

Provenance and DataONE: Facilitating Reproducible Science

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NCEAS

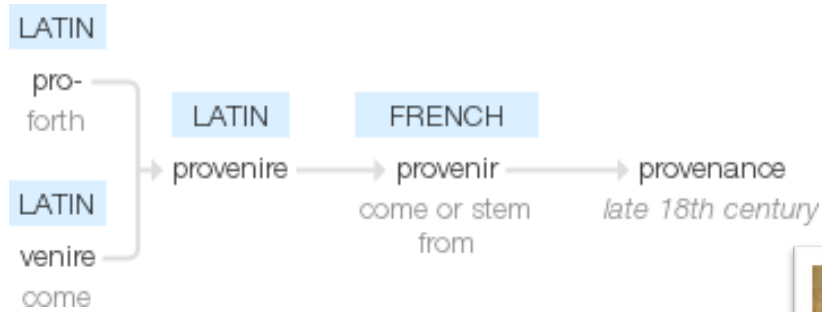
Outline

1. **Overview** on Provenance (*Bertram*)
2. **Searching and Navigating** Provenance (*Lauren*)
3. **Further Details**, “*look behind the scenes*” (*Chris*)

Acknowledgments & special thanks to:

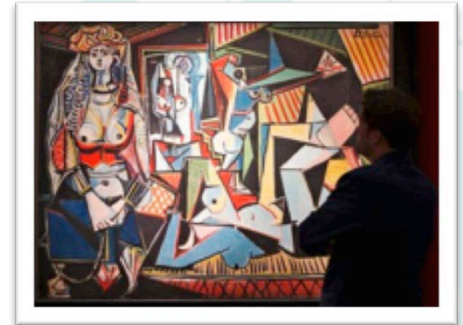
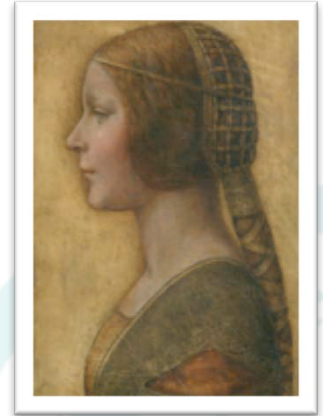
- NSF, DataONE CI Team, WG members (Phases I & II), others contributors (YW)

Provenance



1. The place of **origin** or **earliest known history** of something
2. The **beginning** of something's existence
3. A **record of ownership** of a work of art or an antique, used as a guide to **authenticity** or **quality**

Related terms: lineage, genealogy, pedigree, ...



Computational Provenance

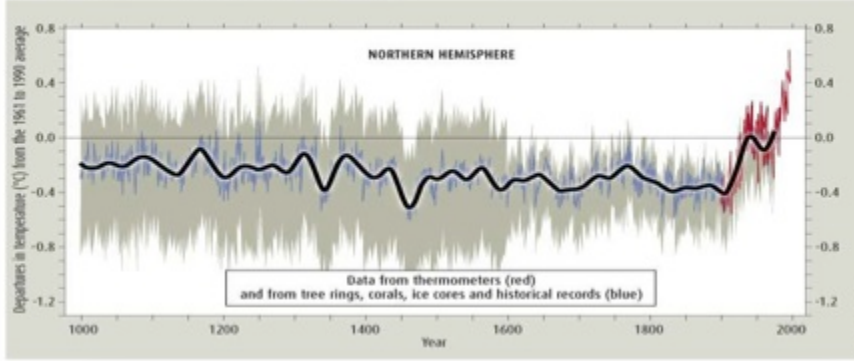
- **Origin and processing history** of an artifact
- usually: data products, figures, ...
- sometimes: workflow & script evolution ...
- **Provenance sightings:**
 - Data science, eScience, CI, Big Data, computational science, 4th paradigm ...
 - Bio(diversity)informatics, ecoinformatics, geoinformatics, ..
 - Computer science, library & information science, ...
 - Scientific workflows & scripts ...
 - Databases, programming languages, ...
 - Privacy vs. provenance, ...



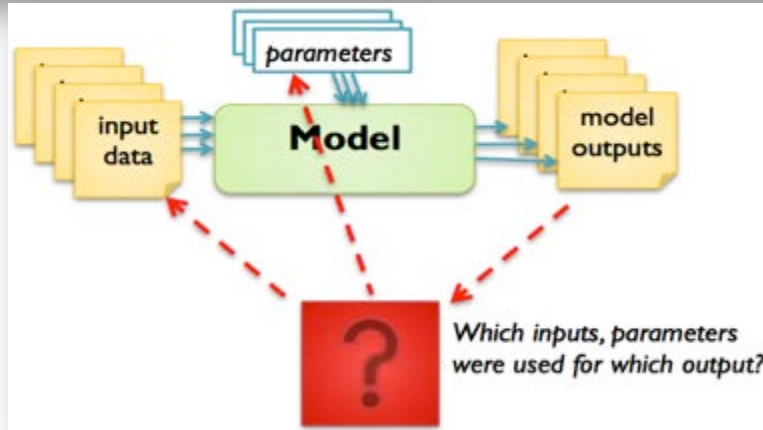
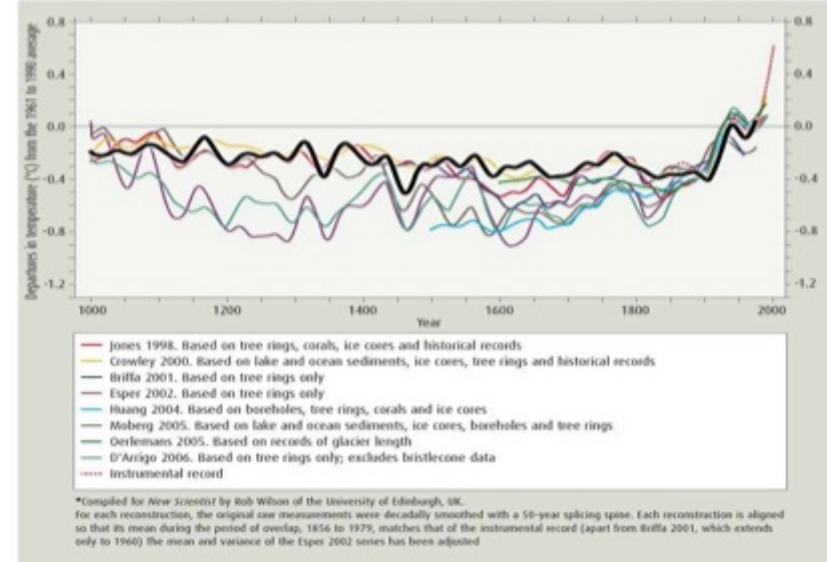
Reproducible Science

