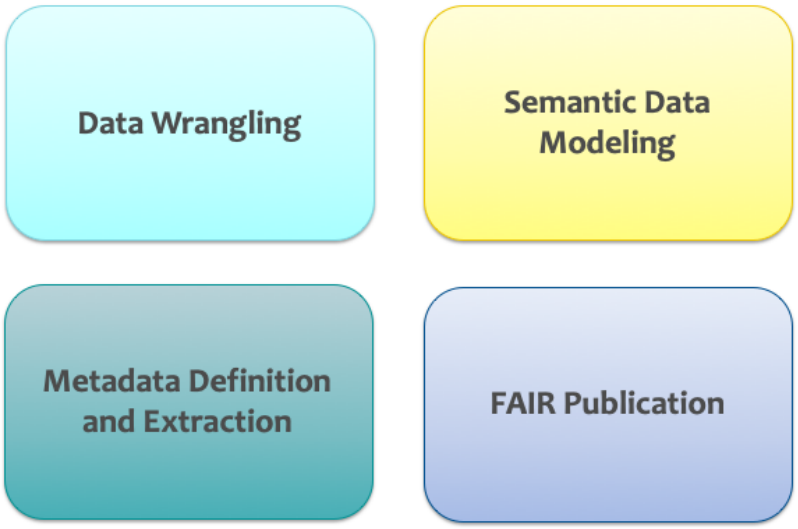
WELCOME: DAY 3

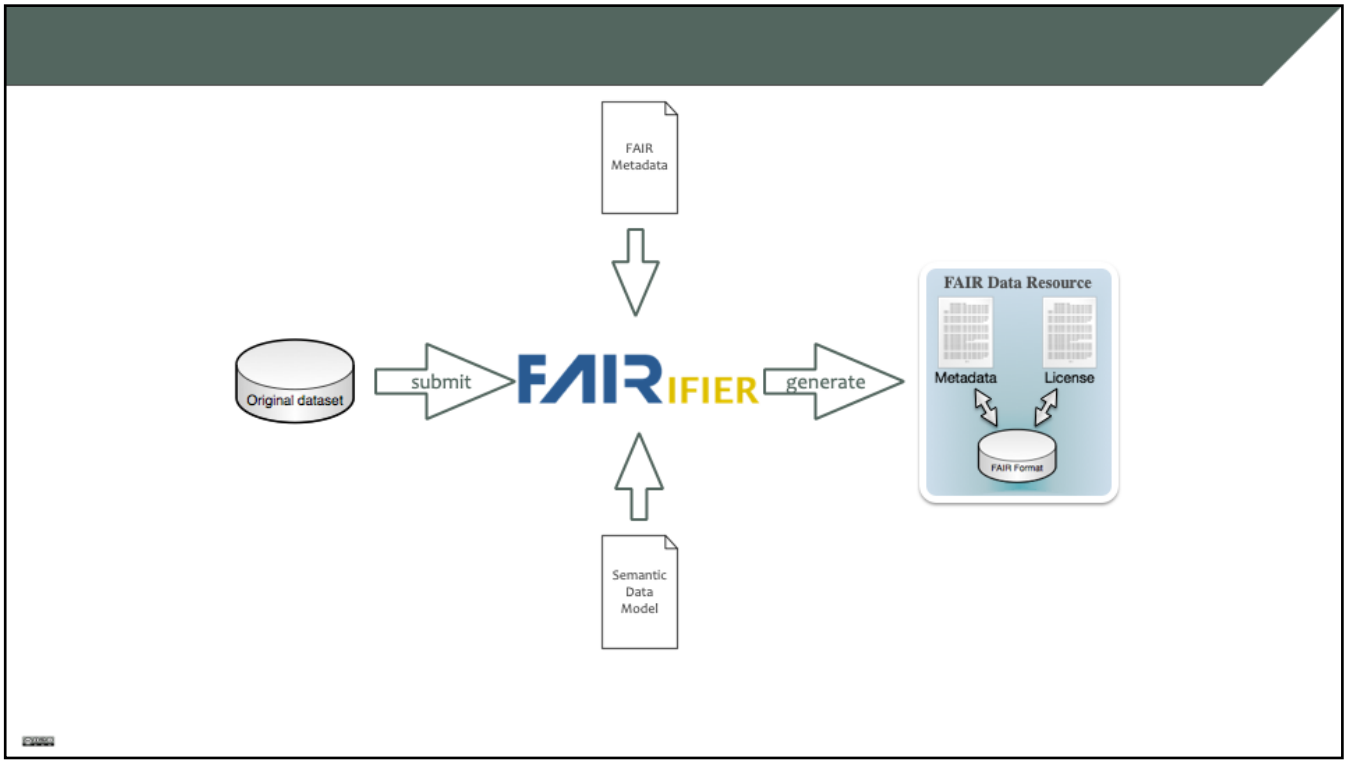
Session 4
FAIRifier

FAIR DATA STEWARDSHIP COURSE

TOWARDS A GO FAIR READINESS PROGRAM

RECAP – FAIRIFIER – MAJOR FUNCTIONALITY BLOCKS




FAIR
Metadata
Original dataset
submit
FAIRIFIER
generate
FAIR Data Resource
Metadata
License
FAIR Format
Semantic
Data
Model

DATA FAIRIFICATION

- **Dataset:**
  - Name: GoNL vcf dump
  - URL: https://molgenis26.target.rug.nl/downloads/gonl_public/variants/release5/
  - Description: http://www.nlgenome.nl/?page_id=9
  - Format: Variant Call Format (VCF) 4.1: http://samtools.github.io/hts-specs/VCFv4.1.pdf
  - Size: 27.896 rows of data

RETRIEVE NON-FAIR DATA

Download compressed file from https://molgenis26.target.rug.nl/downloads/gonl_public/variants/release5/gonl.SV.r5.vcf.gz

Extract file gonl.SV.r5.vcf

ANALYZE AND PREPARE DATASETS

Identify data

ANALYZE AND PREPARE DATASETS

Identify data

```
##fileformat=VCFv4.1
##ALT=<ID=DEL,Description="Deletion">
##FILTER=<ID=Inaccessible,Description="Overlaps a user-input mask">
##FORMAT=<ID=GQ,Number=1,Type=Integer,Description="Genotype quality (#subdomair
##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype">
##INFO=<ID=AC,Number=A,Type=Integer,Description="Allele count in genotypes, for
##INFO=<ID=AF,Number=A,Type=Float,Description="Allele Frequency, for each ALT a
##INFO=<ID=AN,Number=1,Type=Integer,Description="Total number of alleles in cal
##INFO=<ID=CIEND,Number=2,Type=Integer,Description="Confidence interval around
##INFO=<ID=CIPOS,Number=2,Type=Integer,Description="Confidence interval around
##INFO=<ID=DB,Number=0,Type=Flag,Description="dbSNP Membership">
##INFO=<ID=DP,Number=1,Type=Integer,Description="Approximate read depth; some r
##INFO=<ID=END,Number=1,Type=Integer,Description="End position of the variant d
```

ANALYZE AND PREPARE DATASETS

Identify data

VCFv4.1: http://samtools.github.io/hts-specs/VCFv4.1.pdf

```
##fileformat=VCFv4.1
##ALT=<ID=DEL,Description="Deletion">
##FILTER=<ID=Inaccessible,Description="Overlaps a user-input mask">
##FORMAT=<ID=GQ,Number=1,Type=Integer,Description="Genotype quality (#subdomair
##FORMAT=<ID=GT,Number=1,Type=String,Description="Genotype">
##INFO=<ID=AC,Number=A,Type=Integer,Description="Allele count in genotypes, for
##INFO=<ID=AF,Number=A,Type=Float,Description="Allele Frequency, for each ALT a
##INFO=<ID=AN,Number=1,Type=Integer,Description="Total number of alleles in cal
##INFO=<ID=CIEND,Number=2,Type=Integer,Description="Confidence interval around
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##INFO=<ID=DB,Number=0,Type=Flag,Description="dbSNP Membership">
##INFO=<ID=DP,Number=1,Type=Integer,Description="Approximate read depth; some r
##INFO=<ID=END,Number=1,Type=Integer,Description="End position of the variant d
```

ANALYZE AND PREPARE DATASETS

Identify data
Analyze data file

ANALYZE AND PREPARE DATASETS

Identify data
Analyze data file

Although not explicit, in row 108 we can find information about the reference file, which allowed us to ***infer*** that the variant information refers to the human reference genome version 19

According to the VCF spec, the #CHROM column is required and refers to the identifier of the chromosome where the variant occurred

