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# Sharing massive data analysis: from provenance to linked experiment reports

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# Sharing massive data analysis : from provenance to linked experiment reports

Scientific workflows, provenance and linked data to the rescue

Alban Gaignard, PhD, CNRS

Toulouse, 13 november 2018

APSEM 2018

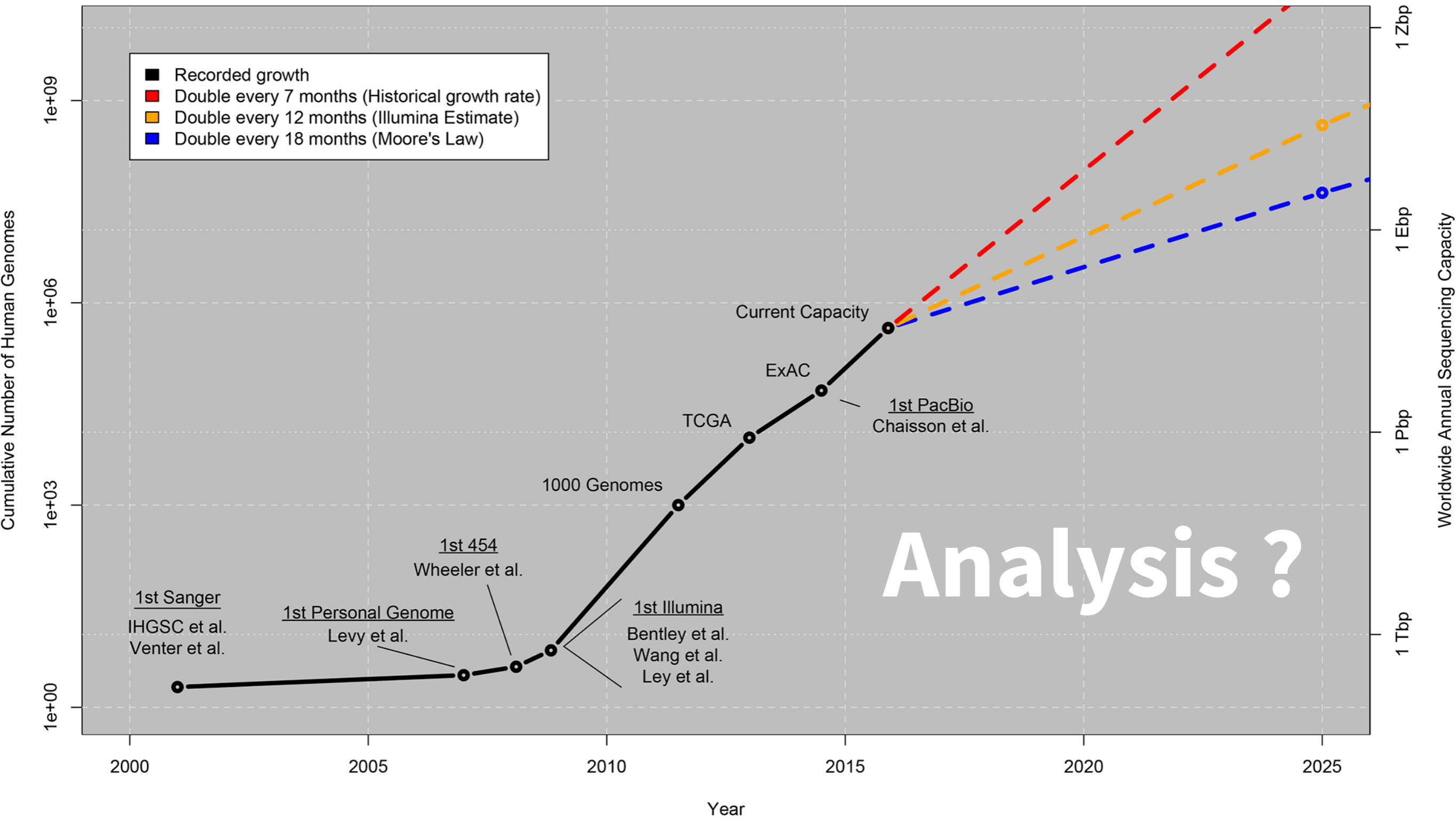


# Reproducibility

at the age of **massive data**

# Massive life science data production

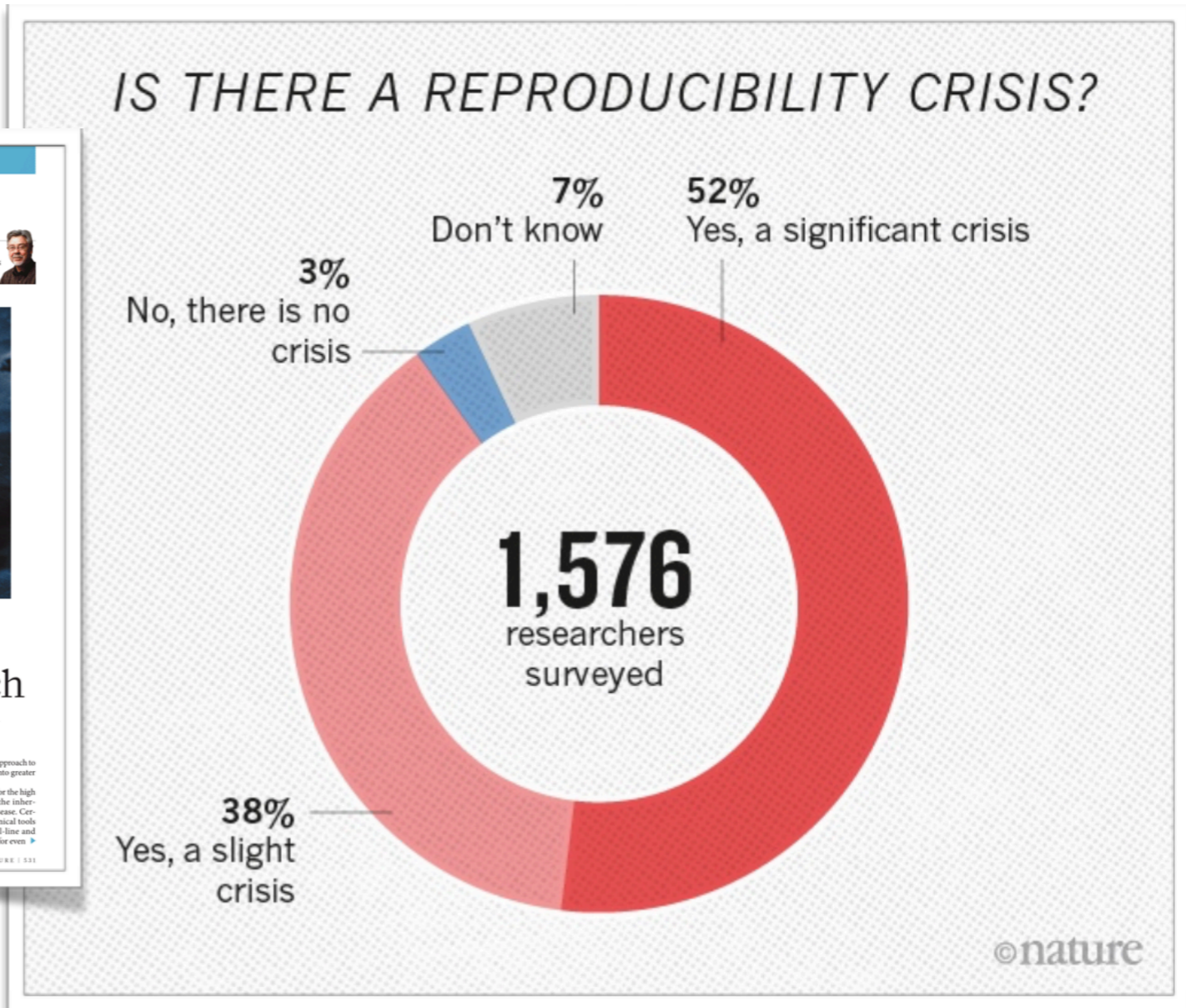
Growth of DNA Sequencing



Analysis ?



# Knowledge production



COMMENT

612 | NATURE | VOL 505 | 30 JANUARY 2014

## NIH plans to enhance reproducibility

Francis S. Collins and Lawrence A. Tabak discuss initiatives that the US National Institutes of Health is exploring to restore the self-correcting nature of preclinical research.

A growing chorus of concern, from scientists and laypeople, contends that the complex system for ensuring the reproducibility of biomedical research is failing and is in need of restructuring<sup>1,2</sup>. As leaders of the US National Institutes of Health (NIH), we share this concern and here explore some of the significant interventions that we are planning.

Science has long been regarded as 'self-correcting' given that it is founded on the shorter term, however, the checks and balances that once ensured scientific fidelity have been hobbled. This has compromised the ability of today's researchers to reproduce others' findings.

Let's be clear: with rare exceptions, we have no evidence to suggest that irreproducibility is about scientific misconduct. In 2011, the Office of Research Integrity of the US Department of Health and Human Services pursued only 12 such cases<sup>3</sup>.

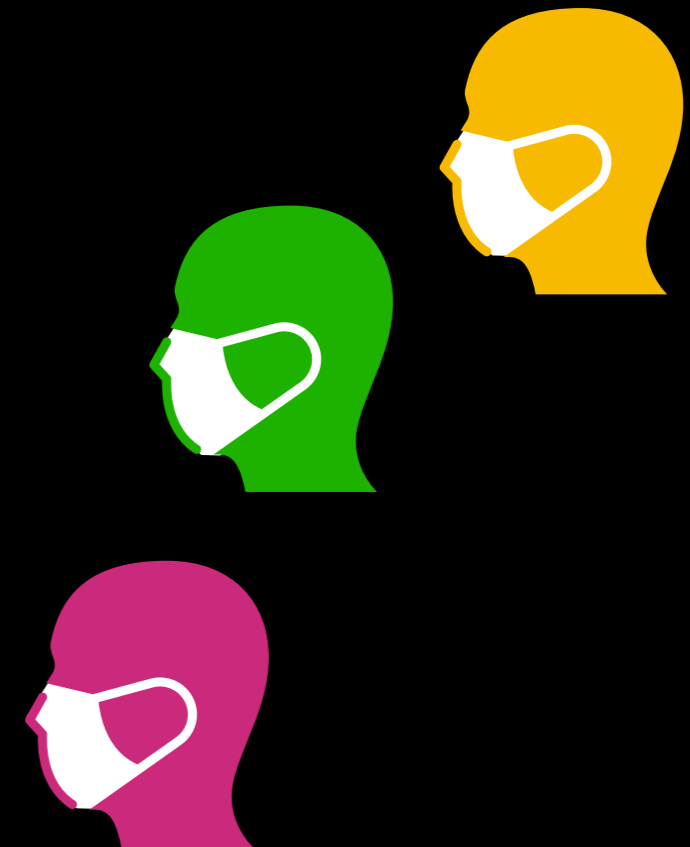
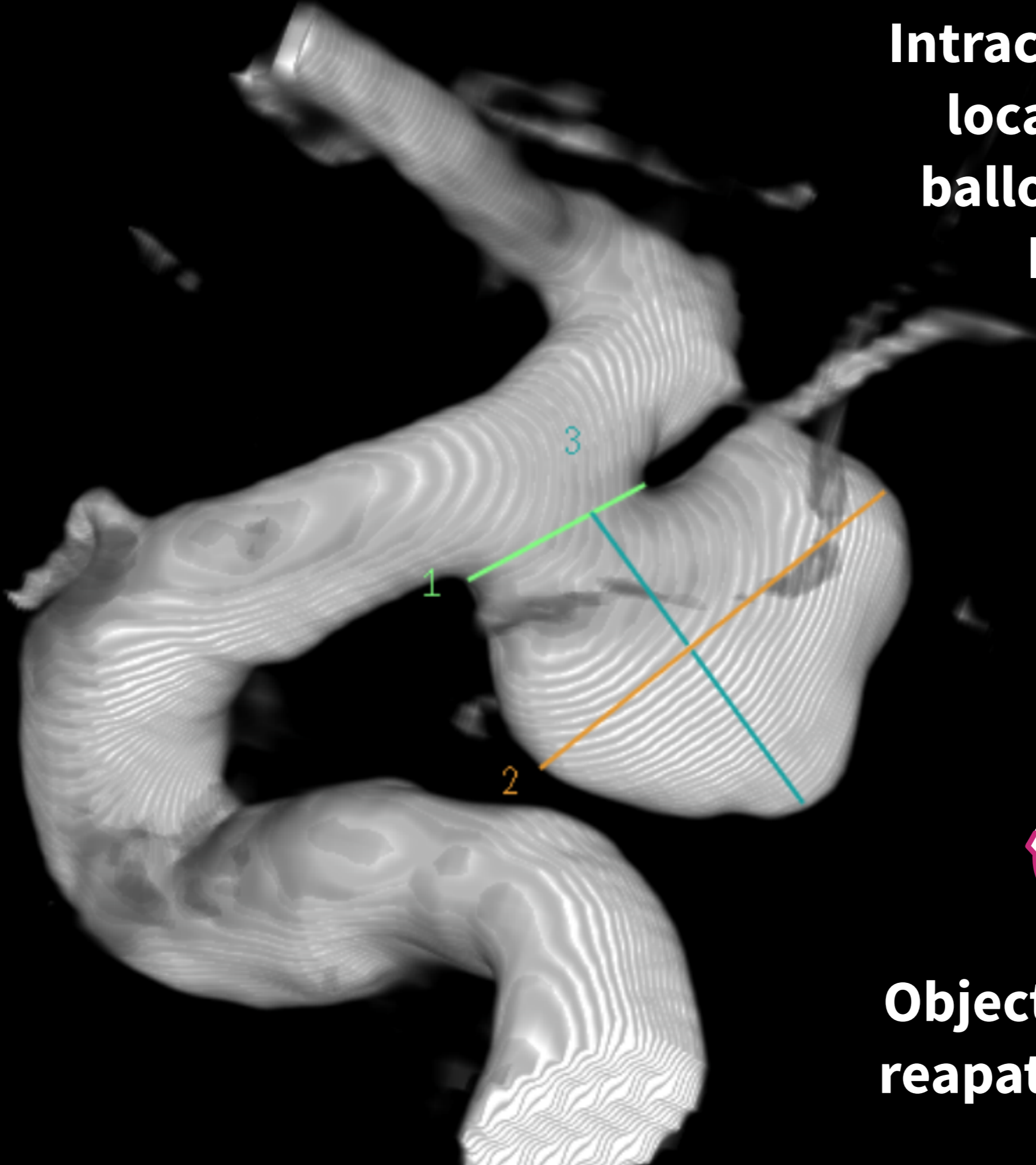
« In 2012, Amgen researchers made headlines when they declared that they had been **unable to reproduce the findings in 47 of 53 'landmark' cancer papers** » (doi:10.1038/nature.2016.19269)

