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Version 6

Populating metadata templates for NCBI submissions using PulseNet 2.0 V.6

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Ruth Timme¹, Maria Balkey¹, Tina Pfefer¹, Candace Bias¹

¹US Food and Drug Administration

GenomeTrakr

Tech. support email: genomeTrakr@fda.hhs.gov



Maria Balkey

US Food and Drug Administration

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We use this protocol and it's working

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Abstract

PURPOSE: to define the standard operating procedure for collecting isolate metadata using PulseNet 2.0 for submission of food/environmental isolates to NCBI.

SCOPE: to provide a standardized procedure to collect isolate metadata using PulseNet 2.0 for submission of food/environmental isolates to NCBI.

RESPONSIBILITIES- SOP Responsible Officials: Ruth Timme, Maria Balkey

The GenomeTrakr Network Management will be responsible to monitor GenomeTrakr submissions processed through PulseNet 2.0 and ensure that all GT labs are familiar with the mandatory metadata fields required for submission of GenomeTrakr sequencing records to NCBI.

V3: Added dropdown menus from controlled vocabulary to sequenced by and project name to metadata template *PulseNet_Bionumerics_Isolate_Metadata*

V4: Changes in metadata template *PulseNet_Bionumerics_Isolate_Metadata*.

- Added dropdown menus from controlled vocabulary to collected_by , SourceCountryState
- Added fields: collected by, isolation source
- Added mapping table of attribute names.
- Remove requirement to send biosample update to NCBI to make changes on sequenced by and project name.

V5: Changes implemented to handle NCBI submissions for GenomeTrakr through the PulseNet 2.0 platform.

V6: New version of spreadsheet with updated dropdown menu. Add values to NCBI Templates

V7: Add GMVS option to download metadata spreadsheet. Mapping serovar to serotype_wgs or serotype.

V8: Add note on serovar mapping. Serovar only maps to serotype_wgs when the WGS prediction for serotype is available. Add PHL_ReceivedDate and WGS_Lab_ReceivedDate to metadata spreadsheet.

Safety warnings

 We will be updating this protocol with each new PulseNet 2.0 upgrade that impacts NCBI submissions

1 Data Ownership

Laboratory scientists that use PN2.0 to submit GenomeTrakr data to NCBI shall be included in the PulseNet NCBI submission group.

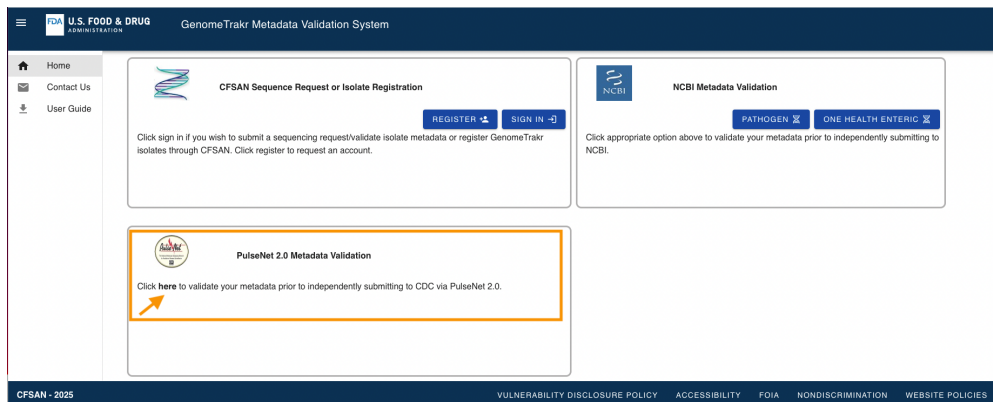
Please reach out to PulseNet to ensure your name is included in this group.

Membership in the PulseNet submission group will grant you the correct privileges for viewing and managing your GenomeTrakr submissions within the NCBI submission portal. If you login to NCBI and ***don't*** see your GenomeTrakr submissions, you likely not a member.

