**Prompt, please read this very carefully**: This document describes the categories that can be assigned to paragraphs from methods sections of taxonomic papers. Section ‘0’ described singleton categories that are outside of the hierarchical classification. Sections ‘1’ and ‘2’ describe the hierarchical classification. The most general categories are ‘organismal features (1)’ and ‘genetic and molecular features (2)’.

All the categories in this document are categories that cover topics of methods sections in taxonomy papers. Please consider each of these categories, both high-level and low-level, and decide whether the paragraph you are given fits into it. After you have done this for all categories, you should have a list of categories for which the paragraph scores ‘1’. The ones you don’t list, I will assume get a ‘0’. For example, the following paragraph:

*"Larvae and adults of Austrolimnius nyctelioides were collected in the Chubut River at Piedra Parada (Argentina,\nChubut province, S 42\u00ba40\u2019\u201370\u00ba05\u2019W, 440 m) and in Nant y Fall creek, Road 17 to Corcovado (Argentina, Chubut\nprovince, 43\u00b013\u2019S\u201371\u00b025\u2019W, 665 m) in the fall and spring of 2004, 2007 and 2011. Specimens were cleared in lactic acid, dissected and mounted on slides for observation and description;\nthe mounting media were Hoyer\u2019s and Polyvinyl-Lactoglycerol (PVLG). Observations (up to 1000 X) and\nillustrations were made using a Leica MZ6 dissecting microscope and DM500 and DMLB compound microscopes,\nall with a camera attached. Photographs were assembled using the freeware software CombineZP (Hadley 2010). "*

Would get a ‘1’ for:

* ‘Sampling location’, because of ‘*were collected in the Chubut River at Piedra Parada (Argentina,\nChubut province, S 42\u00ba40\u2019\u201370\u00ba05\u2019W, 440 m) and in Nant y Fall creek, Road 17 to Corcovado (Argentina, Chubut\nprovince, 43\u00b013\u2019S\u201371\u00b025\u2019W, 665 m)’*
* ‘Specimen storage and preparation’ because of ‘*were cleared in lactic acid, dissected and mounted on slides for observation and description;\nthe mounting media were Hoyer\u2019s and Polyvinyl-Lactoglycerol (PVLG).’* Note, this is only if they are prepared for morphological analysis.
* ‘Imaging’ because of ‘*Observations (up to 1000 X) and\nillustrations were made using a Leica MZ6 dissecting microscope and DM500 and DMLB compound microscopes,\nall with a camera attached. Photographs were assembled using the freeware software CombineZP (Hadley 2010). "*
* ‘Morphological traits’ because of ‘*mounted on slides for observation and description;’* Here the general category ‘Morphological traits’ is assigned rather than more specific ones like ‘qualitative morphoogy’ or ‘quantitative morphology’ because the passage doesn’t specify which it is, and it cannot be inferred.

So for this paragraph, you should return a list as follows:

[‘Sampling location’, ‘Specimen storage and preparation’, ‘Imaging’, ‘Morphological traits’]

After you have made this list, you should double check whether you have not omitted any categories that should have been included, and whether all of the categories you did include are actually mentioned in the paragraph.

Note, there are often boundary cases, where the decision about one or more of the categories is difficult or unclear. Here is a list of further instructions that you should follow in your decisions of such cases:

General instructions:

* At all times, be conservative and careful in your decisions, and only assign a category when you are sure it applies.
* Direct references to information that is in the same paper but not in that particular paragraph, are sufficient to assign ‘1’ to a category. E.g. “*The coordinates of sampling locations are listed in Table 1*.” is sufficient to label that paragraph as ‘1’ for ‘Sampling location’, because we know the information is in table 1 in that paper.
* References to other papers with information are sufficient to label a category as ‘1’. E.g. “*All DNA was sequenced using the methods described in Conix et al*.” is sufficient to label a paragraph as ‘1’ for “SEQUENCING”, because they say they do sequencing and that they follow particular methods than can be checked.
* For any nested category, the higher-level categories apply whenever any of the lower-level ones apply. This is done automatically in the data processing, so there is no need to tick these labels one by one. I.e. it is always sufficient to just tick the most precise category within that branch of the classification tree. E.g. if a paragraph has ‘qualitative morphology’, it does also fall into ‘Morphological traits’, but it is not needed to list this.
* The mere mention of when specimens were collected (e.g. ‘*in march 2017*’) is not enough to tick ‘Sampling’.
* The mere mention of SEM is not sufficient to assign ‘Ultrastructural data’
* The mere mention of ‘Imaging’ does not automatically imply ‘Morphological traits’, as sometimes taxonomists make photo’s but don’t use them as a taxonomic method. For the same reason, the mere mention of ‘photo of habitus’ is not sufficient for ‘qualitative morphological traits’? However, very often imaging will imply ‘Morphological traits’.
* The main aim of the classifier is to know which methods are used in which paper. Hence, very clear, unambiguous references to certain methods, even if they aren’t discussed in detail, are enough to label a category as ‘1’. For example,
  + mention of dissecting and preparing genitalia is enough to tick ‘interbreeding morphology’.
  + *“Samples identification was supervised and checked by Marc Eléaume, crinoid taxonomist at the Muséum national d’Histoire naturelle, Paris, following Clark and Clark (1967) taxonomic description of the species”* is enough to assign ‘Organismal features (Phenotype)
  + “*The units of measurement in this paper are millimetres (mm).*” is enough to assign ‘quantitative morphology’
  + *“Any specimens taken were fixed in 98% ethanol (ETOH) for\nmorphological and molecular analysis and, if enough material was available, some fixed in\nCarnoy’s solution (1:3 of glacial acetic acid to 98% EtOH) for cytological (chromosomal)\nanalysis.”* Is enough to assign “phenotype analysis methods”, “Molecular analysis methods” and “Cytotaxonomy & genome size”.
  + *"Terminology for describing eye coloration in life and webbing formula followed those of Glaw & Vences (1997, 2007)."* is enough for ‘Colour and patterns’