THE HOCKEY STICK: THE ORIGINAL AND LATER VERSIONS

The 2001 IPCC version: "Variations of the Earth's surface temperature over the past 1000 years"
The error bars (in grey) show the 95 per cent confidence range



The IPCC version compared with some other northern hemisphere temperature reconstructions*



Capturing **provenance** is crucial for **transparency**, **interpretation**, **debugging**, ...
=> *repeatable experiments*,
=> *reproducible science*

Scientific Workflows: ASAP!

Automation

wfs to **automate** computational aspects of science

Scaling (exploit and optimize *machine cycles*)

wfs should make use of **parallel compute resources**

wfs should be able handle **large data**

Abstraction, Evolution, Reuse (*human cycles*)

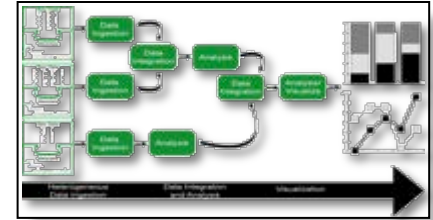
wfs should be easy to (re-)use, evolve, share

Provenance

wfs should capture **processing history, data lineage**

=> traceable data- and wf-evolution

=> **Reproducible Science**



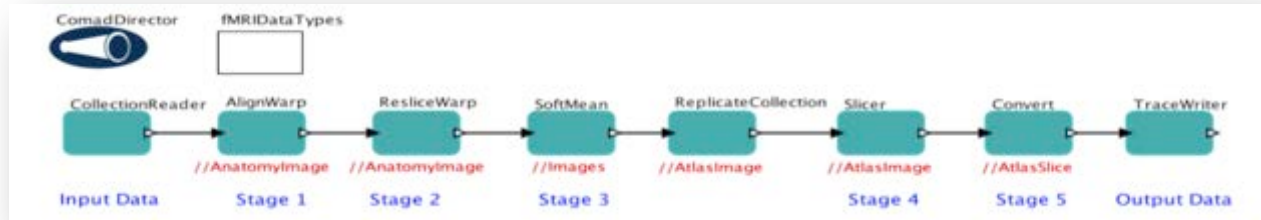
Common Uses of Provenance in Science

- **Audit trail:** trace data generation and possible errors
- **Attribution:** determine ownership and responsibility for data and scientific results
- **Data quality:** from quality of input data, computations
- **Discovery:** enable searching of data, methodologies and experiments
- **Replication:** facilitate repeatable derivation of data to maintain currency

⇒ **Reproducible Science**

Kinds of Provenance

- **Prospective Provenance**
- method/workflow description (“*workflow-land*”)