# Repeat < Replicate < Reproduce < Reuse

Same experiment	Same experiment	Same experiment
Same setup	Same setup	<del>Same setup</del> New ideas,
Same lab	<del>Same lab</del>	<del>Same lab</del> new experiment, some commonalities



# Intracranial aneurysms : localized dilation or ballooning in cerebral blood vessels



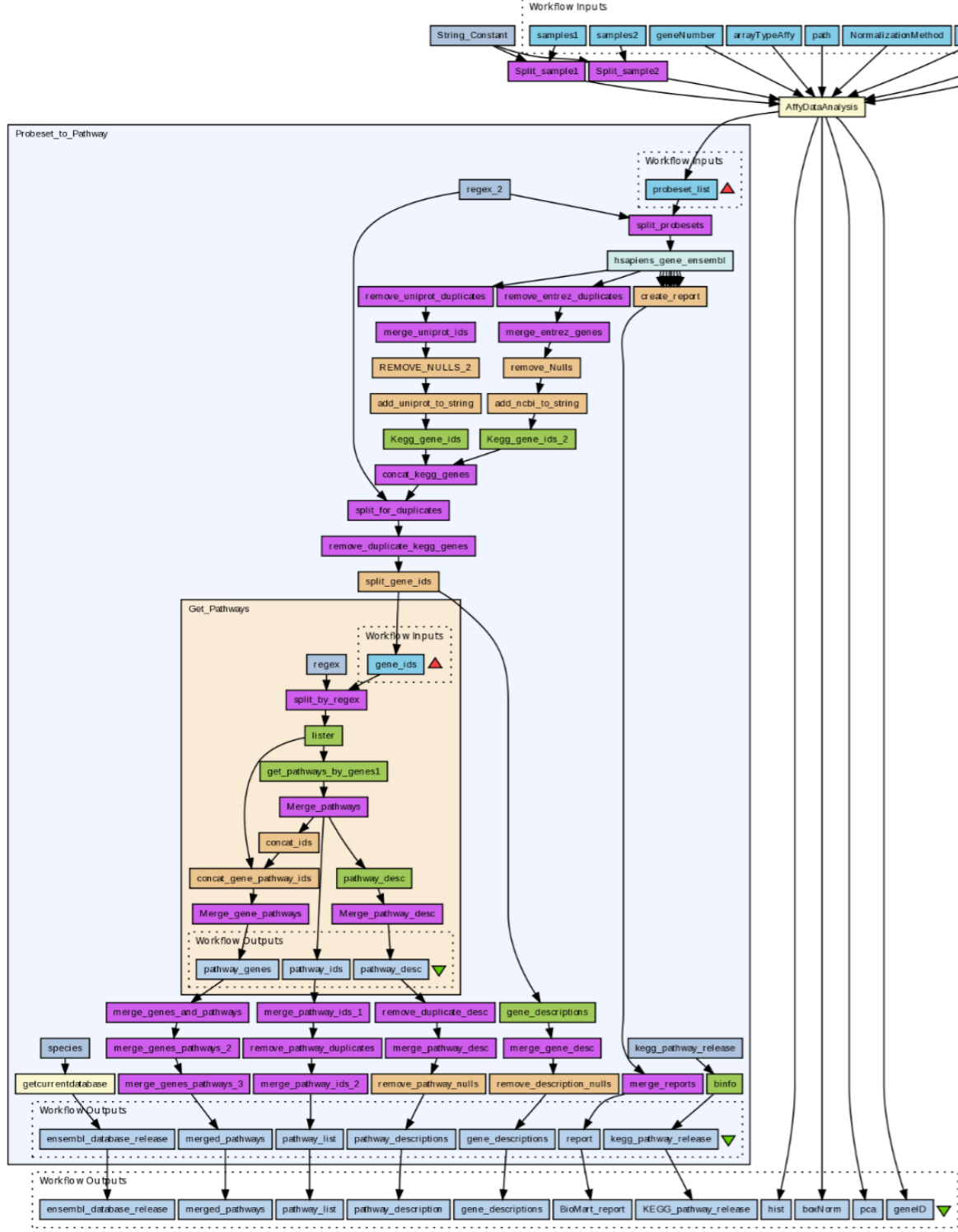
**Objective, systematic,  
reapatable measures ?**

Scientific **workflows** to  
the rescue ...

# What is a workflow ?

« Workflows provide a systematic way of describing the **methods** needed and provide the **interface** between **domain specialists** and **computing infrastructures**. »

« Workflow management systems (WMS) **perform** the complex analyses on a variety of **distributed resources** »



Scientific workflows to enhance **trust** in scientific results :

→ **automate** data analysis (at scale)

→ **abstraction** (describe/share methods)

→ **provenance** (~transparency)

[pdidommaso / awesome-pipeline](#)

A curated list of awesome pipeline toolkits inspired by Awesome Sysadmin

#awesome-list #workflow

228 commits | 1 branch | 0 releases | 42 contributors

Branch: master | New pull request | Create new file | Upload files | Find file | Clone or download

pdidommaso Update README.md | Latest commit #72e6a 25 days ago

CONTRIBUTING.md | Added contributing | 4 years ago

README.md | Update README.md | 25 days ago

EBI README.md

### Awesome Pipeline

A curated list of awesome pipeline toolkits inspired by [Awesome Sysadmin](#)

#### Pipeline frameworks & libraries

- **ActionChain** - A workflow system for simple linear success/failure workflows.
- **Adage** - Small package to describe workflows that are not completely known at definition time.
- **Airflow** - Python-based workflow system created by AirBnB.
- **Anduri** - Component-based workflow framework for scientific data analysis.
- **Antha** - High-level language for biology.
- **Bds** - Scripting language for data pipelines.
- **BioMake** - GNU-Make-like utility for managing builds and complex workflows.
- **BioQueue** - Explicit framework with web monitoring and resource estimation.
- **Bistro** - Library to build and execute typed scientific workflows.
- **Bpipe** - Tool for running and managing bioinformatics pipelines.
- **Briefly** - Python Meta-programming Library for Job Flow Control.
- **Cluster Flow** - Command-line tool which uses common cluster managers to run bioinformatics pipelines.
- **Clusterjob** - Automated reproducibility, and hassle-free submission of computational jobs to clusters.
- **Comps** - Programming model for distributed infrastructures.
- **Conan2** - Light-weight workflow management application.
- **Consecution** - A Python pipeline abstraction inspired by Apache Storm topologies.
- **Cosmos** - Python library for massively parallel workflows.
- **Cromwell** - Workflow Management System geared towards scientific workflows from the Broad Institute.
- **Cuneiform** - Advanced functional workflow language and framework, implemented in Erlang.
- **Dagobah** - Simple DAG-based job scheduler in Python.
- **Dagr** - A scala based DSL and framework for writing and executing bioinformatics pipelines as Directed Acyclic GRaphs.
- **Dask** - Dask is a flexible parallel computing library for analytics.
- **Dockerflow** - Workflow runner that uses Dataflow to run a series of tasks in Docker.
- **Doit** - Task management & automation tool.
- **Drake** - Robust DSL akin to Make, implemented in Clojure.
- **Drake R package** - Reproducibility and high-performance computing with an easy R-focused interface. Unrelated to Factual's Drake.
- **Dray** - An engine for managing the execution of container-based workflows.
- **Fission Workflows** - A fast, lightweight workflow engine for serverless/FaaS functions.



Provenance : a way to **reuse**  
produced & analysed data

## Definition: Oxford dictionary

« The beginning of something's existence; something's origin. »

## Definition: Computer Science

« Provenance information describes the **origins** and the **history of data in its life cycle**. »

« Today, data is often made available on the Internet with **no centralized control over its integrity**: data is constantly being created, copied, moved around, and combined indiscriminately. Because information sources (or different parts of a single large source) may vary widely in terms of quality, it is essential to provide **provenance** and other context information which can **help end users** judge whether query results are **trustworthy**. »



# Representing provenance



## PROV-O: The PROV Ontology

W3C Recommendation 30 April 2013

**This version:**

<http://www.w3.org/TR/2013/REC-prov-o-20130430/>

**Latest published version:**

<http://www.w3.org/TR/prov-o/>

**Implementation report:**

<http://www.w3.org/TR/2013/NOTE-prov-implementations-20130430/>

**Previous version:**

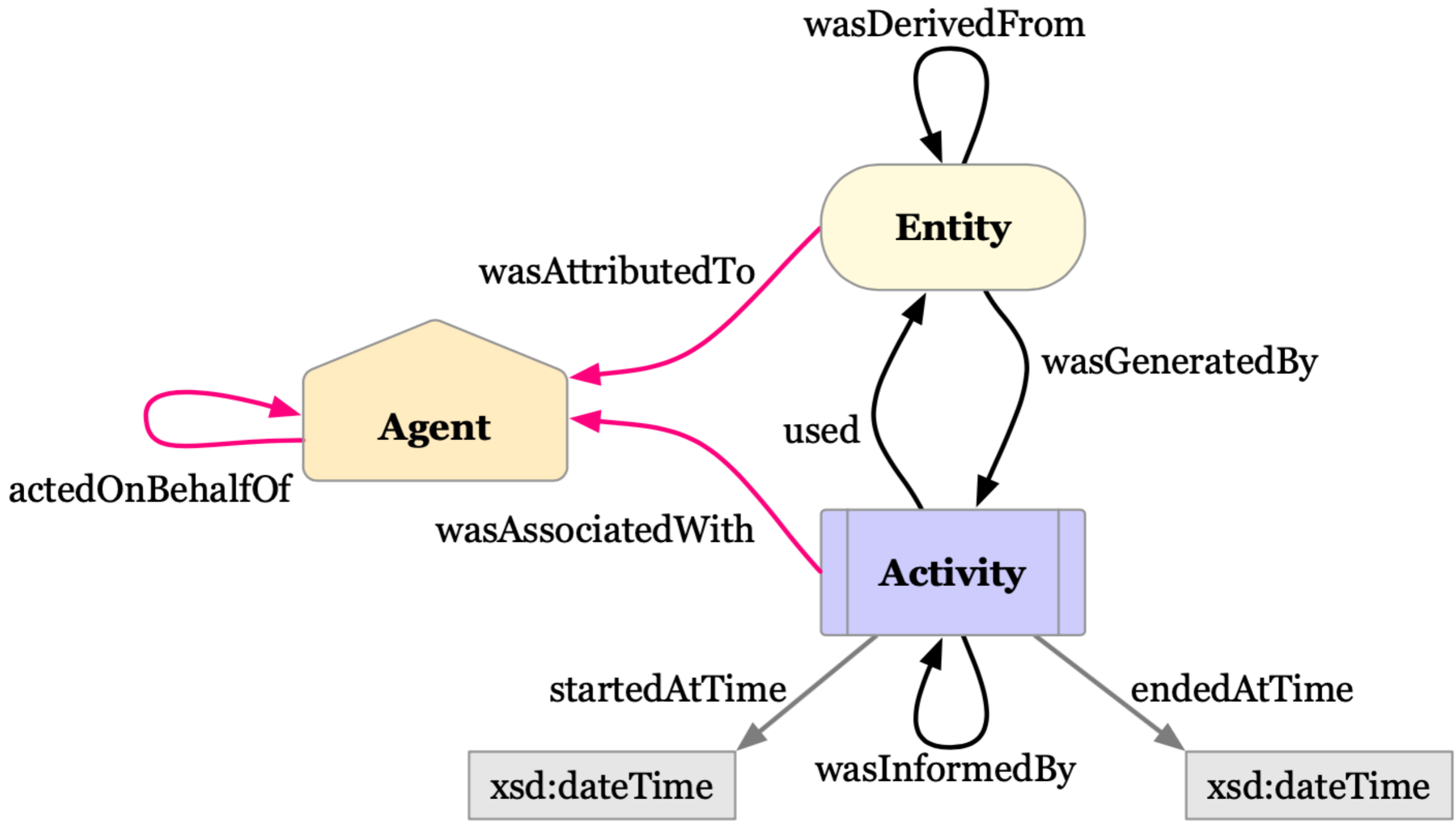
<http://www.w3.org/TR/2013/PR-prov-o-20130312/>

