# SRA XML Specification

Version 1.2 Draft F Oct 04 2010

National Center for Biotechnology Information – National Library of Medicine

EMBL European Bioinformatics Institute

DNA Databank of Japan

# Contents

# 1   Overview

This document summarizes the proposed changes for Release 1.2 of the Sequence Read Archive (SRA) schemas governing XML metadata.  Release 1.2 is an expansion of  Release 1.1, which was in introduced in March 2010.  The goal of this release is to update choices, introduce new features, and specify a usable Analysis object usable for BAM file submissions.  These changes are being introduced with the objective of not invalidating any current valid XML documents.

Major new features in this release are:

- New Analysis schema supports BAM file submissions

- Respecification of processing pipeline and directives

- Reinstantiation of spot descriptor, platform, and processing blocks at the level of SRA Run.

- Addition of choices to many controlled vocabularies

## 1.1  Notice

The features and modalities described in the XML schema DO NOT constitute a statement of features and mechanisms available in the SRA.  The schema changes frequently must precede actual implementation. New feature rollouts and functionality changes are made asynchronously with XML schema changes.

## 1.2  Related Documents

The SRA schema for this release can be obtained from this site:
http://www.ncbi.nlm.nih.gov/viewvc/v1/trunk/sra/doc/SRA_1-2c

## 1.3  Revision History

Draft C reviewed by EBI, DDBJ 28 Sep 2010.

# 2   Explanation of Changes

## 2.1   Changes to All Documents

### 2.1.1   LinkType extended

LinkType redefined to include the a choice of the following link types

- SRA_LINK
- URL_LINK
- XREF_LINK
- ENTREZ_LINK
- DDBJ_LINK
- ENA_LINK

### 2.1.2   New SRA.common.xsd

- SRA.common.xsd factored out of the "COMMON BLOCK" that was included with each SRA schema.  New namespace called com: created for commonly used types. [EBI]

To import this file, do

```
<xs:import schemaLocation="SRA.common.xsd" namespace="SRA.common"/>
```

To use a feature, do

```
<xs:element name="STUDY_ATTRIBUTE" type="com:AttributeType"/>
```

- SRA.*.xsd now imports SRA.common.xsd
- Common Block has been refactored to the SRA.common.xsd under namespace com:
- SpotDescriptorType refactored to SRA.common.xsd
- PlatformType refactored to SRA.common.xsd
- ProcessingType refactored to SRA.common.xsd

## 2.2   Changes to SRA Experiment

### 2.2.1   Add new instrument models

New instrument values have been added to Experiment :

- "Illumina HiSeq 2000" [Illumina],
- "AB SOLiD System 4" [LifeTech],
- "454 GS Junior" [Roche/454],
- "454 GS FLX Titanium" [Roche/454], to succeed "454 Titanium"

- "Illumina Genome Analyzer IIx" [Illumina]

Note that the use of instrument model in Run was deprecated in version 1.1.

## 2.2.2 Changed EXPERIMENT/PLATFORM/ILLUMINA/CYCLE_COUNT

Changed this to optional field to eliminate need to always specify a deprecated field.  [BI]

## 2.2.3 Add new library strategy/library selection combinations

New values for LIBRARY_STRATEGY and LIBRARY_SELECTION have been added to Experiment [EDACC]

- Methylation-Sensitive Restriction Enzyme Sequencing strategy.
<LIBRARY_STRATEGY>MRE-Seq</LIBRARY_STRATEGY>
<LIBRARY_SELECTION>Restriction Digest</LIBRARY_SELECTION>

- Methylated DNA Immunoprecipitation Sequencing strategy.
<LIBRARY_STRATEGY>MeDIP-Seq</LIBRARY_STRATEGY>
<LIBRARY_SELECTION>5-methylcytidine antibody</LIBRARY_SELECTION>

- RNA-Seq strategy
A new choice RNA-Seq  was added to LIBRARY_STRATEGY to support the general choice for sequencing that targets total RNA, with the following new choices for LIBRARY_SELECTION (others are possible):
  - CAGE
  - RACE
  - Size fractionation