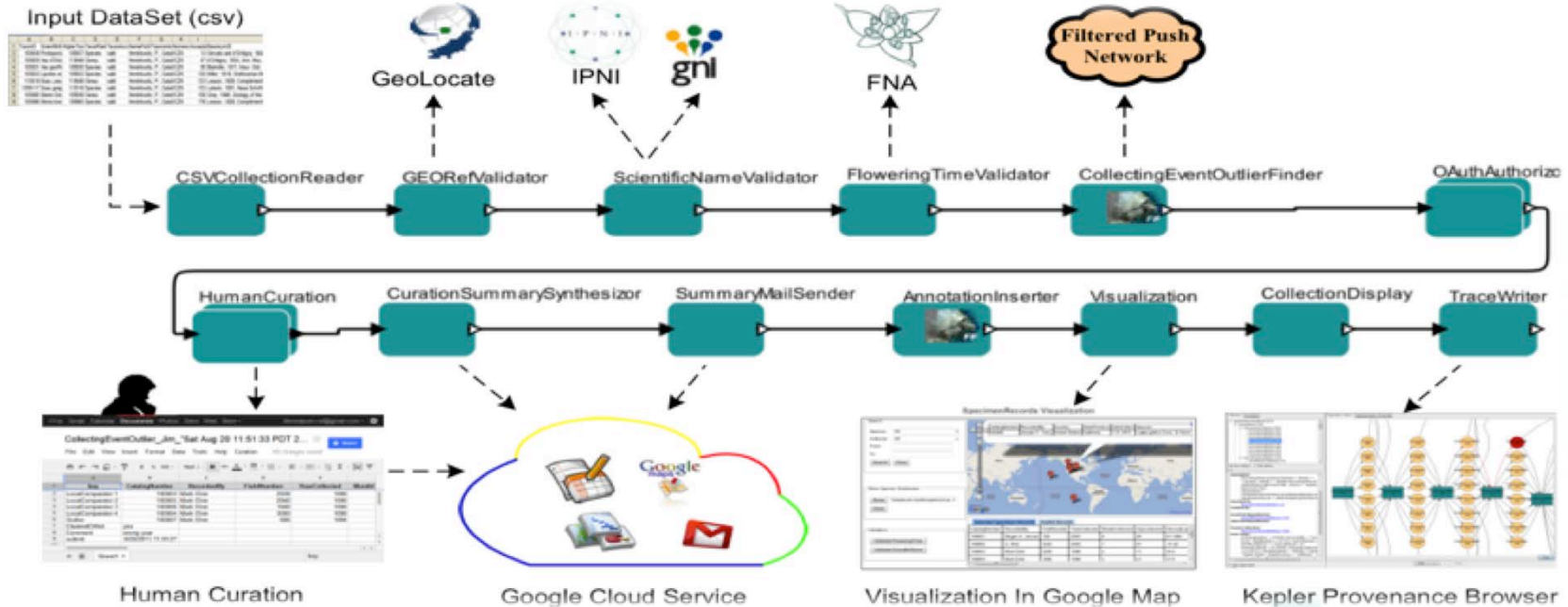


- **Retrospective Provenance**
- runtime provenance tracking (“*trace-land*”)
- Q: Which one is more important?



Prospective Provenance

(A Data Curation Workflow: FilteredPush)



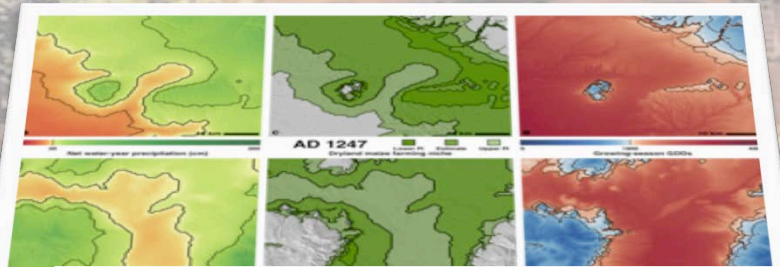
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SKOPE: Synthesized Knowledge Of Past Environments

Bocinsky, Kohler *et al.* study rain-fed maize of **Anasazi**

Four Corners; AD 600–1500. **Climate change** influenced **Mesa Verde Migrations**; late 13th century AD. Uses **network of tree-ring chronologies to reconstruct a spatio-temporal climate** field at a fairly high resolution (~800 m) from AD 1–2000. Algorithm estimates joint information in tree-rings and a climate signal to identify “best” tree-ring chronologies for climate reconstructing.

K. Bocinsky, T. Kohler, A 2000-year reconstruction of the rain-fed maize agricultural niche in the US Southwest. *Nature Communications*. doi:10.1038/ncomms6618



```
203 ## Gene Ontology Statistics are Calculated Here.
204
205 # Gene Ontology Categories that were shown to be relatively Higher (more expressed) in the Experimental Condition.
206 gostatshigher <- higheridrlinkedtogenes[1]
207 higherstatsfilename <- paste(outputDirectory, "/", runName, "_", conditions[1], "_GOStatsHigher_", mytestcond[1], "_v
208 write.table(gostatshigher, file=higherstatsfilename, row.names=FALSE, col.names=FALSE, quote=FALSE, sep="\t")
209 geneListHigherCHR <- gostatshigher$SYMBOL
210 geneListHigherLinkedtoEntrezIds <- select(hgu133plus2.db, keys= geneListHigherCHR, "ENTREZID", "SYMBOL")
211 GOstatsGenesH <- geneListHigherLinkedtoEntrezIds[,2]
212
213 x <- org.Hs.egACCNUM
214 mapped_genes <- mappedkeys(x)
215 xx <- as.list(x[mapped_genes])
216 geneUniverse <- (unique(names(xx)))
```

... implemented as an R Script ...