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**Feature extraction**



**Learning Task**



**Prediction Task**

**Training  
dataset**

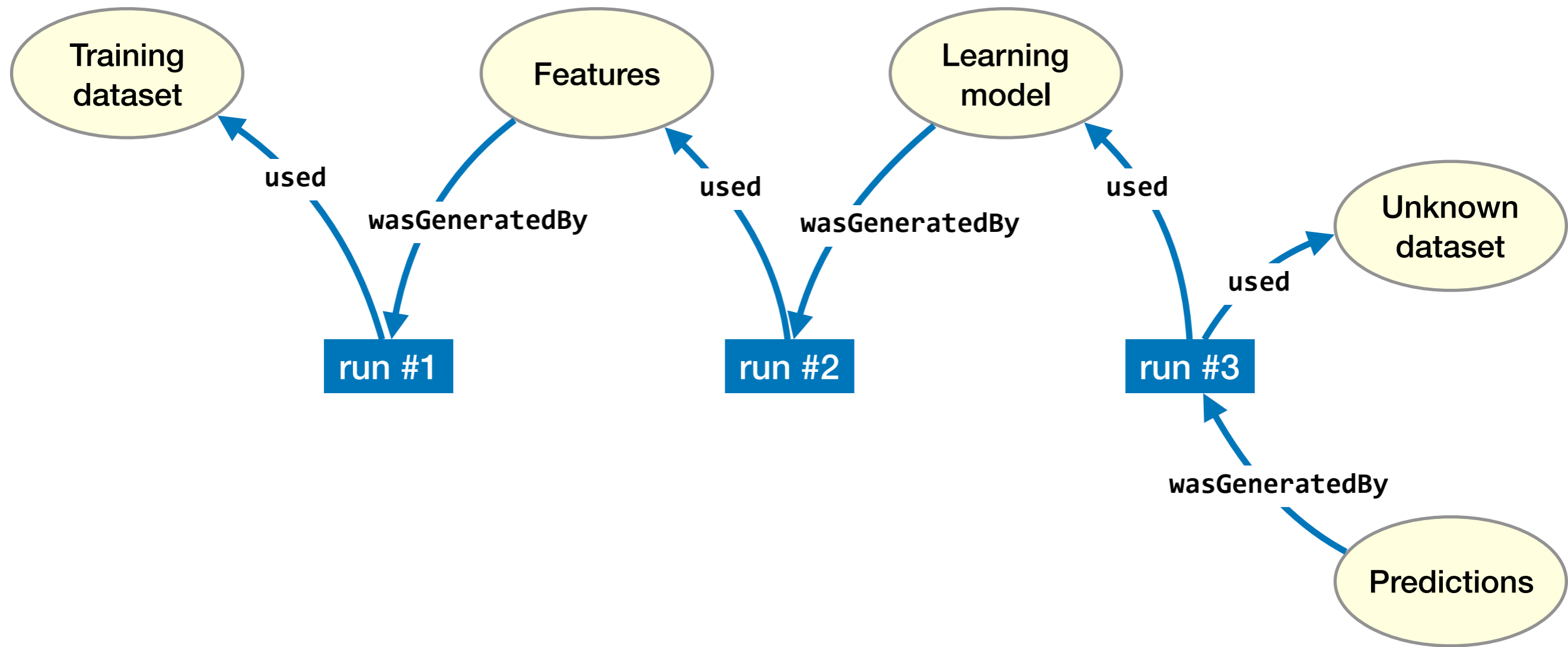
**Features**

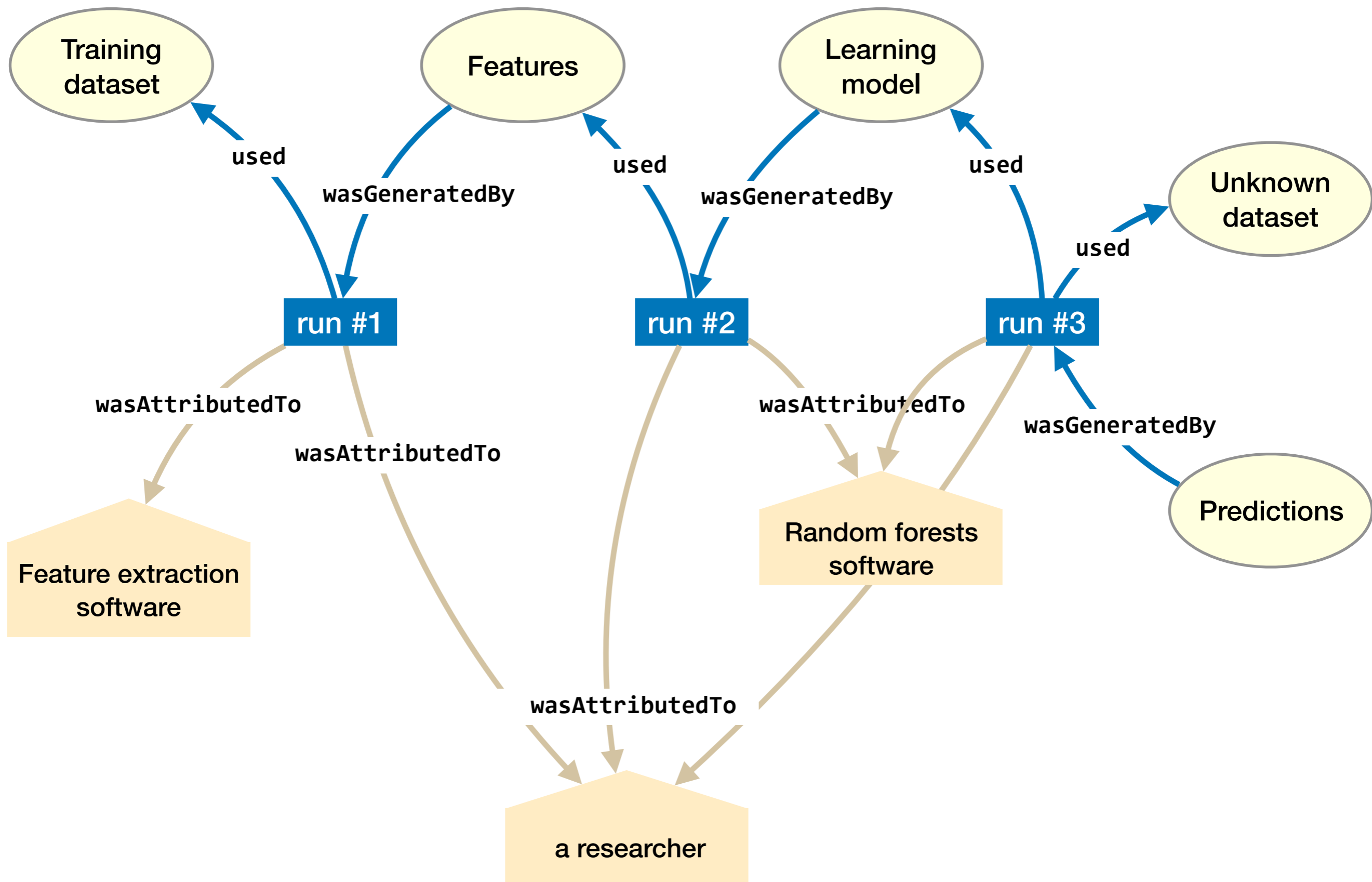
**Learning  
model**

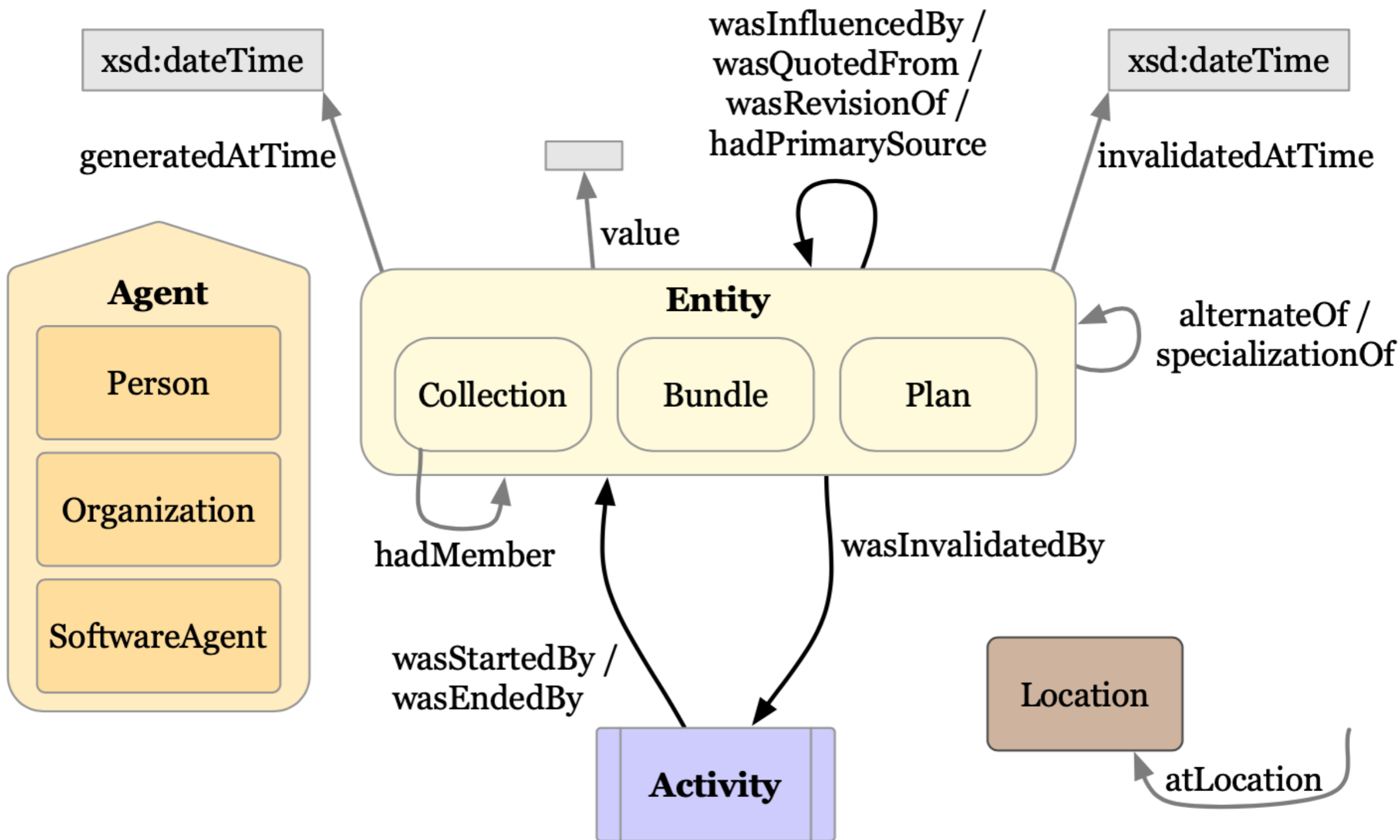
**Unknown  
dataset**

**Predictions**









# Reasoning with provenance



## Constraints of the PROV Data Model

W3C Recommendation 30 April 2013

**This version:**

<http://www.w3.org/TR/2013/REC-prov-constraints-20130430/>

**Latest published version:**

<http://www.w3.org/TR/prov-constraints/>

**Test suite:**

<http://dvcs.w3.org/hg/prov/raw-file/default/testcases/process.html>

**Implementation report:**

<http://www.w3.org/TR/2013/NOTE-prov-implementations-20130430/>

**Previous version:**

<http://www.w3.org/TR/2013/PR-prov-constraints-20130312/> (color-coded diff)

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Please refer to the [errata](#) for this document, which may include some normative corrections.

