* Effective population size
* Readings in the Heredity journal of Nature – papers up on iLearn
* Effective population size has assumptions – the same as HW – ideal population
* When calculating effective population size – all assumptions hold truth except N – population size
* Looking at 3 generations – base population is infinity size and diploid
* Effective population size is the measure of the individuals that are breeding in the population and passing their gamete to the next generation
* With the base population that it is infinite – the smaller the population becomes – the greater the loss of the genetic variation – greater chance of inbreeding – observed heterozygosity will become lower and lower
* Ne measures the loss of genetic drift through inbreeding and low pop size
* So a definition of effective population size – the size of the ideal population that loses genetic variation at the same rate as the population that you are observing – population size not infinite so all population deviates away to some extent from based population of infinite size
* Ne says that this is the size of the ideal population that loses genetic variation at the same rate as the population that you are looking at
* A measurement that you can compare among different organisms of different life history traits
* Two different ways of measuring effective population size:
  + Contemporary effective population size – account for the few most recent generations or over a long time - Can estimate Ne and a lot of measurements through genetic data – if we are using molecular data – want to be as confident as we can that we are measuring neutral parts of the genome (no mutation or selection)
  + Population demography – over a long time
* Heterozygosity can change through time
* As effective size decreases, the pace of the heterozygosity decreases
* Ne is strongly influenced by fluctuations across generation
* Longer term Ne – use harmonic mean would be more precise – more sensitive to lowest N – reflect more of the genetic drift
* Estimate Ne using molecular data
  + Using linkage diseliquibrium – physically unlinked loci will by chance end up in linkage disequilibrium as consequence of small Ne – can use those values of LD to estimate Ne
  + Heterozygosity estimate – not used as much anymore
  + Identify full sibling from molecular data – work out based on full sibling to make out breeding individuals
* LD loci will drive down Ne because Ne is the measure of pair of loci that are not in LD – they’re in LD because of random effect because of small population
* Linear relation between number of chromosomes and Ne/N – can adjust for number of loci that is in LD
* Coalescent – can go back in a pedigree and get more individuals involved – coalescent goes back across generation and on the way of how alleles make up different genotypes at each generation – make inference about Ne at each generation – making inference about drift – enable you to know if the population has gone through bottleneck or not and also the Ne that would be associated with the bottleneck – the funnel shape represents bottleneck
  + Can see that endangered species have gone through genetic bottleneck
* Relationship of genetic correlation (y-axis) and distance class (x-axis) – if individuals did not disperse far from where they were born – there would be a sharp decline of relatedness with distance