- Direct sequencing of methylated fractions sequencing strategy.
<LIBRARY_STRATEGY>MBD-Seq</LIBRARY_STRATEGY>
<LIBRARY_SELECTION>MBD2 protein methyl-CpG binding domain</LIBRARY_SELECTION>
This combination entails  direct sequencing of methylated fractions following enrichment by methyl-CpG binding domain

- Whole exome sequencing strategy
"WXS" (whole exome sequencing) as a library strategy. [ESP-GO]

## 2.2.4 Improved documentation for spot descriptor choices.

## 2.2.5 New Library Source terms

Added TRANSCRIPTOMIC and METAGENOMIC to EXPERIMENT/LIBRARY_DESCRIPTOR/LIBRARY_SOURCE as a way to give further detail to submitters formerly using NON_GENOMIC (which was a holdover choice from the Trace Archive).

## 2.2.6 PLATFORM nodes

Make all the nodes in PLATFORM consistent to allow for  universal query of instrument model.

- EXPERIMENT.PLATFORM.COMPLETE_GENOMICS.INSTRUMENT_MODEL=none
- EXPERIMENT.PLATFORM.PACBIO_SMRT.INSTRUMENT_MODEL=none

## 2.2.7 Change to sample pool descriptor

SAMPLE_DESCRIPTOR.POOL.MEMBER.READ_LABEL made optional, to support pools that are not barcoded (and therefore don't need a read label). [BI]

## 2.2.8 Restored expected_number_runs

The attribute expected_number_runs restored (un-deprecated).  [EDACC]
This field is actually being used on one roadmap project.

## 2.2.9 Added TARGETED_LOCUS

Added "TARGETED_LOCUS" as a library element [HMP]
A controlled list will be offered, to consist initially of
- 16S rRNA
- other

where the submitter can add in free text an alternate locus description.

## 2.2.10       Added POOLING_STRATEGY

Added POOLING_STRATEGY as a library element, to help indicate the sample multiplexing intent of the submitter.  Choices include:
- None
- Simple pool
- Multiplexed samples
- Multiplexed libraries
- Spiked library
- other

## 2.2.11       Added READ_LENGTH property to SPOT_DESCRIPTOR

Added READ_LENGTH attribute to READ_SPEC.  Specify whether the spot should have a default length for the tag.  If provided, the specified number of bases is assigned to this tag regardless of match criteria.  If 0, or not provided, then the tag is "missed" if the match criteria fail.  This was formerly proposed as the "default_length" attribute of EXPECTED_BASECALL_TABLE.  [NCBI]

## 2.2.12       Removed requirement for fields in PROCESSING.QUALITY_SCORES

Removed requirement for deprecated fields in EXPERIMENT.PROCESSING.QUALITY_SCORES [BI]

- <xs:element name="NUMBER_OF_LEVELS" maxOccurs="1" minOccurs="0" type="xs:int"/>
- <xs:element name="MULTIPLIER" maxOccurs="1" minOccurs="0" type="xs:double"/>

## 2.2.13       New PIPELINE spec in PROCESSING

New element PIPELINE in ProcessingType added to describe the pipeline used in processing the data.  This includes a way to specify the sequence of steps in the processing pipeline, programs and their versions, and processing directives.

This was simplified from an earlier proposal, now there is simply a sequence of steps.
Here is an example of an acceptable processing block under SRA 1.2:

```
<PROCESSING>
  <PIPELINE>
    <PIPE_SECTION section_name="base caller">
      <STEP_INDEX>1.0</STEP_INDEX>
      <PREV_STEP_INDEX>NIL</PREV_STEP_INDEX>
      <PROGRAM>454BaseCaller</PROGRAM>
      <VERSION>1.1.01.20</VERSION>
    </PIPE_SECTION>
    <PIPE_SECTION section_name="SRA conversion">
      <STEP_INDEX>1.1</STEP_INDEX>
      <PREV_STEP_INDEX>1.0</PREV_STEP_INDEX>
      <PROGRAM>toSRA</PROGRAM>
      <VERSION>1.34</VERSION>
    </PIPE_SECTION>
  </PIPELINE>
</PROCESSING>
```

## 2.2.14      New PROCESSING_DIRECTIVES spec in PROCESSING

A new feature is the explicit enumeration of treatments to the data applied by the submitter, or requested treatments of the data requested by the submitter to be applied by the Archive.  Initially this will cover the sample multiplexing directives (no demultiplexing, submitter demultiplexed), but will be expanded in the future to track all treatment requests.