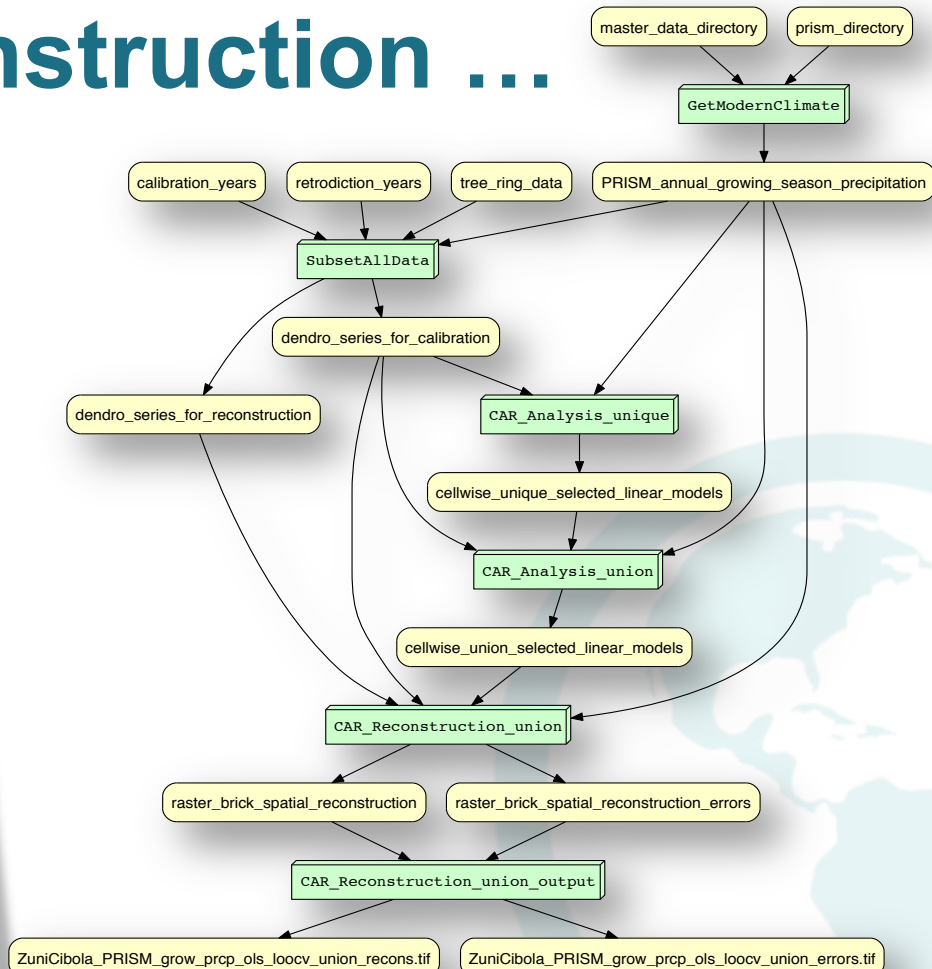
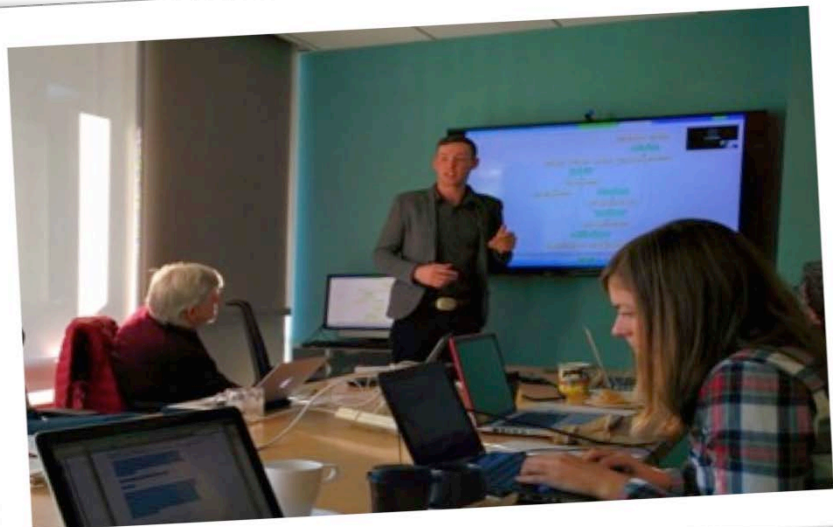
Paleoclimate Reconstruction ...

... explained using YesWorkflow

<https://github.com/yesworkflow-org/>

Kyle B., (computational) archeologist:

"It took me about 20 minutes to comment. Less than an hour to learn and YW-annotate, all-told."



User Comments: YW Annotations

```
188 ## @begin GO_Analysis
189 # @in hgCutoff @as GO_stats_p_value_cutoff
190 # @in higheridrlinkedtogenes @as DEG_list_higher_in_test_condition
191 # @in loweridrlinkedtogenes @as DEG_list_lower_in_test_condition
192 # @out gostatshigher @as GO_stats_gene_list_higher_in_test_condition
193 # @out BP_SummH_File @as GO_stats_BP_higher_in_test_condition
194 # @out CC_SummH_File @as GO_stats_CC_higher_in_test_condition
195 # @out MF_SummH_File @as GO_stats_MF_higher_in_test_condition
196 # @out gostatslower @as GO_stats_gene_list_lower_in_test_condition
197 # @out BP_SummL_File @as GO_stats_BP_lower_in_test_condition
198 # @out CC_SummL_File @as GO_stats_CC_lower_in_test_condition
199 # @out MF_SummL_File @as GO_stats_MF_lower_in_test_condition
200
201 ##### Begin GOStats Block #####
202
203 ## Gene Ontology Statistics are Calculated Here.
204
205 # Gene Ontology Categories that were shown to be relatively Higher (more expressed) in the Experimental Condition.
206 gostatshigher <- higheridrlinkedtogenes[1]
207 higherstatsfilename <- paste(outputDirectory, "/", runName, "_", conditions[1], "_GOStatsHigher_", mytestcond[1], "_vs_", baseline, ".")
208 write.table(gostatshigher, file=higherstatsfilename, row.names=FALSE, col.names=FALSE, quote=FALSE, sep="\t")
209 geneListHigherCHR <- gostatshigher$SYMBOL
210 geneListHigherLinkedtoEntrezIds <- select(hgu133plus2.db, keys= geneListHigherCHR, "ENTREZID", "SYMBOL")
211 GOstatsGenesH <- geneListHigherLinkedtoEntrezIds[,2]
212
213 x <- org.Hs.egACCNUM
214 mapped_genes <- mappedkeys(x)
215 xx <- as.list(x[mapped_genes])
216 geneUniverse <- (unique(names(xx)))
...

```

@begin GO_Analysis

@in hgCutoff

@in ...

