

## GeOMe Help Document

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### Introduction

The Genomic Observatories Meta-Database (GeOMe) is a web-based database which captures metadata on biological samples, used for biodiversity inventories, population studies, and environmental metagenomics. GeOMe assigns persistent identifiers for all samples and sampling events and specifies the set of metadata attributes which satisfy the requirements of the [genomic observatories model](#), including capturing the who, what, where, and when associated with all samples. GeOMe provides instant feedback to users on the quality of their data and packages data for further analysis for use in a laboratory information system (LIMS) using the [Biocode LIMS plugin](#). GeOMe also packages submissions for easy delivery to the Sequence Read Archive (SRA) and Genbank's Nucleotide database.

### Generate Template

Sample metadata is recorded on an Excel Spreadsheet and you can create and customize your own templates under “Tools -> Generate Template”

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On the Generate Template page, you can select columns that you want to include on your spreadsheet. Click on the “DEF” link beside each column name to view the definition of the column name. Columns that are pre-checked and shown in grey, indicate that they are mandatory fields and not able to be un-checked. Columns that are pre-checked and shown in blue indicate they are suggested and can be un-checked. Once you have checked the columns you wish to include in your spreadsheet, press the “Export Excel” button to download an Excel Spreadsheet which you can then use to fill in Sample Metadata.

## GENERATE TEMPLATE

Choose template from dropdown menu *OR* check available column heading below to include in your customized FIMS spreadsheet.

Default

Remove

Export Excel

Select ALL | Select NONE | Save

### DEFAULT COLUMNS

- ☒ phylum DEF
- ☒ principalInvestigator DEF
- ☒ materialSampleID DEF
- ☒ locality DEF
- ☒ decimalLatitude DEF
- ☒ decimalLongitude DEF
- ☒ coordinateUncertaintyInMeters DEF
- ☒ georeferenceProtocol DEF
- ☒ yearCollected DEF
- ☒ monthCollected DEF
- ☒ dayCollected DEF
- ☒ genus DEF
- ☒ species DEF
- ☒ permitInformation DEF
- ☒ basisOfIdentification DEF
- ☒ country DEF
- ☒ lifeStage DEF
- ☒ sex DEF
- ☒ geneticTissueType DEF

- Although there are a lot of field options only four are

#### REQUIRED:

materialSampleID  
principalInvestigator  
phylum  
and either  
decimalLatitude AND decimalLongitude (preferred)  
or  
locality

- Thirteen additional fields are recommended, and thus automatically checked in the default template
- Each individual (organism/sample) is entered in a row in the spreadsheet and must have a unique materialSampleID that is created by the user (your unique sample name)

### DEFINITION

Click on "DEF" next to any of the headings to see the definition of the term.

#### Column Name: locality

URI = urn:locality

Defined\_by = <http://rs.tdwg.org/dwc/terms/locality>

#### Definition:

Local name of site. Something that could be found by Google

## Validate and Load Data

The Validate and Load Data option can be found under "Tools -> Validate and Load Data". The first step is validating your sample metadata. Use the Browse button to browse for your file and select the "Validate" button. After data validation, you can Upload your dataset and include just the metadata or include FASTA or FASTQ metadata.

### FASTA Upload Example

You must create, or select a pre-existing expedition name for your dataset before continuing. Select your FIMS Metadata file, along with a FASTA filename and a Marker name. After selecting the FIMS Metadata file, you must check a box stating that you have visually verified the sample locations on the map at the bottom of the page. The name of your FASTA sequences must match the sample identifiers in the metadata file. Each FASTA file should only include data from a single marker type. If you have multiple markers for the same taxa you must upload multiple FASTA files for a single metadata file, which can be added by clicking on the "+" button.

## VALIDATE AND LOAD DATA

Using this tool you can check for errors in your metadata file and upload your data. The validate tab can be used to ensure that all required fields are completed and that each materialSampleID is unique in your metadata file (in tab delimited text format) while the upload tab will also validate your files and ensure that each materialSampleID is accompanied by a fasta/fastq file of the same name.

Validate

Upload

Results

Data Type(s)

☒ FIMS Metadata
 ☒ Fasta
 ☐ Fastq Metadata

Expedition Name

acaach\_CyB\_JD spreadsheet

☐ New Expedition?

FIMS Metadata

Browse ...

dipnetSample\_Metadata.xlsx

☒ Please verify sample locations on the map below and then check this box

FASTA Data

Browse ...