The English version of this specification is the only normative version. Non-normative [translations](#) may also be available.

## 5.3 Derivations

Derivations with explicit activity, generation, and usage admit the following inference:

### Inference 11 (derivation-generation-use-inference)

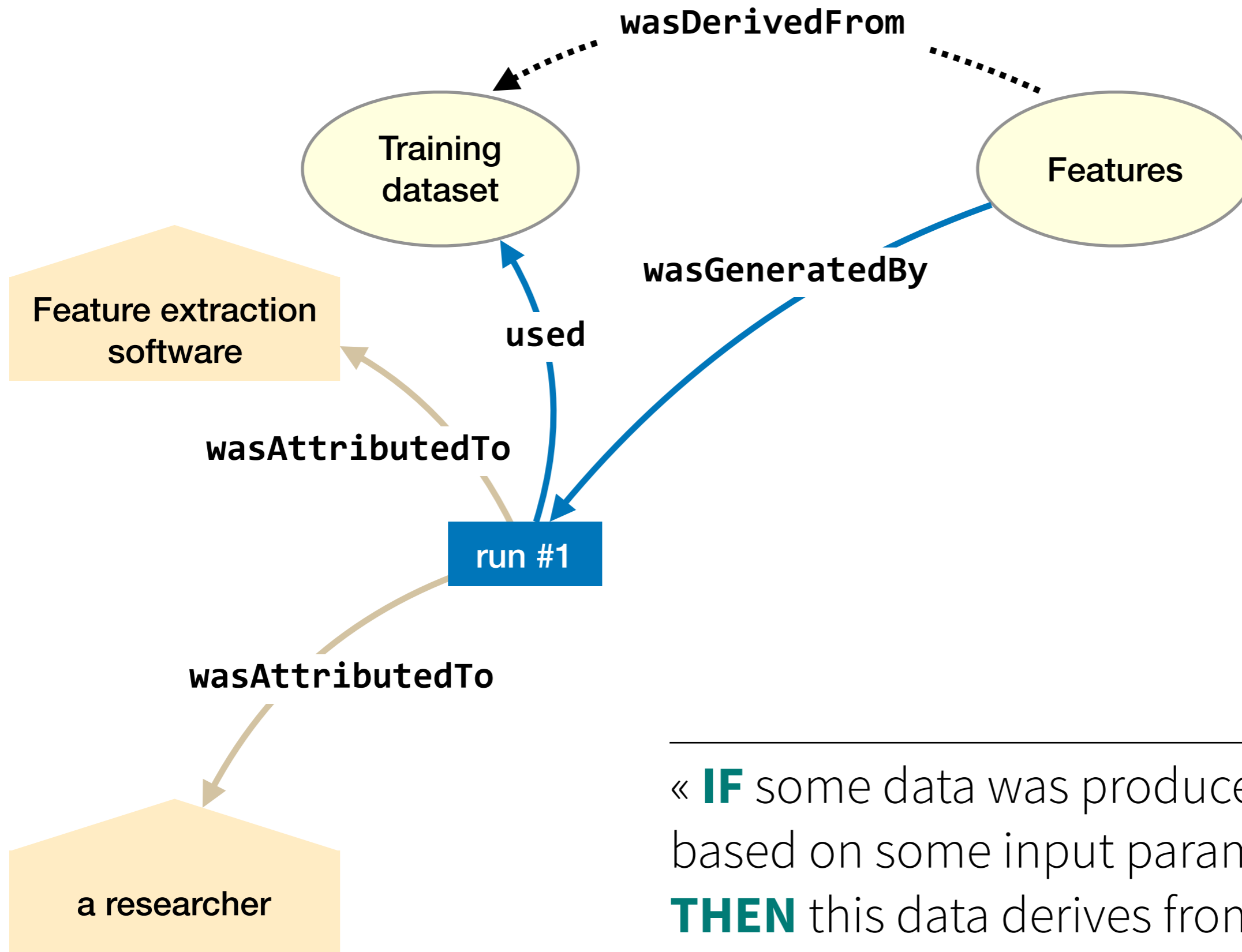
In this inference, none of `a`, `gen2` or `use1` can be placeholders `-`.

**IF** `wasDerivedFrom(_id; e2,e1,a,gen2,use1,_attrs)`, **THEN** there exists `_t1` and `_t2` such that `used(use1; a,e1,_t1,[])` and `wasGeneratedBy(gen2; e2,a,_t2,[])`.

### Inference 15 (influence-inference)

1. **IF** `wasGeneratedBy(id; e,a,_t,attrs)` **THEN** `wasInfluencedBy(id; e, a, attrs)`.
2. **IF** `used(id; a,e,_t,attrs)` **THEN** `wasInfluencedBy(id; a, e, attrs)`.
3. **IF** `wasInformedBy(id; a2,a1,attrs)` **THEN** `wasInfluencedBy(id; a2, a1, attrs)`.
4. **IF** `wasStartedBy(id; a2,e,_a1,_t,attrs)` **THEN** `wasInfluencedBy(id; a2, e, attrs)`.
5. **IF** `wasEndedBy(id; a2,e,_a1,_t,attrs)` **THEN** `wasInfluencedBy(id; a2, e, attrs)`.
6. **IF** `wasInvalidatedBy(id; e,a,_t,attrs)` **THEN** `wasInfluencedBy(id; e, a, attrs)`.
7. **IF** `wasDerivedFrom(id; e2, e1, _a, _g, _u, attrs)` **THEN** `wasInfluencedBy(id; e2, e1, attrs)`. Here, `_a`, `_g`, `_u` **MAY** be placeholders `-`.
8. **IF** `wasAttributedTo(id; e,ag,attrs)` **THEN** `wasInfluencedBy(id; e, ag, attrs)`.
9. **IF** `wasAssociatedWith(id; a,ag,_pl,attrs)` **THEN** `wasInfluencedBy(id; a, ag, attrs)`. Here, `_pl` **MAY** be a placeholder `-`.
10. **IF** `actedOnBehalfOf(id; ag2,ag1,_a,attrs)` **THEN** `wasInfluencedBy(id; ag2, ag1, attrs)`.





---

« **IF** some data was produced by a tool based on some input parameters, **THEN** this data derives from the input parameters »

PROV,  
how-to record/query ?

# Writing PROV statements

```
<Samples/Sample1/VCF/Sample1.hapcaller.g.vcf>  
  a prov:Entity;  
  prov:wasGeneratedBy <http://snakemake-provenance#activity-945311db-8f46-440d-ad05-e8c93832006e>;  
  prov:wasAttributedTo <#haplotypewriter>;  
  rdfs:label "Samples/Sample1/VCF/Sample1.hapcaller.g.vcf";  
  crypto:sha512  
  "28df1599bd0053ac08ce195db5750cf5c5f3a05597695449a2acee49b72245aee290bbc3f9ffcbe0f3f43b8c07156a175a424a25f2de5  
  3c326906340081d1c7b"^^xsd:string ;  
  prov:wasDerivedFrom <BED/capture.extended1000.bed> ;  
  prov:wasDerivedFrom <Samples/Sample1/BAM/Sample1.final.bam> ;  
  prov:wasDerivedFrom <../testdata/dbsnp_138.b37.chr22.recode.vcf.gz> ;  
  prov:wasDerivedFrom <gatkPresent.txt> ;  
  prov:wasDerivedFrom <../testdata/human_g1k_v37.chr22.fasta> ;  
  prov:wasDerivedFrom <../testdata/human_g1k_v37.chr22.dict> ;  
  prov:wasDerivedFrom <Samples/Sample1/BAM/Sample1.final.bai> ;
```

# Writing PROV statements

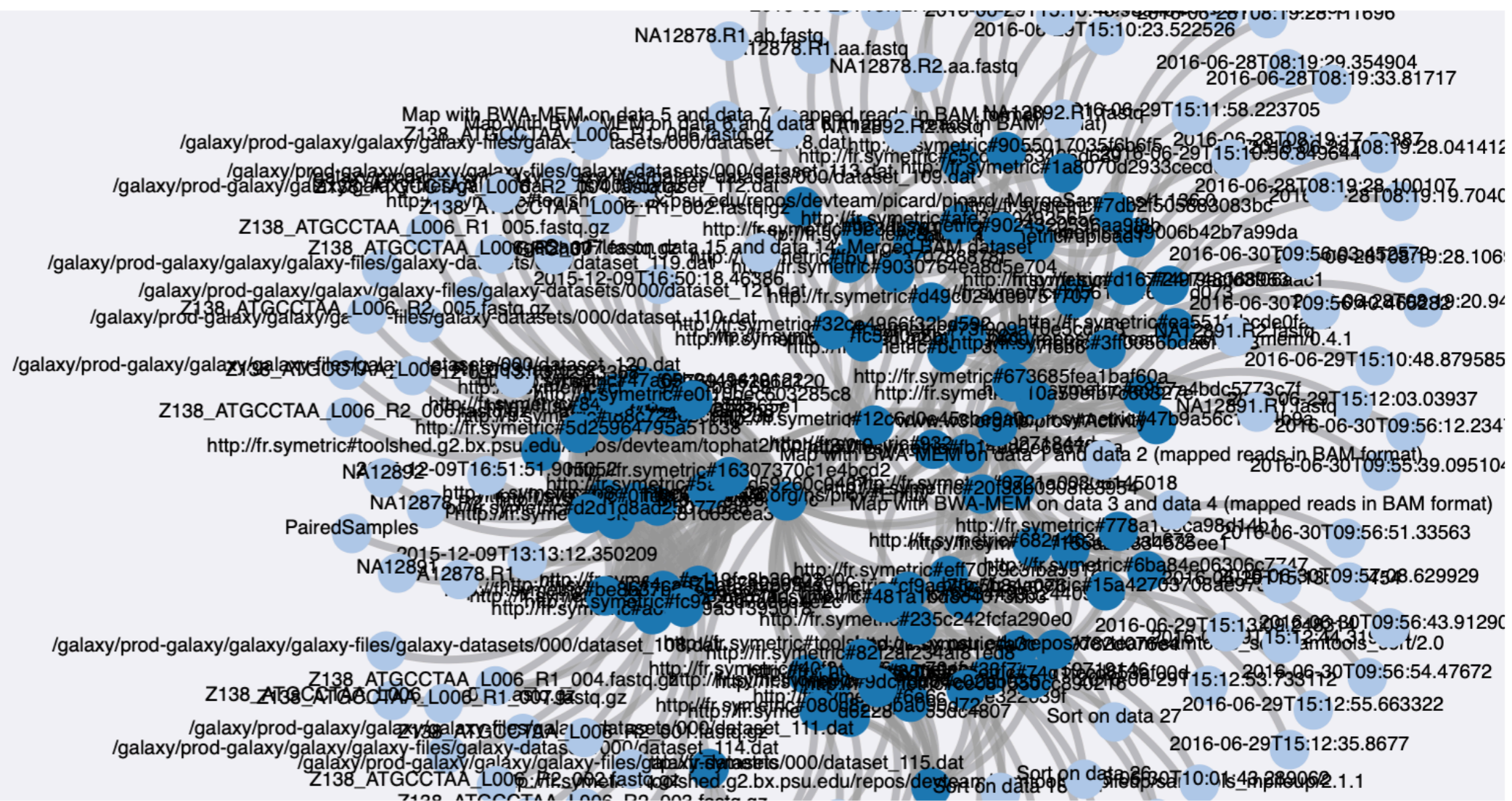
```
<http://snakemake-provenance#activity-945311db-8f46-440d-ad05-e8c93832006e>
a prov:Activity ;
rdfs:comment """
    gatk -Djava.io.tmpdir=Samples/Sample1/VCF -XX:ParallelGCThreads=5 -Xmx3g -T
    HaplotypeCaller -R ../testdata/human_g1k_v37.chr22.fasta
    --emitRefConfidence GVCF -variant_index_type LINEAR
    -variant_index_parameter 128000 -stand_call_conf 30.0 -nct 1
    -rf ReadLength -minRead 0 -maxRead 10000 -S SILENT
    -L:capture,BED BED/capture.extended1000.bed -I
    Samples/Sample1/BAM/Sample1.final.bam --dbsnp:dbsnp,VCF
    ../testdata/dbsnp_138.b37.chr22.recode.vcf.gz -o
    Samples/Sample1/VCF/Sample1.hapcaller.g.vcf
    """ ;
prov:wasAssociatedWith <#haplotypeCaller> ;
prov:startedAtTime "2018-04-04T16:19:57.054054"^^xsd:dateTime;
prov:endedAtTime "2018-04-04T16:19:57.054076"^^xsd:dateTime;
prov:used <BED/capture.extended1000.bed> ;
prov:used <Samples/Sample1/BAM/Sample1.final.bam> ;
prov:used <../testdata/dbsnp_138.b37.chr22.recode.vcf.gz> ;
prov:used <gatkPresent.txt> ;
prov:used <../testdata/human_g1k_v37.chr22.fasta> ;
prov:used <../testdata/human_g1k_v37.chr22.dict> ;
prov:used <Samples/Sample1/BAM/Sample1.final.bai> ;
```