@out BP_Summ1_file

@out ...

@end GO_Analysis

Multi-Scale Synthesis and Terrestrial Model Intercomparison Project (MsTMIP)

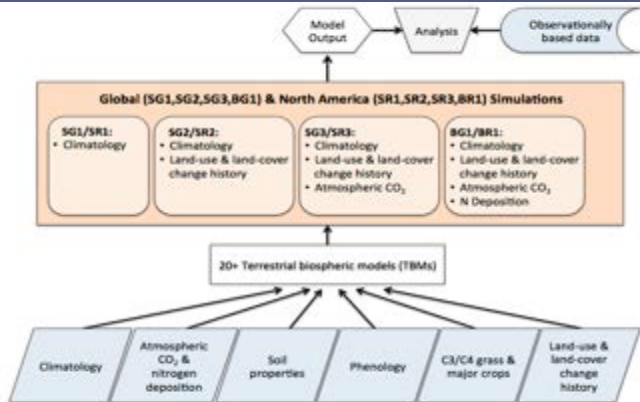


Fig. 1. Schematic of the Multi-Scale Synthesis and Terrestrial Model Intercomparison Project (MsTMIP) framework. Global simulations (SG1,SG2, SG3,BG1) are run at 0.5° by 0.5° resolution; North American simulations (SR1, SR2, SR3, BR1) are run at 0.25° by 0.25° resolution.

The North American Carbon Program Multi-Scale Synthesis and Terrestrial Model Intercomparison Project

D. N. Huntzinger¹, C. Schwalm², A. M. Michalak³, K. Schaefer^{4,5}, A. W. King⁶, Y. Wei⁶, A. Jacobson^{4,7}, S. Liu⁶, R. B. Cook⁶, W. M. Post⁶, G. Berthier⁸, D. Hayes⁶, M. Huang⁹, A. Ito¹⁰, H. Lei^{11,12}, C. Lu¹³, J. Mao⁶, C. H. Peng^{14,15}, S. Peng⁸, B. Poulter⁸, D. Ricciuto⁶, X. Shi⁶, H. Tian¹³, W. Wang¹⁶, N. Zeng¹⁷, F. Zhao¹⁷, and Q. Zhu¹⁵

Provenance

- Externally facing
- Internally facing

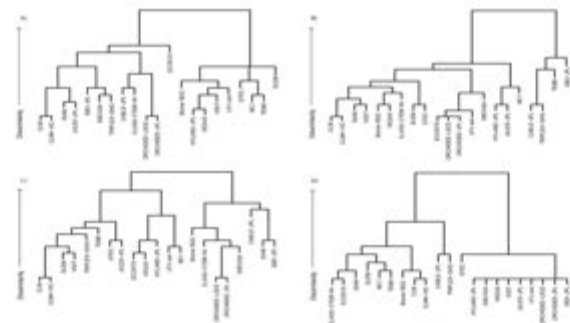
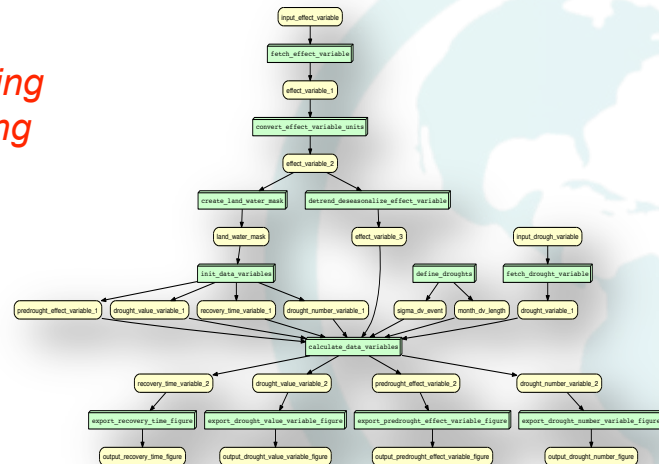
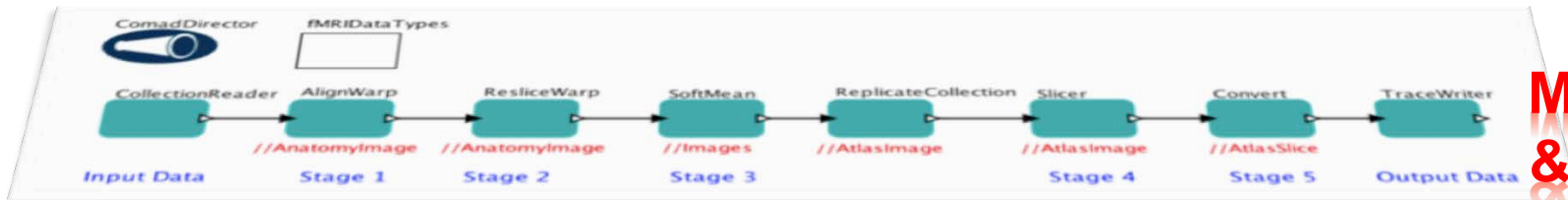


Fig. 3. Dendrogram showing general differences/similarities in how MsTMIP models formulate and parameterize (A) energy, (B) carbon, (C) vegetation, and (D) nitrogen process dynamics. Clusters are determined by Hamming distance. Models in the same "tree" share similar structural model characteristics. For example, models in the "tree" to the left (e.g., ISAM, CABLE-JPL, ORCHIDEE-JPL/LSCCE) in (A) simulate ground heat flux and energy loss storage, while models in the "tree" to the right (e.g., MC1, TEM5, VICIAS) do not. A majority of models separate live carbon into various pools (with exception of 50k-JPL), but they do so in various ways (e.g., left "tree" in (B)). Refer to the Supplement for the binary data used to create this diagram.