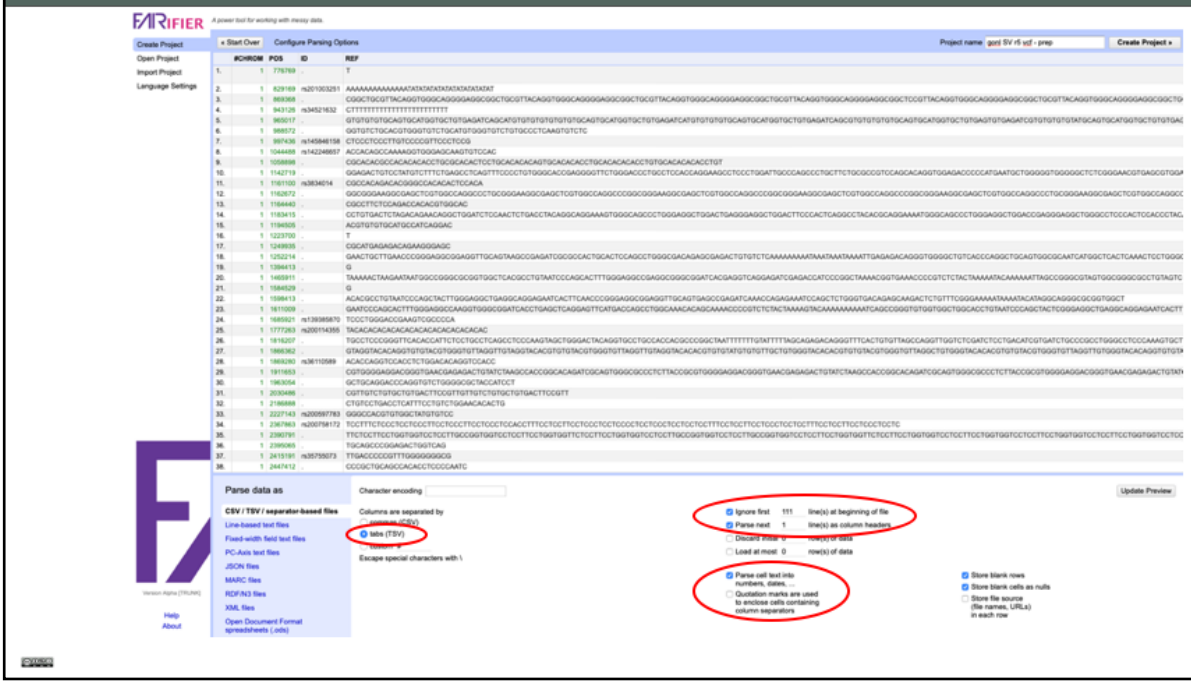
Actual data starting at row 113 with headers at row 112

```
103 ##contig=<ID=GL000193.1,length=189789,assembly=b37
104 ##contig=<ID=GL000194.1,length=191469,assembly=b37
105 ##contig=<ID=GL000225.1,length=211173,assembly=b37
106 ##contig=<ID=GL000192.1,length=547496,assembly=b37
107 ##fileDate=20130429
108 ##reference=file:///home/cog/lfrancioli/resources/hg19/human_g1k_v37.fa
109 ##source=GATKUnifiedGenotyper_2.1.8,Pindel_0.2.4t,MATE-CLEVER_rev.3097f2,123SV_0.9,Breakda
110 ##source=SelectVariants
111 ##source_20130804.1=vcf-annotate(r797) -r INFO/TDT -r INFO/ADOS -r INFO/pop -r INFO/Calle
112 #CHROM  POS ID  REF ALT QUAL    FILTER  INFO
113 1   776769  .   T   <DEL>   .   PASS    AC=8;AF=5.020e-03;AN=1534;CIEND=0,708;CIPOS=-110,
114 1   829169  rs201003251 AAAAAAAAAAAAAATATATATATATATATATATAT   A   .   Inaccessible    A
115 1   869368  .   CGGCTGCGTTACAGGTGGGCAGGGGAGGCGGCTGCGTTACAGGTGGGCAGGGGAGGCGGCTGCGTTACAGGTG
116 1   943126  rs34521632  CTTTTTTTTTTTTTTTTTTTTTTTT   C   .   PASS    AC=121;AF=0.082;AN=15
117 1   965017  .   GTGTGTGTGCAGTGCATGGTGCTGTGAGATCAGCATGTGTGTGTGTGTGCAGTGCATGGTGCTGTGAGATC
118 1   988572  .   GGTGTCTGCACGTGGGTGTCTGCATGTGGGTGTCTGTGCCCTCAAGTGTCTC   G   .   PASS    A
119 1   997436  rs145846158 CTCCCTCCCTTGTCCCCGTTCCCTCCG C   .   Inaccessible    AC=382;AF=0.2
120 1   1044488 rs142246657 ACCACAGCCAAAAGGTGGGAGCAAGTGTCCAC   A   .   PASS    AC=127;AF=0.0
121 1   1058898 .   CGCACACGCCACACACACCTGCGCACACTCCTGCACACACAGTGCACACACCTGCACACACACCTGTGCACAC
122 1   1142719 .   GGAGACTGTCCTATGTCTTTCTGAGCCTCAGTTTCCCCTGTGGGCACCGAGGGGTTCTGGGACCCTGCCTCCA
123 1   1161100 rs3834014   CGCCACAGACACGGGCCACACACTCCACA   C   .   Inaccessible    AC=60;AF=
124 1   1162672 .   GGCGGGAAGGCGAGCTCGTGGCCAGGCCCTGCGGGAAGGCGAGCTCGTGGCCAGGCCCGGCGGGAAGGCGAGC
```

ANALYZE AND PREPARE DATASETS

Identify data
Analyze data file
Prepare dataset – Load dataset into FAIRifier

ANALYZE AND PREPARE DATASETS



ANALYZE AND PREPARE DATASETS

From VCF spec: "***ID - identifier: Semi-colon separated list of unique identifiers where available. If this is a dbSNP variant it is encouraged to use the rs number(s).***"

All	#CHROM	POS	ID	REF
1.	1	776769	.	T
2.	1	829169	rs201003251	AAAAAAAAAAAAAATATATATATATATATATAT
3.	1	869368	.	CGGCTGCGTTACAGGTGGGCAGGGGAGG
4.	1	943126	rs34521632	CTTTTTTTTTTTTTTTTTTTTTTT
5.	1	965017	.	GTGTGTGTGCAGTGCATGGTGCTGTGAGA
6.	1	988572	.	GGTGTCTGCACGTGGGTGTCTGCATGTGG
7.	1	997436	rs145846158	CTCCCTCCCTTGTCCCCGTTCCCTCCG
8.	1	1044488	rs142246657	ACCACAGCCAAAAGGTGGGAGCAAGTGTC
9.	1	1058898	.	CGCACACGCCACACACACCTGCGCACACT
10.	1	1142719	.	GGAGACTGTCCTATGTCTTTCTGAGCCTCA
11.	1	1161100	rs3834014	CGCCACAGACACGGGCCACACACTCCACA

ANALYZE AND PREPARE DATASETS

Data collection: *dbSNP*

Overview | Miscellaneous | RDF/XML | Turtle

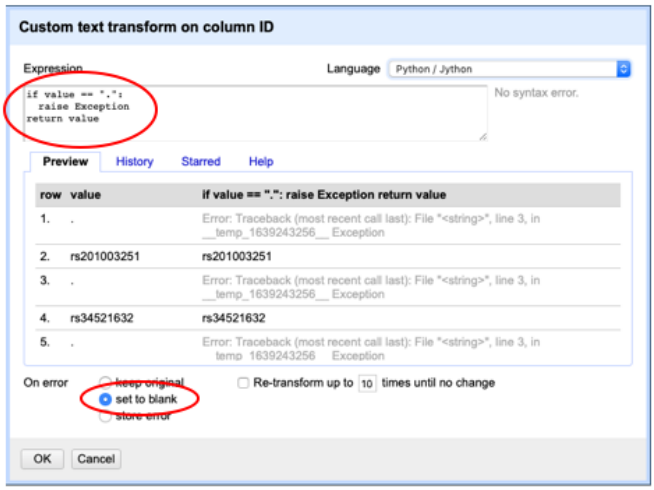
General information

Recommended name	**dbSNP**
Description	The dbSNP database is a repository for both single base nucleotide subsitutions and short deletion and insertion polymorphisms.
Identifier pattern	^rs\d+$
Registry identifier	MIR:00000161

Identification schemes

Namespace	dbsnp
URI	https://identifiers.org/dbsnp

ANALYZE AND PREPARE DATASETS

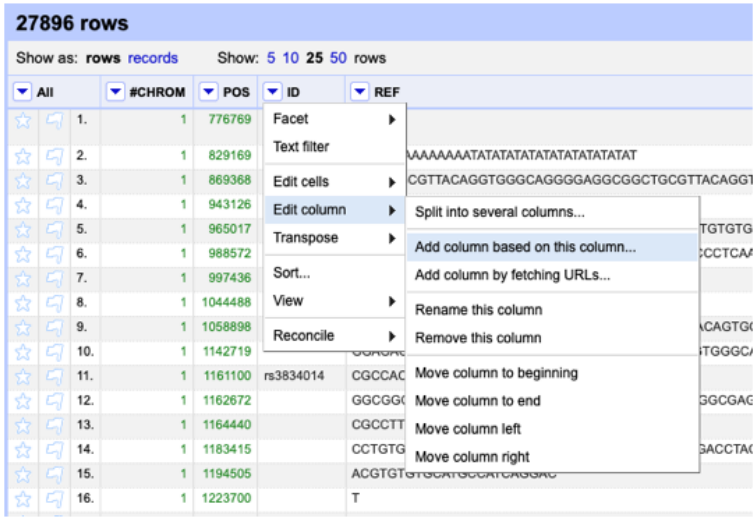


DBSNP URI preparation: remove the . (VCF blank) from the ID column

```
if value == ".":
    raise Exception
return value
```

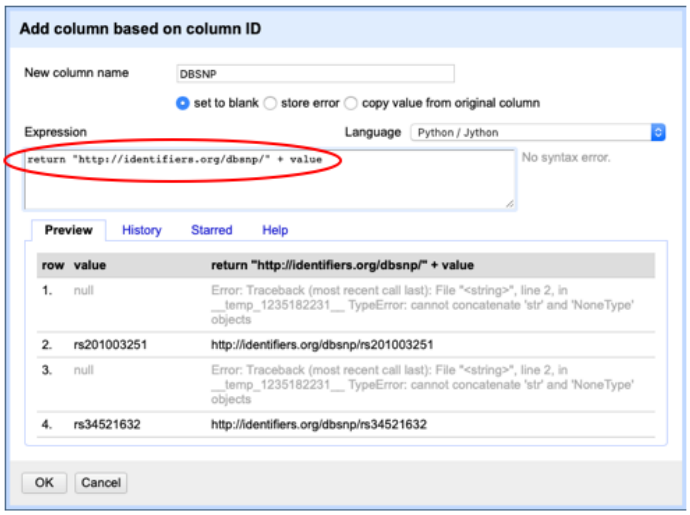
On error: set to blank

ANALYZE AND PREPARE DATASETS



DBSNP URI preparation: create a new column for the DBSNP URIs

ANALYZE AND PREPARE DATASETS



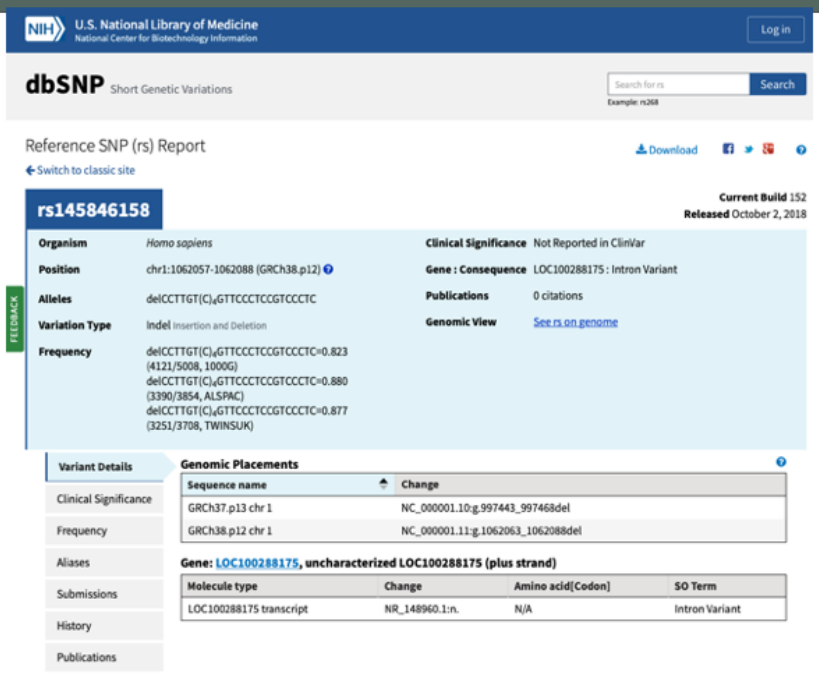
DBSNP URI creation: concatenate the identifiers.org URL with the rs# values