# Querying PROV graphs

```
CONSTRUCT {?x ?p ?y} WHERE {?x ?p ?y}
```

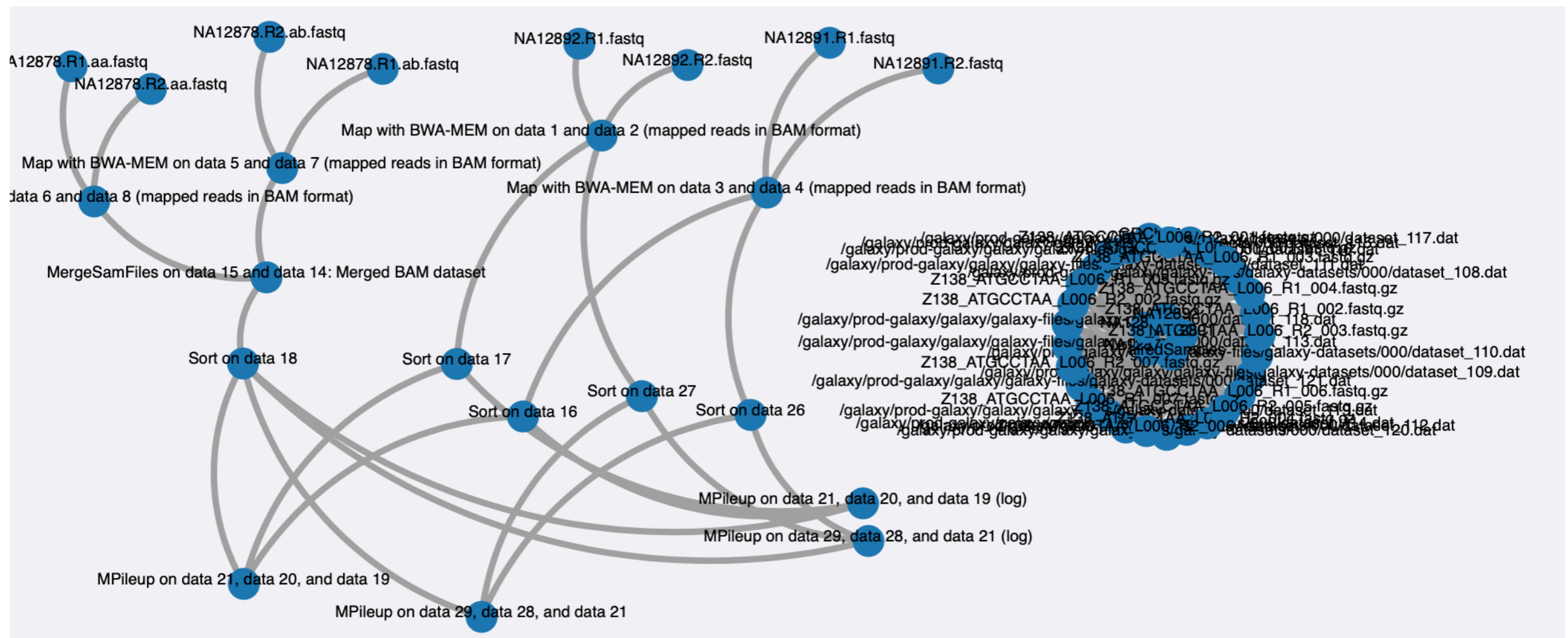
Query



# Querying PROV graphs

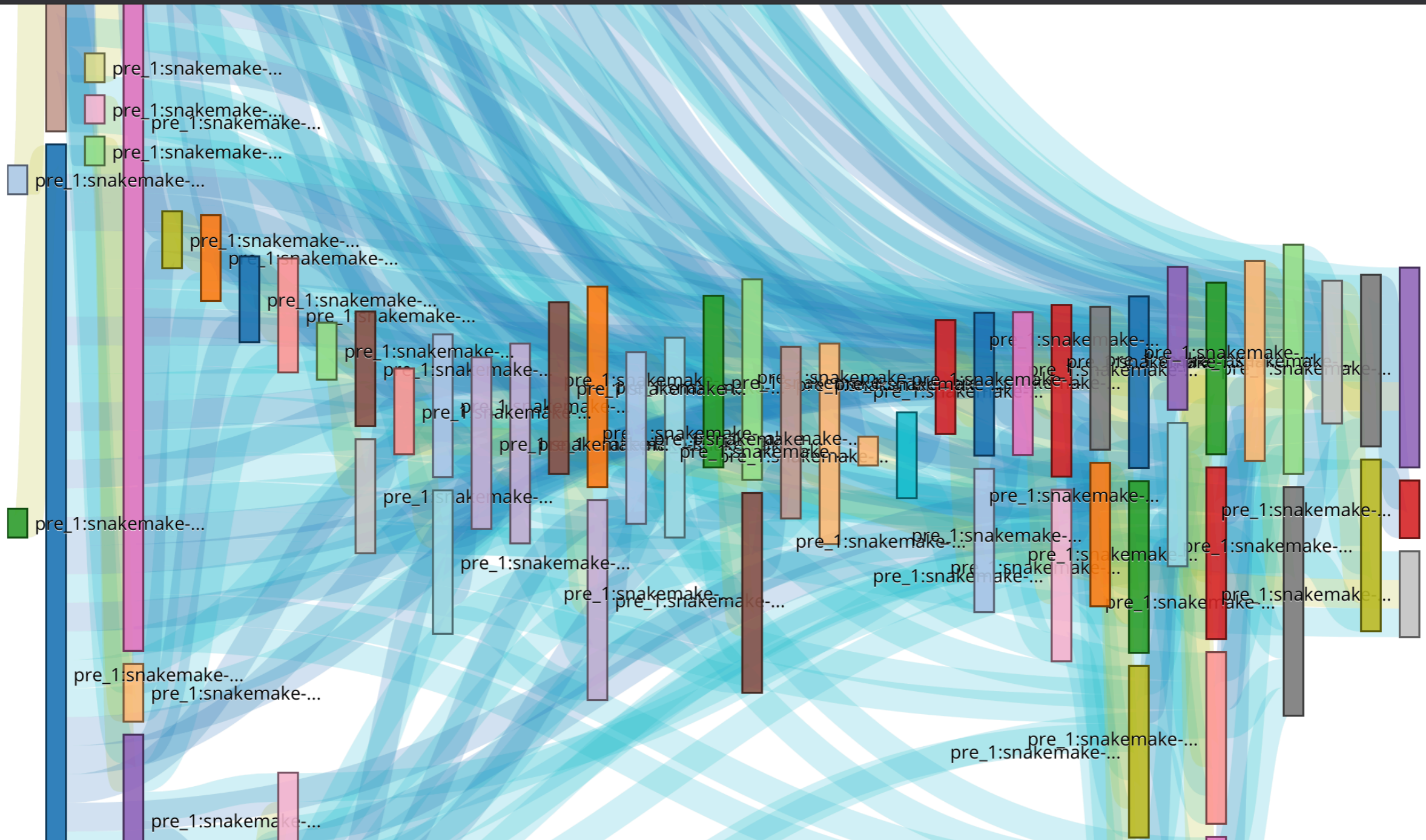
```
PREFIX prov: <http://www.w3.org/ns/prov#>  
CONSTRUCT {  
  ?x prov:wasDerivedFrom ?y  
} WHERE {  
  ?x_uri prov:wasDerivedFrom ?y_uri .  
  ?x_uri rdfs:label ?x .  
  ?y_uri rdfs:label ?y .  
}
```

Query





# PROV store

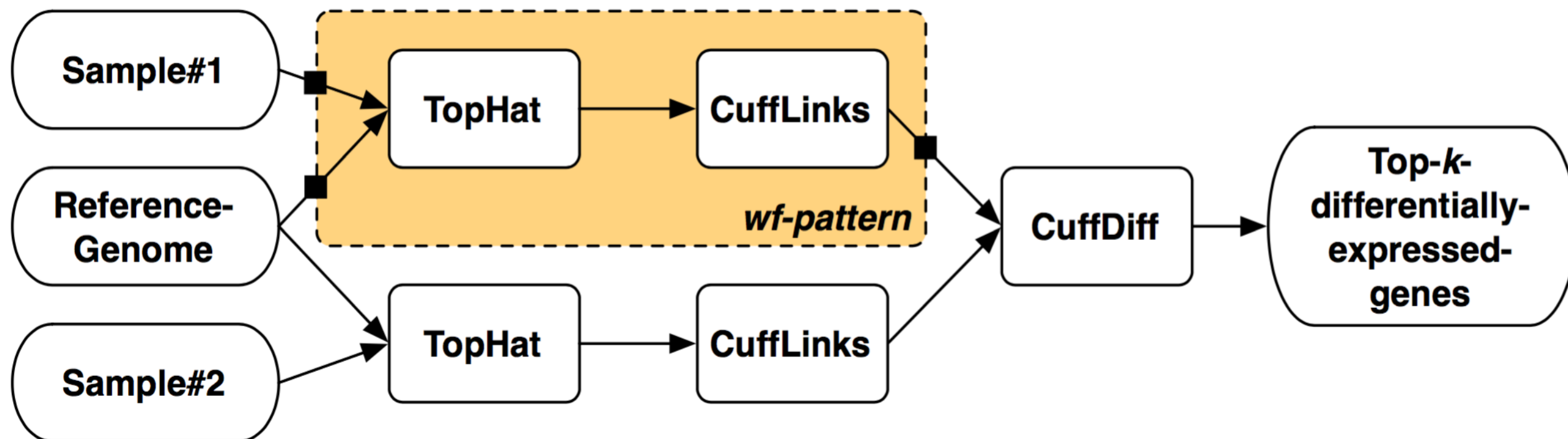


Still open issues ...



