**Prompt, please read this very carefully**: This document gives a list with all the available categories. The explanation and structure of these categories, along with classification instructions, I have already given in the other document.

### Interbreeding

### Grouping & Ranking justification:

### Phylogenetic method (general):

### Biogeography

### Singleton categories

* + 1. Specimen storage location
    2. Sampling location
    3. Abbreviations & terms
    4. Nomenclature & taxonomic history

# Organismal features (Phenotype)

## Phenotype datatypes

### Morphological traits

* + - 1. Quantitative morphology
      2. Qualitative morphology
         1. Colour and patterns
         2. Shape and anatomy
         3. Texture
         4. Ultrastructural data:
      3. Interbreeding morphology

### Behavioural traits:

* + - 1. Acoustic data
      2. Mating behaviour
      3. Feeding behaviour

### Ecological traits

## Phenotype data processing

### Imaging

### Sampling methods

### Specimen storage and preparation

## Phenotype analysis methods

### Non-phylogenetic modelling with morphological data

### Phylogenetic methods with morphological traits

# Genetic and molecular features

## Genetic and molecular datatypes

* + 1. Nuclear dna
    2. Organellar dna (mitochondrial, chloroplast)
    3. Transcriptomic data
    4. Proteomic data
    5. Tandem repeats (Microsatellites, minisatellites)
    6. Whole genomes
    7. Exomes
    8. NGS Genome Wide studies
    9. Epigenetic data
    10. eDNA
    11. Biochemical traits:
        1. Chemotaxonomy:
        2. Cytotaxonomy & genome size:

## Genotype data processing: nucleotide sequencing

### Squencing

### 1st Generation sequencing(sanger sequencing):

### 2nd generation sequencing (NGS):

### 3rd generation sequencing (single molecule sequencing, no PCR amplification):

## Molecular analysis methods

### Non-phylogenetic molecular methods

* + - 1. Distance & barcoding
      2. allele sharing-based (haplowebs) approaches
      3. Fixed alternative character states
      4. Clustering methods (structure, structurama, baps, dapc):
      5. Interbreeding assessed through molecular data

### Phylogenetic Species delimitation

### Phylogenetic tree reconstruction methods

* + - 1. Distance based (neighbour joining, UPGMA)
      2. Character based methods
      3. Consensus and supertree methods

### Machine learning methods