2 Metadata SampleSheet preparation

Populate the metadata spreadsheet form before uploading your sequencing run or linking NCBI sequencing records within PulseNet 2.0.

Please download the metadata template from the GenomeTrakr MetadataValidation System (GMVS) and review the included guidelines before filling out the spreadsheet.



CDC PulseNet 2.0 Metadata Sheet Upload

Click below to browse and attach the PulseNet 2.0 metadata sample sheet. Click the **Validate** button after attaching. If needed, click the  button to download the latest template. The latest version number is **2.0**. If you currently have a template, you can find the version number at the top of the Instructions tab.

* There is a known issue with Microsoft Excel version **build 2308** not allowing vertical scroll on drop-down menus with a mouse after performing a horizontal scroll. Please contact your local IT to get upgraded to a different build if you experience this issue with a GMVS metadata template.



Click to attach the PulseNet 2.0 metadata sample spreadsheet



Only xlsx accepted

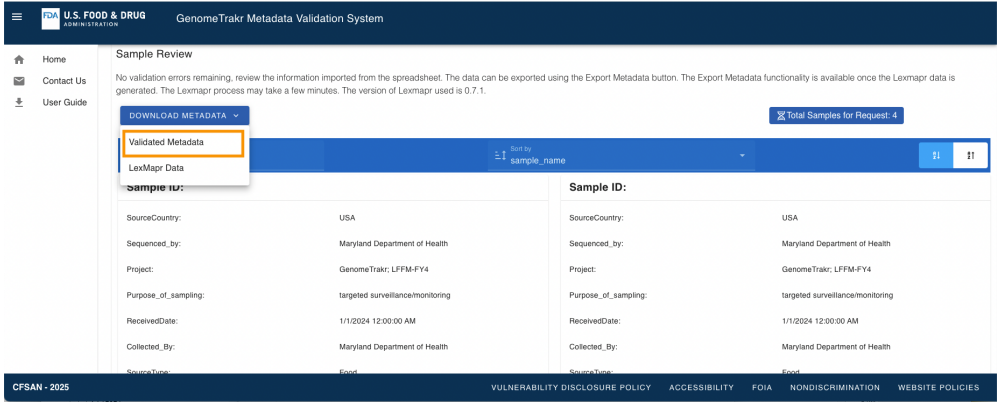
Click to download metadata spreadsheet

Search and Select Lab Name Conducting Validation.

 VALIDATE

 CANCEL

Once you have filled out the template, validate spreadsheet at GMVS. If the metadata is validated, you will have the option **Download Metadata** and click on Validated Metadata. The Validated file is ready for upload to PN 2.0.



U.S. FOOD & DRUG ADMINISTRATION GenomeTrakr Metadata Validation System

Sample Review

No validation errors remaining, review the information imported from the spreadsheet. The data can be exported using the Export Metadata button. The Export Metadata functionality is available once the Lexmapr data is generated. The Lexmapr process may take a few minutes. The version of Lexmapr used is 0.7.1.

DOWNLOAD METADATA Total Samples for Request: 4

- Validated Metadata**
- LexMapr Data

Sort by: sample_name

sample id:	Sample ID:
SourceCountry: USA	SourceCountry: USA
Sequenced_by: Maryland Department of Health	Sequenced_by: Maryland Department of Health
Project: GenomeTrakr: LFFM-FY4	Project: GenomeTrakr: LFFM-FY4
Purpose_of_sampling: targeted surveillance/monitoring	Purpose_of_sampling: targeted surveillance/monitoring
ReceivedDate: 1/1/2024 12:00:00 AM	ReceivedDate: 1/1/2024 12:00:00 AM
Collected_By: Maryland Department of Health	Collected_By: Maryland Department of Health

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Import metadata according PulseNet Instructions

Note

In order to access PulseNet Instructions, make sure you have successfully logged in at the SAMS Partner Portal.