Finally, here is another example paragraph:

'*In each river (see Table 1) three sampling points were selected, placed up, middle and\ndownstream. Applying the sampling and laboratory protocols established by MAGRAMA (2011),\nmacroinvertebrate were collected in May, July and September (2013) by volunteers, supervised by members of the\nAsociación de Ciencias Ambientales (ACA). They used a surber net (500 µm mesh size), working in a 100m length\nsection of good access and fordable section and distributing 20 subsamples in a proportional way between six\nhabitat types: hard substrates (large and small rocks), vegetal substrates (detritus, river shore with plants and\nsubmerged macrophytes) and sands and/or another fine sediments. In the field, samples of macroinvertebrates were\nfixed with 4 % formalin. In the laboratory the specimens were separated with a binocular microscope and preserved\nin 70 % ethanol. Subsequently, the individuals belonging to this family were identified\nto species level. Epibionts on the surface of the Hydraenidae beetles were observed and counted on each\nanatomical unit under stereoscopic and light microscopes. To identify the protozoan epibionts, they were isolated\nand treated using the Fernández-Leborans & Castro de Zaldumbide (1986) silver carbonate technique as well as\nmethyl green, Grenacher’s carmin and haematoxilin techniques. Light microscope images were obtained using\nKS300 Zeiss IMAGE ANALYSIS and AXIOVISION softwares to identify the epibiont species. Statistical\nanalyses were performed using the STATGRAPHICS programme.'*

For this paragraph, you should return:

* ‘sampling location’, because of ‘*In each river (see Table 1) three sampling points were selected, placed up, middle and\ndownstream*.’
* ‘sampling’, because of ‘*Applying the sampling and laboratory protocols established by MAGRAMA (2011)’*
* ‘Ecological traits’ because of ‘*in a proportional way between six\nhabitat types: hard substrates (large and small rocks), vegetal substrates (detritus, river shore with plants and\nsubmerged macrophytes) and sands and/or another fine sediments.’*
* ‘Specimen storage and preparation’ because of ‘*samples of macroinvertebrates were\nfixed with 4 % formalin’.*
* ‘Quantitative morphology’ because of ‘*Epibionts on the surface of the Hydraenidae beetles were observed and counted’.*
* ‘Imaging’ because of ‘*Light microscope images were obtained using\nKS300 Zeiss IMAGE ANALYSIS and AXIOVISION softwares to identify the epibiont species’*
* ‘Non-phylogenetic modelling with morphological data’ because of ‘*Statistical\nanalyses were performed using the STATGRAPHICS programme.’*

Hence, for this paragraph, you should return: [‘sampling location’, ‘sampling’, ‘Ecological traits’, ‘Specimen storage and preparation’, ‘Quantitative morphology’, ‘Imaging’, ‘Non-phylogenetic modelling with morphological data’]

# Categories outside the main classification

### Interbreeding

*Assign this category when: any mention or use of interbreeding related data or reasoning, be it molecular or phenotypic. This includes morphological descriptions of genitalia, hybridization experiments, or biogeographical discussions reflecting on potential for interbreeding. This category is ‘1’ automatically if category 2.1.1.3 (‘interbreeding morphology) is ‘1’.*