return "http://identifiers.org/dbsnp/" + value

ANALYZE AND PREPARE DATASETS

#CHROM	POS	ID	DBSNP	REF
1	776769			T
1	829169	rs201003251	http://identifiers.org/dbsnp/rs201003251	AAAAAAAAAAAAAATATATATATATATATATATATAT
1	869368			CGGCTGCGTTACAGGTGGGCAGGGGAGGCGGCTGCGTTACAGGTGGGCAG
1	943126	rs34521632	http://identifiers.org/dbsnp/rs34521632	CTTTTTTTTTTTTTTTTTTTTTTT
1	965017			GTGTGTGTGCAGTGCATGGTGCTGTGAGATCAGCATGTGTGTGTGTGTGC
1	988572			GGTGTCTGCACGTGGGTGTCTGCATGTGGGTGTCTGTGCCCTCAAGTGTCTC
1	997436	rs145846158	http://identifiers.org/dbsnp/rs145846158	CTCCCTCCCTTGTCCCCGTTCCCTCCG
1	1044488	rs142246657	http://identifiers.org/dbsnp/rs142246657	ACCACAGCCAAAAGGTGGGAGCAAGTGTCCAC
1	1058898			CGCACACGCCACACACACCTGCGCACACTCCTGCACACACAGTGCACACACC
1	1142719			GGAGACTGTCCTATGTCTTTCTGAGCCTCAGTTTCCCCTGTGGGCACCGAGG
1	1161100	rs3834014	http://identifiers.org/dbsnp/rs3834014	CGCCACAGACACGGGCCACACACTCCACA
1	1162672			GGCGGGAAGGCGAGCTCGTGGCCAGGCCCTGCGGGAAGGCGAGCTCGTGG
1	1164440			CGCCTTCTCCAGACCACACGTGGCAC
1	1183415			CCTGTGACTCTAGACAGAACAGGCTGGATCTCCAACTCTGACCTACAGGCAG
1	1194505			ACGTGTGTGCATGCCATCAGGAC

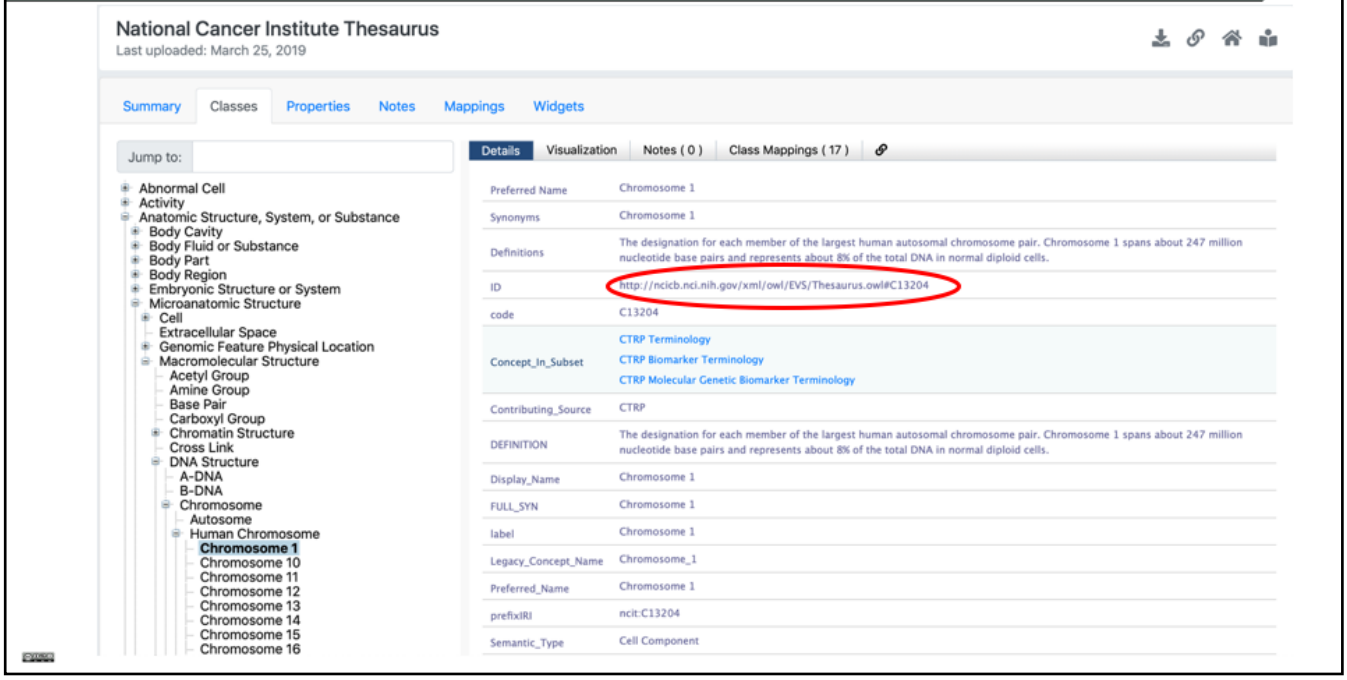
ANALYZE AND PREPARE DATASETS



ANALYZE AND PREPARE DATASETS

All		#CHROM	POS	ID	REF
1.		1	776769	.	T
2.		1	829169	rs201003251	AAAAAAAAAAAAAATATATATATATATATATAT
3.		1	869368	.	CGGCTGCGTTACAGGTGGGCAGGGGAGG
4.		1	943126	rs34521632	CTTTTTTTTTTTTTTTTTTTTTTTT
5.		1	965017	.	GTGTGTGTGCAGTGCATGGTGCTGTGAGA
6.		1	988572	.	GGTGTCTGCACGTGGGTGTCTGCATGTGC
7.		1	997436	rs145846158	CTCCCTCCCTTGTCCCCGTTCCCTCCG
8.		1	1044488	rs142246657	ACCACAGCCAAAAGGTGGGAGCAAGTGTC
9.		1	1058898	.	CGCACACGCCACACACACCTGCGCACACT
10.		1	1142719	.	GGAGACTGTCCTATGTCTTTCTGAGCCTCA
11.		1	1161100	rs3834014	CGCCACAGACACGGGCCACACACTCCACA

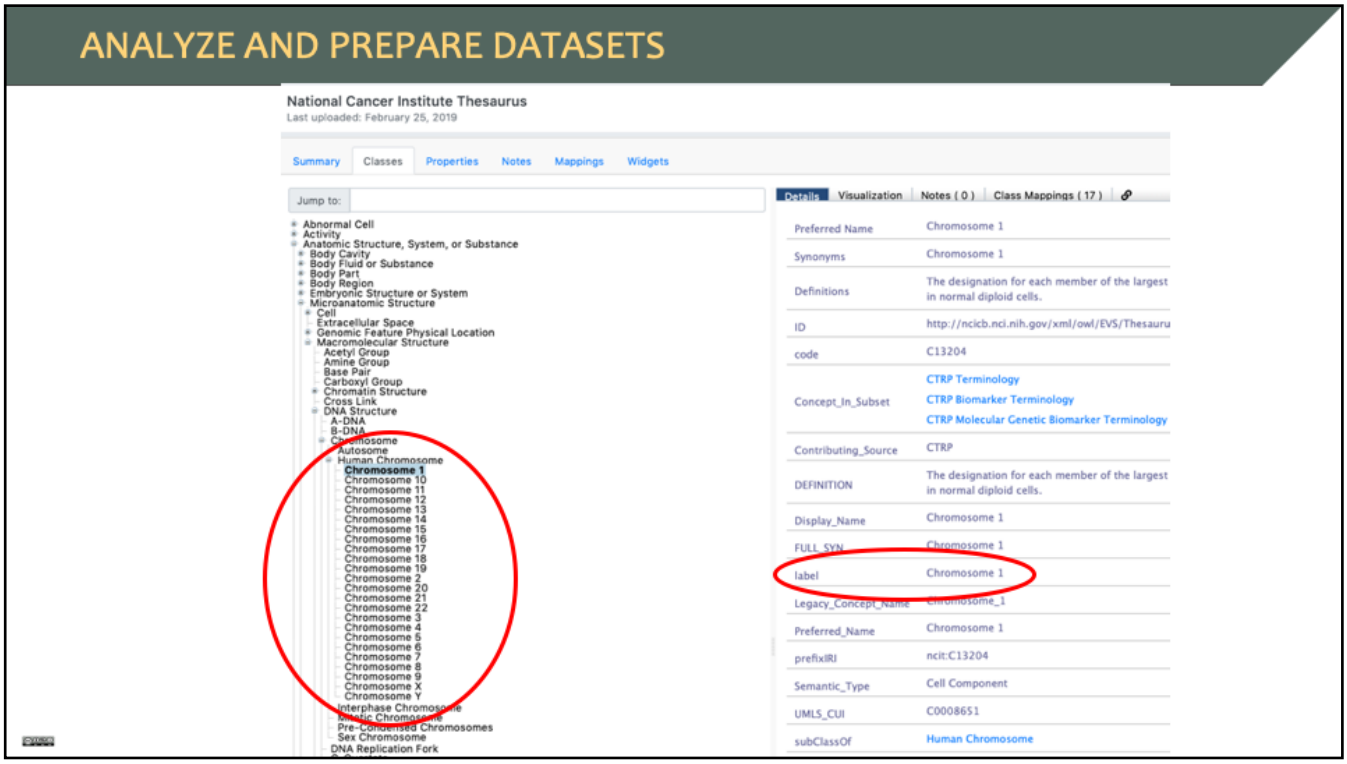
ANALYZE AND PREPARE DATASETS



ANALYZE AND PREPARE DATASETS

- **We should try to match the data we have (in the #CHROM column) with the correspondent chromosome identifiers;**
- **This is the role of the reconciliation service;**
- **The goal is to reconcile our chromosome names with the chromosome labels from the NCI Thesaurus.**
  - However, there is no public SPARQL endpoint offered by NCI;
  - The BioPortal SPARQL endpoint is bandwidth limited;
- **One possible solution is to create our own reconciliation service based on a RDF file.**