3 Creation of NCBI Submission Templates

Before submitting data to NCBI, set up **sample specific** submission templates in PulseNet 2.0 according to [PulseNet Instructions](#), following GenomeTrakr mapping guidelines included in this protocol.

Map each field name to the corresponding field value as described in steps

⇒ [go to step #3.1](#) for Food isolates

⇒ [go to step #3.2](#) for Food Facility inspection isolates

⇒ [go to step #3.3](#) for Animal isolates

⇒ [go to step #3.4](#) for Farm or other environmental isolates.

Make sure to add the the GenomeTrakr-required fields to each template depending on the source type designation, using the **Add Field** functionality in the Pipeline Template section.

The creation of NCBI Submission Templates in PulseNet 2.0 will only be done once, then the saved templates can be used for all future submissions.

3.1 NCBI Template for Food Isolates

If the Strain name is mapped to the WGS_id, ensure the Submitter Provided Unique ID is mapped to the key.

If the Strain name is mapped to the key, ensure the Submitter Provided Unique ID is mapped to the WGS_id.

If adding OHE package fields, please use OHE package nomenclature as indicated below.

A	B	C
Field Name	Field Type	Field Value
Strain name	Mapping	WGS_id OR Key
Sample name	Mapping	Key
Submitter Provided Unique ID	Mapping	WGS_id OR Key
SPUID namespace	Value	GenomeTrakr



A	B	C
BioProject accession	Mapping	BioProject
Author	Mapping	Sequenced_by
Serovar	Mapping	Serotype_wgs*
SourceType	Mapping	SourceType
<i>Isolate Name Alias if SourceType equals Human</i>	<i>Value</i>	<i>missing</i>
Isolate Name Alias if SourceType does not equal Human	Mapping	Key
Isolation source if SourceType does not equal Human	Mapping	SourceSite, TypeDetails
<i>Isolation source if SourceType equals Human</i>	<i>Value</i>	<i>missing</i>
<i>Geographical origin if SourceType equals Human</i>	<i>Value</i>	<i>missing</i>
Geographical origin if SourceType does not equal Human	Mapping	Geo_loc_name
Organism name	Mapping	Genus, Species
<i>Collection / isolation date if SourceType equals Human</i>	<i>Value</i>	<i>missing</i>
Collection / isolation date if SourceType does not equal Human	Mapping	IsolatDate YYYY-mm
<i>Collected by if SourceType equals Human</i>	<i>Value</i>	<i>missing</i>
Collected by if SourceType does not equal Human	Mapping	Collected_By
Instrument model	Mapping	Instrument_Model



A	B	C
Library strategy	Value	WGS
Library source	Value	GENOMIC
Library selection	Value	RANDOM
Library layout	Value	PAIRED
Library name	Mapping	Library
Project name	Mapping	Project
<i>Sequenced by if SourceType equals Human</i>	<i>Value</i>	<i>missing</i>
Sequenced by if SourceType does not equal Human	Mapping	Sequenced_by
ADD FIELD...		
intended_consumer	Mapping	Intended_consumer
food_origin	Mapping	Food_origin
food_processing_method	Mapping	Food_processing_method
purpose_of_sampling	Mapping	Purpose_of_sampling

*Map -Serovar- to missing if WGS prediction (Serotype_wgs) is not available.

Save submission template according to [PulseNet Instructions](#) as -**GenomeTrakr-FoodGroup**-.

3.2 NCBI Template for **Food Facility Environment Isolates**

If the Strain name is mapped to the WGS_id, ensure the Submitter Provided Unique ID is mapped to the key.

If the Strain name is mapped to the key, ensure the Submitter Provided Unique ID is mapped to the WGS_id.



If adding OHE package fields, please use OHE package nomenclature as indicated below.