### Grouping & Ranking justification:

*Assign this category whenever decisions about recognising groups of organisms are made, this category applies.This is often about species, but can also be about other ranks. This category also often applies when authors discuss species concepts, as these are typically invoked to justify grouping or ranking criteria.*

### Phylogenetic method (general):

*Assign this category whenever authors use phylogenetic methods or reasoning. This can range from inferring trees using genetic data to talking about morphological traits being homologies. This category is ‘1’ whenever 2.3.3, 3.3.2 and 3.3.3 are ‘1’, but also sometimes when there is insufficient information to assign any of these.*

### Biogeography

*This is a datatype that can be either investigated using molecular data or other kinds of data. Assign this category whenever distributions, ranges, phylogeography, endemism,... of groups are investigated and compared. It does not apply when it is merely mentioned where one group occurs. I.e. there has to be some indication that it will be used in taxonomic reasoning.*

### Other singleton categories

* + 1. Specimen storage location

*Applies whenever authors mention where the material they used or collected is stored.*

* + 1. Sampling location

*Applies whenever authors mention where the material they used was collected, even if they didn’t collect it themselves. This includes vague descriptions like ‘the area of the border checkpoint Kapitan Andreevo, Bulgaria’ as well as precise coordinates. This also includes mention of the type locality if they used the type.*

* + 1. Abbreviations & terms

*Applies whenever authors specify the terms and abbreviations they will use, even if these are not mentioned explicitly there. It does not apply when there merely are abbreviations for natural history museums between brackets. It applies, for example, when the authors write something like ‘terms for hindleg morphology were taken from Conix et al. (2005)’.*

* + 1. Nomenclature & taxonomic history

*Applies whenever authors report on investigation of synonymy and nomenclatural history. It also applies when the authors give an overview of the various taxonomic sources of these taxa through history.*

# Organismal features (Phenotype)

## Phenotype datatypes

### Morphological traits

* + - 1. Quantitative morphology

*This category applies whenever any morphological features are counted or measured. It does not apply when behavioural traits, such as bird song, are measured or counted.*

* + - 1. Qualitative morphology

*This category applies whenever non-quantitative morphology is used, for example the general shape of an organ or body-part, the way body-parts fit together, or colours and patterns. Often, one of the subcategories will apply.*

* + - * 1. Colour and patterns

*This category includes all mention of the color of an organism or body-part, but also things like opacity, hue and patterns.*

* + - * 1. Shape and anatomy

*This category includes all mentions of the general shape of body parts, but also the way organs or body parts fit together.*

* + - * 1. Texture

*This category includes all mentions of the texture of body parts.*

* + - * 1. Ultrastructural data:

*This category includes all mention of imaging beyond what can be obtained through optical microscopy—typically at the (sub)cellular level. For instance, mention of axonemes, microvilli, pollen morphology...*

* + - 1. Interbreeding morphology

*This applies whenever there is any mention of interbreeding-related morphology. E.g. “The genitalia were dissected using method X and mounted on…” is enough to label it as ‘1’.*

### Behavioural traits:

*This category applies whenever the authors use behavioural data in their taxonomic reasoning, ranging from mating behaviour and song to foraging behaviour.*

* + - 1. Acoustic data

*This category applies whenever the other measure sound, like bird calls and bird song.*

* + - 1. Mating behaviour

*This category applies whenever the authors talk about the behaviours of organism related to mating, interbreeding and reproduction.*

* + - 1. Feeding behaviour

*This category applies whenever the authors talk about the behaviours of organism related to feeding or finding nourishment.*

### Ecological traits

*This category applies whenever the authors talk about the habitat or ecological niche of an organism, or when they use features of the environment in their taxonomic reasoning.*

## Phenotype data processing

### Imaging

*This category applies whenever images, drawings or visual data of organisms are created. This includes making and editing photographs, and using microscopes. It does not include making representations of phylogenetic trees.*

### Sampling methods

*This category applies whenever any details about the sampling, apart from the location, are given. This includes methods for catching organisms as well as precise sample sizes, duration of sampling, etc.*

### Specimen storage and preparation

*This category applies whenever the authors talk about how collected organisms were stored, or how they were prepared for morphological investigation, such as microscopy or observation of particular body parts.*

## Phenotype analysis methods

*This category applies whenever the authors analyse morphological or other phenotypic data for analysis. This can be phylogenetic or non-phylogenetic analysis.*

### Non-phylogenetic modelling with morphological data

*This category includes multivariate regressions, PCA and other statistical methods to investigate phenotypic data that are not phylogenetic*. In other words, any non-phylogenetic analysis of phenotypic data falls in this category.