ANALYZE AND PREPARE DATASETS

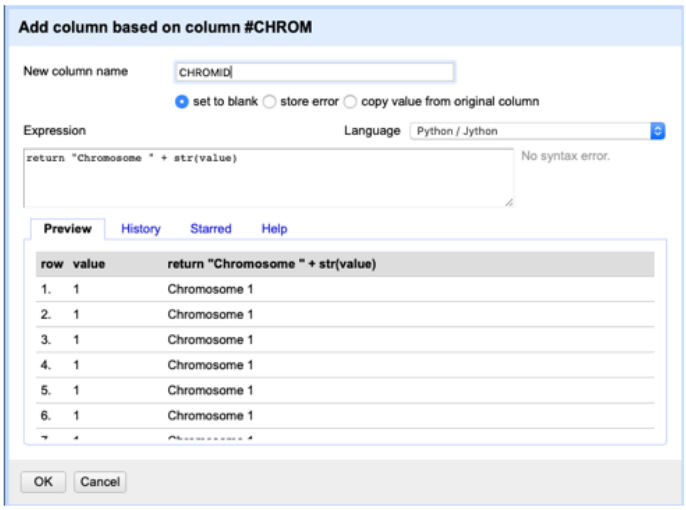


From the BioPortal UI we already know that all chromosomes are subclasses of the class “Human Chromosome” with URI:

http://ncicb.nci.nih.gov/xml/owl/EVS/Thesaurus.owl#C13203

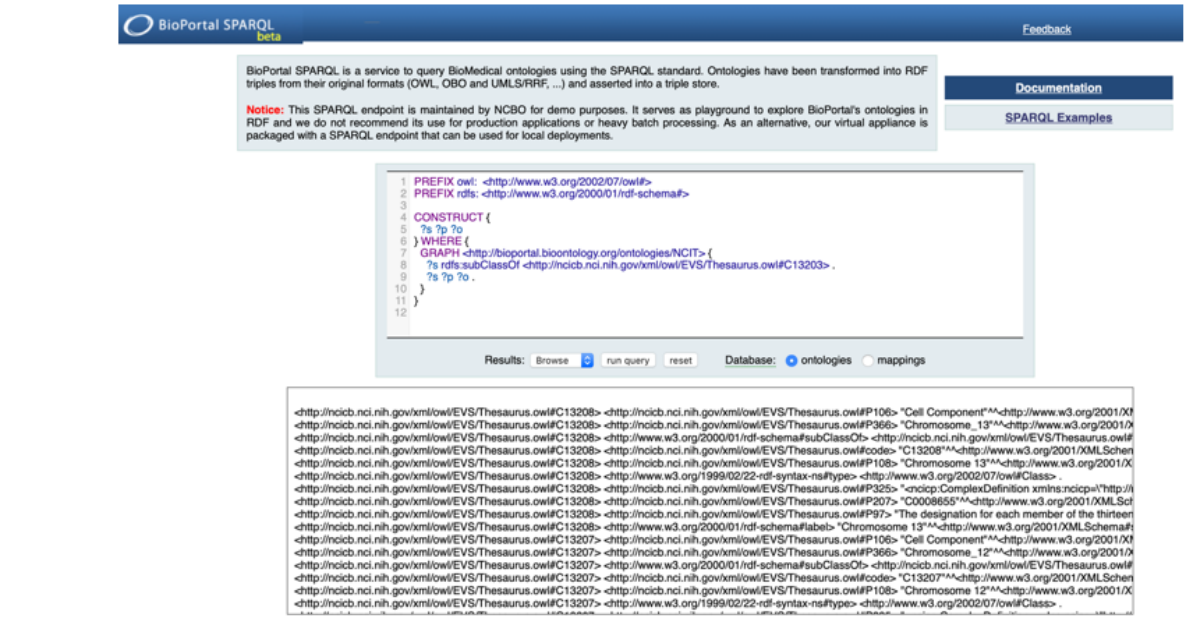
We can also see that the chromosome label is in the format “Chromosome “ + the chromosome number/letter.

ANALYZE AND PREPARE DATASETS



Chromosome URI preparation: add Chromosome ID column appending "Chromosome"

ANALYZE AND PREPARE DATASETS

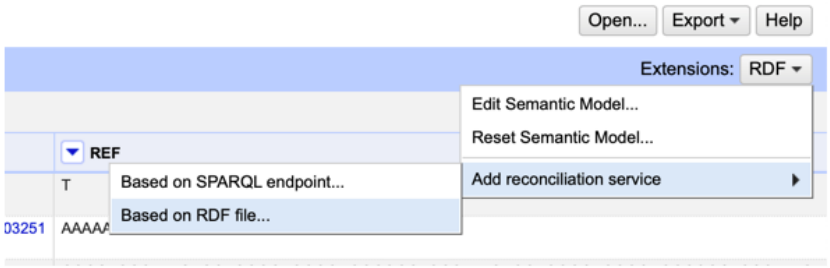


Chromosome URI preparation: run the SPARQL query on BioPortal SPARQL endpoint

Run the SPARQL query on http://sparql.bioontology.org/:

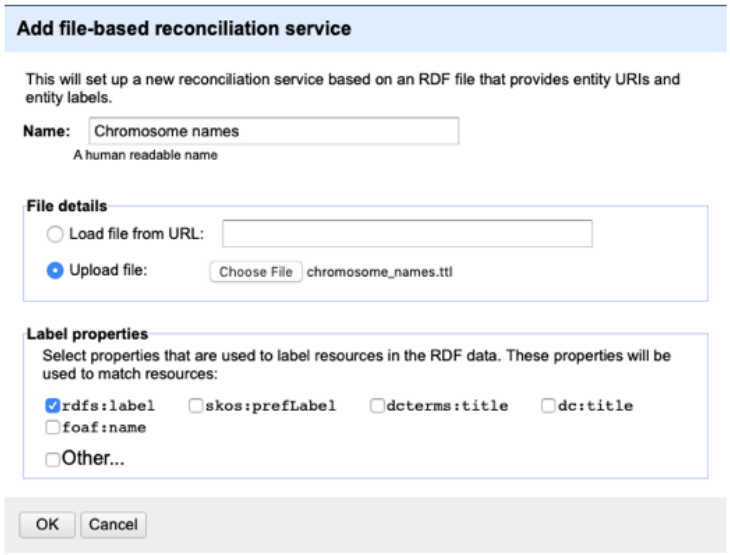
```
PREFIX owl:  <http://www.w3.org/2002/07/owl#>
PREFIX rdfs: <http://www.w3.org/2000/01/rdf-schema#>

CONSTRUCT {
  ?s ?p ?o
} WHERE {
  GRAPH <http://bioportal.bioontology.org/ontologies/NCIT> {
    ?s rdfs:subClassOf
<http://ncicb.nci.nih.gov/xml/owl/EVS/Thesaurus.owl#C13203> .
    ?s ?p ?o .
  }
}
```

ANALYZE AND PREPARE DATASETS



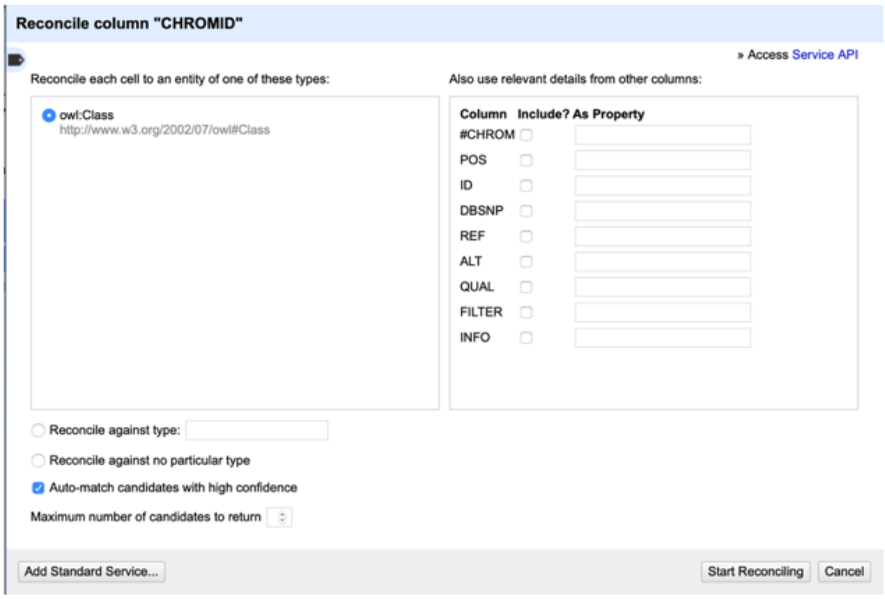
Chromosome URI preparation: add a new reconciliation service based on our RDF file

