DATA DRIVEN COLLABORATION: A SOCIAL CONSTRUCT FOR MULTIDISCIPLINARY SCIENTIFIC DISCOVERY

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  - See: Design Unbound: Designing for Emergence in a White Water World, Brown and Pendleton-Jullian, MIT Press
- Rob Schuler
- Karl Czajkowski
- Hongsuda Tangmunarunkit

What does it mean to have a scientific result

- Others have to “know” about it
  - What is the scope and scale of “knowing”
- Others have to be able to validate it
  - Reproduce the method and achieve the same result
  - Achieve the same result via a different method
  - Reuse the result in a new method

“Non-reproducible single occurrences are of no significance to science.”

Karl Popper, 1959. The logic of scientific discovery. Hutchinson, London, United Kingdom.

How do we create a scientific result

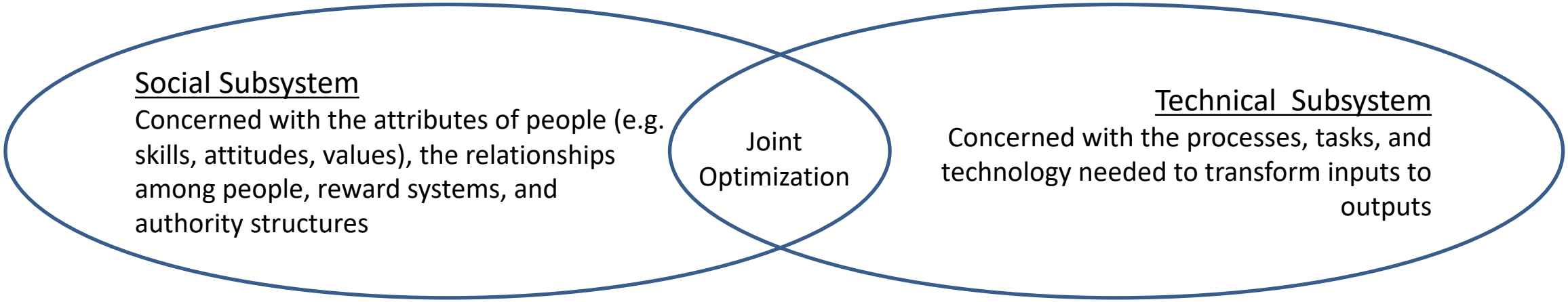
Any time scientists disagree, it's because we have insufficient data. Then we can agree on what kind of data to get; we get the data; and the data solves the problem. Either I'm right, or you're right, or we're both wrong. And we move on. That kind of conflict resolution does not exist in politics or religion.

Neil deGrasse Tyson

- Science is about communities arguing over data
  - How do those communities form
  - How do communities argue: knowledge capture and communication

Data driven multidisciplinary collaboration is a adaptive socio-technical eco-system

- How do manage social and technical subsystems
- How do we optimize across the ecosystem across time and space



Man-computer symbiosis … aims are 1) to let computers facilitate formulative thinking …., and 2) to enable men and computers to cooperate in making decisions and controlling complex situations without inflexible dependence on predetermined programs.

Licklider, 1960

Militello, e. al.. (2013). Sources of variation in primary care clinical workflow: Implications for the design of cognitive support. Health informatics journal.

Top down or bottom Up: The TIM^n perspective

- Tribes
- Institutions
- Markets
- Networks

Ronfeldt, David, Tribes, Institutions, Markets, Networks: A Framework About Societal Evolution. Santa Monica, CA: RAND Corporation, 1996.

Traditional eScience projects look like markets built around episodic exchange of papers/data (publication)

Transformational science requires networks.

Community of practice

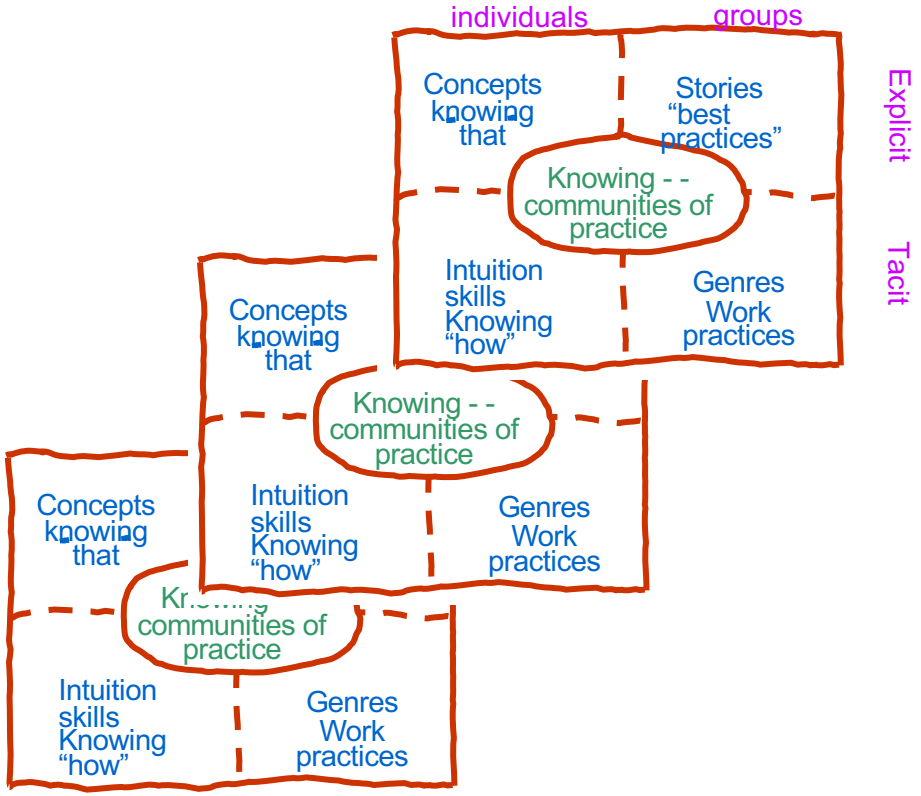
A group of people….

- With diverse viewpoints, role, etc.
- Engaged in joint work
- Over a significant period of time ,
- In which they build things, solve problems, learn , invent, and negotiate meaning,
- And evolve a way of talking and reading each other!

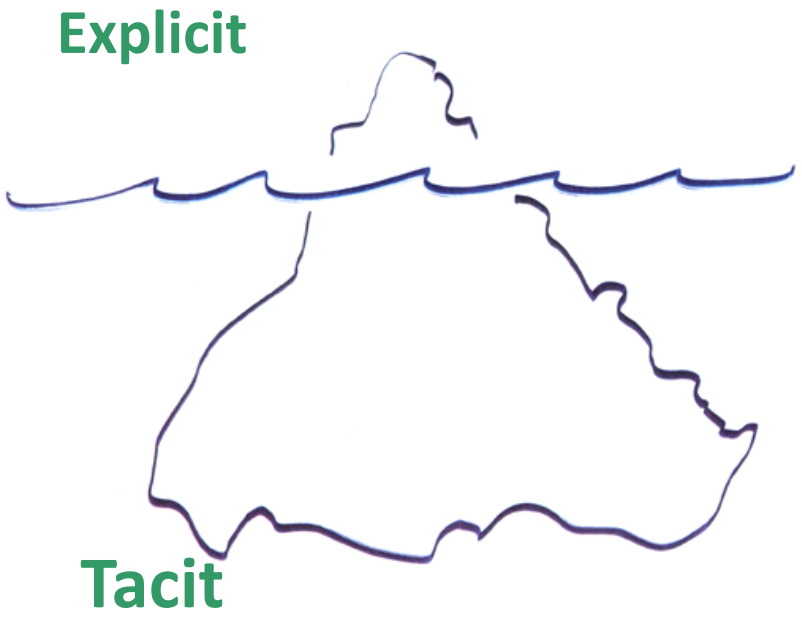
Networks of practice for transformational science

- Multiple communities working together in integrated, dynamic, adaptive and open collaboration

VS.



Dimensions of knowledge (jsb)

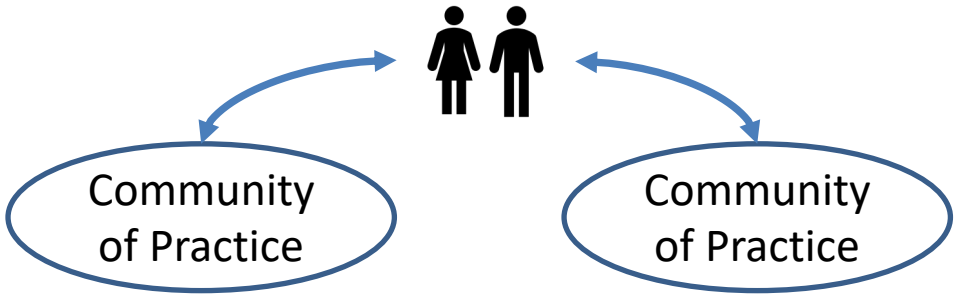


- Learning as enculturation into a practice - learning to be.
- the tacit dimension can't be completely converted to explicit
  - but some of it can - consider the doing of science.

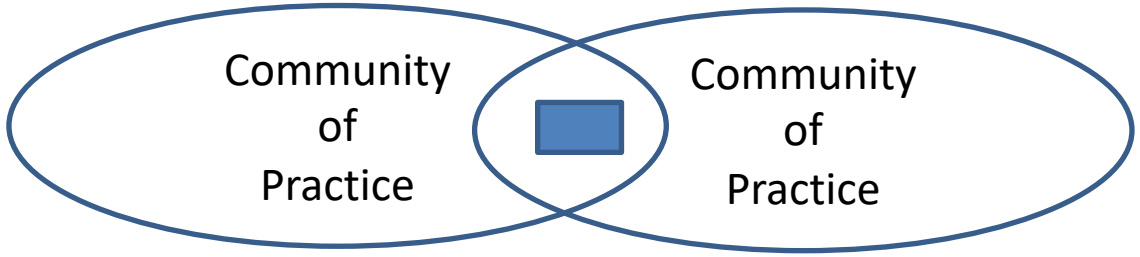
Knowledge flow across communities of practice

- Boundary objects and knowledge brokers

Translator/Knowledge Broker



Boundary object



Information used in different ways by different communities. Boundary objects are plastic, interpreted differently across communities but with enough immutable content to maintain integrity.