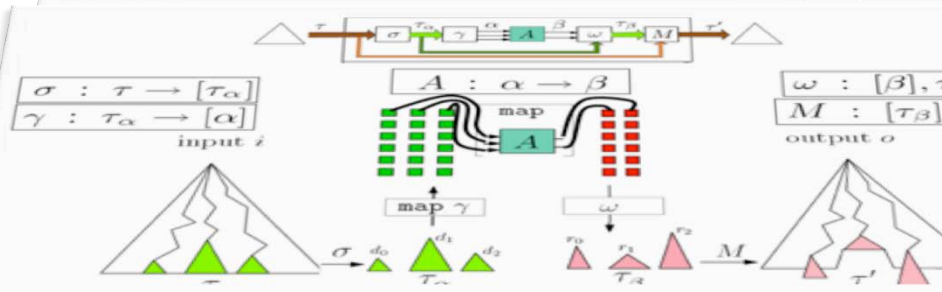
Scientific Workflow Research



Modeling & Design

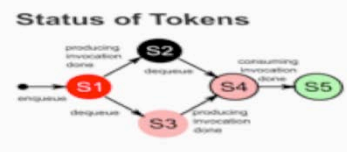
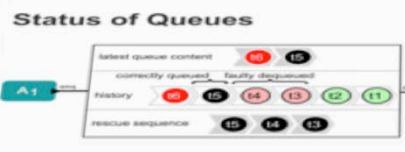
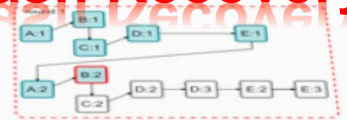
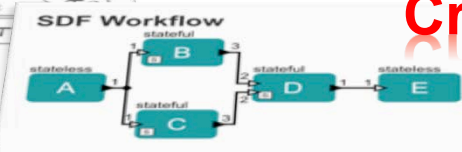


Provenance



Parallel Execution

Fault-Tolerance, Crash Recovery



Wait, there is more ...

<https://goo.gl/53OCdW>

- **Fine-grained vs coarse-grained** provenance
- **Black-box vs white-box** provenance

- **Standards:**
- OPM → PROV
- D-OPM → ProvONE

- **Database Community:**
- why-, where-, how-, why-not provenance
- links to causality
- ... logical derivations, proofs, ...



Live Demonstration



Facilitate reproducible science

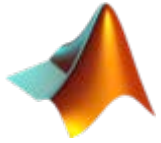
- Creating and managing provenance information
- Communicating script and model workflows
- Storing and sharing
- Using provenance information for search



Creating and managing provenance information



Investigator tools (ITK)



Matlab DataONE Toolbox



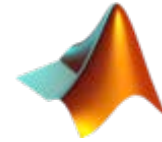
Recordr R Library



Java YesWorkflow Tool



Functions being added



<code>record()</code>
<code>startRecord()</code>
<code>endRecord()</code>
<code>listRuns()</code>
<code>deleteRuns()</code>
<code>viewRun()</code>
<code>publish()</code>

<code>set()</code>
<code>get()</code>
<code>saveConfig()</code>
<code>loadConfig()</code>
<code>listConfig()</code>

See: [Run Manager API](#) document



Example: R programming

```
1 # Generate map of locations by type
2 library(recordr)
3 recordr <- new("Recordr")
4 pkg <- record(recordr, "./hcdbSites.R", "locations-by-type-png")
```



R: managing script runs



> **listRuns (recordr)**

Script	StartTime	EndTime	PublishedTime	Tag	RunID
hcdbSites.R C85A ...	2015-05-07T18:53:09Z	2015-05-07T18:53:09Z	unpublished	locations-by-type-png	

> **deleteRuns (recordr, "locations-by-type-png")**

C85A188-B72E-49F1-AEF4-7BFC24DA186B

> **viewRun (recordr, "locations-by-type-png")**

... details about the run listed here ...

> **publishRun (recordr, "locations-by-type-png")**

C85A188-B72E-49F1-AEF4-7BFC24DA186B



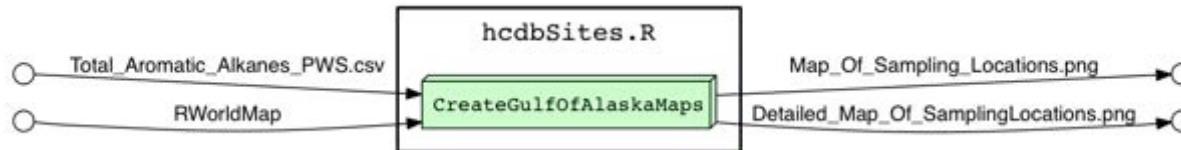
Communicating workflow provenance



YesWorkflow tool



```
1 # @begin CreateGulfOfAlaskaMaps
2 # @in hcdb @as Total_Aromatic_Alkanes_PWS.csv
3 # @in world @as RWorldMap
4 # @out map @as Map_Of_Sampling_Locations.png
5 # @out detailMap @as Detailed_Map_Of_SamplingLocations.png
... mapping code is here ...
25 # @end CreateGulfOfAlaskaMaps
```