**Reuse** instead of  
**re-execution** ?

# RNA-seq data analysis workflow



<i>TopHat</i>	1 sample	300 samples
Input data	2 x 17 Gb	10.2 Tb
1-core CPU	170 hours	5.9 years
32-cores CPU	32 hours	14 months
Output data	12 Gb	3.6 Tb

**Compute and storage intensive**

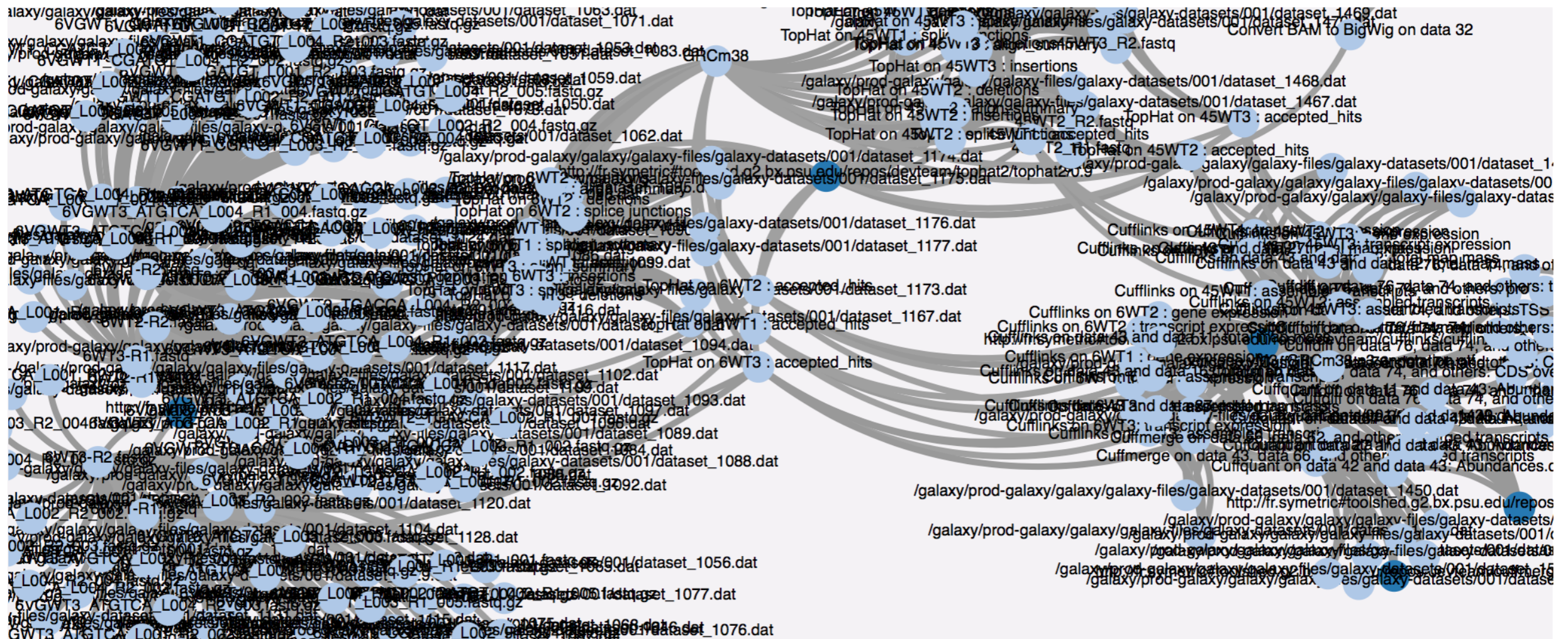
**Avoid duplicated storage / computing**

# Is provenance enough for reuse ?

**Too fine-grained**  
**No domain concepts**

```
11 a prov:Bundle, prov:Entity;  
12 prov:wasAttributedTo <#galaxy2prov>;  
13 prov:generatedAtTime "2016-04-14T18:18:37.000409"^^xsd:dateTime;  
14 .  
15  
16 <#72486b583fe152f0>  
17 a prov:Activity ;  
18 prov:wasAssociatedWith <#cat1> ;  
19 prov:startedAtTime "2015-12-15T12:54:50.749845"^^xsd:dateTime;  
20 prov:endedAtTime "2015-12-15T12:55:57.016799"^^xsd:dateTime;
```

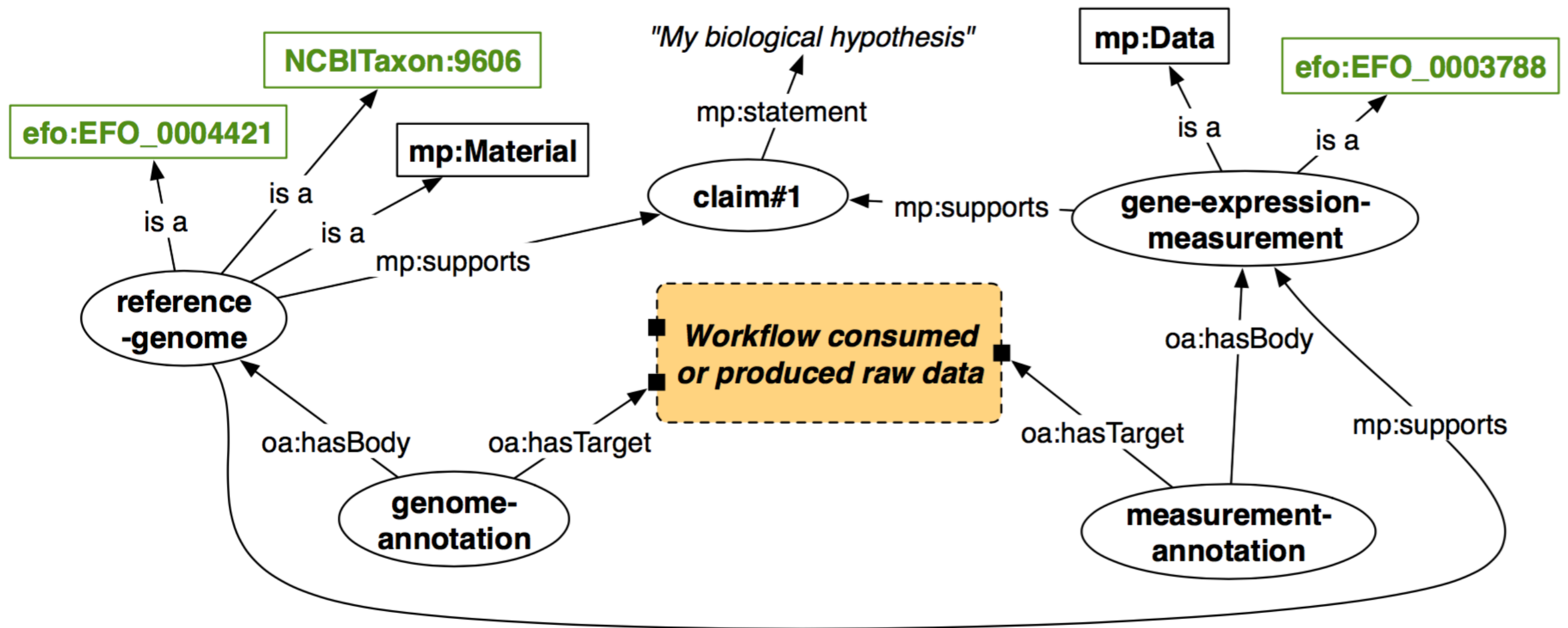
Visualise





# Human & machine-tractable report needed !

Annotated paper's "**Material & Methods**" with links to **some** workflow artifacts (algorithms, data).



# Problem statement & objectives

## Problem statement

Scientific workflows produce massive raw results. Their publication into curated query-able linked data repositories requires lot of time and expertise.

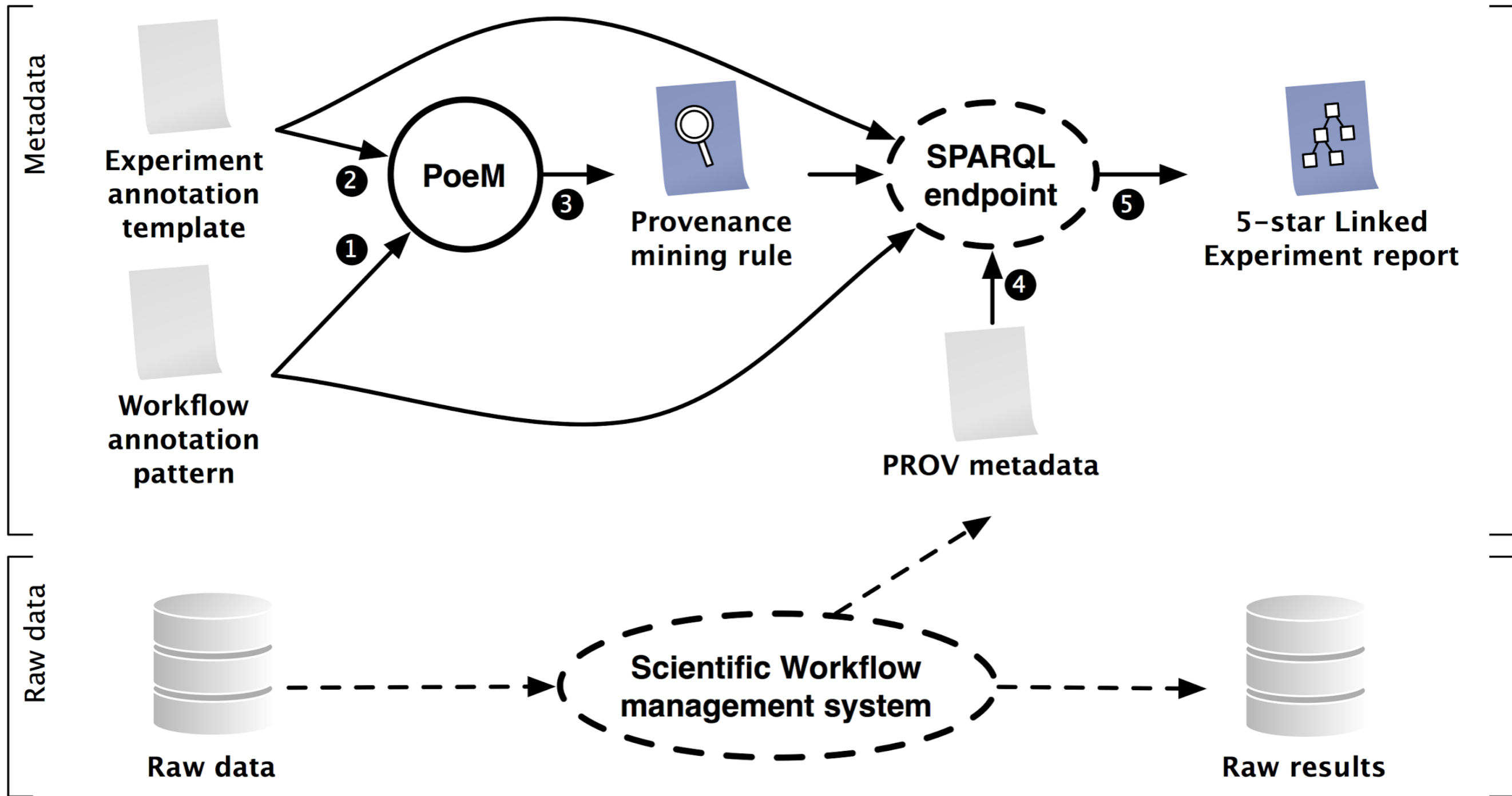
**Can we exploit provenance traces to ease the publication of scientific results as Linked Data ?**

## Objectives

(1) Leverage annotated workflow patterns to generate **provenance mining rules**.

(2) Refine provenance traces into **linked experiment reports**.

# Approach



# PoeM: generating Provenance Mining rules ③

**Input** :  $W$  : Workflow annotated pattern ①,  
 $S_1$  : First step of  $W$ ,  
 $S_2$  : Last step of  $W$ ,  
 $A$  : Annotation template ②.

**Output:** *Rule*: Provenance mining rule.

1 **begin**

2  $IN_{S_1} \leftarrow getInputs(S_1)$

3  $OUT_{S_2} \leftarrow getOutputs(S_2)$

4

5  $provGraph \leftarrow genDataLineage(OUT_{S_2}, IN_{S_1})$

6  $reportGraph \leftarrow bindReportTargets(provGraph, A)$

7

8  $Rule \leftarrow \frac{provGraph.edge_1 \wedge \dots \wedge provGraph.edge_N}{reportGraph}$

SPARQL Property path  
SPARQL Basic graph pattern  
SPARQL Construct query

# Demo

poem.univ-nantes.fr

## PoeM: Provenance Mining for scientific linked data publishing

Contact : Alban Gaignard, Hala Skaf, Audrey Bihouee, {firstname.lastname}@univ-nantes.fr.

[For demonstration purpose only.](#)

This web page illustrates our semi-automated **approach** for mining provenance traces and assembling linked experiment reports. PoeM generates Semantic Web rules from (i) annotated workflow patterns, (ii) domain-specific annotations, and (iii) provenance traces of a workflow run. The rules finally match provenance subgraphs and produce linked experiment reports.

We illustrate our approach in the context of an RNAseq bioinformatics **workflow**.

This work reuses existing linked open vocabularies, namely [PROV-O](#), [P-PLAN](#), [Micropublications Ontology](#), [Experimental Factors Ontology](#), and [EDAM](#).

This demo is supported by the [Corese](#) Semantic Web factory, [Apache Jena](#), [D3.js](#), [Codemirror.js](#) and [Twitter Bootstrap](#).