Star, Susan Leigh, and James R. Griesemer. "Institutional Ecology, `Translations' and Boundary Objects: Amateurs and Professionals in Berkeley's Museum of Vertebrate Zoology, 1907-39." *Social Studies of Science* 19, no. 3

Data as a boundary object

- Must be findable by network of practice,
- Must be accessible across the network while following norms of the community
- Must be interpretable by other community (interoperable)
  - The bits
  - The terms we use to describe
  - The relationships between elements

Where have we seen these requirements before…..

FAIR data…

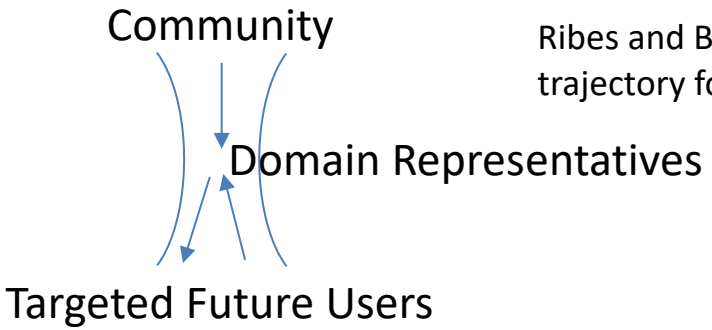
- Findable
  - identified by a unique identifier, characterized by rich metadata
- Accessible
  - standard protocol with access control, metadata accessible even when the data is not,
- Interoperable
  - by standardized terms to describe it
- Reusable
  - Accurate and relevant attributes.

FAIR collaboration

- Data as boundary object → Create FAIR data at every part of a scientific investigation
  - Enable “long tail” science organized around data
- Requires accurate descriptions of data
  - Characteristics of data element
  - Relationships between data elements
- Question: How do we create and maintain these metadata and relationships in a collaborative environment?

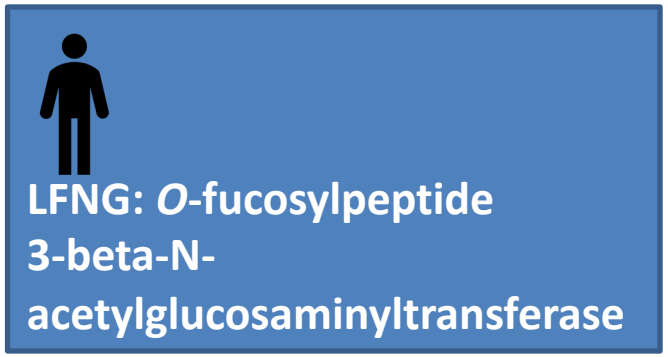
Collaboration is an evolutionary process

- Data interoperability, e.g. structure and meaning is time-dependent



Ribes and Bowker. "A learning trajectory for ontology building.", 2005

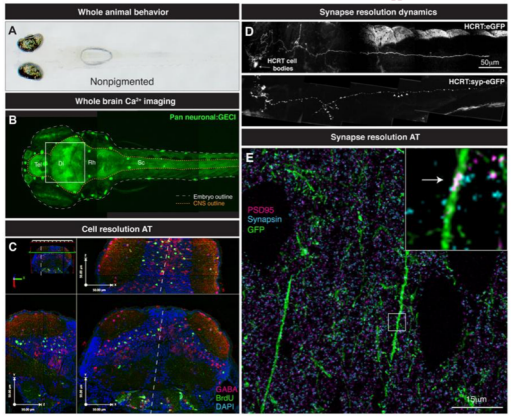
- Any evaluation of FAIRness is ill-posed unless we specify community and point in time!



Tacit Knowledge in data driven collaboration

- Data captures core knowledge of community/network of practice
  - Explicit knowlege
- Tacit knowledge required as well
  - Workflow systems
  - ”Web” and interaction analytics

Difficulty of managing large, complex collections of data throughout research activities

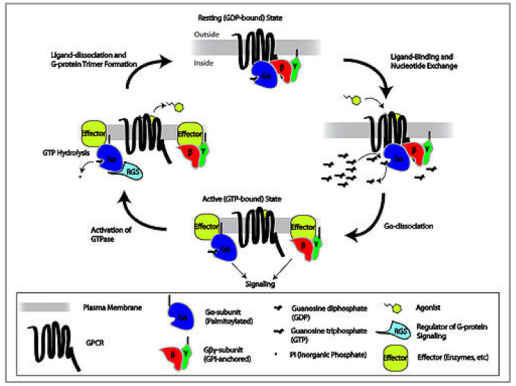


Synaptome: complex, in-vivo, longitudinal experiment

"When the Sloan Digital Sky Survey started work in 2000, its telescope in New Mexico collected more data in its first few weeks than had been amassed in the entire history of astronomy." (Economist 2010)

"Large amounts of data are generated using a variety of innovative technologies and the limiting step is accessing, searching and integrating this data." (Claus, Underwood, 2002)

- 50% or more time spent on **data wrangling**; (Kandel et al 2011)
- threaten **validity** of results and (10%) **reproducibility**; (Begley, Ellis 2012)
- and sparsity of **sharing**; (Borgman 2011)

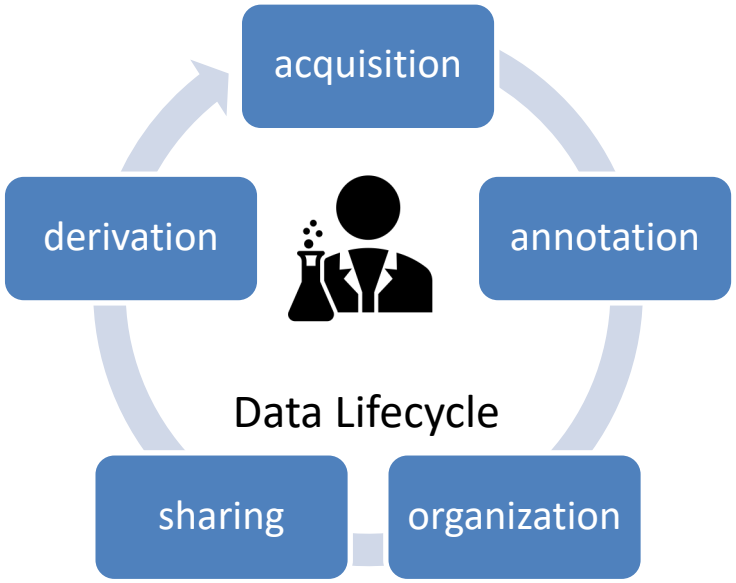


GPCR: pharma drug discovery

Turn scientists into active participants throughout the data lifecycle

~~tossing it over the fence~~

✓ "self serve" data curation



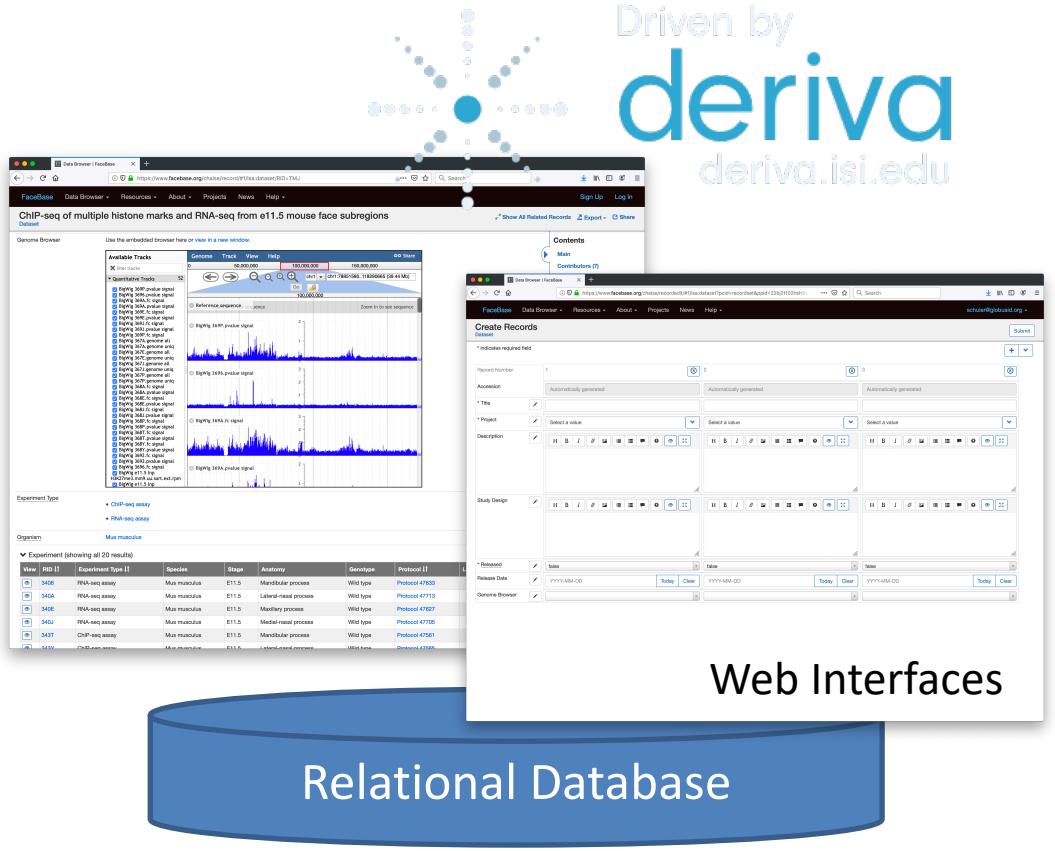
REPLACE:

- spreadsheets,
- "meaningful" filenames,
- inefficient EAV models,…

WITH:

- well-formed relational models…

but… how to evolve model?