Marker

CO1

?

FASTA Data

Browse ...

Marker

CO2

?

-

+

**Instructions:**

- The name of your fasta sequences must match the materialsampleIDs in the metadata file
- You can include multiple taxa in a single fasta/metadata file
- Each fasta file should only include data from a single marker type (e.g. CO1, CYB, etc)
- If you have multiple markers for the same taxa you must upload multiple fasta files for a single metadata file.
- We recommend Fasta files names should follow this format  
markerabbreviation\_usertaxaabbreviation.fa

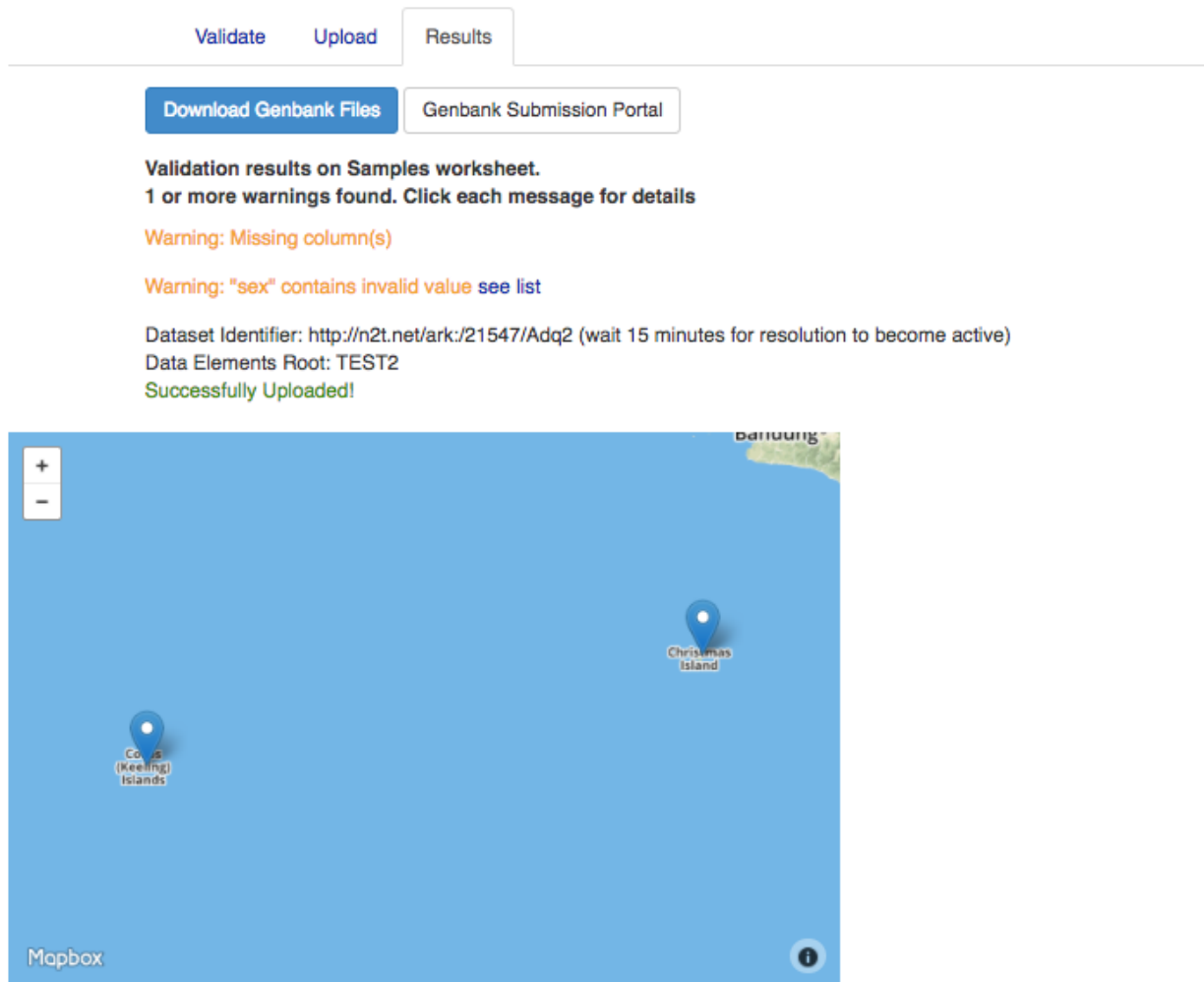
## FASTQ Upload Example

The FASTQ Upload example follows the same protocols as the FASTA upload example. The following points should be followed when uploading FASTQ data:

- FIMS will accept single and paired end read data
- Each FASTQ file should contain reads from a single individual
- Names of fastq files must match the materialsampleIDs in the metadata file up to the file extension (e.g., R1.fq.gz, .1.fq, etc)
- The actual fastq sequence files will not be uploaded here and stored on the FIMS system. Instead the metadata file will be uploaded and stored here.
- For validation purposes a text file of the fastq file names (one name per line and including the file extension) will be uploaded here. If you are uploading PE data there should be two file names per sample. This process ensures that required fields are complete, that each materialsampleID is unique, and that the materialsampleIDs match the fastq file names.
- Once uploading is complete the FIMS system will produce two files (SRA metadata and BioSample attributes files) that will ease the upload process to NCBI's Short Read

Archive (SRA). When these files are downloaded a set of simple instructions are included that will speed your SRA submission.

Once you have validated and uploaded FASTQ file, a screen is presented that shows you two buttons and your validation results. One button enables you to download pre-generated Genbank submission files. The second button is available which opens a browser window taking you to Genbank's SRA Portal.



### GeOMe R Package

A link is available under the tools menu which takes you to the GeOMe R package github page, located at <https://github.com/DIPnet/fimsR-access>. More instructions are available at that link.

### Browse Expeditions

The "Browse Expeditions" option shows all available uploaded expeditions that are part of GeOMe. This pages shows you the number of samples, FASTA sequences, and FASTQ metadata

provided for each sample. Here you have the option of downloading CSV, FASTA, or FASTQ formatted metadata.



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## EXPEDITION BROWSER

In this system an "Expedition" includes the metadata (and Sanger sequences if applicable) from a single dataset. The GUID is the globally unique persistent identifier for the expedition and should be acknowledged in the original publication of the dataset and accredited when any part of that dataset is downloaded for reuse.

Expedition Title	Samples	Fasta Sequences	Fastq Metadata	GUID	
Acanthurus_reversus_RADSeq_Sanger spreadsheet	30	83	9	<a href="http://n2t.net/ark:/21547/AgX2">http://n2t.net/ark:/21547/AgX2</a>	<a href="#">Download</a>
Acanthurus_olivaceus_rangewide_Sanger&RADSeq	673	1156	52	<a href="http://n2t.net/ark:/21547/AEW2">http://n2t.net/ark:/21547/AEW2</a>	<a href="#">Download</a>
Celexa_CO1_cb spreadsheet	150	150	0	<a href="http://n2t.net/ark:/21547/AFX2">http://n2t.net/ark:/21547/AFX2</a>	<a href="#">Download</a>
Celsan_CO1_cb spreadsheet	109	109	0	<a href="http://n2t.net/ark:/21547/AFW2">http://n2t.net/ark:/21547/AFW2</a>	<a href="#">Download</a>
Centropyge_Cytb_DiBattista2016 spreadsheet	157	156	0	<a href="http://n2t.net/ark:/21547/Agg2">http://n2t.net/ark:/21547/Agg2</a>	<a href="#">Download</a>
Ceparg_CyB_MG spreadsheet	775	775	0	<a href="http://n2t.net/ark:/21547/AFM2">http://n2t.net/ark:/21547/AFM2</a>	<a href="#">Download</a>
Ctestr_CYB_JE spreadsheet	531	531	0	<a href="http://n2t.net/ark:/21547/AGI2">http://n2t.net/ark:/21547/AGI2</a>	<a href="#">Download</a>
Diaspp_A68_HL spreadsheet	310	310	0	<a href="http://n2t.net/ark:/21547/AGA2">http://n2t.net/ark:/21547/AGA2</a>	<a href="#">Download</a>
Diaspp_CO1_HL spreadsheet	13	13	0	<a href="http://n2t.net/ark:/21547/AFz2">http://n2t.net/ark:/21547/AFz2</a>	<a href="#">Download</a>
Echdia_CytB_HL spreadsheet	25	25	0	<a href="http://n2t.net/ark:/21547/AFt2">http://n2t.net/ark:/21547/AFt2</a>	<a href="#">Download</a>
Eucmet_CO1_HL spreadsheet	30	30	0	<a href="http://n2t.net/ark:/21547/AFw2">http://n2t.net/ark:/21547/AFw2</a>	<a href="#">Download</a>
Gilgoburna_Dinnet test 1C spreadsheet	2	2	0	<a href="http://n2t.net/ark:/21547/Al2">http://n2t.net/ark:/21547/Al2</a>	<a href="#">Download</a>