Show input annotations

Show provenance trace

Show generated rule

Show resulting report

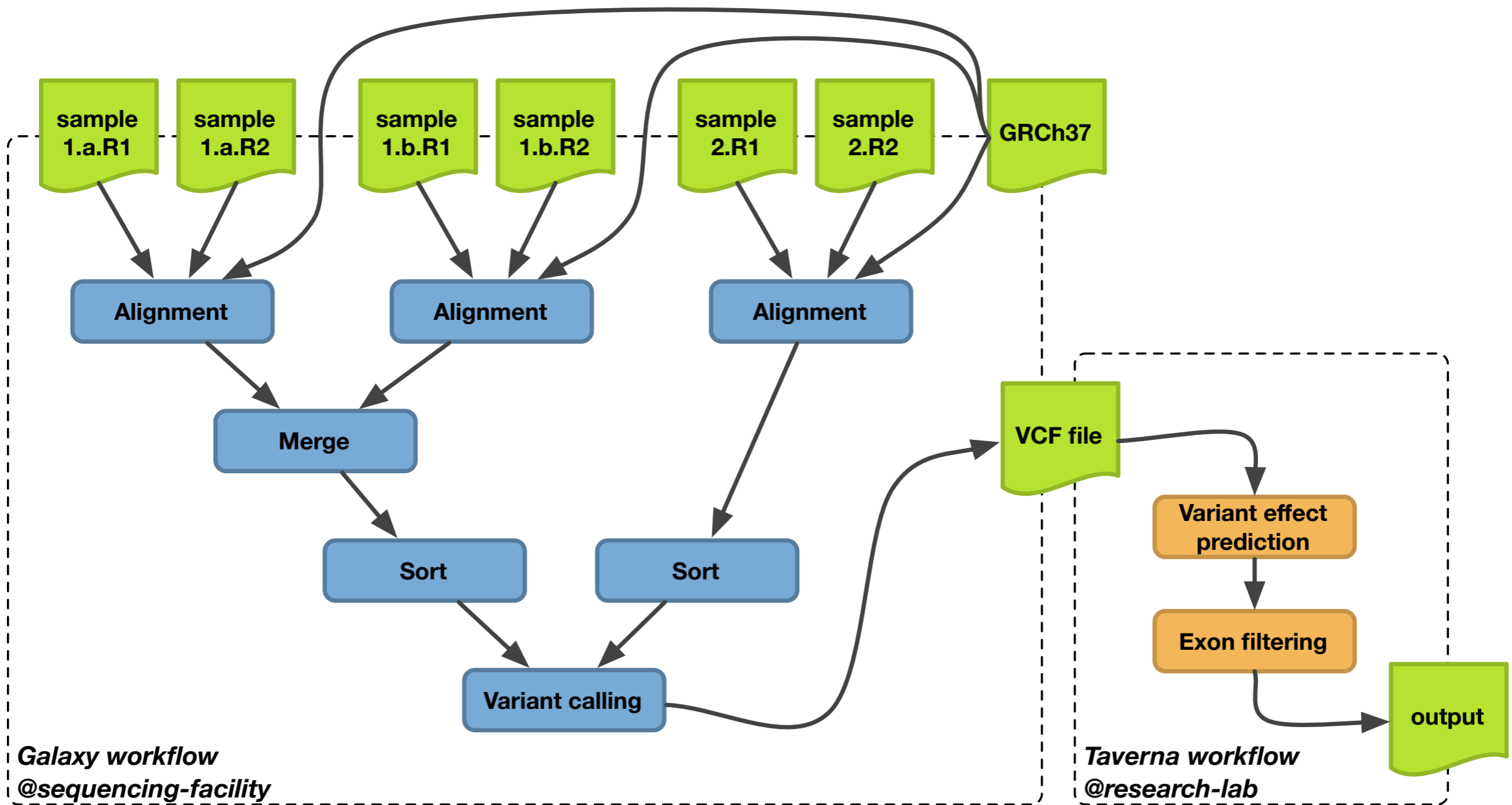
## Resulting linked experiment report

```
1 @prefix void: <http://rdfs.org/ns/void#> .
2 @prefix mp: <http://purl.org/mp/> .
3 @prefix edam: <http://edamontology.org/> .
4 @prefix sym: <http://fr.symetric/vocab#> .
5 @prefix xsd: <http://www.w3.org/2001/XMLSchema#> .
6 @prefix rdfs: <http://www.w3.org/2000/01/rdf-schema#> .
7 @prefix p-plan: <http://purl.org/net/p-plan#> .
8 @prefix efo: <http://www.ebi.ac.uk/efo/> .
9 @prefix ncbitaxon: <http://purl.org/obo/owl/NCBITaxon> .
10 @prefix oa: <http://www.w3.org/ns/oa#> .
```



Provenance  
in **multi-site** studies ?

Multi-site studies → ≠ workflow engines !



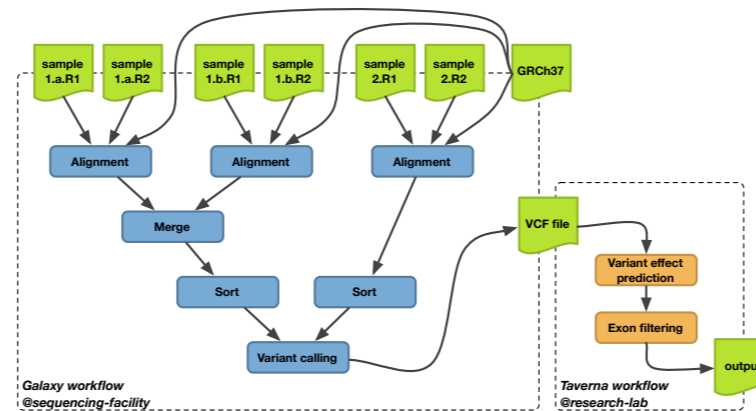
Galaxy workflow  
@sequencing-facility

Taverna workflow  
@research-lab



Scattered provenance capture ?

# Provenance issues



« Which alignment algorithm was used when predicting these effects ? »

« A new version of a reference genome is available, which genome was used when predicting these phenotypes ? »

**Need for an overall tracking of provenance over both Galaxy and Taverna workflows !**

# Provenance « heterogeneity »

---

Galaxy PROV predicates	counts
prov:wasDerivedFrom	118
rdf:type	76
rdfs:label	62
prov:used	61
prov:wasAttributedTo	34
prov:wasGeneratedBy	33
prov:endedAtTime	26
prov:startedAtTime	26
prov:wasAssociatedWith	26
prov:generatedAtTime	1

---

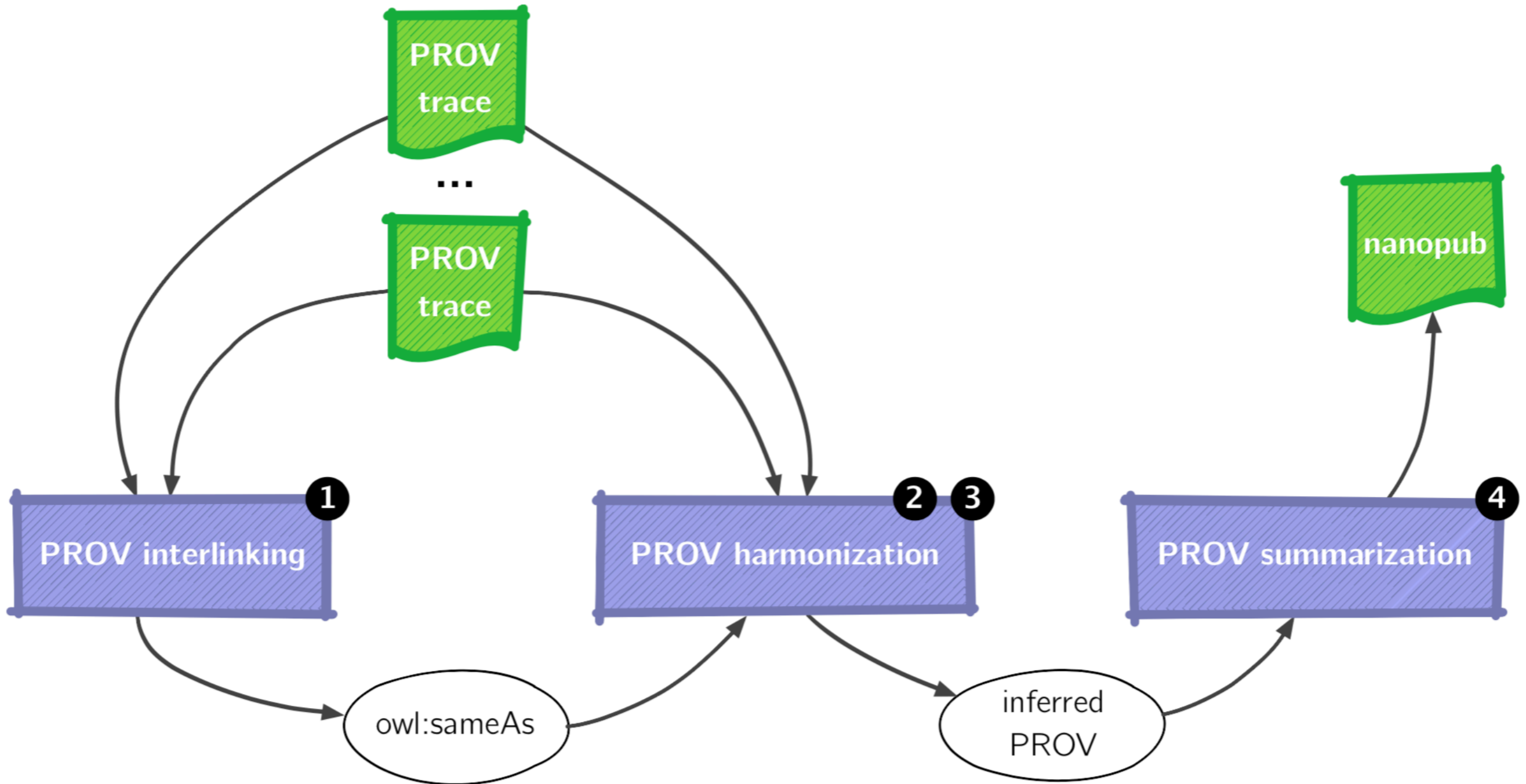
---

Taverna PROV predicates	counts
rdf:type	54
rdfs:label	13
prov:atTime	8
wfprov:describedByParameter	6
rdfs:comment	6
prov:hadRole	6
prov:activity	5
dcterms:hasPart	4
prov:agent	4
prov:endedAtTime	4
prov:hadPlan	4
prov:qualifiedAssociation	4
prov:qualifiedEnd	4
prov:qualifiedStart	4
prov:startedAtTime	4
prov:wasAssociatedWith	4
tavernaprov:content	3
wfprov:usedInput	3
wfprov:wasEnactedBy	3
wfprov:wasOutputFrom	3

---

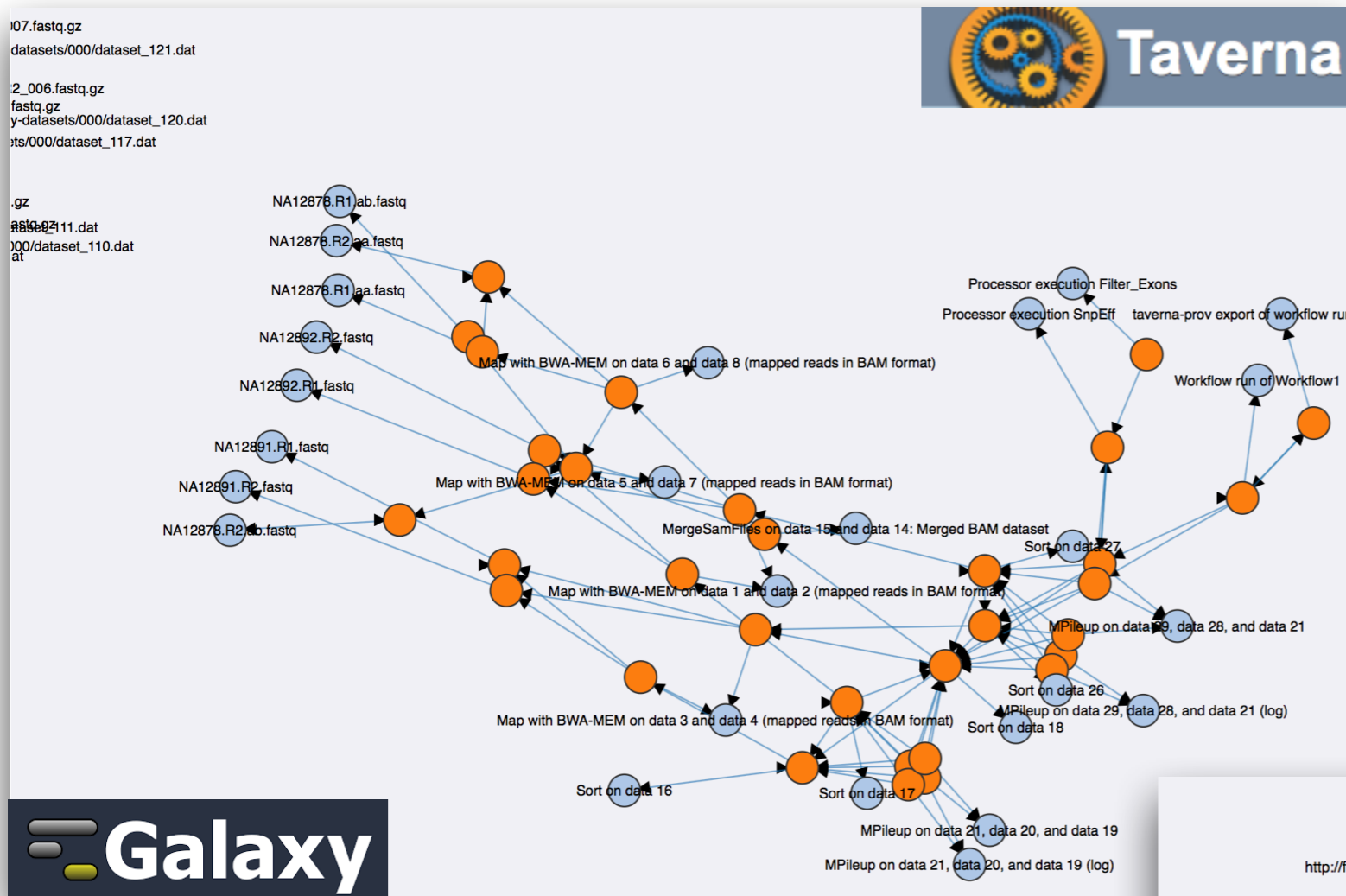
**How to reconcile these provenance traces ?**