(Schuler, Czajkowski, Kesselman 2014; Schuler, Czajkowski, Kesselman 2016; Bugacov et al 2017)

Scientific asset management system

Discovery Environment for Relational Information and Versioned Assets (DERIVA)

- Data Driven Collaboration
  - Think of it as a “photo manager” for scientific data
  - Maintain FAIR data from creation through publication
- Captures data and relationships between data
  - Catalog to capture relationships between data
  - Object store to hold data
- Can rapidly change to follow changes in scientific knowledge

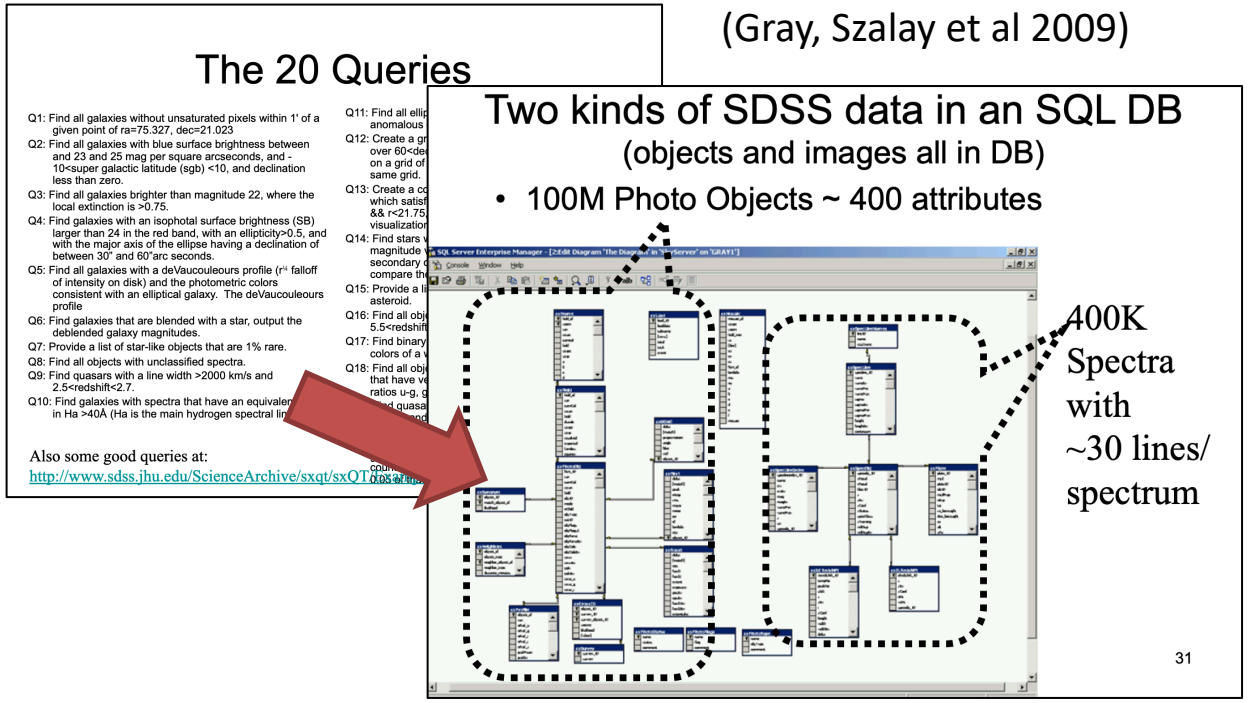
DERIVA promotes FAIR data production

- F: providing rich metadata using an Entity-Relationship model to express relationships between diverse data elements;
- A: offering rich access control and access to metadata via standard HTTP web service interfaces;
- I: integrating with standardized terms defined by collaborators, consortium or communities; and
- R: supporting dynamic model evolution so that the data presented accurately represents the current structure and state of knowledge within an investigation.

The “20 questions” approach, gets it started, but we need more agile methods throughout formative phases

- Drive database and system design by ~20 key queries

(Gray, Szalay et al 2009)



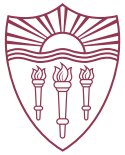
http://jimgray.azurewebsites.net/talks/SciData.ppt

However…

“Database technology has had limited uptake [in science and data science], in part due to the overhead in designing a schema…

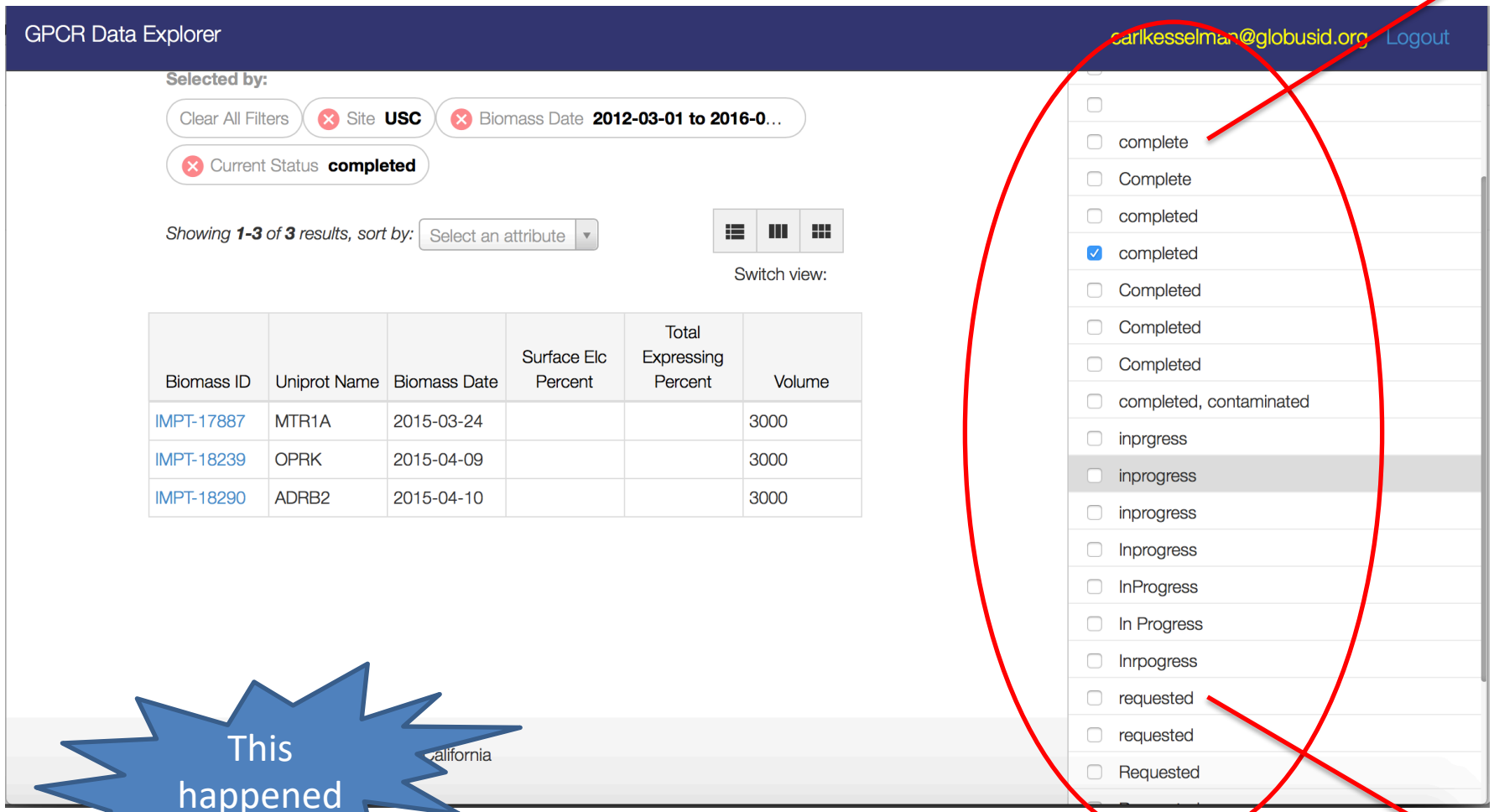
Changing data and changing requirements make it difficult to amortize these upfront costs…”

(Jain et al 2016)

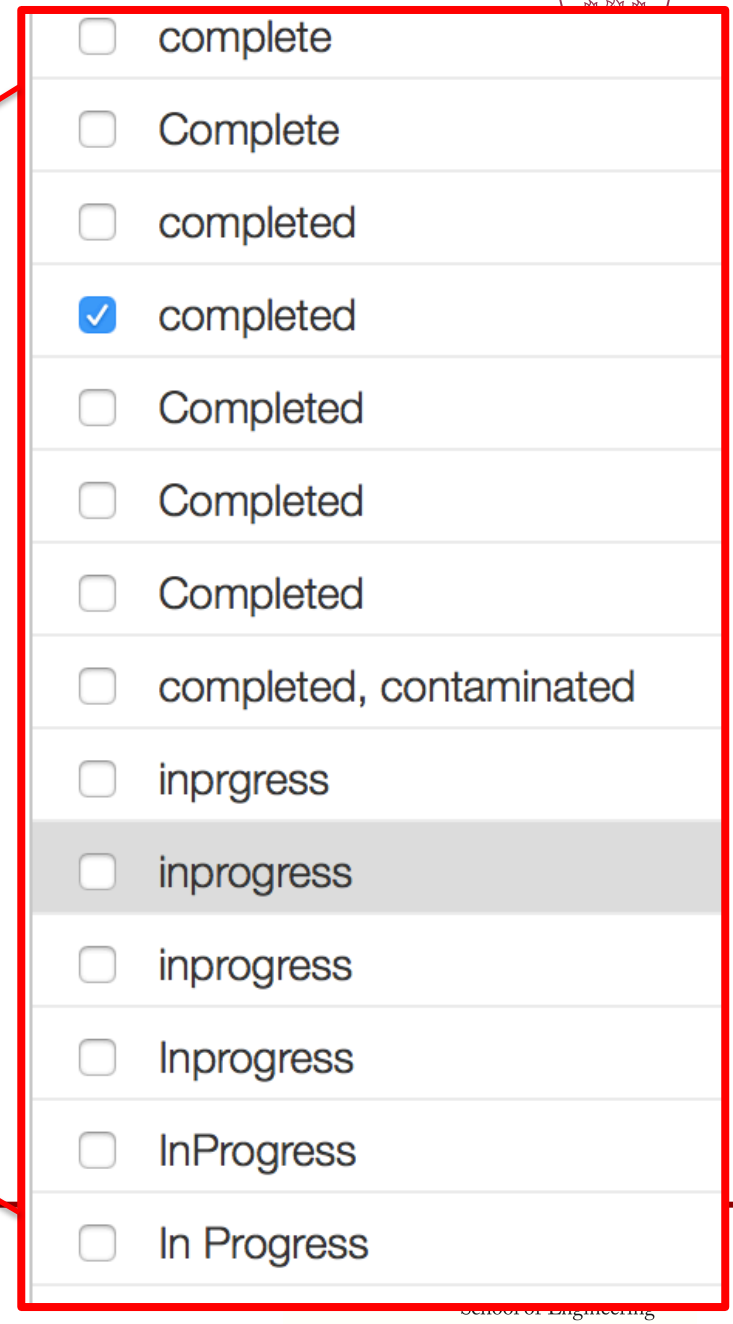


- “Everyone starts with the same schema: <stuff/>. Then they refine it.”
  - J. Widom

Suboptimal schema leads to suboptimal data: e.g., “messy” data!



