

EMBL Nucleotide Sequence Database Group : SRA metadata update instructions

This page last changed on May 05, 2010 by richardg.

SRA Metadata Updates

- Update of any SRA metadata objects are possible.
- For updating an object, you need a submission.XML and the XML(s) for the corresponding objects
- You can only update objects within your center_name space
- This instructions page is divided into two sections. (1) XML background information and (2) Step-by-step guide to carrying out the update.

1. XML Information

- The update submission.XML:
 - This submission.XML is not accessioned or stored; it is just used for the update transaction (a pseudo submission)
 - For example: to update a sample, you need to provide submission.XML and a sample.XML
 - In the submission.XML you have to use the MODIFY action, instead of ADD
 - In the submission.XML @alias and @center_name attributes are mandatory
 - Please retain the empty attribute **target** as this is required by the schema [submission.XML template for an update](#)

```
<?xml version="1.0" encoding="UTF-8"?>
<SUBMISSION_SET>
  <SUBMISSION alias="anUpdate" center_name="YourCenterName" >
    <ACTIONS>
      <ACTION>
        <MODIFY source="sample.xml" target=""/>
      </ACTION>
    </ACTIONS>
  </SUBMISSION>
</SUBMISSION_SET>
```

- The SRA meta-data object (Study/Sample/Experiment/Run/Analysis) to be updated:
 - Either @alias or @accession are mandatory in any SRA meta-data object which need to be updated
 - The @alias should be unique within the submitting centre and should be provided exactly as provided in the original submission. Alternatively, the corresponding accession can be given
 - @center_name can be provided to help validate the @alias
 - Either @refname or @accession are mandatory if the object is referenced in others
 - @refname should be unique with in the @refcenter
 - If @accession is given, it should be provided with the correct prefix
 - For STUDY objects, PROJECT_ID cannot be updated to zero ('0') from an already- assigned a non-negative value
 - For SAMPLE objects, TAX_ID cannot be updated to zero ('0') from an already-assigned non-negative value

An update scenario

SAMPLE original value (original XML)

```
<SAMPLE accession="ERS000011"
  alias="Solexa sequencing of Saccharomyces paradoxus strain W7 random 200 bp library">
```

```

<SAMPLE_NAME>
  <TAXON_ID>580234</TAXON_ID>
  <COMMON_NAME>Saccharomyces paradoxus</COMMON_NAME>
</SAMPLE_NAME>
<DESCRIPTION>Solexa sequencing of Saccharomyces
paradoxus strain W7 random 200 bp library</DESCRIPTION>
</SAMPLE>

```

SAMPLE to be updated (new sample.XML meant for update)

Example 1: Using the sample object's accession:

```

<SAMPLE accession="ERS000011" >
  <TITLE>Saccharomyces paradoxus W7</TITLE>
  <SAMPLE_NAME>
    <TAXON_ID>580234</TAXON_ID>
    <COMMON_NAME>Saccharomyces paradoxus</COMMON_NAME>
    <ANONYMIZED_NAME>Saccharomyces paradoxus</ANONYMIZED_NAME>
  </SAMPLE_NAME>
  <DESCRIPTION>Solexa sequencing of Saccharomyces
paradoxus strain W7 random 200 bp library</DESCRIPTION>
  <SAMPLE_ATTRIBUTES>
    <SAMPLE_ATTRIBUTE>
      <TAG>strain</TAG>
      <VALUE>W7</VALUE>
    </SAMPLE_ATTRIBUTE>
    <SAMPLE_ATTRIBUTE>
      <TAG>SAMPLE-TITLE</TAG>
      <VALUE>Saccharomyces paradoxus W7</VALUE>
    </SAMPLE_ATTRIBUTE>
  </SAMPLE_ATTRIBUTES>
</SAMPLE>

```

OR

Example 2: Using the sample object's original alias:

```

<SAMPLE
alias="Solexa sequencing of Saccharomyces paradoxus strain W7 random 200 bp library">
  <TITLE>Saccharomyces paradoxus W7</TITLE>
  <SAMPLE_NAME>
    <TAXON_ID>580234</TAXON_ID>
    <COMMON_NAME>Saccharomyces paradoxus</COMMON_NAME>
    <ANONYMIZED_NAME>Saccharomyces paradoxus</ANONYMIZED_NAME>
  </SAMPLE_NAME>
  <DESCRIPTION>Solexa sequencing of Saccharomyces
paradoxus strain W7 random 200 bp library</DESCRIPTION>
  <SAMPLE_ATTRIBUTES>
    <SAMPLE_ATTRIBUTE>
      <TAG>strain</TAG>
      <VALUE>W7</VALUE>
    </SAMPLE_ATTRIBUTE>
    <SAMPLE_ATTRIBUTE>
      <TAG>SAMPLE-TITLE</TAG>
      <VALUE>Saccharomyces paradoxus W7</VALUE>
    </SAMPLE_ATTRIBUTE>
  </SAMPLE_ATTRIBUTES>

```

```
</SAMPLE>
```

2. Step-By-Step Guide to Updating

1. Decide which objects (study, sample, experiment, run or analysis) need updating and obtain the latest XML for these objects. This can be taken from the ENA Browser:

For a single object -

<http://www.ebi.ac.uk/ena/data/view/<accession>&display=xml&download&filename=<filename.xml>>

e.g. <http://www.ebi.ac.uk/ena/data/view/ERS000001&display=xml&download&filename=sample.xml>

For a range of objects -

<http://www.ebi.ac.uk/ena/data/view/<accession>&display=xml&download&filename=<filename.xml>>

e.g. <http://www.ebi.ac.uk/ena/data/view/ERS000001-ERS000001&display=xml&download&filename=sample.xml>

Please note that when creating an XML from multiple objects, you will need to flank the XML with an element SET (STUDY_SET, SAMPLE_SET, EXPERIMENT_SET, RUN_SET, ANALYSIS_SET). For example: <SAMPLE_SET>multiple samples</SAMPLE_SET>

If your data is private, you can request the latest XML from datasubs@ebi.ac.uk stating the objects you wish it for.

2. Edit the XML so that it contains the new/amended metadata.

3. Generate a submission.xml (or copy from section 1 above). This is used to submit the amended XMLs and is not accessioned. It requires an alias (e.g., "update20100505_experiment") and must use the MODIFY command (rather than ADD). You must also use your center_name acronym.

4. Go to the SRA submission services page: <https://www.ebi.ac.uk/ena/submit/drop-box/submit/>

5. Browse for your submission.xml and the relevant updated XMLs.

6. Enter your drop-box details and submit.

7. If the update is successful, the receipt will return **true**. If there was a problem, the receipt will return **false** - please check the errors at the bottom of the page. If you cannot rectify the issues or understand the error message(s), please contact datasubs@ebi.ac.uk explaining the problem and attaching the XMLs and errors.