A	B	C
Field Name	Field Type	Field Value
Strain name	Mapping	WGS_id OR Key
Sample name	Mapping	Key
Submitter Provided Unique ID	Mapping	WGS_id OR Key
SPUID namespace	Value	GenomeTrakr
BioProject accession	Mapping	BioProject
Author	Mapping	Sequenced_by
Serovar	Mapping	Serotype_wgs*
SourceType	Mapping	SourceType
<i>Isolate Name Alias if SourceType equals Human</i>	<i>Value</i>	<i>missing</i>
Isolate Name Alias if SourceType does not equal Human	Mapping	Key
Isolation source if SourceType does not equal Human	Mapping	SourceSite, TypeDetails
<i>Isolation source if SourceType equals Human</i>	<i>Value</i>	<i>missing</i>
<i>Geographical origin if SourceType equals Human</i>	<i>Value</i>	<i>missing</i>
Geographical origin if SourceType does not equal Human	Mapping	Geo_loc_name
Organism name	Mapping	Genus, Species
<i>Collection / isolation date if SourceType equals Human</i>	<i>Value</i>	<i>missing</i>
Collection / isolation date if SourceType does not equal Human	Mapping	IsolatDate YYYY-mm



A	B	C
<i>Collected by if Source Type equals Human</i>	<i>Value</i>	<i>missing</i>
Collected by if Source Type does not equal Human	Mapping	Collected_By
Instrument model	Mapping	Instrument_Model
Library strategy	Value	WGS
Library source	Value	GENOMIC
Library selection	Value	RANDOM
Library layout	Value	PAIRED
Library name	Mapping	Library
Project name	Mapping	Project
<i>Sequenced by if Source Type equals Human</i>	<i>Value</i>	<i>missing</i>
Sequenced by if Source Type does not equal Human	Mapping	Sequenced_by
ADD FIELD...		
facility_type	Mapping	Facility_type
food_type_processed	Mapping	Food_type_processed
purpose_of_sampling	Mapping	Purpose_of_sampling

*Map -Serovar- to missing if WGS prediction (Serotype_wgs) is not available.

Save submission template according to [PulseNet Instructions](#) as
-GenomeTrakr-FoodFacilityEnvironment-.

3.3 NCBI Template for **Animal Isolates**

If the Strain name is mapped to the WGS_id, ensure the Submitter Provided Unique ID is mapped to the key.

If the Strain name is mapped to the key, ensure the Submitter Provided Unique ID is mapped to the WGS_id.

If adding OHE package fields, please use OHE package nomenclature as indicated below.



A	B	C
Field Name	Field Type	Field Value
Strain name	Mapping	WGS_id OR Key
Sample name	Mapping	Key
Submitter Provided Unique ID	Mapping	WGS_id OR Key
SPUID namespace	Value	GenomeTrakr
BioProject accession	Mapping	BioProject
Author	Mapping	Sequenced_by
Serovar	Mapping	Serotype_wgs*
SourceType	Mapping	SourceType
<i>Isolate Name Alias if SourceType equals Human</i>	Value	missing
Isolate Name Alias if SourceType does not equal Human	Mapping	Key
Isolation source if SourceType does not equal Human	Mapping	SourceSite, TypeDetails
<i>Isolation source if SourceType equals Human</i>	Value	missing
<i>Geographical origin if SourceType equals Human</i>	Value	missing
Geographical origin if SourceType does not equal Human	Mapping	Geo_loc_name
Organism name	Mapping	Genus, Species
<i>Collection / isolation date if SourceType equals Human</i>	Value	missing
Collection / isolation date if SourceType does not equal Human	Mapping	IsolatDate YYYY-mm



A	B	C
<i>Collected by if Source Type equals Human</i>	<i>Value</i>	<i>missing</i>
Collected by if Source Type does not equal Human	Mapping	Collected_By
Instrument model	Mapping	Instrument_Model
Library strategy	Value	WGS
Library source	Value	GENOMIC
Library selection	Value	RANDOM
Library layout	Value	PAIRED
Library name	Mapping	Library
Project name	Mapping	Project
<i>Sequenced by if Source Type equals Human</i>	<i>Value</i>	<i>missing</i>
Sequenced by if Source Type does not equal Human	Mapping	Sequenced_by
ADD FIELD...		
host	Mapping	Host
animal_env	Mapping	animal_env
purpose_of_sampling	Mapping	Purpose_of_sampling

*Map -Serovar- to missing if WGS prediction (Serotype_wgs) is not available.