This happened



Unconstrained Domain

Numerous steps to evolve even “simple” database

1 Measures + Specimens

ID	A	B	Litter	Anatomy	Age
73	abc	def	YC1	Mandible	E10.5
74	mno	pqr	YC1	Mandible	E10.5
75	stu	vxy	YC1	Maxila	E8.5

2 Cleaning (not pictured)

3

Measures

ID	A	B	FK
73	abc	def	1
74	mno	pqr	1
75	stu	vxy	2

ID	Litter	Anatomy	Age
1	YC1	Mandible	E10.5
2	YC1	Maxila	E8.5

Specimens

4

Measures

ID	A	B	FK
73	abc	def	1
74	mno	pqr	1
75	stu	vxy	2

Vocabulary

Anatomy	Age
Mandib	E10.5
Maxila	E8.5

ID	Litter	Anatomy	Age
1	YC1	Mandible	E10.5
2	YC1	Maxila	E8.5

Specimens

Open challenges for schema evolution remain…

Current situation:

1. Coordination of numerous SQL operations
2. Data migration, decoupled
3. Operations outside scope of SQL

(non-trivial manual effort, human error)

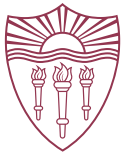
What scientists need are:

1. Operations closer to the scientific domain (fewer and less complex)
2. Streamlined operations (for transforming data and schema)
3. Seamless use of general-purpose languages for specialized transforms
4. Efficient expression evaluation

Schema evolution is … Transformation of a database schema that preserves instance data

(Roddick 1995)

Requirements distilled from reported and observed uses of databases in science



1. Define and alter tables of domain concepts
2. Create or change relationships between domain concepts
3. Capture categories of domain concepts (combine or separate sets)
4. Partition or merge tables of domain concepts (normalize/denormalize)
5. Express new concepts that were embedded in others (reify concepts)
6. Integrate data from external sources (external DBs, spreadsheets,…)
7. Increase the semantic coherence of data (align values, new domains,…)

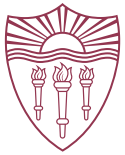
Emerging "Database Evolution Languages" help, but the level of abstraction is still close to SQL

- Database Evolution Language (DEL)
  - *Schema Modification Operators* (SMOs) – the operations of the DEL
  - Recent Examples: PRISM, BIDEL
- Primary contribution
  - schema *versioning* (backward compatibility) for enterprise and web information systems
  - Do not provide significantly higher level of abstraction to users

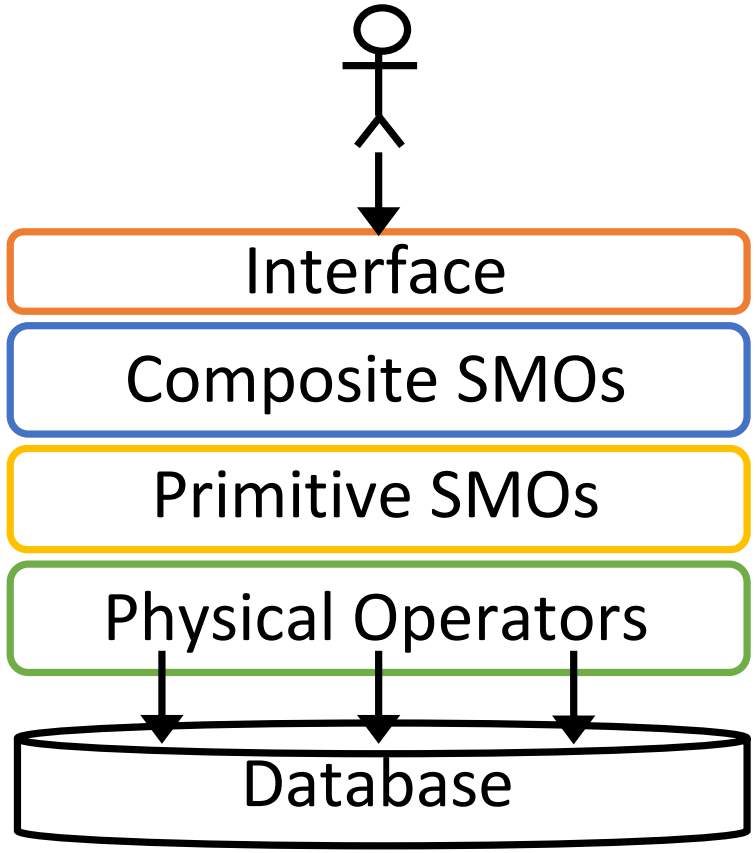
Schema Modification Operators (SMO) Syntax
CREATE TABLE R(a,b,c)
DROP TABLE R
RENAME TABLE R INTO T
COPY TABLE R INTO T
MERGE TABLE R, S INTO T
PARTITION TABLE R INTO S WITH $cond$, T
DECOMPOSE TABLE R INTO S(a,b), T(a,c)
JOIN TABLE R,S INTO T WHERE $cond$
ADD COLUMN d [AS $const \mid func(a,b,c)$] INTO R
DROP COLUMN c FROM R
RENAME COLUMN b IN R TO d

PRISM++ (Curino, Moon, Zaniolo, Deutsch 2013)

Our approach: An open, extensible DEL based on an algebra of primitive and composite SMOs

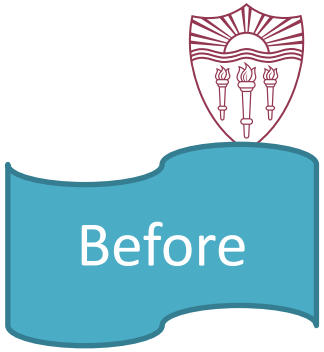


- **Primitive SMO**: indivisible operators, extended definitions of more common relational operators
- **Composite SMO**: defined as a functional composition over other (primitive or composite) SMOs
- **Algebraic expressions** can be decomposed and *rewritten into semantically equivalent*, more efficient expressions.
- **Embed in general-purpose language** with user programs *translated into the algebra*.



Conceptual overview of the approach

Problem scenario: free text “tags” of gene names…



Assays: Table of genetic assays

ID	A	B	List_of_Genes
73	abc	def	Msx1, Foxc2, Sox9
74	mno	pqr	Tgfb3, Sox9, Bmp4, …
…	…	…	…

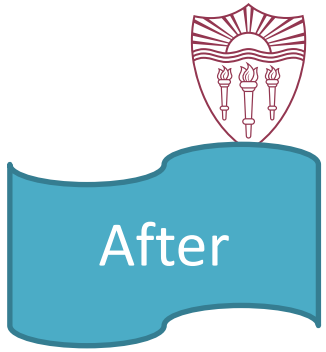
PROBLEM
Free text listing of gene names related to the assay records

Objective: to extract the free text “List_of_Genes” in a normalized and semantically aligned association with the canonical term set.

Genes: Table of canonical terms

ID	Term	Synonyms
1	Msx1	…
2	Tgfb3	…
3	Foxc2	…
4	Sox9	…
5	Bmp4	…
…	…	…

Problem scenario: free text “tags” of gene names…



Assays: Table of genetic assays

ID	A	B	~~List_of_Genes~~
73	abc	def	~~Msx1, Foxc2, Sox9~~
74	mno	pqr	~~Tgfb3, Sox9, Bmp4, …~~
…	…	…	~~…~~

Assay_Genes: Table of semantically aligned assay to gene name association

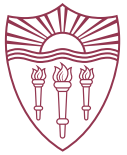
Assay	Gene
73	Msx1
73	Foxc2
73	Sox9
74	Tgfb3
74	Sox9
74	Bmp4
…	…

Genes: Table of canonical terms

ID	Term	Synonyms
1	Msx1	…
2	Tgfb3	…
3	Foxc2	…
4	Sox9	…
5	Bmp4	…
…	…	…

Objective: to extract the free text “List_of_Genes” in a normalized and semantically aligned association with the canonical term set.

Tagify: normalize and semantically align free form tags…



d Tagify$_a$ r

Iteratively apply composite SMO definitions until we have an expression of only primitive SMOs

Input:
d: `Genes`
r: `Assays`

Parameters:
a: `List_of_Genes`
(others omitted for brevity)

Result:
Computes association table

Tagify: normalize and semantically align free form tags…

$$d \text{ Tagify}_a\ r \mapsto d \text{ Align}_a\ (\text{Atomize}_a\ r)$$ (Tagify definition)

Input:
d: `Genes`
r: `Assays`

Parameters:
a: `List_of_Genes`
(others omitted for brevity)

Result:
Computes association table

Tagify: normalize and semantically align free form tags…

$$d \text{ Tagify}_a\ r \mapsto d \text{ Align}_a\ (\text{Atomize}_a\ r) \quad \text{(Tagify definition)}$$

$$\mapsto d \text{ Align}_a\ (\mu\ (\text{Reify}^{\text{Sub}}{}_a\ r)) \quad \text{(Atomize definition)}$$

Input:
d: `Genes`
r: `Assays`

Parameters:
a: `List_of_Genes`
(others omitted for brevity)

Result:
Computes association table

Tagify: normalize and semantically align free form tags…

d Tagify$_a$ r $\mapsto$ d Align$_a$ (Atomize$_a$ r) (Tagify definition)

$\mapsto$ d Align$_a$ (μ (Reify$^{Sub}{}_a$ r)) (Atomize definition)

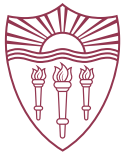
$\mapsto$ d Align$_a$ (μ ($\pi_{key(r),a}$ r)) (ReifySub definition)

Input:
d: `Genes`
r: `Assays`

Parameters:
a: `List_of_Genes`
(others omitted for brevity)

Result:
Computes association table

Tagify: normalize and semantically align free form tags…



d Tagify$_a$ r $\mapsto$ d Align$_a$ (Atomize$_a$ r) (Tagify definition)

$\mapsto$ d Align$_a$ (μ (Reify$^{\text{Sub}}{}_a$ r)) (Atomize definition)

$\mapsto$ d Align$_a$ (μ ($\pi_{\text{key(r)},a}$ r)) (ReifySub definition)

$\mapsto$ $\varrho_{\text{t/a}}$ ($\pi_{\text{-a,-s}}$ (μ ($\pi_{\text{key(r)},a}$ r)) $\bowtie_{\equiv}$ d) (Align definition)

Input:
d: `Genes`
r: `Assays`

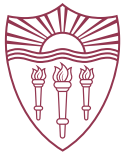
Parameters:
a: `List_of_Genes`
(others omitted for brevity)

Result:
Computes association table

Collaborative Metadata Management

- ERMRest: A web service for managing metadata and relationships between data assets
  - Everything is a resource with a URI and interface
- Entity/Relationship modeling

Data API



- All operations mapped into URL:

  `ermrest/catalog/1@Y-1Z4B/entity/foo/bar/x::gt::7`

  – Queries can be viewed as naming data

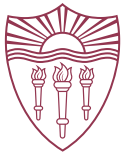
  – Tables exchanges as CSV or JSON

- Operate on whole or partial entity, projections, aggregates
- Joins, filter-based row selection, column projection, configurable sort order, and pagination.
- Insertion, update, or deletion of data in one table at a time.