### Phylogenetic methods with morphological traits

*Assign this category whenever the authors use phenotypic data for phylogenetic reasoning or analysis.*

# Genetic and molecular features

*This category applies whenever authors use molecular data, often in the shape of genetic data, in their taxonomic methods.*

## Genetic and molecular datatypes

### Nuclear dna

*This category applies whenever authors use, analyse, sequence or include nuclear dna.*

### Organellar dna (mitochondrial, chloroplast)

*This category applies whenever authors use, analyse, sequence or include organellar dna, often from chloroplasts or mitochondria.*

### Transcriptomic data

*This category applies whenever authors use, analyse, sequence or include data derived from the transcriptome, be it RNA content or information of gene expression.*

### Proteomic data

*This category applies whenever authors use, analyse, sequence or include information derived from the proteome. This is often in the form of allozyme analysis in older taxonomic work.*

### Tandem repeats (Microsatellites, minisatellites)

*This category applies whenever authors use, analyse, sequence or include tandem repeats. Useful terms here include ‘short tandem repeats’, ‘SSR’, ‘STR’, and ‘simple sequence repeats’.*

### Whole genomes

### Exomes

*This category applies whenever authors use, analyse, sequence or include data derived only from the exome.*

### NGS Genome Wide studies

### Epigenetic data

*This category applies whenever authors use, analyse, sequence or include epigenetic data.*

### eDNA

*This category applies whenever authors use, analyse, sequence or include so-called environmental dna, i.e. DNA taken from environmental samples such as soil, water, air or sediment.*

### Biochemical traits:

* + - 1. Chemotaxonomy:

*This category applies whenever authors use, measure or analyse, chemical data, such as metabolites or pheromones.*

* + - 1. Cytotaxonomy & genome size:

*This category applies whenever authors use, measure or analyse* *cytological data, such as karyotypes, genome sizes or chromosome numbers.*

## Genotype data processing: nucleotide sequencing

*This category applies whenever authors describe processing and preparing molecular data for analysis. This often consists in sequencing dna but need not be restricted to that.*

### Squencing

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

*This category applies whenever authors describe sequencing data using methods from the first generation of sequencing, most typically sanger sequencing.*

### 2nd generation sequencing (NGS):

*This category applies whenever authors describe sequencing data using methods from the second generation of sequencing, often called ‘next generation sequencing’.*

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

*This category applies whenever authors describe sequencing data using methods from the third generation of sequencing, typically not requiring amplification.*

## Molecular analysis methods

### Non-phylogenetic molecular methods

* + - 1. Distance & barcoding

*This applies whenever distances are calculated incl. simply counting the number of substitutions, even if only the NJ tree is mentioned. It does not apply automatically when barcodes are merely mentioned. Of course, it might, and often does, apply with barcodes too.*

* + - 1. allele sharing-based (haplowebs) approaches

*This category applies whenever authors focus on identifying shared alleles, often in the shape of haplowebs.*

* + - 1. Fixed alternative character states

*This category applies whenever the authors use fixed molecular character states that differ between groups or lineages in their taxonomic reasoning and analysis.*

* + - 1. Clustering methods (structure, structurama, baps, dapc):

*This category applies whenever authors analyse molecular data using a clustering method. It also includes population-genetic methods using the HWP*.

* + - 1. Interbreeding assessed through molecular data

*This category applies whenever authors measure or reason about reproductive isolation, and interbreeding on the basis of molecular data.*

### Phylogenetic Species delimitation

*This category applies whenever authors try to identify or define species boundaries using molecular data to infer evolutionary relationships between groups (such as populations). This is distinct from traditional phylogenetic tree inference, which is not directly aimed at inferring species boundaries. Helpful terms include General mixed yule coalescent (GMYC), Poisson tree process (PTP), Multi-species coalescent, SpeDeSTEM, BP&P, Brownie, SNAPP, mPTP, \*BEAST.*

### Phylogenetic tree reconstruction methods

*This category applies whenever the authors try to reconstruct a phylogenetic tree on the basis of molecular data.*

* + - 1. Distance based (neighbour joining, UPGMA)

*This category applies whenever the authors infer a phylogenetic tree on the basis of genetic distance data.*

* + - 1. Character based methods

*This category applies whenever the authors infer a phylogenetic tree on the basis of molecular characters, often nuclear or organellar genes, and uften using Bayesian inference or maximum likelihood.*

* + - 1. Consensus and supertree methods

*This category applies when authors use consensus tree methods to summarize multiple phylogenetic trees with the same taxon set, or supertree methods to combine phylogenetic trees with overlapping but non-identical taxon sets. These approaches often involve integrating data from different sources to produce a single, representative phylogenetic tree.*

### Machine learning methods

*This category applies using machine learning algorithms to analyse large datasets and draw taxonomic conclusions, be it identification or recognising new taxa.*