## *2.3  Changes to Study*

### 2.3.1  New STUDY_TYPE choices

- Exome Sequencing
- Pooled Clone Sequencing.

These were requested by Sanger/EBI.

### 2.3.2  CENTER_NAME deprecated

The submission and ownership is adequately tracked in the related SUBMISSION object, and the STUDY@center_name attribute.

### 2.3.3  RELATED_STUDIES

RELATED_STUDIES is intended to be used as a mechanism to bind the record to the emerging BioProject record (successor to genomeprj record), as well as binding to other resources that track studies (GEO and dbGaP at NCBI, and EGA and ArrayExpress at EBI).   This feature should replace the use of PROJECT_ID, a holdover from the Trace Archive, and which has been deprecated.

In order to negotiate a design error in SRA 1.1, a new branch choice has been created called

RELATED_STUDY which should be used in preference to the currently effective STUDY, which is now deprecated.  The link to a named database was implemented (XRefLinkType) in order to constrain the choice of related project to a named database.

```
<xs:element name="RELATED_STUDY" maxOccurs="unbounded" minOccurs="1">
  <xs:complexType>
    <xs:sequence>
      <xs:element name="RELATED_LINK" type="com:XRefType"
        minOccurs="1" maxOccurs="1">
        <xs:annotation>
          <xs:documentation>
            Related study or project record from a list of supported databases.
            The study's information is derived from this project record rather
            than stored as first class information.
          </xs:documentation>
        </xs:annotation>
      </xs:element>
      <xs:element name="IS_PRIMARY" type="xs:boolean"
       minOccurs="1" maxOccurs="1">
        <xs:annotation>
          <xs:documentation>
            Whether this study object is designated as the primary source
            of the study or project information.
          </xs:documentation>
        </xs:annotation>
      </xs:element>
    </xs:sequence>
  </xs:complexType>
</xs:element>
```

## *2.4 Changes to Sample*

There are no changes to SRA Sample in this revision.

## *2.5 Changes to Submission*

In SUBMISSION, added required "schema" attribute to MODIFY action
in order to force submitter to specify the namespace of the intended
target.  "target" is made optional, and will be ignored.  Henceforth,
the MODIFY source file will contain all the needed references. [BI]

## *2.6 Changes to Run*

### 2.6.1 Replicated descriptors at Run level

- Replicated SPOT_DESCRIPTOR at the level of Run.  If specified at Run, it will override the setting at the level of Experiment.
- Replicated PLATFORM at the level of Run.   If specified at Run, it will override the setting at the level of Experiment.
- Replicated PROCESSING at the level of Run.   If specified at Run, it will override the setting at the level of Experiment.

### 2.6.2 New Filetype support

- Added bam as a filetype for RUN.
- Added kar as a supported filetype for RUN, as native SRA format in serialized form.

## *2.7 Respecified ANALYSIS object*

### 2.7.1 Removed deprecated branches:

- ANALYSIS_TYPE/REPORT
- ANALYSIS_FILES/FILE/filetype/.pdf
- ANALYSIS_FILES/FILE/filetype/.sam  (will be delivered in .bam only)

### 2.7.2 Specified REFERENCE_ALIGNMENT branch

The ANALYSIS/ANALYSIS_TYPE/REFERENCE_ALIGNMENT has been completely specified in order to serve as the metadata container for alignment files delivered in BAM format.

## *2.8 New SRA Package Object*

A new schema SRA.package.xsd has been introduced in order to provide a container for any combination of SRA XML documents, and to allow for applications using SRA objects to aggregate them in any form.  SRA packages are not now supported for submission, but eventually will be used in preference to tar archive files.