# Approach



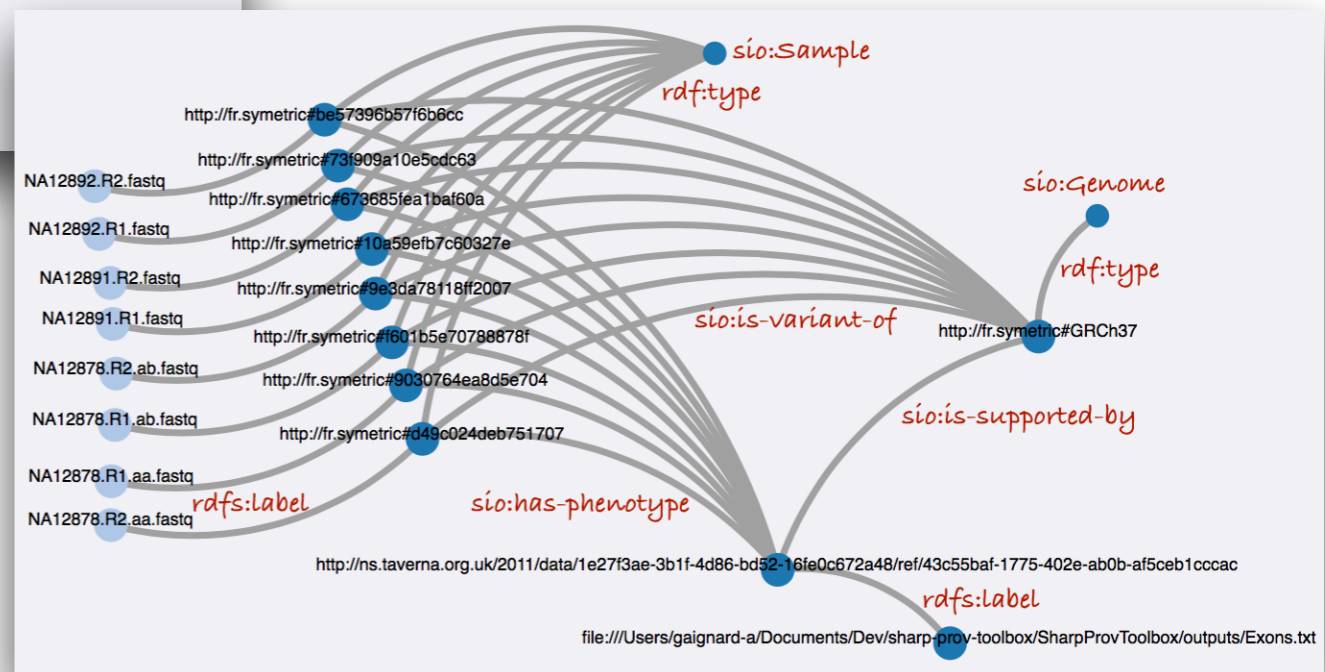


# Results



Linked experiment report with Nanopublication, domain-specific concepts

Reconciled provenance as an « influence graph »



# Summary

# Take home message & perspectives

- **Scientific Workflows** → automation, abstraction, provenance
- Standards for **provenance representation** and **reasoning**
- Better handle **multi-site studies** (ESWC'17 satellite event paper)
- Linked experiment reports = **contextualized** and **summarized** provenance (TaPP'16 paper)
- Distributed data analysis → **Distributed provenance, reasoning** ?
- **Learning patterns** in provenance graphs ?
- **Predicting domain-specific annotation** for workflow results ?  
What about trust ?

# Acknowledgments



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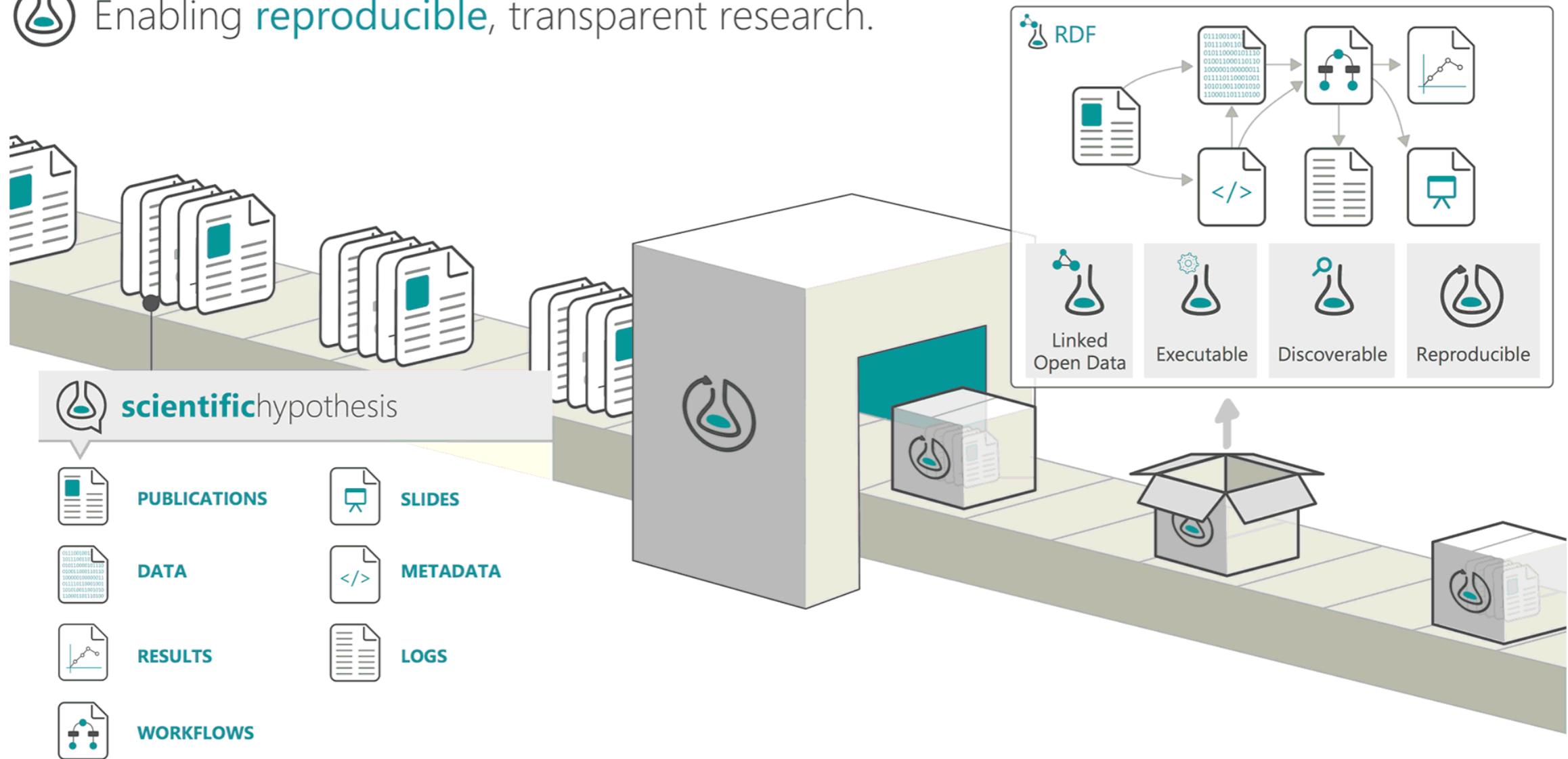
GDR  **MadICS**  
action **ReproVirtuFlow**

Backup slides



# Research Objects

 Enabling **reproducible**, transparent research.



Sean Bechhofer, Iain Buchan, David De Roure, Paolo Missier, John Ainsworth, Jiten Bhagat, Phillip Couch, Don Cruickshank, Mark Delderfield, Ian Dunlop, Matthew Gamble, Danus Michaelides, Stuart Owen, David Newman, Shoaib Sufi, Carole Goble (2013) **Why Linked Data is Not Enough for Scientists**, *Future Generation Computer Systems* **29**(2), February 2013, Pages 599-611, ISSN 0167-739X, <https://doi.org/10.1016/j.future.2011.08.004>

Khalid Belhajjame, Jun Zhao, Daniel Garijo, Matthew Gamble, Kristina Hettne, Raul Palma, Eleni Mina, Oscar Corcho, José Manuel Gómez-Pérez, Sean Bechhofer, Graham Klyne, Carole Goble (2015) **Using a suite of ontologies for preserving workflow-centric research objects**, *Web Semantics: Science, Services and Agents on the World Wide Web*, <https://doi.org/10.1016/j.websem.2015.01.003>

schema.org Action

# Action

Canonical URL: <http://schema.org/Action>

## [Thing](#) > [Action](#)

An action performed by a direct agent and indirect participants upon a direct object. Optionally happens at a location with the help of an inanimate instrument. The execution of the action may produce a result. Specific action sub-type documentation specifies the exact expectation of each argument/role.

See also [blog post](#) and [Actions overview document](#).

Usage: Between 100 and 1000 domains

[\[more...\]](#)

Property	Expected Type	Description
<b>Properties from <a href="#">Action</a></b>		
<a href="#">actionStatus</a>	<a href="#">ActionStatusType</a>	Indicates the current disposition of the Action.
<a href="#">agent</a>	<a href="#">Organization</a> or <a href="#">Person</a>	The direct performer or driver of the action (animate or inanimate). e.g. <i>John</i> wrote a book.
<a href="#">endTime</a>	<a href="#">DateTime</a>	The endTime of something. For a reserved event or service (e.g. FoodEstablishmentReservation), the time that it is expected to end. For actions that span a period of time, when the action was performed. e.g. John wrote a book from January to <i>December</i> .  Note that Event uses startDate/endDate instead of startTime/endTime, even when describing dates with times. This situation may be clarified in future revisions.

<u><b>error</b></u>	<u>Thing</u>	For failed actions, more information on the cause of the failure.
<u><b>instrument</b></u>	<u>Thing</u>	The object that helped the agent perform the action. e.g. John wrote a book with <i>a pen</i> .
<u><b>location</b></u>	<u>Place</u> or <u>PostalAddress</u> or <u>Text</u>	The location of for example where the event is happening, an organization is located, or where an action takes place.
<u><b>object</b></u>	<u>Thing</u>	The object upon which the action is carried out, whose state is kept intact or changed. Also known as the semantic roles patient, affected or undergoer (which change their state) or theme (which doesn't). e.g. John read <i>a book</i> .
<u><b>participant</b></u>	<u>Organization</u> or <u>Person</u>	Other co-agents that participated in the action indirectly. e.g. John wrote a book with <i>Steve</i> .
<u><b>result</b></u>	<u>Thing</u>	The result produced in the action. e.g. John wrote <i>a book</i> .
<u><b>startTime</b></u>	<u>DateTime</u>	The startTime of something. For a reserved event or service (e.g. FoodEstablishmentReservation), the time that it is expected to start. For actions that span a period of time, when the action was performed. e.g. John wrote a book from <i>January</i> to December.  Note that Event uses startDate/endDate instead of startTime/endTime, even when describing dates with times. This situation may be clarified in future revisions.
<u><b>target</b></u>	<u>EntryPoint</u>	Indicates a target EntryPoint for an Action.