**fTitle/Abstract Removal Criteria**

* Non-Animals
  + Plants
  + Fungi
* Microbiology
  + Bacteria
  + Viruses
  + Protists
  + Cellular
* Humans
  + Medical
  + Anthropology
  + Archeology
  + Public Health
* Non-Wildlife
  + Agriculture
  + Domesticated
    - Any farm animals
    - Pets (Dogs, Cats)
  + Veterinary
* Non-Genetic
  + Physiology
  + Anatomy
  + Chemistry
  + Physics
  + Toxicology
* Species identification
* Ancient
  + Paleontology
  + < 1800
* Phylogenetics
* Epigenetics
  + Methylation
* Environmental DNA
  + Water
  + Sediment
* Non-temporal
* **Non-Genomic (should be last exclusion criterion)**
  + **Microsatellites (should be included, write microsats in notes)**
  + Allozymes
  + STRs

**Title/Abstract Inclusion Criteria**

* Genomic
  + SNPS
  + Exomes
  + Whole genome
  + Exons
  + Mitochondrial
  + Etc.
* Wildlife
  + Vertebrates
  + Invertebrates
  + Reproduction in wild
* Contemporary Samples
  + > 1800
* Temporal Sampling
  + Multiple genetic samples from different time points
* Empirical or theoretical or review

**Accepted Paper Content to Record**

\*Only need to record this information if your subject area is subject #1 and it is an EMPIRICAL study.

Columns should be filled out as thoroughly as possible (only leave blank if the information is not available). If you have questions about the content of a column or a particular paper, post on Teams in the “Literature Review - Compiling Data” channel and tag the channel so that everyone can see the post and give feedback.

Look at the highlighted row at the top of the “diversity\_accepted” excel spreadsheet in the OneDrive working\_group folder for an example of how to fill out these columns.

|  |  |  |
| --- | --- | --- |
| Column | Options | Description |
| subject[1:4] | Adaptation  Connectivity  Diversity  Popsize | The subject the paper is focused on by order of focus. As an example, a paper is focused on Adaptation, but also talks about gene flow/connectivity. Adaptation is subject\_1 and connectivity is subject\_2. All four subjects may not be present. |
| system | Freshwater  Marine  Terrestrial  Other | The general system that is being studied. Correlated to the study animal.  If the organism spends part of its life cycle in different habitats (e.g. catadramous, anadramous, semi-aquatic insects, amphibians) or lives in an “in-between” environment (e.g. riparian/estuarine/euryhaline), mark as other for now. |
| taxonomic\_group | The class of the study organism |  |
| country\_sampled | The country the samples were collected in |  |
| Location\_sampled | The location (as described in the paper) samples were collected at | Only record if given. Should be as specific as possible (if someone were to look this up, would be able to identify the location on Google Maps).  Order of location should match order of samples in year\_sampled & num\_sampled columns. If only one site was collected at (e.g. same site for historical & contemp samples) then only list the site once. Otherwise, the location each time point was collected at should be listed, separated by commas.  If multiple locations were collected at one time point (e.g. Site A & Site B were both collected in 2007) then both sites should be listed, separated by periods (ex: Site A.Site B,next time point).  If you have lat/lon denote it in the column.  If you have so many sampling locations (esp connectivity studies!) that it isn’t easy to parse them apart, write in column instead: “see paper, fig/table # for location/coordinates” |
| Year\_sampled | Year.Month.Date (as specific as given in the paper) | The data should be input as XXXX.XX.XX (Year.Month.Date). If month/date is not available, put 01 in the appropriate column. (Ex. Sampling in 1992: 1992.01.01; sampling in August 1975 (1975.08.01))  If collected from multiple time points, separate with a comma (ex: 1992.01.01,1993.01.01,1995.01.01)  Should be recorded with the most recent sample FIRST, followed by the next most recent sample, etc. |
| Number\_sampled  **\*NOTE: It is VERY important that the sample order in location\_sampled,time\_sampled,number\_sampled matches up!!** All columns should have the same number of commas (the only exception is if the same locations were used for all time points, then location\_sampled may only have one location or several locations separated by periods). | Number of individuals sampled at each time point. | Order of location should match order of samples in year\_sampled & location\_sampled columns. This is very important!!  The sample size for each time point should be listed, separated by commas.  If multiple locations were collected at one time point (e.g. 12 individuals at Site A & 24 individuals at Site B were all collected in 2007) then both sites should be listed, separated by periods (ex: 12.24,next time point). |
| Generation\_time | Generation time of study organism (in days). | Record if reported in paper. If not reported in paper, look up on own (literature search, life history trait database (fishbase, etc)). If the generation time comes from a source other than the original study, make sure to record where you got the generation time from (in notes column). |
| Study\_design | Opportunistic  Pre-designed | Opportunistic: Not all samples were collected by researchers; instead, opportunistically used museum samples/archived samples to ask and answer research questions.  Pre-designed: The study was designed from the start to use temporal data (e.g. the researchers collected all/most samples on their own). |
| Type\_Change | Anthropogenic  Natural | Is the study investigating genomic change due to a natural process (natural disaster, “normal” environmental variability, disease, etc.) or due to an anthropogenic process (harvesting, habitat loss, climate change, etc.). |
| Driver\_Process (multiple columns to allow for multiple drivers) | Climate Change  Competition  Disease  Environmental Variation  Habitat Loss  Human Exploration  Invasive Species  Natural Disaster | Main pressure driving observed change. Will be multiple columns in case more than one driver is being investigated. Should be ordered primary, secondary, tertiary, etc. |
| Length\_Process | Acute  Chronic | How long has pressure driving change been around for?  Acute: Pressure driving change is short-lived (0-10 generations).  Chronic: Pressure driving change is long-term (>10 generations). |
| Data\_Type | mtDNA sequence  Nuclear sequence  SNP  Microsat | What type of data was incorporated in the study. |
| Tissue\_Type | Bone  Skin  Scale  Hair  Muscle  Gills  Liver  Kidney | For historical samples only. What tissue was DNA extracted from? |
| Preservation\_Method | DESS  Dried  Ethanol  Formalin  Frozen  Propanol  DMSO  Spirits  Ethanol, frozen  Spirits, frozen  DESS, frozen | For historical samples only. How were the tissues preserved prior to inclusion in the study? |
| Extraction\_Method | Qiagen  Omega [other proprietary]  Tin\_etal\_2004  deBruyn\_etal\_2011 | For historical samples only. How was DNA extracted?  If DNA was extracted with a standard kit (Qiagen, etc.) write that. If extraction followed a “home brew” kit/process write the paper cited in a similar method to examples (Tin\_etal\_2004, etc.). |
| Sequencing\_Platform | Illumina HiSeq  Illumina MiSeq  Illumina NextSeq  Illumina-BeadXPress SNP assay  Ion Torrent  Nanopore  PacBio  Sanger  454-pyrosequencing | What sequencing platform was used? |
| Library\_Prep\_Method (Genotyping\_Method?) | Exome capture  PCR  RAD  RNA  Shotgun  Targeted sequence capture  Whole genome | How was the DNA prepared for sequencing?  If primers were used to target mtDNA/microsatellites, put PCR in the column. |

