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### Document Information

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## SRA XML Schema 1.4 Release Notes

Final – 10 May 2012

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## Overview

This document summarizes the proposed changes for Release 1.4 of the Sequence Read Archive (SRA) schemas governing XML metadata. This schema will be used by the SRA archive instances and has been developed under the auspices of the International Nucleotide Sequence Database Collaboration (INSDC, insdc.org).

Release 1.4 is an expansionary change over Release 1.3, which was introduced in August 2011. These changes are being introduced with the objective of not invalidating any currently valid XML documents.

Major new features in this release are:

- Addition of new instrument platform, CAPILLARY, and new instrument models
- Enhancement of choices for library and experiment
- Introduction of an IDENTIFIERS block to track multiple active and inactive accessions and IDs.
- Support for BAM file submission through SRA Run

## Notice

The features described in the SRA 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. Each SRA implementation by INSDC partners may impose additional business rules not reflected in the schema.

## 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\\_1-4](http://www.ncbi.nlm.nih.gov/viewvc/v1/trunk/sra/doc/SRA_1-4)

[Using the SRA Identifier Block.pdf](#)

## Revision History

Draft D- 2012-04-20 submitted for approval by INSDC partners

Draft E- 2012-04-30 submitted for approval by INSDC partners

Draft F- 2012-05-07 submitted for approval by INSDC partners

Draft G- 2012-05-09 submitted for approval by INSDC partners

Final – 2012-05-10 approved for release by INSDC partners

## Explanation of Changes

### Introduction of IDENTIFIERS block to all documents

An IDENTIFIERS block of IdentifierType has been added to all documents. This block is intended to give more flexibility in how IDs are tracked. IDs include primary and secondary accessions, equivalent records in other databases, submitter primary and secondary names for records. The number of IDs is unbounded. Whether they are active or not (replaced or deprecated) can be indicated. A uuid (universally unique ID) ID type is supported, although this will not be used by INSDC SRA archives.

### Changes to PlatformType

#### Add new platform CAPILLARY

This platform choice is intended to support handling of Traces in the SRA. The instrument model choices are:

- AB 3730xL Genetic Analyzer
- AB 3730 Genetic Analyzer
- AB 3500xL Genetic Analyzer

- AB 3500 Genetic Analyzer
- AB 3130xL Genetic Analyzer
- AB 3130 Genetic Analyzer
- AB 310 Genetic Analyzer

### **Add new instrument models**

New instrument values have been added to Platform block :

- Remove “none” as an instrument model for Complete Genomics, PacBio
- Correct name for AB 5500, 5500xl instruments
- Add 454 FLX+
- Add AB SOLiD 3.0 plus
- Add Illumina HiSeq 2500
- Add Illumina HiScanSQ
- Add Ion Proton

### **Changes to LibraryDescriptorType**

#### **Added Library Strategies**

- WGA (whole genome amplification) to replace some instances of RANDOM
- Added miRNA-Seq for micro RNA and other small non-coding RNA sequencing
- Added Tn-Seq for gene fitness determination through transposon seeding.

#### **Added Library Selections**

- Added MDA (multiple displacement amplification)
- Added Padlock Probes capture strategy to be used in conjunction with Bisulfite-Seq

#### **Make LibraryName optional**

The LibraryName field is not needed except from bulk submitters who may submit multiple experiments per library.

#### **Added options to TARGETED\_LOCI**

The PROBE\_SET block was made optional (a technical change). In addition, the following items were added to the locus attribute:

- 18S ribosomal RNA
- RBCL
- matK
- COX1
- ITS1-5.8S-ITS2

## **Changes to RunType**

### **New Filetypes Added**

In order to support submission reference alignments in BAM format, the filetypes table has been augmented with these new filetypes:

- BAM header
- Reference fasta
- Complete Genomics native

### **Title block added**

The TITLE block will allow for expansion of run to include all sequencing for the experiment or to include a certain logical fraction. The TITLE block can be used to distinguish which fraction.

## **Changes to ExperimentType**

### **SPOT\_DESCRIPTOR made optional in Experiment**

The SPOT\_DESCRIPTOR block is used by the loader to cognate the input data during load into the SRA. If the data are never transformed, then it can serve as the permanent map of the layout of the reads in the run. In order to refactor information needed for loading or interpreting the read layout, this block should be used in the RUN instead. For BAM loads it is not needed at all.

### **Modify GapDescriptorType**

Some changes to the schema for the GapDescriptor have been implemented in order to better support Complete Genomics libraries. There are as yet no deposited experiments with GapDescriptor blocks in them, so this change will be benign.

## Changes to Submission

The SUBMISSION/FILES block has been deprecated. Use the DATA\_BLOCK/FILES instead.

## Deprecated Fields

SRA 1.4 contains the following fields, branches, and options that should no longer be used in current submissions.

