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# GenFS Metadata Cleanup Challenge protocol

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**Protocol status:** Working
**We use this protocol and it's working**

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## Abstract

This protocol provides guidance for submitting bulk BioSample updates to NCBI for the GenFS Metadata Cleanup Challenge exercise.

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# Timeline/Workflow for the 2024 Metadata Cleanup Challenge

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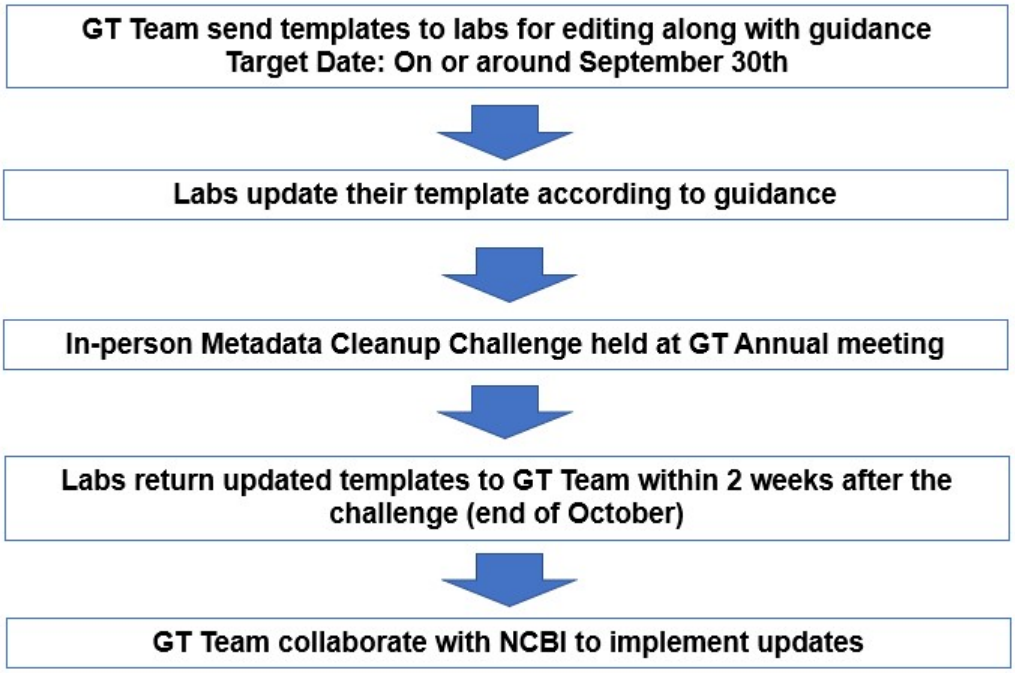



2 **Overview and scope of exercise**

**Timeframe:** focus on submissions between September 2023-August 2024. Your lab is welcome to include submission outside this timeframe.

**Scope:** review and curate entries for the following attributes, which are core requirements within the One Health Enteric package:

**Focus on these attributes:**

- source_type
- collected_by
- sequenced_by
- project_name
- host (for human and animal isolates)
- food_origin (for food isolates)
- isolation_source

## Guidance for preparing the update file

3 **Steps 4 and 5 describe the required format for the bulk update file.**

4 **For labs in the GenomeTrakr network:**
We have generated a bulk metadata update template for every laboratory that has a BioProject linked to the GenomeTrakr umbrella BioProject at NCBI (**PRJNA593772**).

Pick up your metadata template here: **DOCS: metadata hackathon/2024 Hackathon Template Pickup**.

**General instructions for generating a template of current metadata for a given BioProject or set of BioProjects:**

<Enter SRA Run selector instructions>

5 **Prepare the update file:**

- Updates should be put into one bulk update file per lab, or per lab/organism, or some other aggregation.
- **Rows:** The first row, or header, must contain the column names. Each subsequent row must contain exactly one BioSample and its updatable fields, or attributes. Each row must contain exactly the same number of columns.
- **Columns:** The column names should be attribute names **(full name or harmonized name)** included in the One Health Enteric package. The first column should contain the BioSample accession (eg SAMN123456789)
- **File format:** tab-delimited text file using the file suffix .tsv or .txt. If you use Microsoft Excel for editing, export the final template into this format.