**Procedure for Recording Data**

Each topic group has their own Excel spreadsheet that contains all the accepted papers relevant to their topic. The format of the Excel spreadsheets are identical. Papers that the topic group is responsible for recording data for are found at the top of the spreadsheet (e.g. papers that are empirical and have their topic in the “subject\_1” column). All other papers that are relevant to the subject topic are found below.

It is up to each topic group to decide how to divide up the papers. The initials for the person who ends up recording data for each paper should go in the “Recorder” column. Groups may add columns to the spreadsheet, but these should go at the end (after the “Notes” column).

There may be some papers that do not fit our criteria for the literature review. If you encounter a paper that should be rejected (does not use historical samples, etc.), change the decision column to “reject” and input the appropriate rejection reason in the removal\_criteria column. Delete the entries in the study\_type and subject columns.

If you need to re-assign a paper (e.g. upon reading realize that it is appropriate for a category it hadn’t been categorized in), add the appropriate subject to one of the subject columns and copy and paste the row over to the appropriate spreadsheet. If your topic group was responsible for recording data from that paper (was subject\_1), still record the data (do NOT change the subject\_1 column unless absolutely necessary). Once you copy the row over to the new excel spreadsheet, let the appropriate topic group know.

**Best Practices Section Questions**

\* These questions will form the basis of each individual best practices section. As such, they should be kept in mind as papers are being read. We have no “formal” columns to record information on these questions, but columns can be added to the end of individual section spreadsheets as groups see fit to do so.

1. How does marker choice and the number of loci impact inferential ability and statistical power?
2. What are common sampling schemes (number of samples, number of time points, sample sizes, etc.)? How might sampling schemes be best designed to optimize inferential ability and statistical power?
3. Are there species- or population-specific attributes that may influence one’s ability to detect change?
4. What types of analyses/metrics are commonly used? What types of analyses/software/metrics might you recommend?
5. Are there limitations or common pitfalls researchers should be aware of when designing temporal genomics studies investigating your particular subject?
6. Are there important differences between terrestrial, freshwater, and marine systems that should be kept in mind when designing these types of temporal genomics studies?