Save submission template according to [PulseNet Instructions](#) as **-GenomeTrakr-AnimalHost-**.

3.4 NCBI Template for **Farm Environment Isolates**

If the Strain name is mapped to the WGS_id, ensure the Submitter Provided Unique ID is mapped to the key.

If the Strain name is mapped to the key, ensure the Submitter Provided Unique ID is mapped to the WGS_id.



If adding OHE package fields, please use OHE package nomenclature as indicated below.

A	B	C
Field Name	Field Type	Field Value
Strain name	Mapping	WGS_id OR Key
Sample name	Mapping	Key
Submitter Provided Unique ID	Mapping	WGS_id OR Key
SPUID namespace	Value	GenomeTrakr
BioProject accession	Mapping	BioProject
Author	Mapping	Sequenced_by
Serovar	Mapping	Serotype_wgs*
SourceType	Mapping	SourceType
<i>Isolate Name Alias if SourceType equals Human</i>	<i>Value</i>	<i>missing</i>
Isolate Name Alias if SourceType does not equal Human	Mapping	Key
Isolation source if SourceType does not equal Human	Mapping	SourceSite, TypeDetails
<i>Isolation source if SourceType equals Human</i>	<i>Value</i>	<i>missing</i>
<i>Geographical origin if SourceType equals Human</i>	<i>Value</i>	<i>missing</i>
Geographical origin if SourceType does not equal Human	Mapping	Geo_loc_name
Organism name	Mapping	Genus, Species
<i>Collection / isolation date if SourceType equals Human</i>	<i>Value</i>	<i>missing</i>
Collection / isolation date if SourceType does not equal Human	Mapping	IsolatDate YYYY-mm

A	B	C
<i>Collected by if Source Type equals Human</i>	<i>Value</i>	<i>missing</i>
Collected by if Source Type does not equal Human	Mapping	Collected_By
Instrument model	Mapping	Instrument_Model
Library strategy	Value	WGS
Library source	Value	GENOMIC
Library selection	Value	RANDOM
Library layout	Value	PAIRED
Library name	Mapping	Library
<i>Project name</i>	<i>Mapping</i>	<i>Project</i>
<i>Sequenced by if Source Type equals Human</i>	<i>Value</i>	<i>missing</i>
Sequenced by if Source Type does not equal Human	Mapping	Sequenced_by
ADD FIELD...		
env_local_scale	Mapping	Env_local_scale
env_medium	Mapping	Env_medium
purpose_of_sampling	Mapping	Purpose_of_samplin g

*Map -Serovar- to missing if WGS prediction (Serotype_wgs) is not available.

Save submission template according to [PulseNet Instructions](#) as **-GenomeTrakr-FarmEnvironment-**.

4 NCBI Submissions

Submit data to NCBI according to [PulseNet Instructions](#), if you have several submissions from different sample types, make sure to group records accordingly and select the appropriate custom **NCBI GenomeTrakr-labeled Template**. If NCBI accessions are not available at PulseNet 2.0 in 1 business day, please contact NCBI (**pd-help@ncbi.nlm.nih.gov**) and PulseNet to troubleshoot issues with submissions.



Contact GenomeTrakr by email genometrakr@fda.hhs.gov if issues with submissions are delayed for more than 3 days. GenomeTrakr can support urgent submissions if needed.