ANALYZE AND PREPARE DATASETS



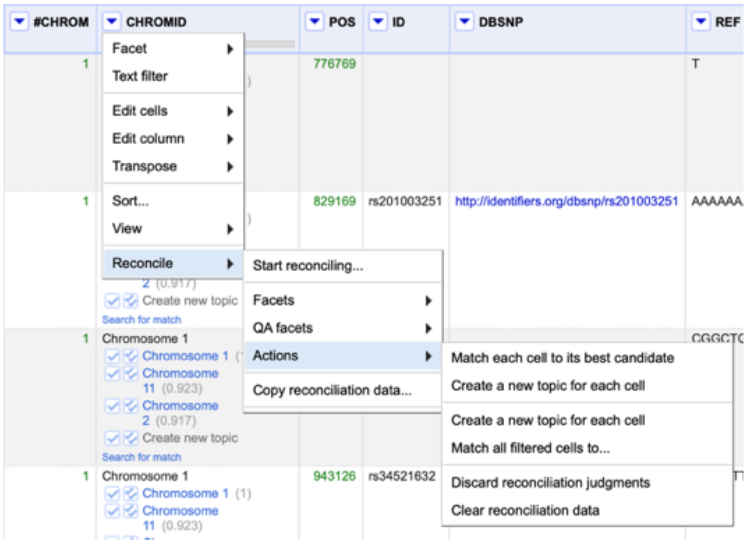
Chromosome URI preparation: add a new reconciliation service based on our RDF file

ANALYZE AND PREPARE DATASETS



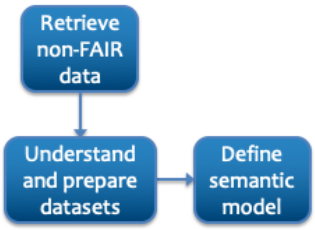
Chromosome URI preparation: start reconciliation using our new reconciliation service

ANALYZE AND PREPARE DATASETS

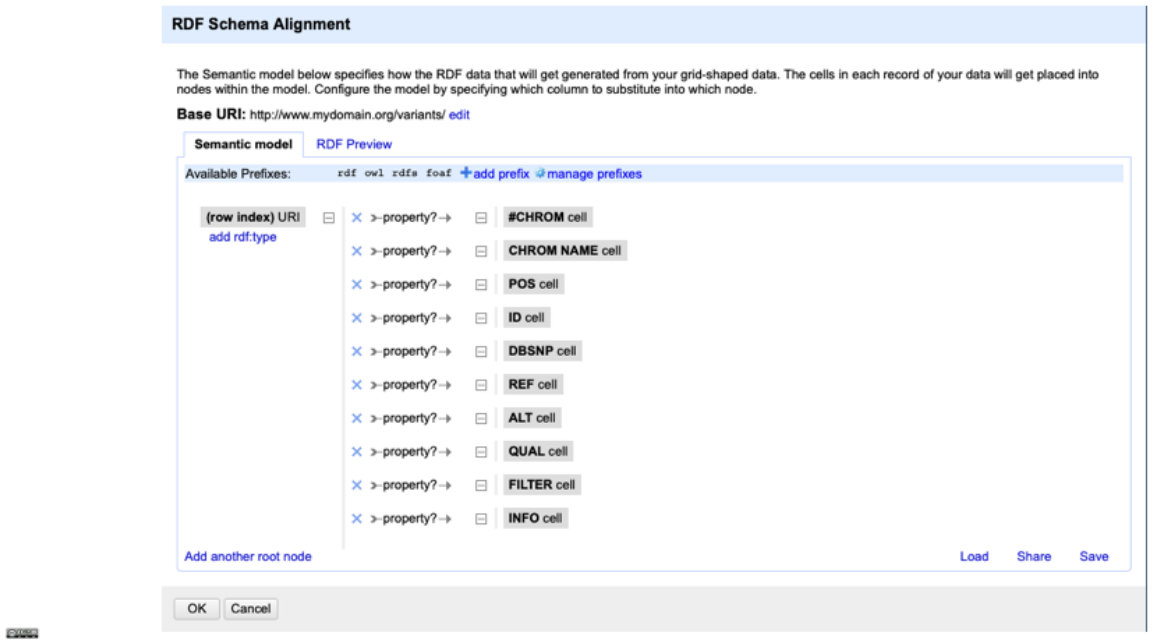


Chromosome URI preparation: match all cells to their best candidate

FAIRIFICATION WORKFLOW

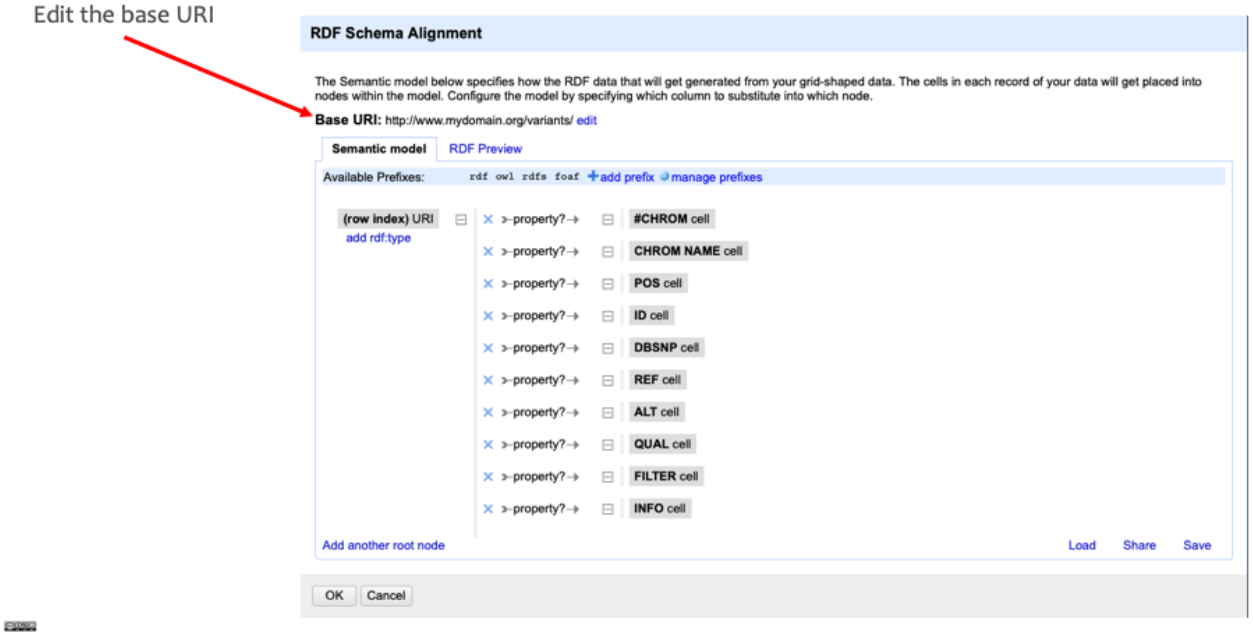


DEFINE SEMANTIC MODEL



DEFINE SEMANTIC MODEL

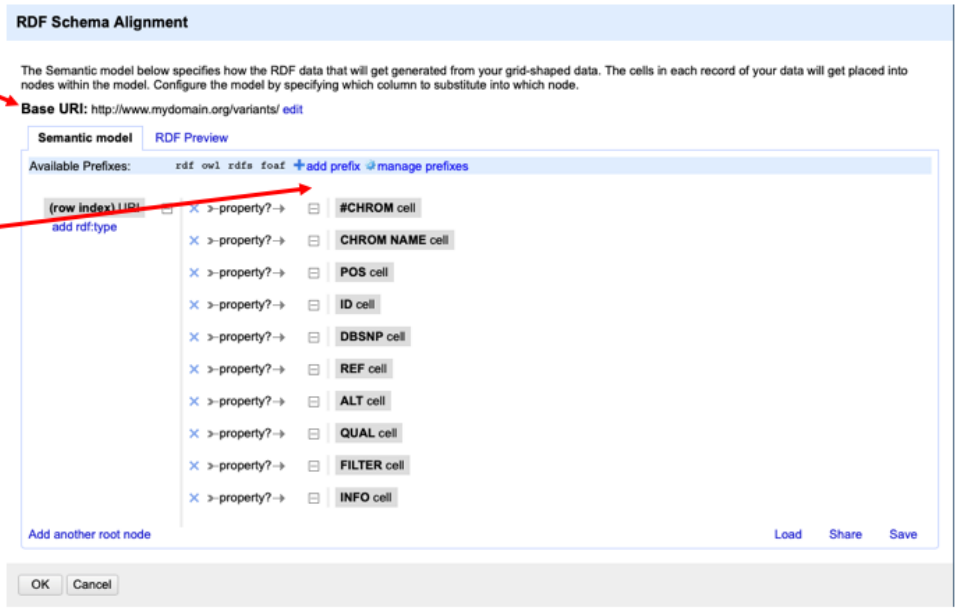
Edit the base URI



DEFINE SEMANTIC MODEL

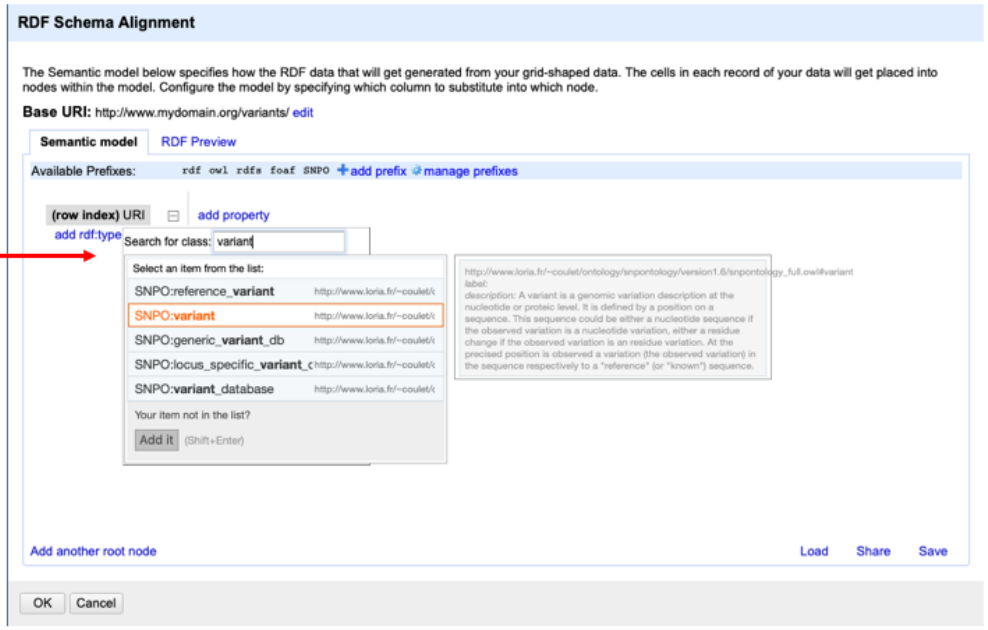
Edit the base URI

Add SNPO prefix: http://data.bioontology.org/ontologies/SNPO/submissions/4/download?apikey=8b5b7825-538d-40e0-9e9e-5ab9274a9aeb