**FYI:**

- Only those columns where at least one record has a replacement value need to be supplied.
- If a field is blank in the update file, and has an actual value in NCBI BioSample, that will be taken as "replace current value with NULL".
- If a field in a record already has a value in NCBI BioSample that will not be changed, then the field should be filled in with its current value.
- If a field is new to the BioSample, it will be added. A blank field whose attribute does not currently exist in the BioSample record will not be added.

5.1 **What fields/attributes can be included in the bulk update file?**

- collected_by
- geo_loc_name

- food_origin
- host
- project_name
- sequenced_by
- source_type
- isolation_source
- collection_date
- purpose_of_sampling
- env_local_scale
- env_medium
- animal_env
- env_broad_scale
- facility_type
- intended_consumer
- food_type_processed
- food_processing_method

### 5.2 What fields CANNOT be updated in the bulk update file?

DO NOT include the following attributes in this bulk update file. Changes to the following fields can be managed separately at NCBI by writing to **biosamplehelp@ncbi.nlm.nih.gov**.

- changes to organism species names
- changes to strain name, isolate, or sample_name
- changes to linked BioProject

Basically, anything to do with tracking biosamples cannot be updated using the bulk update channel.
To make changes to any of the below fields, please write directly to **pd-help@ncbi.nlm.nih.gov**

- **biosample_acc/BioSample** – This is the primary key of the entire BioSample system - Keep this accession in the first column, but DO NOT EDIT OR UPDATE ENTRIES.
- **bioproject_acc/BioProject -** This change requires additional processing on NCBI end, please separately write to **pd-help@ncbi.nlm.nih.gov** for this kind of change request.
- **strain** or **isolate** – This change requires additional processing on NCBI end, please separately write to **pd-help@ncbi.nlm.nih.gov** for this kind of change request.
- **sample_name** – Submitter's name for the biosample. This is published on the BioSample report.
- **attribute package** – This requires validation of all the fields together. Please request this kind of change separately at **pd-help@ncbi.nlm.nih.gov** .
- **center name** – This is a property of SRA and cannot be changed using the bulk update channel.

- **organism** - Change to the BioSample species (the identification of the isolate). Please request this kind of change separately at **pd-help@ncbi.nlm.nih.gov** .
- ***Salmonella* serovar/serotype** - Because of the way Salmonella are stored in NCBI taxonomy, changing the serovar (even when the species stays as *Salmonella enterica*) requires special handling. Please request this kind of change separately at **pd-help@ncbi.nlm.nih.gov**.
- Any kind of SRA to BioSample, BioSample to BioProject, or SRA to BioProject mapping. Please write separately to **pd-help@ncbi.nlm.nih.gov** for this kind of change request.
- Any of the **computed fields** in Pathogen Detection (epi_type, min_same, min_diff, computed_types, or amr/virulence analysis outputs). These attributes cannot be updated by the record owner.

## Guidance for making corrections and updates within the file

6 **Steps 7-9:** These steps cover required fields. In your Excel template, ensure there's an entry in these columns for every row. If information is missing, then choose one of the null terms, "Not Applicable, Not Collected, Not Provided, Missing, or Restricted Access".

7 **source_type**

Review your entries, ensure every record has an source_type entry. Make corrections where needed.

human
animal
food
environmental
other
Not Applicable
Not Collected
Not Provided
Missing
Restricted Access

NCBI and US pathogen surveillance coordinators have a *strict* controlled vocabulary for this attribute, only the above terms are allowed.

8 **project_name**

Review the entries in this column, make corrections where needed and populate all missing fields. For US surveillance, please choose the coordinating body that best the isolate.

GenomeTrakr
GenomeTrakr; LFFM-FY1
GenomeTrakr; LFFM-FY2
GenomeTrakr; LFFM-FY3
GenomeTrakr; LFFM-FY4
GenomeTrakr; LFFM-FY5
NARMS
NARMS Cecal
NARMS Retail Meat
PulseNet
USDA-FSIS
Vet-LIRN
NAHLN
USDA-ARS

If you would like to create another term to communicate membership in another project or network, feel free to do that! Enter you new term directly into the update template. If you would like this term added to the picklist, send this term to **genomeTrakr@fda.hhs.gov,** and we'll add it to the next update.