Fine grain access control

- ACL = (resource, permission, roles)
  - schema, table, column, or reference
  - access permission (e.g., insert, update, etc.)
  - a set of user or group identity
- ACL is associated with a resource in the hierarchy:
  - catalog, schema, table, column, and constraint
- ACLs are inherited simplifying management
- Static and dynamic policy specifications

Snapshots and history



- Logical snapshots at every catalog mutation
  - Prior values are stored in the catalog
  - Snapshot ID created for every snapshot
- Catalog URI can include snapshot ID

  `–ermrest/catalog/1@Y-1Z4B/entity/foo/bar/x`
- History Management
  - Range Discovery, Truncation, Policy Amendment, Data Redaction

Persistent identifiers

- Every entity ERMRest has unique ID (RID)
  - Assigned by catalog, can be used as foreign-key
- Every version of entire catalog has a unique ID.
- Query with snapshot ID uniquely names a entity set
  - ERMRest URI with snapshot ID
- RID and Snapshot ID uniquely name an specific version of entity
- Support for identifiers from community controlled vocabulary
  - E.g. Uberon, Schema.org, RRIDs

Evolving applications with schema

- Hard problem in general
  - In practice, schema are broken to accommodate applications.
- Pragmatic solutions:
  - Loose coupling around interchange format
  - Model introspection and dynamic interfaces

Big data bags

- A packaging format for encapsulating
  - Payload: arbitrary content
  - Tags: metadata describing the payload
  - Checksums: supports verification of content

Chard, Kyle, et al. "I'll take that to go: Big data bags and minimal identifiers for exchange of large, complex datasets." *2016 IEEE International Conference on Big Data (Big Data)*. IEEE, 2016

```
Bio_data_bag/
|-- data
| \-- genomic
|   \-- 2a673.fastq
|   \-- 2a673.fastq
| -- manifest-md5.txt
|     afbfa23123bfa data/genomic/2a673.fasta
| -- bagit.txt
      Contact-Name: John Smith
```

Making Bags big

- Manifest lists all content and checksums
- Available content contained in “data” directory
- Content may be “missing”
  - Missing content must be listed in “fetch.txt”
  - Fetch entries list local name in data directory, and URL of where to fetch data
- Have created tool for creating, validating and materializing bags

Rich metadata for Bags

Open Knowledge Foundation Table Schema

```
{
  "name": "Method",
  "schema": {
    "fields": [
      {
        "name": "id",
        "title": "A globally unique ID",
        "type": "string",
        "constraints": { "required": true, "unique": true}
      },
    ],
    "missingValues": [ "" ], "primaryKey": "id"
  }
},
```

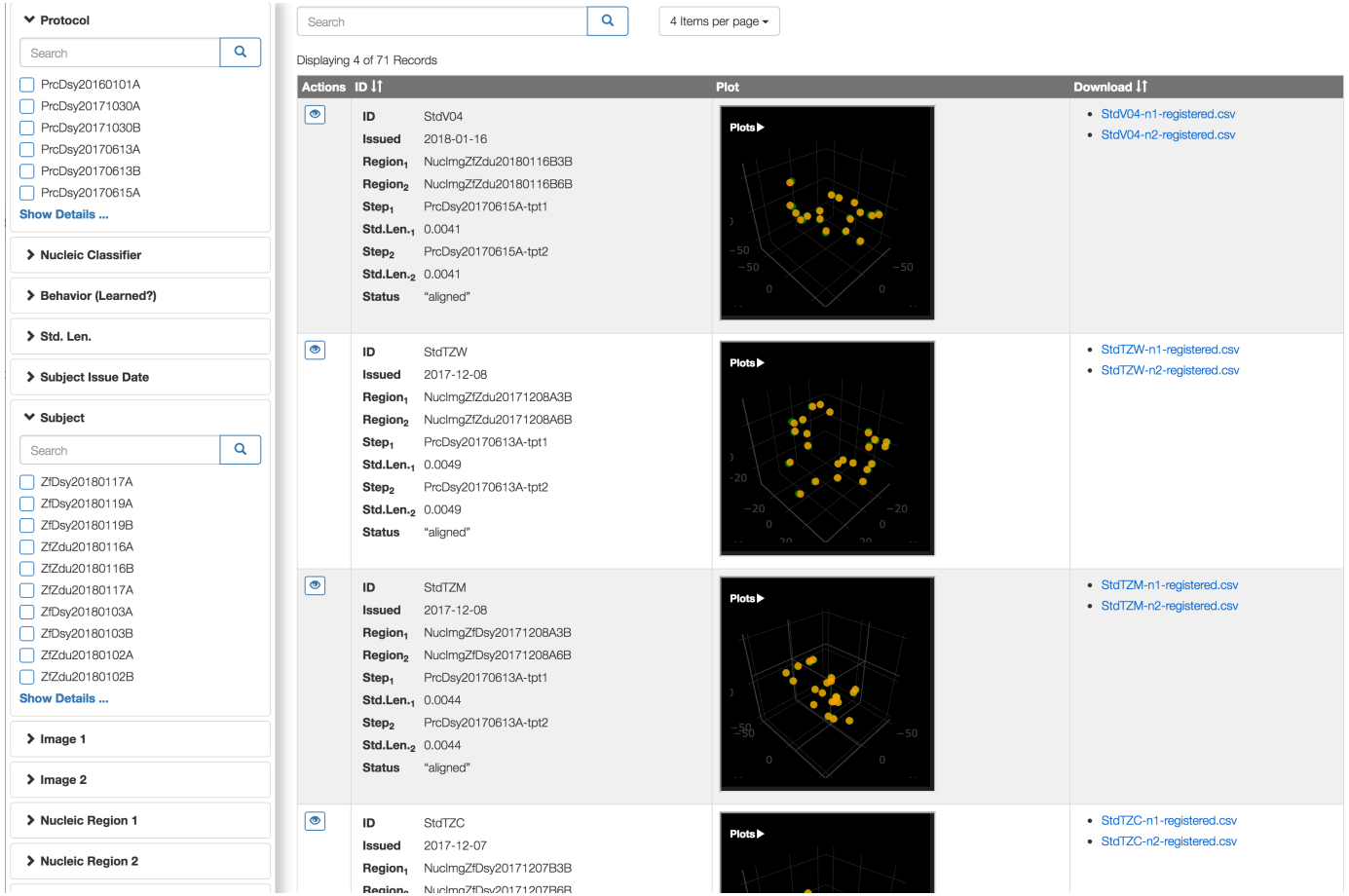
Research Objects

```
{
  "@context": {
     "@vocab": "http://purl.org/dc/terms/",
     "dcmi":
"http://purl.org/dc/dcmitype/Dataset"
  },
  "@id":  "../../data/numbers.csv",
  "@type": "dcmi:Dataset",
  "title": "CSV files of beverage
consumption",
 ”description": "A CSV file listing the number
of cups consumed per person.”
}
```

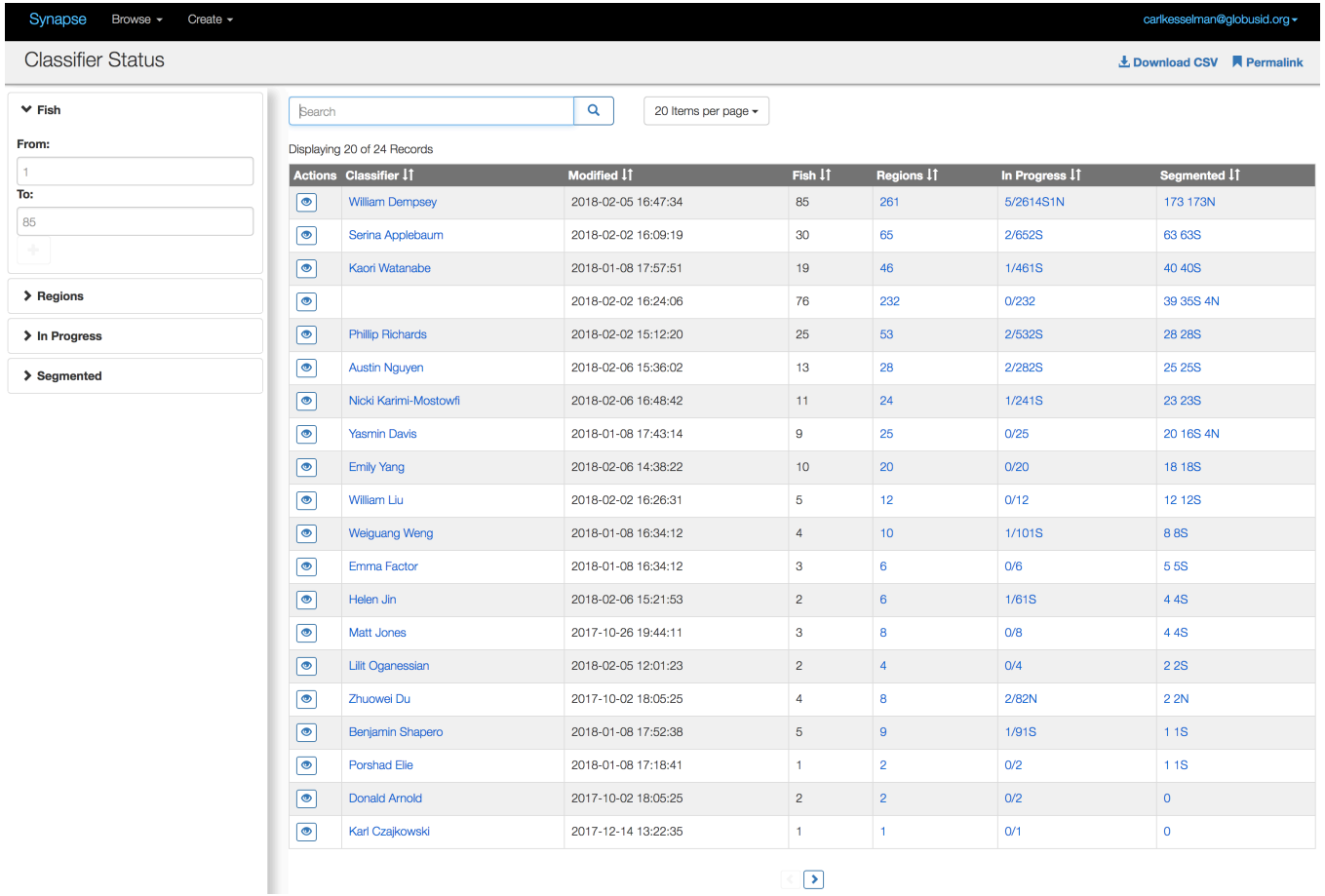
Chaise – An adaptive model-driven Web user interface