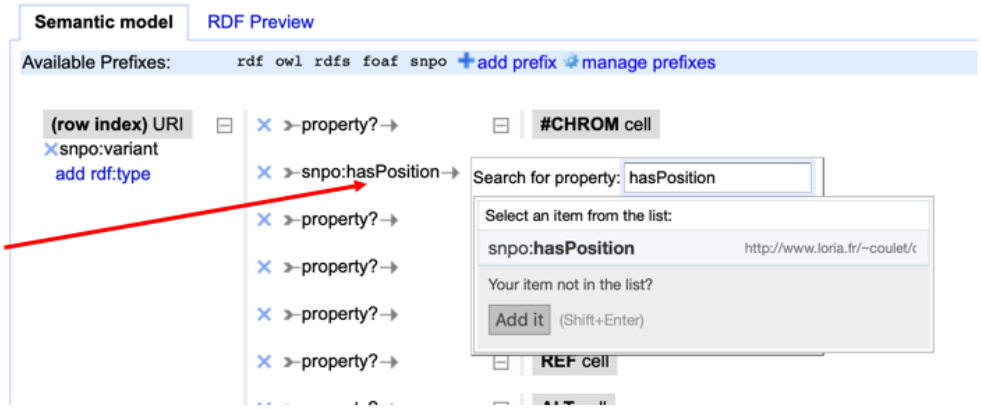
DEFINE SEMANTIC MODEL

Add snpo:variant as rdf:type



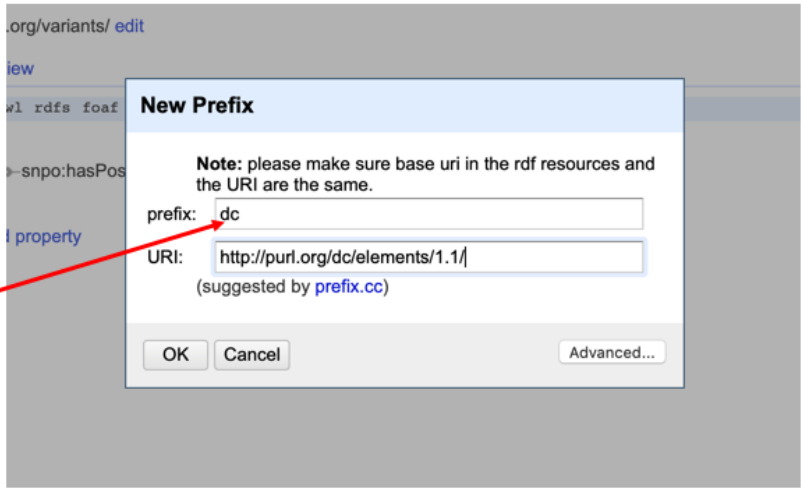
DEFINE SEMANTIC MODEL

Add ***snpo:hasPosition*** as the predicate relating variant and CHROMID

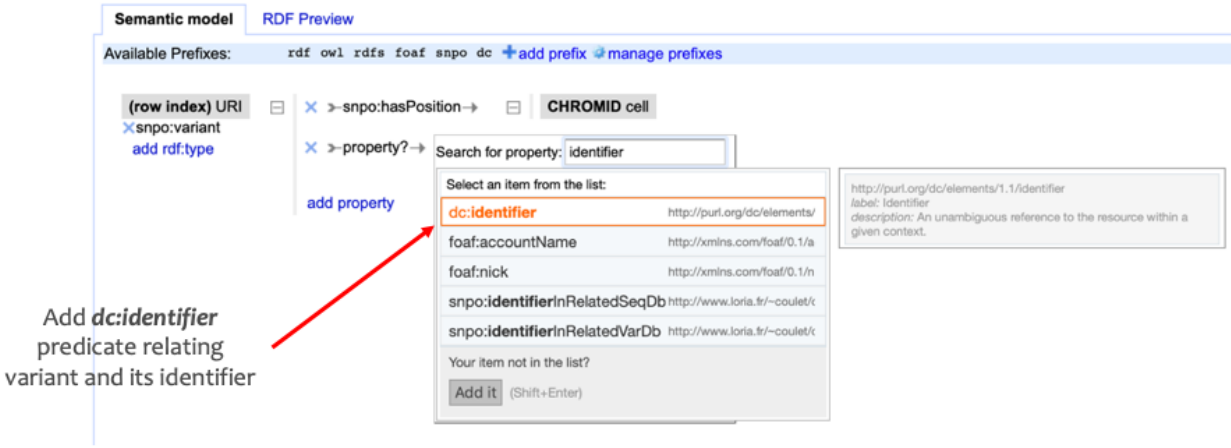


DEFINE SEMANTIC MODEL

Add Dublin Core prefix



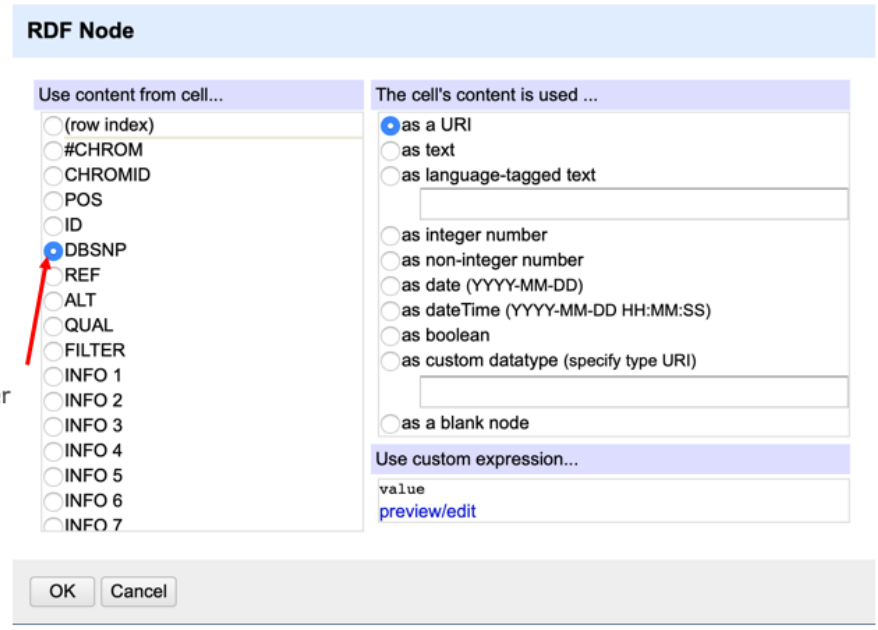
DEFINE SEMANTIC MODEL



Add ***dc:identifier*** predicate relating variant and its identifier

DEFINE SEMANTIC MODEL

Add ***dc:identifier*** predicate relating variant and its identifier



DEFINE SEMANTIC MODEL

Semantic model | **RDF Preview**

This is a sample `Turtle` representation of (up-to) the *first 10* rows

```
@prefix rdf: <http://www.w3.org/1999/02/22-rdf-syntax-ns#> .
@prefix owl: <http://www.w3.org/2002/07/owl#> .
@prefix rdfs: <http://www.w3.org/2000/01/rdf-schema#> .
@prefix foaf: <http://xmlns.com/foaf/0.1/> .
@prefix dc: <http://purl.org/dc/elements/1.1/> .
@prefix snpo: <http://data.bioontology.org/ontologies/SNPO/submissions/4/download?apikey=8b5b7825-538d-40e0-9e9e-5ab9274a9aeb%20> .


<http://www.mydomain.org/variants/0> a <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#variant> ;
        <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#hasPosition> <http://www.mydomain.org/variants/Chromosc

<http://www.mydomain.org/variants/1> a <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#variant> ;
        <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#hasPosition> <http://www.mydomain.org/variants/Chromosc
        dc:identifier <http://identifiers.org/dbsnp/rs201003251> .

<http://www.mydomain.org/variants/2> a <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#variant> ;
        <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#hasPosition> <http://www.mydomain.org/variants/Chromosc

<http://www.mydomain.org/variants/3> a <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#variant> ;
        <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#hasPosition> <http://www.mydomain.org/variants/Chromosc
        dc:identifier <http://identifiers.org/dbsnp/rs34521632> .

<http://www.mydomain.org/variants/4> a <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#variant> ;
        <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#hasPosition> <http://www.mydomain.org/variants/Chromosc

<http://www.mydomain.org/variants/5> a <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#variant> ;
        <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#hasPosition> <http://www.mydomain.org/variants/Chromosc

<http://www.mydomain.org/variants/6> a <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#variant> ;
```