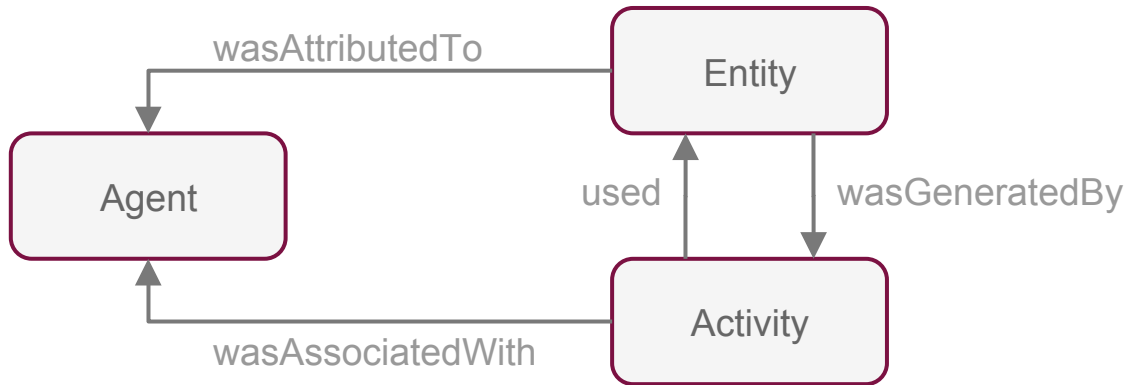


Storing and sharing provenance information



Using a common model

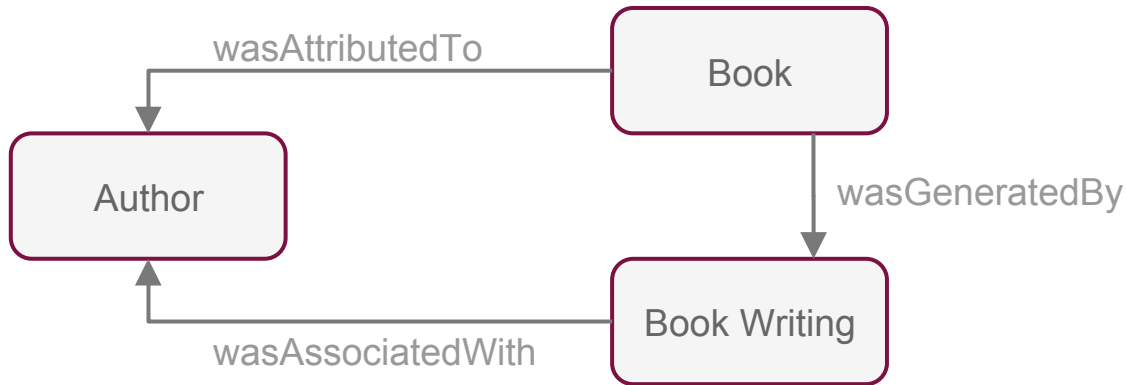
W3C has published the 'PROV' family of recommendations