Include more than one term? Separate with "; ", for example, "GenomeTrakr; USDA-ARS".

9 **collected_by** and **sequenced_by**

Review the entries in both of these columns, make corrections where needed, and populate any missing fields.

Ensure terms are standardized across all your records. Check the **sequenced_by** picklist in the current One Health Enteric package file for your standardized laboratory name.

Send updates, corrections, or additions to your laboratory name to **genomeTrakr@fda.hhs.gov** and we'll make corresponding updates to the picklist terms.

10 **Steps 11-13:** For this exercise we're focused on two conditionally required attributes:
1. **host** should be populated for isolates derived from human or animal samples
2. **food_origin** should be populated for isolates derived from food products, or other commercial products sampled for pathogens (medical products, cosmetics, tattoo ink, etc).

Use the **source_type** column to filter for these sample types, first for animal/human samples (step 11 + 12), then for food samples (step 13).

11 **host**

***FOR HUMAN and ANIMAL ISOLATES ONLY***

**Host** is a required for host associated human and animal isolates.
Use the **source_type** column to identify human and animal isolates (filter in Excel for human and animal).

Use the entries in the **isolation_source** column to help determine what the **host** entry should be**.**

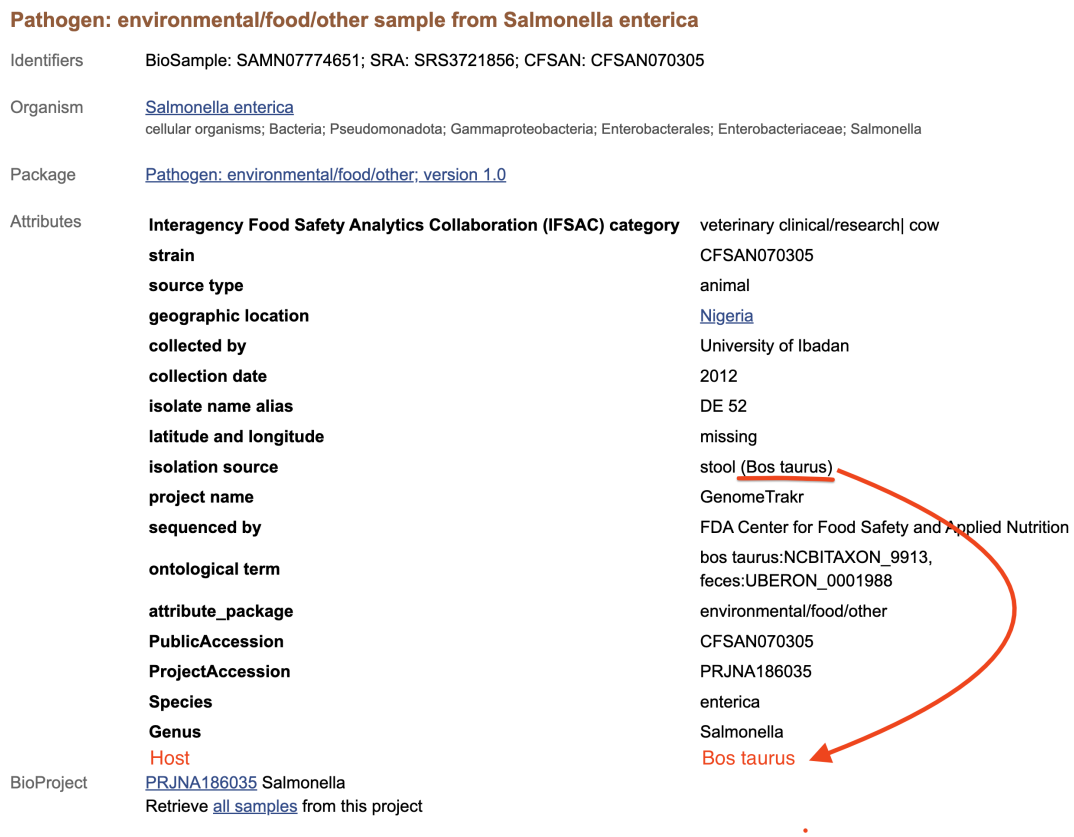
Where possible, enter a scientific or binomial name, for example *Homo sapiens* or *Bos taurus*.
If scientific name is unknown, use a common name recognized by the **NCBI taxonomy database** (porcine, bovine, etc).