DEFINE SEMANTIC MODEL

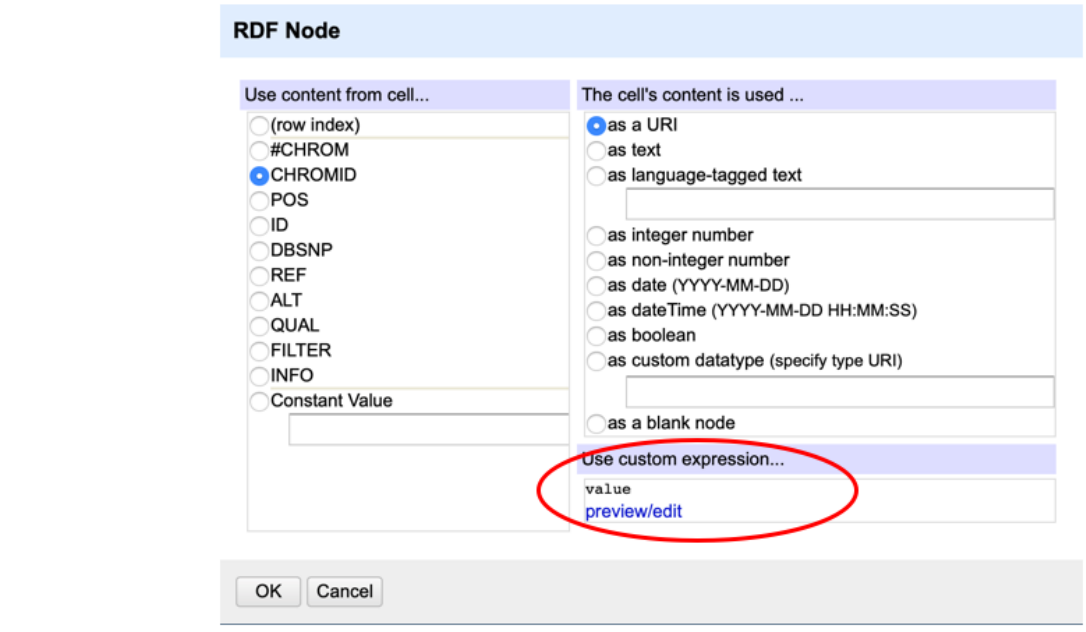
Semantic model | **RDF Preview**

This is a sample `Turtle` representation of (up-to) the *first 10* rows

```
@prefix rdf: <http://www.w3.org/1999/02/22-rdf-syntax-ns#> .
@prefix owl: <http://www.w3.org/2002/07/owl#> .
@prefix rdfs: <http://www.w3.org/2000/01/rdf-schema#> .
@prefix foaf: <http://xmlns.com/foaf/0.1/> .
@prefix dc: <http://purl.org/dc/elements/1.1/> .
@prefix snpo: <http://data.bioontology.org/ontologies/SNPO/submissions/4/download?apikey=8b5b7825-538d-40e0-9e9e-5ab9274a9aeb%20> .


<http://www.mydomain.org/variants/0> a <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#variant> ;
        <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#hasPosition> <http://www.mydomain.org/variants/Chromosc

<http://www.mydomain.org/variants/1> a <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#variant> ;
        <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#hasPosition> <http://www.mydomain.org/variants/Chromosc
        dc:identifier <http://identifiers.org/dbsnp/rs201003251> .

<http://www.mydomain.org/variants/2> a <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#variant> ;
        <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#hasPosition> <http://www.mydomain.org/variants/Chromosc

<http://www.mydomain.org/variants/3> a <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#variant> ;
        <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#hasPosition> <http://www.mydomain.org/variants/Chromosc
        dc:identifier <http://identifiers.org/dbsnp/rs34521632> .

<http://www.mydomain.org/variants/4> a <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#variant> ;
        <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#hasPosition> <http://www.mydomain.org/variants/Chromosc

<http://www.mydomain.org/variants/5> a <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#variant> ;
        <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#hasPosition> <http://www.mydomain.org/variants/Chromosc

<http://www.mydomain.org/variants/6> a <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#variant> ;
```

We have an issue. The chromosome URI is not the one from NCIT but it is using our domain. We need to fix it.

DEFINE SEMANTIC MODEL



DEFINE SEMANTIC MODEL

Preview URI values

General Refine Expression Language (GREL)

```
cell.recon.match.id
```

No syntax error.

row	value	cell.recon.match.id	resolved against the base URI
1.	Chromosome 1	http://ncicb.nci.nih.gov/xml/owl/EVS/Thesaur	http://ncicb.nci.nih.gov/xml/owl/EVS/Thesaur
2.	Chromosome 1	http://ncicb.nci.nih.gov/xml/owl/EVS/Thesaur	http://ncicb.nci.nih.gov/xml/owl/EVS/Thesaur
3.	Chromosome 1	http://ncicb.nci.nih.gov/xml/owl/EVS/Thesaur	http://ncicb.nci.nih.gov/xml/owl/EVS/Thesaur
4.	Chromosome 1	http://ncicb.nci.nih.gov/xml/owl/EVS/Thesaur	http://ncicb.nci.nih.gov/xml/owl/EVS/Thesaur
5.	Chromosome 1	http://ncicb.nci.nih.gov/xml/owl/EVS/Thesaur	http://ncicb.nci.nih.gov/xml/owl/EVS/Thesaur
6.	Chromosome 1	http://ncicb.nci.nih.gov/xml/owl/EVS/Thesaur	http://ncicb.nci.nih.gov/xml/owl/EVS/Thesaur

DEFINE SEMANTIC MODEL

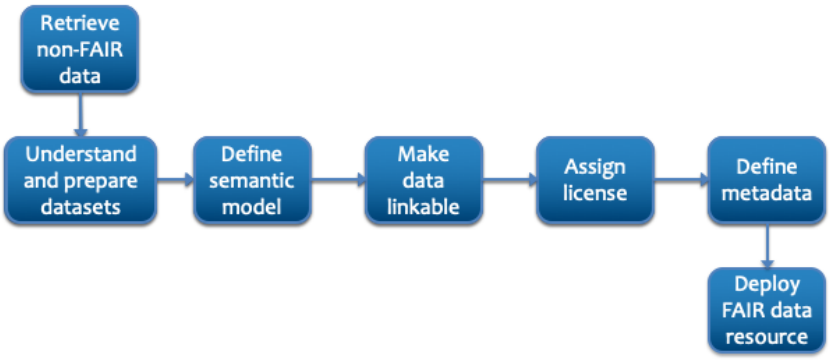
Semantic model | **RDF Preview**

This is a sample `Turtle` representation of (up-to) the *first 10* rows

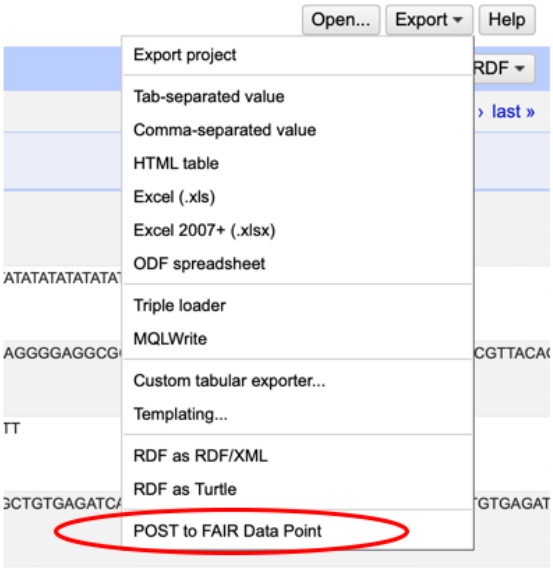
```
@prefix rdf: <http://www.w3.org/1999/02/22-rdf-syntax-ns#> .
@prefix owl: <http://www.w3.org/2002/07/owl#> .
@prefix rdfs: <http://www.w3.org/2000/01/rdf-schema#> .
@prefix foaf: <http://xmlns.com/foaf/0.1/> .
@prefix dc: <http://purl.org/dc/elements/1.1/> .
@prefix snpo: <http://data.bioontology.org/ontologies/SNPO/submissions/4/download?apikey=8b5b7825-538d-40e0-9e9e-5ab9274a9aeb%20> .

<http://www.mydomain.org/variants/0> a <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#variant> ;
        <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#hasPosition> <http://ncicb.nci.nih.gov/xml/owl/EVS/Thes

<http://www.mydomain.org/variants/1> a <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#variant> ;
        <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#hasPosition> <http://ncicb.nci.nih.gov/xml/owl/EVS/Thes
        dc:identifier <http://identifiers.org/dbsnp/rs201003251> .

<http://www.mydomain.org/variants/2> a <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#variant> ;
        <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#hasPosition> <http://ncicb.nci.nih.gov/xml/owl/EVS/Thes

<http://www.mydomain.org/variants/3> a <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#variant> ;
        <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#hasPosition> <http://ncicb.nci.nih.gov/xml/owl/EVS/Thes
        dc:identifier <http://identifiers.org/dbsnp/rs34521632> .

<http://www.mydomain.org/variants/4> a <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#variant> ;
        <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#hasPosition> <http://ncicb.nci.nih.gov/xml/owl/EVS/Thes

<http://www.mydomain.org/variants/5> a <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#variant> ;
        <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#hasPosition> <http://ncicb.nci.nih.gov/xml/owl/EVS/Thes

<http://www.mydomain.org/variants/6> a <http://www.loria.fr/~coulet/ontology/snpontology/version1.6/snpontology_full.owl#variant> ;
```

