* Connectivity
* 30 mcqs – 9 – 6 pm
* Landscape genetics – analysis of genetic or demographic connectivity across the landscape – looking at relationship between different environmental variable – if dealing with patches of distribution, refer to them as matrix – how the environmental and behavioural components of the organisms in the matrix influence the connectivity among habitat patches
* Landscape genetics make use of neutral genetic data – loci we might be analysing that is not under selection – may not be coding – but some approaches do look for selection of loci that are under selection or linked to them – can tell what selective pressure might be if we find those selected loci
* Different way of connectivity definition – genetic connectivity - deal with gene flow – movement of alleles across landscape
* Demographic connectivity – movement of individuals across the landscape
* Can analysis genetic data at a range of hierarchy
  + Genes – allelic diversity
  + Individuals
  + Groups of individuals in a habitat fragments – refer to as populations
  + Species – can be lots of populations
* When dealing with individuals, might use the genotypic array within the individuals – can tell paternity or relatedness – move to population can tell genetic structure – species deal with biogeography or speciation
* Analysis of population level and analysis at the individual levels
* Important to come up with hierarchal levels – 3 broad categories
  + Genotypic analyses – look at individuals – a whole bunch of loci – will have genotypes at different loci – based on genotype can ask questions about relatedness between individuals – genotypes are shuffled at each generation – share half of alleles with each parent so in one generation shuffling of alleles can be picked up – across single generation based on genotypes of the interested loci – short time
  + Genic analyses – measure allele frequencies at population level – calculate allele frequencies in one population and compare with another population – change as the consequence of gene flow or genetic drift – long scale rather than genetic shuffling – look at the process that shapes differences in population throughout long timescale – medium time
  + Genealogical analyses – take account of new variants – when they arise and how they accumulate – slow process – based on mutation – date back very long in time – long time
* Population levels
  + All individuals within habitat patches – population
  + Differences between population
* F-statistics – look at how inbreeding impacts individual level with a population and how drift results in differences between population – based on loci assumed to be neutral
  + FIS: within patches – IS = individual in subpopulation
  + FST: level of differences because of drift among patches
* FIS is the a measure of inbreeding within a patch – it’s not inbreeding coefficient – positive FIS there are other processes that can explain it, not only inbreeding
* FST is the genetic divergence between populations
* Pop D is not in HW because red and blues are not interbreeding because of the stream
  + Population sub-division so if we calculate assuming HW – will get more homozygotes than expected – but it’s not because of inbreeding – because of the stream that divides them – need to consider genetic structure – Wahlund Effect
  + When see large FIS – can try FST to investigate
  + Genetic structure may not always be known – especially when sampling is very broad
* The level of genetic differentiation increases when effective population size get smaller – random genetic drift – neutral loci
* Random genetic drift driving the genetic divergence between population at neutral loci – the smaller the pop size, the quicker the divergence, the higher the Fst
* When FST is lower than 0.35 – connectivity that allows advantageous allele to move among different patches
* Fst lower than 0.2 – sufficient gene flow to avoid harmful local breeding
* All depending on effective pop size
* Often apply with straight line genetic distance
  + If fst increases within distance, geographic distance inhibits gene flow – pattern of isolation by distance
* Most organsims do not traverse in straight line – different environmental feature facilitates their movements across the landscape
  + Resistance
  + Make GIS technology
  + Put high resistance value when it is unlikely that the species can cross that environment
  + Put together to determine paths that facilitate or inhibit movements of organisms
* Demographic connectivity – at a landscape scale, too costly, too time-consuming, or impractical to measure dispersal – genetic is a good solution
* 3 different analytical approaches according to timescales
  + Patches assuming HW
  + Get the alleles frequencu
  + What is the likelihood of the individual belonging to a population
  + Identify individual movement patterns among population or habitat patches – the migrants
  + Can work out the dispersal distances of parent-offspring