When **host** is completely unknown, provide one of NCBI's null values:
Not Applicable
Not Collected
Not Provided
Missing
Restricted Access

12 **isolation_source**

**For human and animal isolates: remove all taxonomic references included in **isolation_source**.**
This information should solely reside in **host**.

Example edit to both **isolation_source** and **host**:



**Pathogen: environmental/food/other sample from Salmonella enterica**

| | | |
|---|---|---|
| Identifiers | BioSample: SAMN07774651; SRA: SRS3721856; CFSAN: CFSAN070305 | |
| Organism | Salmonella enterica<br>cellular organisms; Bacteria; Pseudomonadota; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Salmonella | |
| Package | Pathogen: environmental/food/other; version 1.0 | |
| Attributes | **Interagency Food Safety Analytics Collaboration (IFSAC) category** | veterinary clinical/research\| cow |
| | **strain** | CFSAN070305 |
| | **source type** | animal |
| | **geographic location** | Nigeria |
| | **collected by** | University of Ibadan |
| | **collection date** | 2012 |
| | **isolate name alias** | DE 52 |
| | **latitude and longitude** | missing |
| | **isolation source** | stool (Bos taurus) |
| | **project name** | GenomeTrakr |
| | **sequenced by** | FDA Center for Food Safety and Applied Nutrition |
| | **ontological term** | bos taurus:NCBITAXON_9913, feces:UBERON_0001988 |
| | **attribute_package** | environmental/food/other |
| | **PublicAccession** | CFSAN070305 |
| | **ProjectAccession** | PRJNA186035 |
| | **Species** | enterica |
| | **Genus** | Salmonella |
| | Host | Bos taurus |
| BioProject | PRJNA186035 Salmonella<br>Retrieve all samples from this project | |

## 13 food_origin

****FOR FOOD OR OTHER PRODUCTS ONLY****

Sort or filter on the **source_type** column to identify the "**food**" isolates.

Food and other products have two attributes describing geographic location information:
**geo_loc_name**: geographic location where the sample was physically collected
**food_origin**: geographic *origin* of food product or other product sampled for pathogens

Check location data in **geo_loc_name:**

- If the location information in **geo_loc_name** reflects the *state or country of origin for* the food product (e.g. "India", reflecting an imported food product sampled in the US), move this geographic information to **food_origin.**
- If your isolates contain the location where the sample was collected (**e.g. port of entry, US state of grocery store, etc)**, leave **geo_loc_name** as is. Populate **food_origin** with the country or state of origin.

If **food_origin** is unknown, provide one of NCBI's null values:
Not Applicable
Not Collected
Not Provided
Missing
Restricted Access

## OPTIONAL: bring your records up to OHE standards

14 Review and populate the other conditionally required fields for OHE sub-packages. Filter on **source_type** to locate these categories:

**animal samples,** source_type = animal
animal_env

**food product samples,** source_type = food
intended_consumer
food_processing_method

**facility inspection samples,** source_type = environmental
facility_type
food_type_processed

**farm/environment samples,** source_type = environmental
env_broad_scale
env_medium
env_local_scale

## Finalize the update file and submit the bulk template!

15 Check for duplications - ensure there are no double BioSample entries.

15.1 Bring your template to the October 16th, 2024 GenomeTrakr metadata cleanup challenge - finalize edits at the hackathon.

15.2 Remove columns that you're not updating. Ensure that the BioSample accession is retained in Column 1 and strain is kept for tracking the update.

**Keep**
Biosample
strain

**Remove**
package name
Title
Center_Name
Release_Date
Bioproject
Run
sample_name

15.3 Save as a tab-delimited .tsv file and transfer the .tsv file to protocols.io:
**DOCS: metadata hackathon/2024 Hackathon Template Submission**