<http://ncicb.nci.nih.gov/xml/owl/EVS/Thesaurus.owl#C13204>

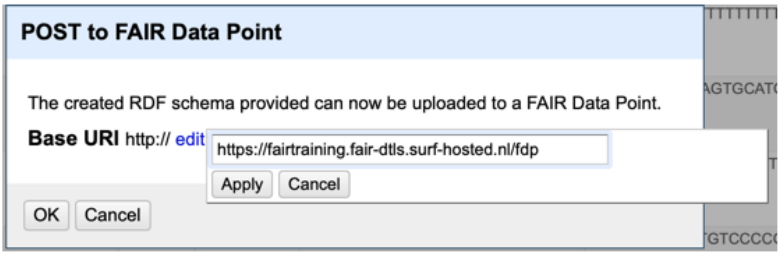
FAIRIFICATION WORKFLOW



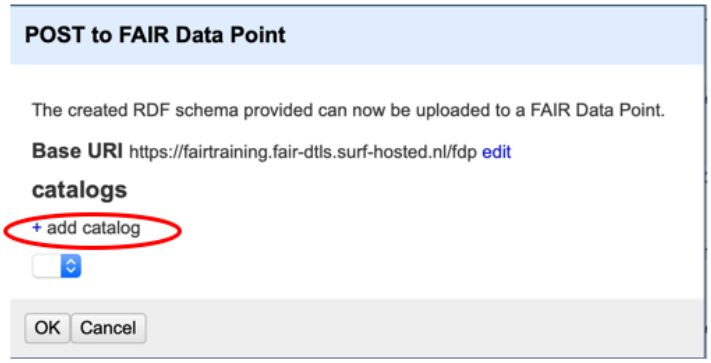
PUBLISH TO FAIR DATA POINT



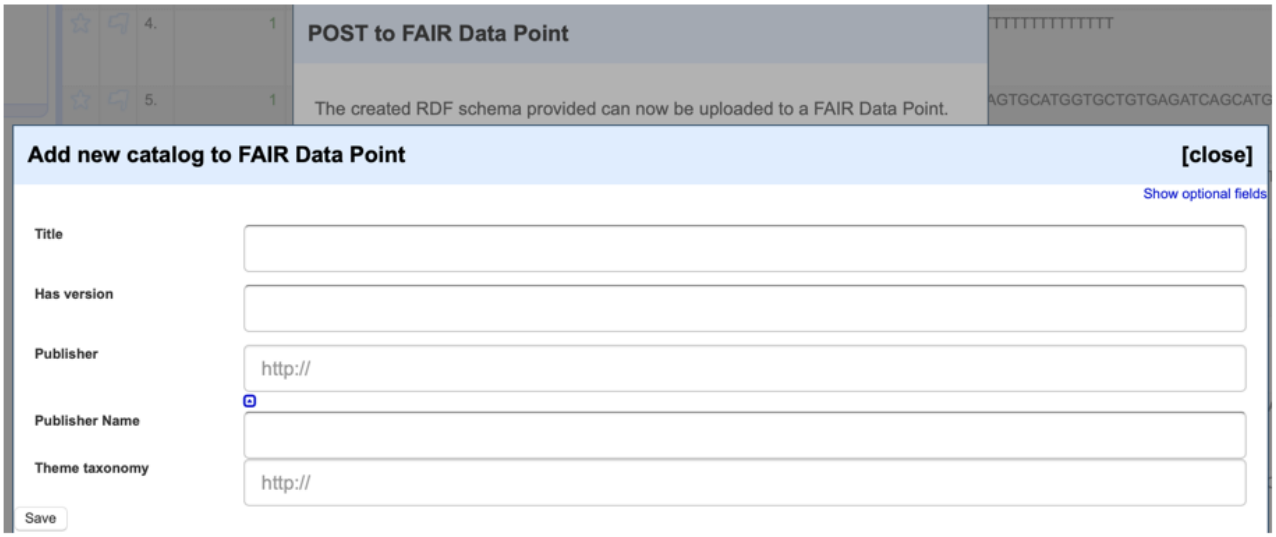
PUBLISH TO FAIR DATA POINT



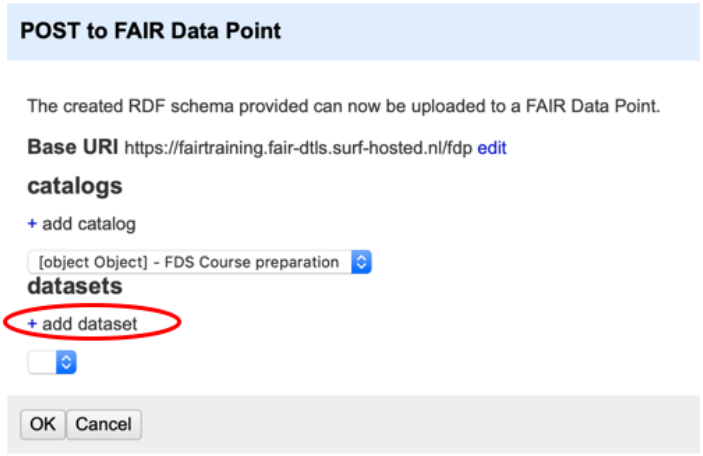
PUBLISH TO FAIR DATA POINT – ADD CATALOG



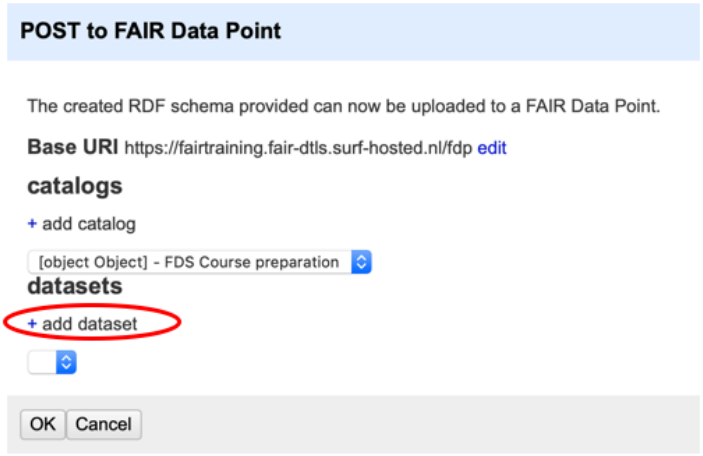
PUBLISH TO FAIR DATA POINT – ADD CATALOG



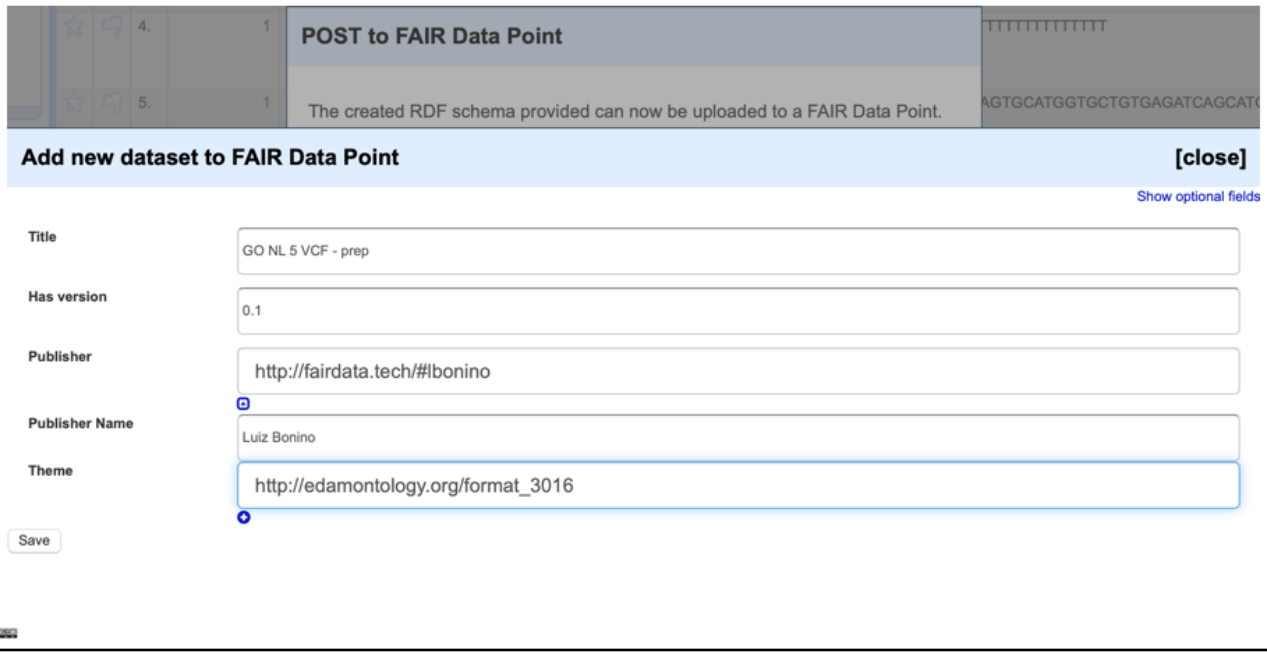
PUBLISH TO FAIR DATA POINT – ADD DATASET



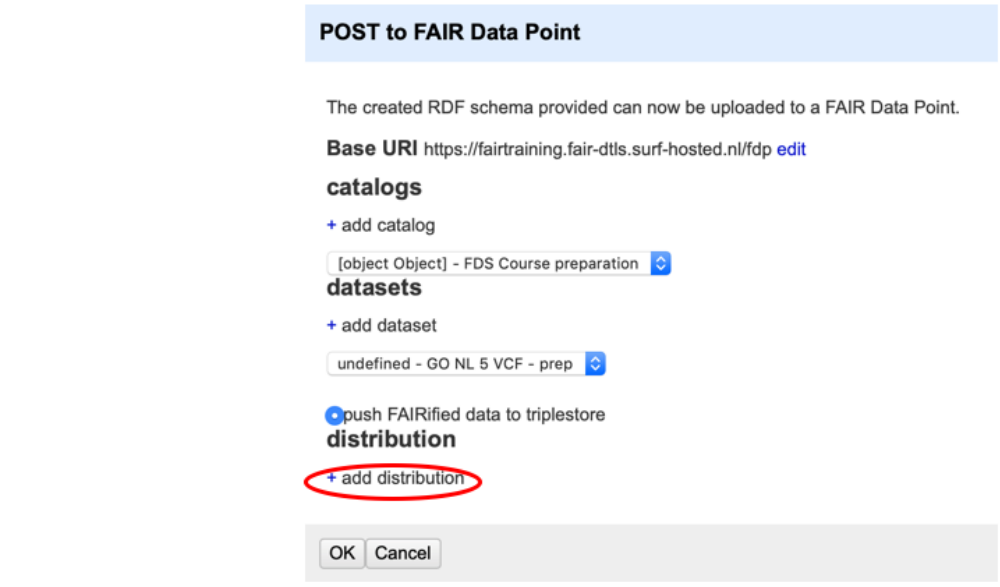
PUBLISH TO FAIR DATA POINT – ADD DATASET



PUBLISH TO FAIR DATA POINT – ADD DATASET



PUBLISH TO FAIR DATA POINT – ADD DISTRIBUTION



Q&A – CONTACT INFO

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Associate Professor BioSemantics – LUMC

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Skype: **luizolavobonino**

Web: **www.go-fair.org**