See w3.org/TR/prov-o/

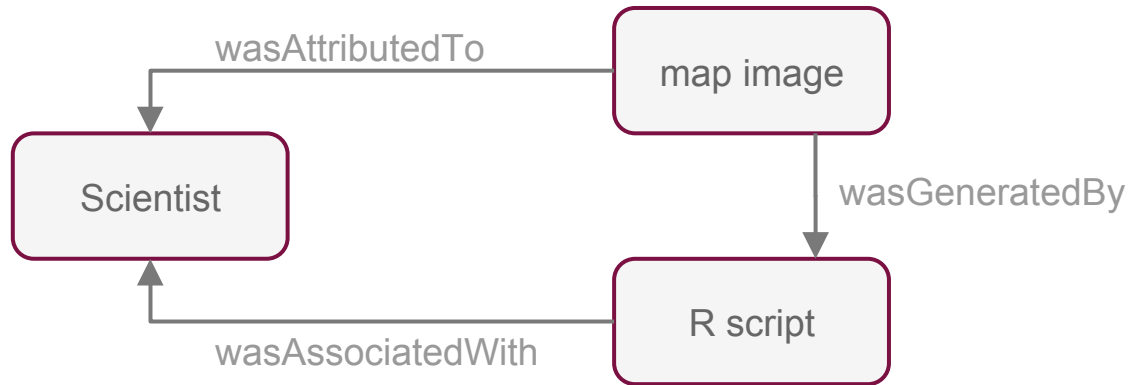
Using a common model

Example: Book writing activity



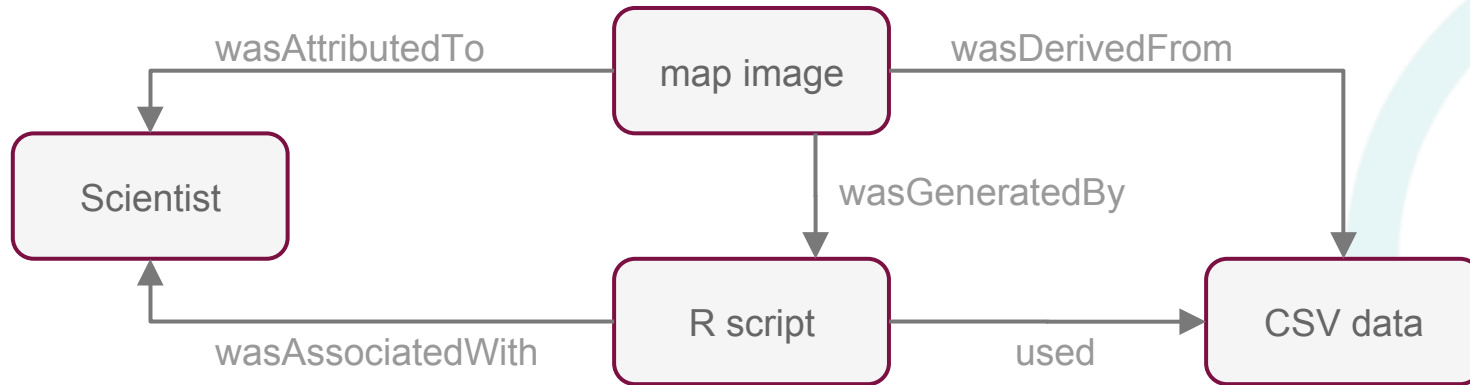
Using a common model

Example: Scientific workflow



Using a common model

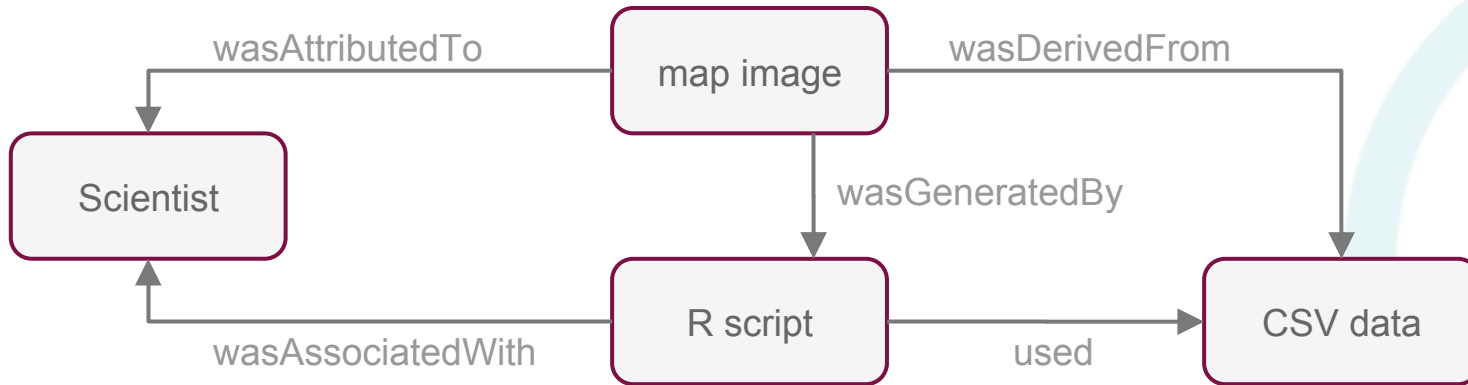
Example: Scientific workflow



Using a common model

Example: Scientific workflow

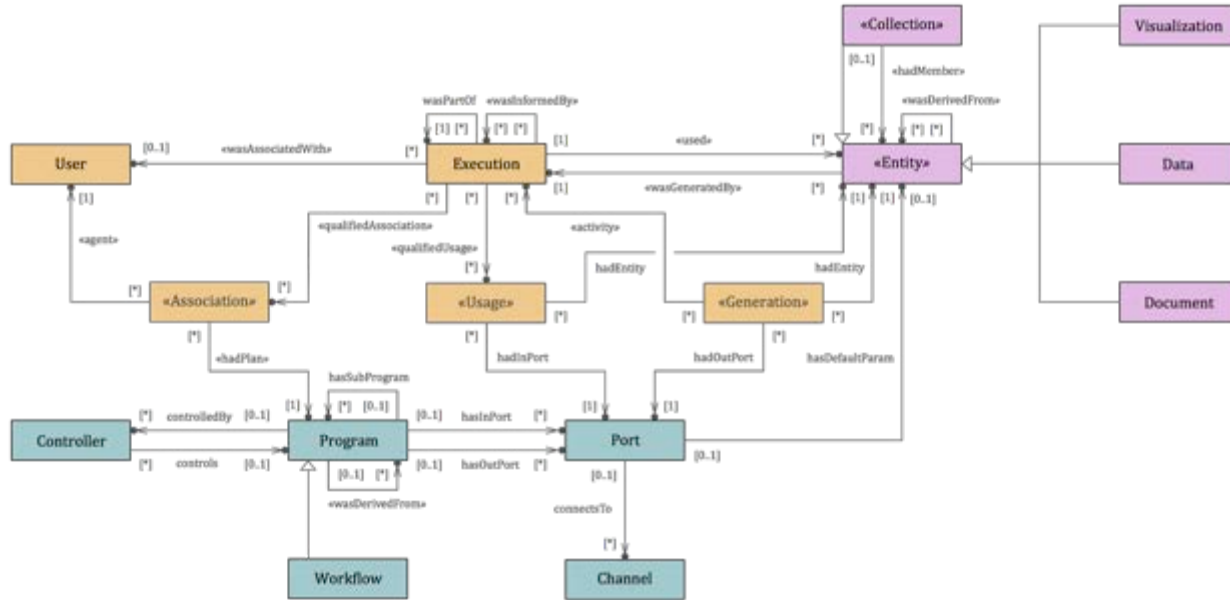
< “map image” wasDerivedFrom “CSV data” >



Using a common model

- W3C PROV model : very generic, universal
- Tracking provenance in scientific workflows
requires specialization of PROV
- The ProvONE model extends PROV to
provide this

ProvONE builds on W3C PROV



Using provenance information for search



Facilitating search



DataONE harvests provenance information and indexes it