- How little can we assume?
  - discovery, analysis, visualization, editing, sharing and collaboration over tabular data (ERMRest).
- Makes almost no assumptions about data model
  - Introspect the data model from ERMrest.
  - Use heuristics, for instance, how to flatten a hierarchical structure into a simplified presentation for searching and viewing.
  - Schema annotations are used to modify or override its rendering heuristics, for instance, to hide a column of a table or to use a specific display name.
  - Apply user preferences to override, for instance, to present a nested table of data in a transposed layout.

Management of all scientific assets

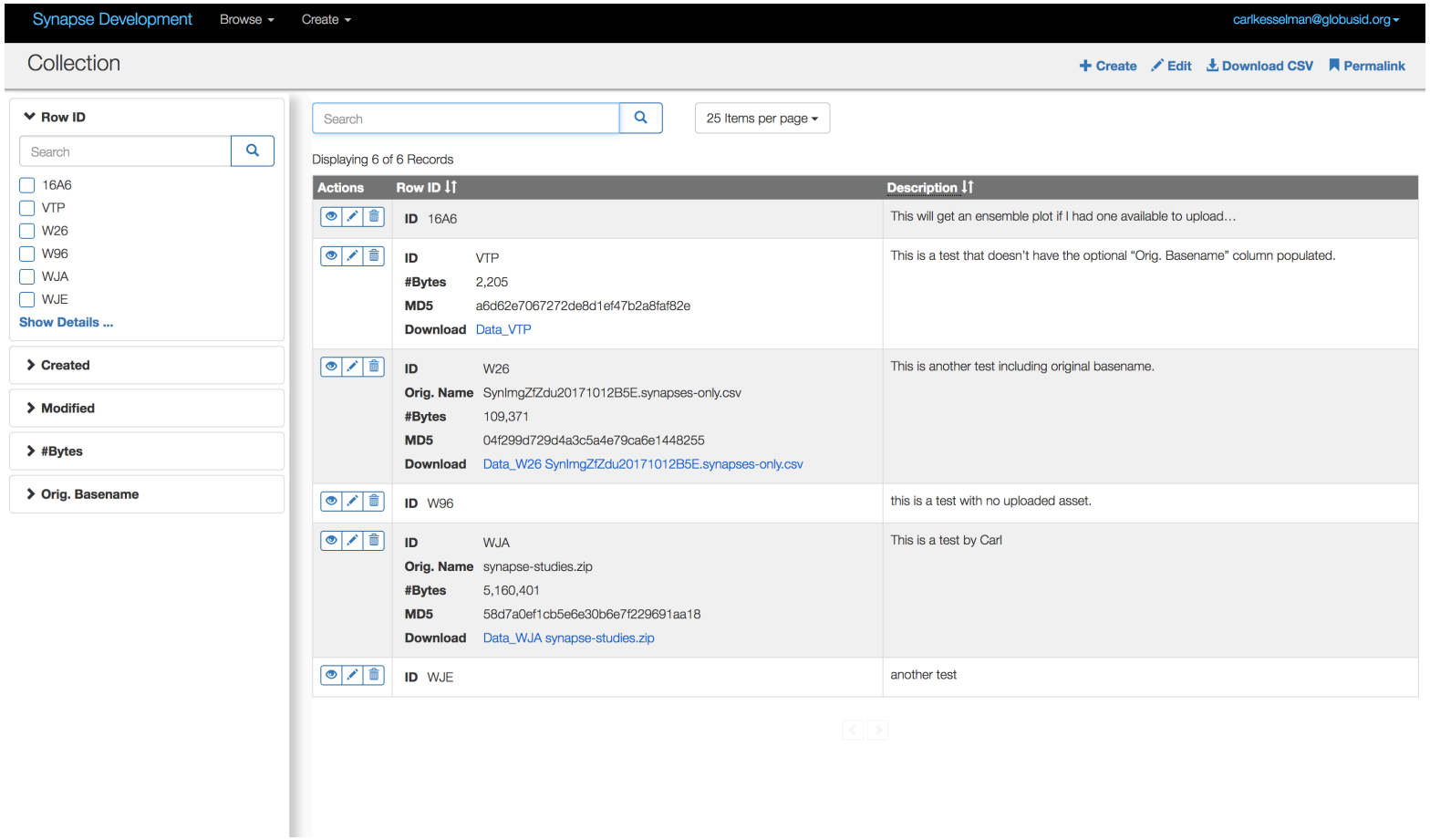


Dashboards to track progress

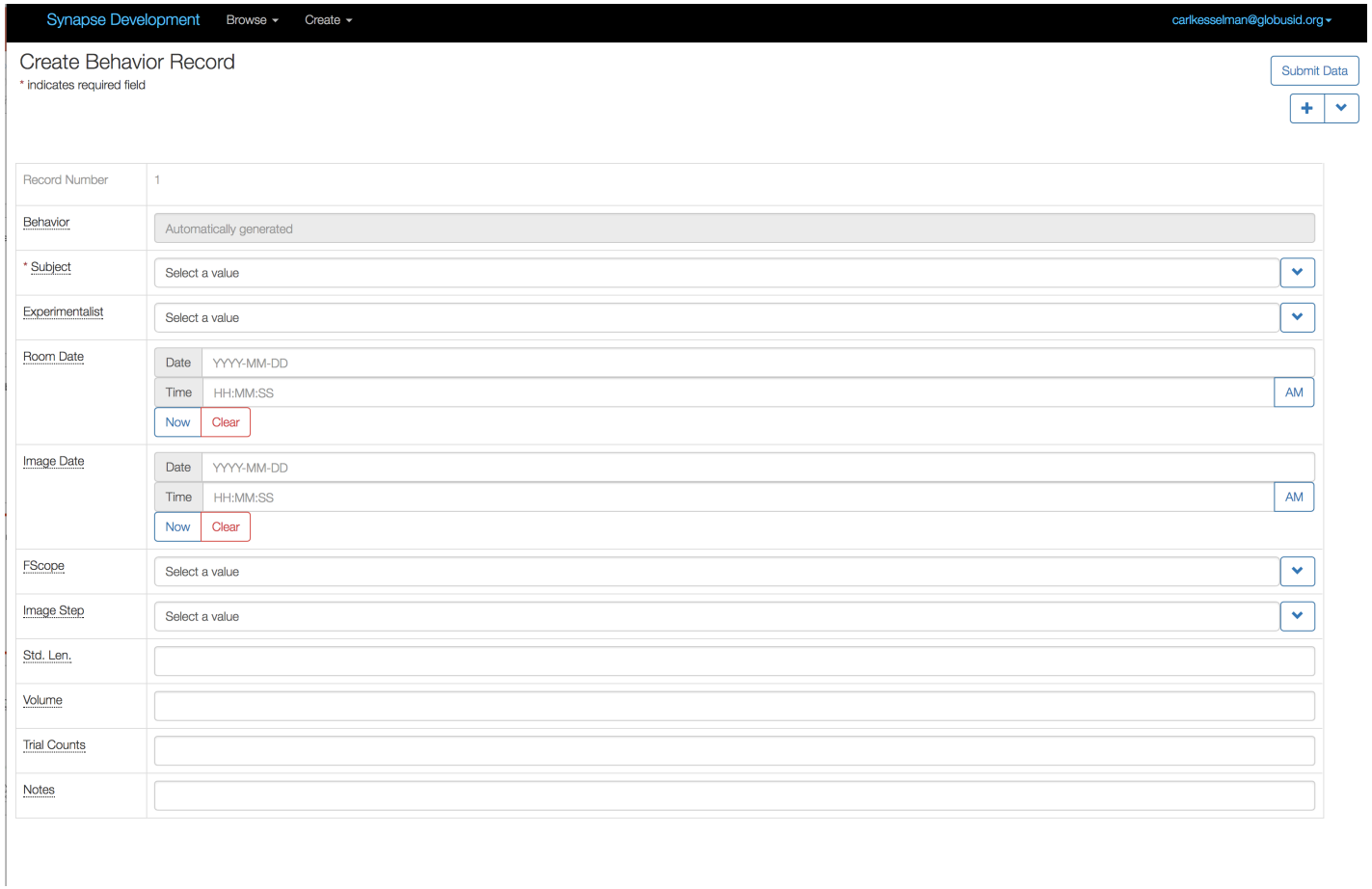


Actions	Classifier	Modified	Fish	Regions	In Progress	Segmented
	William Dempsey	2018-02-05 16:47:34	85	261	5/2614S1N	173 173N
	Serina Applebaum	2018-02-02 16:09:19	30	65	2/652S	63 63S
	Kaori Watanabe	2018-01-08 17:57:51	19	46	1/461S	40 40S
		2018-02-02 16:24:06	76	232	0/232	39 35S 4N
	Phillip Richards	2018-02-02 15:12:20	25	53	2/532S	28 28S
	Austin Nguyen	2018-02-06 15:36:02	13	28	2/282S	25 25S
	Nicki Karimi-Mostowfi	2018-02-06 16:48:42	11	24	1/241S	23 23S
	Yasmin Davis	2018-01-08 17:43:14	9	25	0/25	20 16S 4N
	Emily Yang	2018-02-06 14:38:22	10	20	0/20	18 18S
	William Liu	2018-02-02 16:26:31	5	12	0/12	12 12S
	Weiguang Weng	2018-01-08 16:34:12	4	10	1/101S	8 8S
	Emma Factor	2018-01-08 16:34:12	3	6	0/6	5 5S
	Helen Jin	2018-02-06 15:21:53	2	6	1/61S	4 4S
	Matt Jones	2017-10-26 19:44:11	3	8	0/8	4 4S
	Lilit Oganessian	2018-02-05 12:01:23	2	4	0/4	2 2S
	Zhuowei Du	2017-10-02 18:05:25	4	8	2/82N	2 2N
	Benjamin Shapero	2018-01-08 17:52:38	5	9	1/91S	1 1S
	Porshad Elie	2018-01-08 17:18:41	1	2	0/2	1 1S
	Donald Arnold	2017-10-02 18:05:25	2	2	0/2	0
	Karl Czajkowski	2017-12-14 13:22:35	1	1	0/1	0