Field	Notes
/STUDY/DESCRIPTOR/CENTER NAME	1
/STUDY/DESCRIPTOR/PROJECT ID	2
/EXPERIMENT/@expected number reads	
/EXPERIMENT/@expected number spots	
/EXPERIMENT/DESIGN/LIBRARY DESCRIPTOR/LIBRARY SOURCE[NON GENOMIC]	4
/EXPERIMENT/DESIGN/SPOT DESCRIPTOR/SPOT DECODE METHOD	
/EXPERIMENT/DESIGN/SPOT DESCRIPTOR/SPOT DECODE SPEC/NUMBER OF READS PER SPOT	
/EXPERIMENT/LIBRARY/LIBRARY DESCRIPTOR/LIBRARY SOURCE[NON GENOMIC]	4
/EXPERIMENT/LIBRARY/SPOT DESCRIPTOR/SPOT DECODE METHOD	
/EXPERIMENT/LIBRARY/SPOT DESCRIPTOR/SPOT DECODE SPEC/NUMBER OF READS PER SPOT	
/EXPERIMENT/PLATFORM/ABI SOLID/COLOR MATRIX	
/EXPERIMENT/PLATFORM/ABI SOLID/COLOR MATRIX CODE	
/EXPERIMENT/PLATFORM/ABI SOLID/CYCLE COUNT	
/EXPERIMENT/PLATFORM/ABI SOLID/INSTRUMENT MODEL[AB SOLiD 5500]	5
/EXPERIMENT/PLATFORM/ABI SOLID/INSTRUMENT MODEL[AB SOLiD 5500x1]	5
/EXPERIMENT/PLATFORM/ABI SOLID/SEQUENCE LENGTH	
/EXPERIMENT/PLATFORM/HELICOS/FLOW COUNT	
/EXPERIMENT/PLATFORM/HELICOS/FLOW SEQUENCE	
/EXPERIMENT/PLATFORM/ILLUMINA/CYCLE COUNT	
/EXPERIMENT/PLATFORM/ILLUMINA/CYCLE SEQUENCE	
/EXPERIMENT/PLATFORM/ILLUMINA/SEQUENCE LENGTH	
/EXPERIMENT/PLATFORM/LS454/FLOW COUNT	
/EXPERIMENT/PLATFORM/LS454/FLOW SEQUENCE	
/EXPERIMENT/PLATFORM/LS454/KEY SEQUENCE	
/EXPERIMENT/PROCESSING/BASE CALLS	6
/EXPERIMENT/PROCESSING/BASE CALLS/BASE CALLER	
/EXPERIMENT/PROCESSING/BASE CALLS/SEQUENCE SPACE	
/EXPERIMENT/PROCESSING/QUALITY SCORES	6
/EXPERIMENT/PROCESSING/QUALITY SCORES/@qtype[other]	
/EXPERIMENT/PROCESSING/QUALITY SCORES/@qtype[phred]	
/EXPERIMENT/PROCESSING/QUALITY SCORES/MULTIPLIER	
/EXPERIMENT/PROCESSING/QUALITY SCORES/NUMBER OF LEVELS	
/EXPERIMENT/PROCESSING/QUALITY SCORES/QUALITY SCORER	
/RUN/@instrument model	7
/RUN/@run file	
/RUN/@total data blocks	
/RUN/DATA BLOCK/@format code	
/RUN/DATA BLOCK/@number channels	
/RUN/DATA BLOCK/@total reads	
/RUN/DATA BLOCK/@total spots	
/RUN/PLATFORM/ABI SOLID/COLOR MATRIX	
/RUN/PLATFORM/ABI SOLID/COLOR MATRIX CODE	
/RUN/PLATFORM/ABI SOLID/CYCLE COUNT	
/RUN/PLATFORM/ABI SOLID/INSTRUMENT MODEL[AB SOLiD 5500]	
/RUN/PLATFORM/ABI SOLID/INSTRUMENT MODEL[AB SOLiD 5500x1]	

/RUN/PLATFORM/ABI SOLID/SEQUENCE LENGTH	
/RUN/PLATFORM/HELICOS/FLOW COUNT	
/RUN/PLATFORM/HELICOS/FLOW SEQUENCE	
/RUN/PLATFORM/ILLUMINA/CYCLE COUNT	
/RUN/PLATFORM/ILLUMINA/CYCLE SEQUENCE	
/RUN/PLATFORM/ILLUMINA/SEQUENCE LENGTH	
/RUN/PLATFORM/LS454/FLOW COUNT	
/RUN/PLATFORM/LS454/FLOW SEQUENCE	
/RUN/PLATFORM/LS454/KEY SEQUENCE	
/RUN/SPOT DESCRIPTOR/SPOT DECODE METHOD	
/RUN/SPOT DESCRIPTOR/SPOT DECODE SPEC/NUMBER OF READS PER SPOT	
/SUBMISSION/ACTIONS/ACTION/HOLD/@HoldForPeriod	
/SUBMISSION/FILES	8

## Notes

1. Use document header attribute @center\_name
2. Use STUDY/RELATED\_STUDIES/RELATED\_STUDY
3. n/a
4. Use TRANSCRIPTOMIC or METAGENOMIC or METATRANSCRIPTOMIC
5. Use AB 5500 Genetic Analyzer or AB 5500xl Genetic Analyzer
6. Use PIPELINE
7. Use PLATFORM\*/INSTRUMENT\_MODEL
8. Use DATA\_BLOCK/FILES/FILE/filetype, DATA\_BLOCK/FILES/FILE/checksum

## Future Planned Revisions

The next revision, SRA 1.5, will be contracting revision (one that potentially invalidates current documents). The main changes will be to remove deprecated fields. This will involve migration of data in anticipation of future schema changes. The SRA 1.5 schema release will follow soon after SRA 1.4 is deployed.

## Figures, Tables and Boxes Appendix (do not delete)

Place numbered figures, tables and boxes (referred to from the main text) below.

“In-line” figures (e.g. equations) and tables should be placed within the main text in their desired final location. Boxes can have a single level of sections; the titles for these sections should be marked up in “Box subhead” style.