Step-by-step tutorial: generating metadata and submitting to LIMS

Each data item submitted to the LIMS requires a metadata file. The LIMS system provides tools to generate these metadata files. If you are generating metadata for less than three (< 3) samples, it's recommended that you use the metadata form, as this will be the fastest method to produce your metadata files. If you are generating metadata for more than three (> 3) samples, it's recommended that you use the metadata batch processor to generate your metadata files. This tutorial provides step-by-step instructions for both methods.

Metadata Form (< 3 samples)

1. Go to the LIMS metadata form.
2. Enter information to the required fields (those with a blue asterisk)
    1. **Required fields summary**:
        1. LIMS Account: The LIMS account is your account name: you can see this at the top right corner of the page. If you enter a non-existent account name, the system will tell you the account is invalid when you submit the form.
        2. Experimental ID: The experimental ID is the serial number analog for your sample. If you previously characterized your sample in the LIMS and are now submitting additional characterization information (e.g. you previously submitted an NMR spectrum and now you're submitting a mass spectrum), you **must** use the same experimental ID. If this is a new sample, then click the “Generate ID” button to generate a new unique identifier.
        3. Component: The simplest kind of molecule/chemical species as understood by the LIMS. Specify your component by common name or PubChem CID number (the latter is preferred!) and mark its component class: monomer, solvent, catalyst, or additional reagent (i.e. other).
        4. Experiment, Synthesis Dates: The date the experiment (characterization) was performed and the date the sample was synthesized. Recommendation: use the calendar tool over manual entry.
        5. Exp. Synopsis: A brief synopsis, or summary, of what's going on in this experiment. Recommendation: include a truncated version of your methods and instrument parameters here.
        6. Synthesis Platform: Indicate where/how the sample was synthesized.
        7. Instrument: Indicate the instrument from which the data you are submitting was acquired.
        8. Data File(s): Indicate which instrument data files are included as part of this metadata submission.
        9. Data Category: Indicate the manner in which the data should be interpreted (i.e., is this a spectrum, or a chromatogram, or a mean squared displacement measurement?). Data categories are used to distinguish between different data representations that might be available from a singular raw data source file.
        10. Data Integrity: Indicate whether the identity or identities of the component(s)/polymer(s)/composite is confirmed. In other words: have you confirmed that your sample is as you've described above? If so, mark it as verified. If not, mark it as unverified.
        11. Data Availability: Indicate whether the data is accessible to all qualified BioPACIFIC MIP users or whether it should be restricted. For the LIMS beta phase, all data

should be marked as available to all users.

2. **Conditional fields summary**:
    1. Polymer: If your sample is a polymer (i.e. an assembly of multiple components), then you will provide the common name or abbreviation (or, if available, PubChem CID number) in this field. You must also provide information concerning the following:
        1. *Polymer components*: Indicate which components belong to/were used to construct the specified polymer.
        2. *Component ratios*: Indicate the ratios of these components, expressed as either mass or mole ratios.
        3. *Chemical formula*: Provide the chemical formula, with repeating units indicated appropriately.
        4. *Molecular weight*: Provide the molecular weight in g/mol.
        5. *Polymerization mechanism(s)*: Indicate which mechanism(s) was/were employed to construct the polymer.
3. After completing all of the required fields for your sample, click “Generate Metadata File”.
4. If there are no validation errors, you should see the something similar to the following at the top of the metadata form: 
5. Click on the “Download Metadata” button. This will ask you to download your formatted metadata JSON file (to either a location of your choosing, your Downloads folder, or another location – whichever is specified by your browser settings).
6. Move/copy/save the JSON file to the LIMS Transfer folder location on the instrument. Ask the project scientist and/or laboratory technicians overseeing the lab for more information.
7. Copy the instrument data files to the LIMS Transfer folder. The name of each file must match exactly with the names of the data (and context, if provided) files in the metadata file. If the file names do not match, they will not be transferred to the LIMS.
8. At this point, you're finished! The system utilities of the instrument computer will take care of the rest, sending your metadata, data, and context (if provided) files to the LIMS. After a successful transfer, the files will be archived in a separate “archive” folder inside the LIMS Transfer folder.

Metadata Batch (> 3 samples)

1. Go to the LIMS metadata batch processor.

From:
https://bpm-wiki.cnsi.ucsb.edu/ - **NSF BioPACIFIC MIP Wiki**

Permanent link:
https://bpm-wiki.cnsi.ucsb.edu/doku.php?id=lims-guide-data-prep-tutorial&rev=1681153843

Last update: **2023/04/10 19:10**