

New concept proposal

Data Processing

Author	Eelke van der Horst, Femke Kopmels	Date last updated	31/10/2023	
Project	General interest	Contact	DCC	
Dataset release	2024.1	Consulted expert	-	

1 Rationale

An essential part of scientific disciplines is processing the data produced by assays to retrieve an analysis result. Especially in data-intensive domains such as omics, data processing makes up a significant part of the experiment. Usually, individual processing and analysis steps are chained together into a (bioinformatics) pipeline. As part of data processing, data may be transformed from one format or structure to another, or may be subjected to computing to produce aggregates and other analysis results. To evaluate and reproduce these results, metadata on the data processing steps, such as the software/script that was used, is required.

2 Comparison to other standards/data models

2.1 OBI and EFO

OBI has a 'data transformation' class (OBI:0200000) that has the synonym 'data processing'. It is defined as "A planned process that produces output data from input data". EFO imports this class. This class is equivalent to the proposed concept, and its subclasses may be used as terms to indicate the type of data processing.

2.2 EDAM

Most items under EDAM's Operation (EDAM:operation_0004) are data processing steps, and may be used as code to indicate the particular type of processing.

2.3 SIO

The Semanticscience Integrated Ontology (SIO) has an 'information processing' class that is similar to data processing but broader, since it also includes 'data collection'.









3 Concept information

•	concept			Contextualized description	• •	Stand ard	Value set or subset	Cardinality for composed Of
	Processing	· •	Processing	a process that produces output data from input data				
composedOf		coded information specifying the concept		code specifying the nature of data processing		OBI or other	for EDAM: descendant of EDAM:operation_000 4 Operation ; for OBI: descendant of: OBI:0200000 data transformation	1:1
composedOf		software associated to the concept		software used for data processing	Software			0:1
composedOf		input associated to the concept	input	input data file	Data File			0:n

SPHN Swiss Personalized Health Network	2 4

								_	SPHN
composedOf	output	output associated to the concept	output	output data file	Data File			0:n	
composedOf	start datetime	datetime at which the concept started		datetime at which the data processing started	temporal			0:1	
composedOf	quality control metric	quality control metric associated to the concept	control metric	quality control metric related to the output of the data processing	Quality Control Metric			0:n	
composedOf	predecess or	a preceding process associated to the concept	or	process preceding this data processing	Data Processing; Assay		RO:000208 7 immediatel y preceded by		
composedOf	standard operating procedure	standard operating procedure associated to the concept	operating procedure	standard operating procedure that was followed for this data processing	Standard Operating Procedure			0:1	

-		_		Cardinality for concept to Source System
Data Processing	0:n	1:1	0:n	1:1

SPHN Swiss Personalized Health Network	3 4



4 Impact on the SPHN Dataset

Optional (if existing concepts need to be adapted because of this new concept, state here the currently released version of the existing concept and the proposed adapted version)

5 Discussion

Data Processing can be used for any data processing step for which the used software should be indicated, such as BCL to FASTQ conversion. The Data Processing concept can be used to indicate sub-steps of a broader process when there is a need to provide metadata for individual steps.

Usually, a data processing step has at least one input file. However, there are cases where intermediate files between steps are not known or important. Therefore, the minimum cardinality is 0.

6 Example

Genome annotation (a data processing step in a genomics pipeline)

code: EDAM:operation 0362 |Genome annotation|

processing datetime: 2023-06-26

input:

name: ExampleFile1

data provider institute: EXAMPLE01

output:

name: ExampleFile2

data provider institute: **EXAMPLE01**

predecessor:

code: EDAM:operation_3182 |Genome alignment|



