* eDNA – shared by different organisms – characterise community – sampled from the environment
* Filter DNA from water – fresh and marine
* Collected from soils – PCR to amplify
* Meta-barcoding – take environmental sample – barcoding uses sequences that genes are conserved enough in the same species and different species – eg. use CO1 which is mitochondria genome – large database of CO1 sequences so can link to species
* CO1 isn’t the only one – 16S/12S
* PCR to amplify – can gene sequence – can do bulk coding with next generation sequencing – match with large database – give lists of species that are present in the area – community composition
* Eg. compare 3 different methods of detecting shark – underwater camera, diving, and Edna – number of sharks species – eDNA has fewer samples – eDNA detected more species – efficient for species present
* iDNA – insect carried DNA – the ones that feed from blood – blood has host DNA – bird blood cell has nucleus so higher DNA
* eg. mosquitoes sampling – capture mosquitoes and extract DNA from gut
* eg. leeches are quite efficient too
* community composition and functional diversity – consequences of environmental change on functional diversity
* Eg. Liu et al looking at relationship between fungal diversity and drought resilience of grass land plants
* eRNA – taking environmental samples and then transcriptomic to answer questions of functional diversity – which genes are upregulated – enzymes act on RNA segments – revert RNA back to cDNA – cDNA fragments represent the genes that are switched on – PCR amplified and then sequence – qPCR – get estimation of quantity of the DNA in the sample – quantify extend to which different genes are switched on in the sample
* Absence is related to