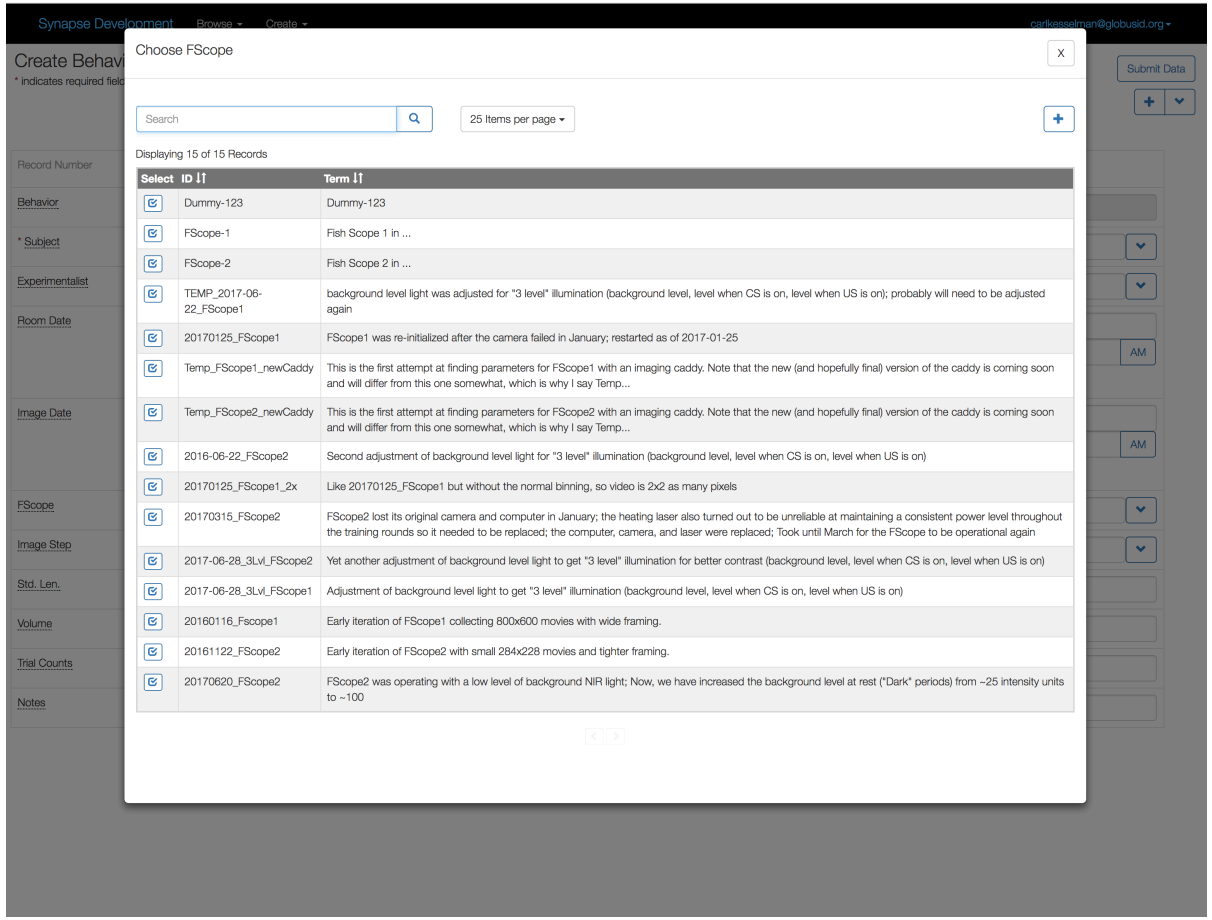
Dynamic data collections with global IDs



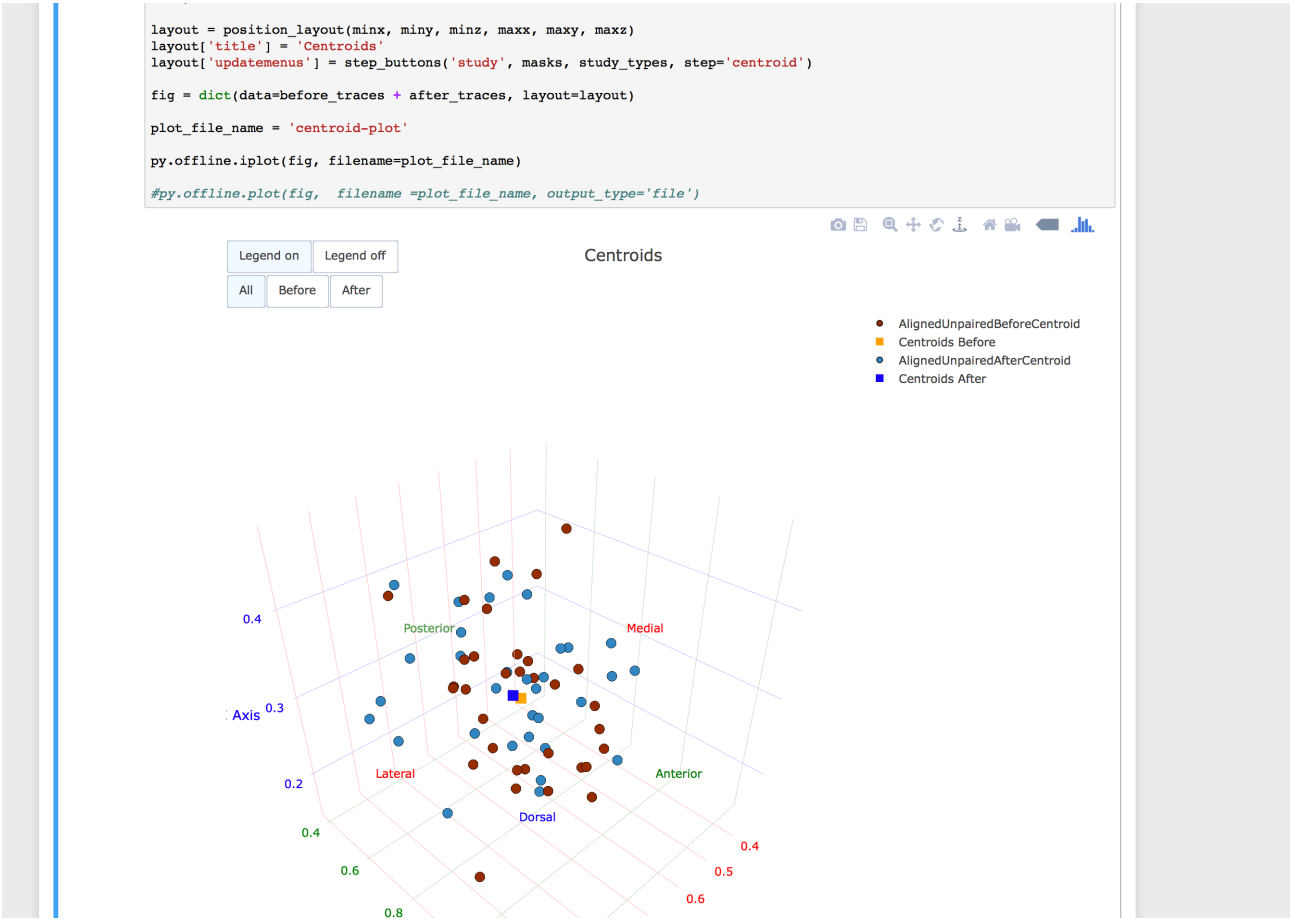
Model driven data entry…



With controlled vocabulary.



Web services interface can be used to pull data directly from catalog. Notice that all data assests are versioned (BeforeURL), and that we have the exact snapshot version of the data catalog and code, allowing us to perform RDA compliant persistent search.



Interaction with the notebook allows us to plot data. Plots can be placed into catalog as an asset that is part of the study.

In vivo replacement of damaged bladder urothelium by Wolffian duct epithelial cells

Diya B. Joseph, Anoop S. Chandrashekar, Lisa L. Abler, Li-Fang Chu, James A. Thomson, Cathy Mendelsohn, and Chad M. Vezina

PNAS August 14, 2018 115 (33) 8394-8399; published ahead of print July 30, 2018
https://doi.org/10.1073/pnas.1802966115

Edited by Marianne Bronner, California Institute of Technology, Pasadena, CA, and approved July 2, 2018 (received for review February 19, 2018)

Significance

When the bladder's specialized epithelial lining is damaged by infection or injury, its own basal and intermediate cell progenitors are called upon to restore a functional barrier. Here we show that when these progenitor cells are depleted in conditional *Dnmt1* mutant mice,

Methods

Data Dissemination.

To increase rigor, reproducibility, and transparency, raw image files and other data generated as part of this study were deposited into the GUDMAP consortium database and are fully accessible at: https://doi.org/10.25548/W-QXXC (**25**).

Conditional *Dnmt1* Mutants.

