File S1

Calculating coancestry coefficients

Calculating coancestry coefficients from the admixture F-model (AFM). The frequency of allele u in subpopulation A is simply the average of the indicator variables x_{ijku},

$$p_{Aju} = \frac{1}{2n_A}\sum_{i=1}^{n_A}(x_{ij1u} + x_{ij2u}). \quad \text{(Eq. S1)}$$

The frequency p_{Aju} is a random variable, with expectation (over the flow of neutral alleles through a pedigree structure that we consider fixed) q_{ju}. The covariance among subpopulations A and B is

$$\text{Cov}(p_{Aju}, p_{Bju}) = \mathrm{E}[(p_{Aju} - p_{ju})(p_{Bju} - p_{ju})] = \mathrm{E}(p_{Aju}p_{Bju}) - q_{ju}^2 = (q_{ju} - q_{ju}^2)\theta_{AB}^{\mathcal{P}}, \quad \text{(Eq. S2)}$$

where the last equality follows (at the limit of low mutation rate) by noting that identity by state follows either from identity by descent, or by the two distinct alleles in the ancestral population being identical by state,

$$\mathrm{E}(x_{i'ju}x_{iju}) = q_{ju}^2 + \theta_{ii'}(q_{ju} - q_{ju}^2) \quad \text{(Eq. S3)}$$

and substituting the definitions of p_{Aju} (Eq. S1) and $\theta_{AB}^{\mathcal{P}}$ (Eq. 1 in the main text) into Equation S1.

In the AFM, it holds that

$$\text{Cov}(p_{Aju}, p_{Bju}) = \text{Cov}\left(\sum_{k=1}^{n_L}\kappa_{Ak}z_{kju}\,,\ \sum_{k=1}^{n_L}\kappa_{Bk}z_{kju}\right). \quad \text{(Eq. S4)}$$

Because the lineages are independent, Cov($z_{kju}, z_{k'ju}$)=0 for all $k \neq k'$. Thus, Equation S4 reduces to

$$\text{Cov}(p_{Aju}, p_{Bju}) = \sum_{k=1}^{n_L}\kappa_{Ak}\kappa_{Bk}\text{Var } z_{kju} = \sum_{k=1}^{n_L}\kappa_{Ak}\kappa_{Bk}\frac{q_{ju} - q_{ju}^2}{a_k + 1}. \quad \text{(Eq. S5)}$$

Combining this with Eq. S2 yields

$$(q_{ju} - q_{ju}^2)\theta_{AB}^{\mathcal{P}} = \sum_{k=1}^{n_L}\kappa_{Ak}\kappa_{Bk}\frac{q_{ju} - q_{ju}^2}{a_k + 1}, \quad \text{(Eq. S6)}$$

and hence

$$\theta_{AB}^{\mathcal{P}} = \sum_{k=1}^{n_L}\frac{\kappa_{Ak}\kappa_{Bk}}{a_k + 1}. \quad \text{(Eq. 12, main text)}$$

Calculating coancestry coefficients from a pedigree. If the complete pedigree is known, it is easy to calculate coancestry coefficients for each pair of individuals using the recursive formula (Lynch and Walsh 1998),

$$\theta_{ii'} = \frac{\theta_{is(i')} + \theta_{id(i')}}{2} = \frac{\theta_{s(i)s(i')} + \theta_{s(i)d(i')} + \theta_{d(i)s(i')} + \theta_{d(i)d(i')}}{4} \text{ for } i \neq i',$$

$$\theta_{ii} = \frac{1 + \theta_{s(i)d(i)}}{2}. \quad (\text{Eq. S7})$$

Above, $s(i)$ and $d(i)$ are the sire and dam of individual i, respectively. We used this formula for calculating the true value of $\boldsymbol{\theta}^{\mathcal{P}}$ in our simulated data sets.

References

Lynch, M., and B. Walsh, 1998 *Genetics and analysis of quantitative traits*. Sinauer Associates Incorporated, New York.