## Query

The GeOME query interface enables users to filter on geographic information, any word string as part of the metadata (e.g. "Moorea"), Darwin core terms, expedition names, or any other column that is part of the GeOME specification. The Query interface returns results either in map form or table form, selectable by clicking on the "Map" or "Table" buttons on the upper right corner of the interface. The "Download" link enables metadata download of the queried results.

## Accession Numbers and Sample Identifiers

When you submit your work for publication you may be asked for Genbank accession numbers, dataset identifiers, or even sample identifiers. GeOME creates identifiers for physical samples and datasets, as well as automatically syncing sequence read archive SRA numbers. The following information describes how to handle these identifiers.

### Physical Sample Identifiers

As you may have seen, you can obtain a globally unique form of the materialSampleID in the "bcid" column at the end of the row of metadata when you download a CSV file and it looks like:

ark:/21547/Apj2Acaoli\_262

The above follows the same principal of reporting a doi, where you just put doi: and some string following it. if you want it resolvable, then you can report it with the resolver in front of it, like:

[https://n2t.net/ark:/21547/Apj2Acaoli\\_262](https://n2t.net/ark:/21547/Apj2Acaoli_262)

#### Dataset/Expedition Identifiers

You can find dataset identifiers by going to "Tools -> Browse Expeditions" and you'll see a column called "GUID" that if you click on will bring you to information about your expedition.

E.g. <https://n2t.net/ark:/21547/Apc2>

#### Sequence Identifiers

For nextgen sequences that have followed the GeOMe path described in this document you can enter the resolvable GUID for the materialSample and find links to the BioProject and BioSample identifier, e.g. check out the following record:

[http://n2t.net/ark:/21547/le2Acaoli\\_CAS44](http://n2t.net/ark:/21547/le2Acaoli_CAS44)

GeOMe currently doesn't link Genbank Accession identifiers for FASTA data submissions, so these will need to be researched independently.

## Cheat sheet for uploading your DIPnet data to the NCBI Short Read Archive (SRA)

After submitting your metadata to DIPnet two files will be produced the bioSample-attributes.tsv and the sra- metadata.tsv files and you will be directed to SRA to upload your data. There are several steps but the creation of those two files will streamline the process significantly!

If you don't already have a NCBI account you will need to create one. If you do have an account then sign in using the tab at the top right corner of page.

After you sign in start a new submission

### **Step 1:** Submitter

Enter your personal information

**Step 2: General Info**

You will be asked two important questions here:

1. Did you already register a BioProject for this data set?
2. Did you already register BioSamples for this

data set?

In the majority of cases the answer to both

questions will be NO

The following instructions are based on the user answering “NO” to both of the above questions.

**Step 3: Project Info**

Fill in project information. For example:

Project Title: *Acanthurus\_reversus\_RADSeq\_data*

Project Description: RADSeq data for the reef fish *Acanthurus reversus*

Relevance: Evolution

Is your project part of a larger initiative that is already registered with NCBI?

Most likely No

External links: Add if relevant

Select your grants: If relevant

**Step 4: Biosample type**

Here you choose your sample type. Most DIPnet members will check either “Invertebrates” OR “Model organism or animal sample” for vertebrates.

**Step 5: Biosample attributes**

Upload the bioSample-attributes file (.tsv) produced by GeOMe. You may see additional warnings or error messages produced by the SRA validator. You must fix error messages. In some cases, you may safely ignore warnings. For example, we have seen cases for users working in marine system where locality is often based on nearby terrestrial locations, and the SRA responds with a warning that the locality is invalid since it is located in the warning. This particular message may be ignored for marine users where this is intentional.

**Step 6: SRA metadata**

Check the Upload a file option and upload the sra-metadata file (.tsv) produced by GeOMe

**Step 7: Files**

Follow the directions on SRA and upload your files. You will be asked to download the latest version of Aspera Connect. This will speed upload tremendously. Once Aspera is installed go directly to the Choose Files option, choose your zipped folder, and Aspera will automatically



open.

**Step 8:**

Overvi

ew

Submit

!