COLONY2 methods for sibling assignments assuming a polygamous mating structure. The Pearson correlation coefficient and p-value (as computed by `scipy.stats.pearsonr`) are reported.



References

Crow, James F., and Carter Denniston. "Inbreeding and variance effective population numbers." *Evolution* (1988): 482-495.

Jones, Owen R., and Jinliang Wang. "COLONY: a program for parentage and sibship inference from multilocus genotype data." *Molecular ecology resources* 10.3 (2010): 551-555.

Wang, Jinliang. "A new method for estimating effective population sizes from a single sample of multilocus genotypes." *Molecular Ecology* 18.10 (2009): 2148-2164.

Waples, Robin S., and Ryan K. Waples. "Inbreeding effective population size and parentage analysis without parents." *Molecular ecology resources* 11.s1 (2011): 162-171.