Mice were housed as previously described (**26**). All procedures performed on mice were approved by the University of Wisconsin–Madison Animal Care and Use Committee and were carried out in accordance with the Guide for the Care and Use of Laboratory Animals. *Shh*^{cre} alleles (B6.Cg*Shh*$^{tm1(EGFP/cre)Cjt/J}$) (**11**) were used to conditionally inactivate *Dnmt1* using *Dnmt1flox* alleles (B6.129S4-*Dnmt1*$^{tm2Jae/Mmucd}$) in *Shh* lineage cells marked

In vivo replacement of damaged bladder urothelium by Wolffian duct epithelial cells

COLLECTION

RID	W-QXXC
Title	In vivo replacement of damaged bladder urothelium by Wolffian duct epithelial cells
Description	Figures and data relating to the PNAS 2018 paper titled “In vivo replacement of damaged bladder urothelium by Wolffian duct epithelial cells” by Joseph et al.
Details	The following table shows the mapping of figures and image record IDs (RID) presented in the paper.

Figure	Reference	Additional Images
1A	W-QXXW	W-QXZ4, W-QY2C
1B	W-QY34	W-QY38, W-QY3C
1C	W-QY66	W-QY6T, W-QY86
1D	W-QY8Y	W-QY9A, W-QYA6
1E	W-QYB6	W-QYBP, W-QZ6T
1F	W-QYC2	W-QYCE, W-QYCT
1G	W-QYDP	W-QYDY, W-QYEA
1H	W-QYEP	W-QYF2, W-QYFE
1I	W-QYGP	W-QYH2, W-QYHE
1J	W-QYHT	W-QYJ6, W-QYJJ
1K	W-QYKP	W-QYM2, W-QYME

Contents

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Specimen Collection (25)

In vivo replacement of damaged bladder urothelium by Wolffian duct epithelial cells

COLLECTION

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Require DOI?	Yes
Persistent ID	https://doi.org/10.25548/W-QXXC
Principal Investigator	Chad Vezina
Data Provider	University of Wisconsin
Consortium	GUDMAP
Creation Time	2018-05-17 21:19:14
Last Modified Time	2018-07-09 22:13:01

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He Slide Collection (showing all 13 results)

View More

View	RID	Thumbnail	Name	Species	Tissue	Age Stage	Gender	Image File
	W-R01Y		Urogenital sinus from Control embryo (Shhcre/+; Dnmt1flox/+) (1 of 3)	Mus musculus	urogenital sinus	18.5 embryonic days	Male	20160826ShhcreDnmtiLOFME18.5U
	W-R02A		Urogenital sinus from Control embryo (Shhcre/+; Dnmt1flox/+) (2 of 3)	Mus musculus	urogenital sinus	18.5 embryonic days	Male	20160826ShhcreDnmtiLOFME18.5U
	W-R02P		Urogenital sinus from Control embryo (Shhcre/+; Dnmt1flox/+) (3 of 3)	Mus musculus	urogenital sinus	18.5 embryonic days	Male	20160826ShhcreDnmtiLOFME18.5U
	W-R02Y		Urogenital sinus from Conditional Dnmt1 embryo (Shhcre/+; Dnmt1flox/flox) (1 of 3)	Mus musculus	urogenital sinus	18.5 embryonic days	Male	20160826ShhcreDnmtiLOFME18.5U
	W-R036		Urogenital sinus from Conditional Dnmt1 embryo (Shhcre/+; Dnmt1flox/flox) (2 of 3)	Mus musculus	urogenital sinus	18.5 embryonic	Male	20160826ShhcreDnmtiLOFM

GUDMAP/RBK Resources | Search | Create | Dev-Only search | Dashboards (requires login) | Help | Feedback | carlkesselman@globusid.org

Whole-mount 3D views of the huma

COLLECTION

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RID	Q-3K5A
Title	Whole-mount 3D views of the
Description	A collection of human embryo Related to JASN https://doi.o
Require DOI?	Yes
Persistent ID	https://doi.org/10.25548/BU
Record Status Detail	Complete
Curation Status	Release
Principal Investigator	Andrew McMahon, USC
Data Provider	University of Southern California
Consortium	GUDMAP
Creation Time	2017-09-23 02:18:02
Last Modified Time	2018-05-23 03:39:13

e Kidney Organogenesis.

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- IF Slide Collection (13)
- IF Video Collection (0)
- Sequencing Study Collection (0)

He Slide Collection (no results found) — Add | View More

Actions	RID	Thumbnail	Name	Species	Tissue	Age Stage	Gender	Image File	Record Stat
No Results Found									

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X

Share Link

https://dev.gudmap.org/chaise/record/#2/Common:Collection/RID=Q-3K5A

Citation

Andrew McMahon *GUDMAP Consortium* https://doi.org/10.25548/BURB-6P44 (2017).

Download Citation:

BibTex

In vivo replacement of damaged bladder urothelium by Wolffian duct epithelial cells

COLLECTION

RID W-QXXC

Title In vivo replacement of damaged bladder urothelium by Wolffian duct epithelial cells

Description Figures and data relating to the PNAS 2018 paper titled “In vivo replacement of damaged bladder urothelium by Wolffian duct epithelial cells” by Joseph et al.

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1B	W-QY34	W-QY38, W-QY3C
1C	W-QY66	W-QY6T, W-QY86
1D	W-QY8Y	W-QY9A, W-QYA6
1E	W-QYB6	W-QYBP, W-QZ6T
1F	W-QYC2	W-QYCE, W-QYCT
1G	W-QYDP	W-QYDY, W-QYEA
1H	W-QYEP	W-QYF2, W-QYFE
1I	W-QYGP	W-QYH2, W-QYHE
1J	W-QYHT	W-QYJ6, W-QYJJ

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Main
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Specimen Collection (25)
IF Slide Collection (0)
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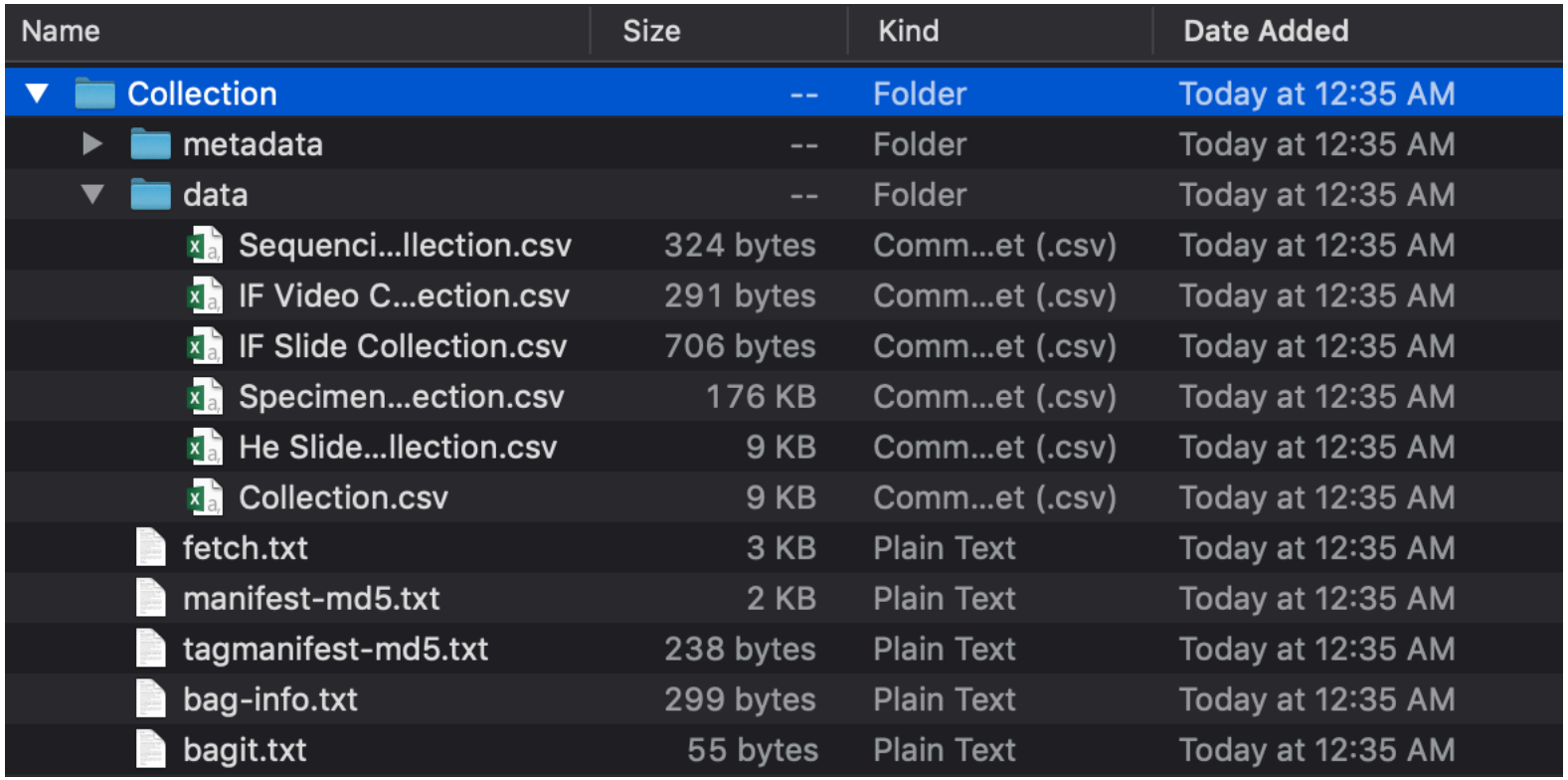
Sequencing Study Collection (0)



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data	--	Folder	Today at 12:35 AM
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bag-info.txt	299 bytes	Plain Text	Today at 12:35 AM
bagit.txt	55 bytes	Plain Text	Today at 12:35 AM

Summary

- Think of eScience infrastructure as part of socio-technical system
  - Design for the interface across communities of practice
- Validated this approach with Deriva across many domains and scales
  - Craniofacial dysmorphia, protein structure database, molecular atlas, kidney reconstruction, dynamic synapse mapping, optimization models, pancreatic beta cell modeling, developmental biology, …
- Other platform approaches possible
  - E.g. L. Trani, M. Atkinson, D. Bailo, R. Paciello, R. Filgueira, Establishing core concepts for information-powered collaborations, FGCS 89 (2018) 421–437.
- For more information: www.derivacloud.org

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deriva.isi.edu