UNIVERSITY of WASHINGTON

Advancing Declarative Query for Data-Intensive Science

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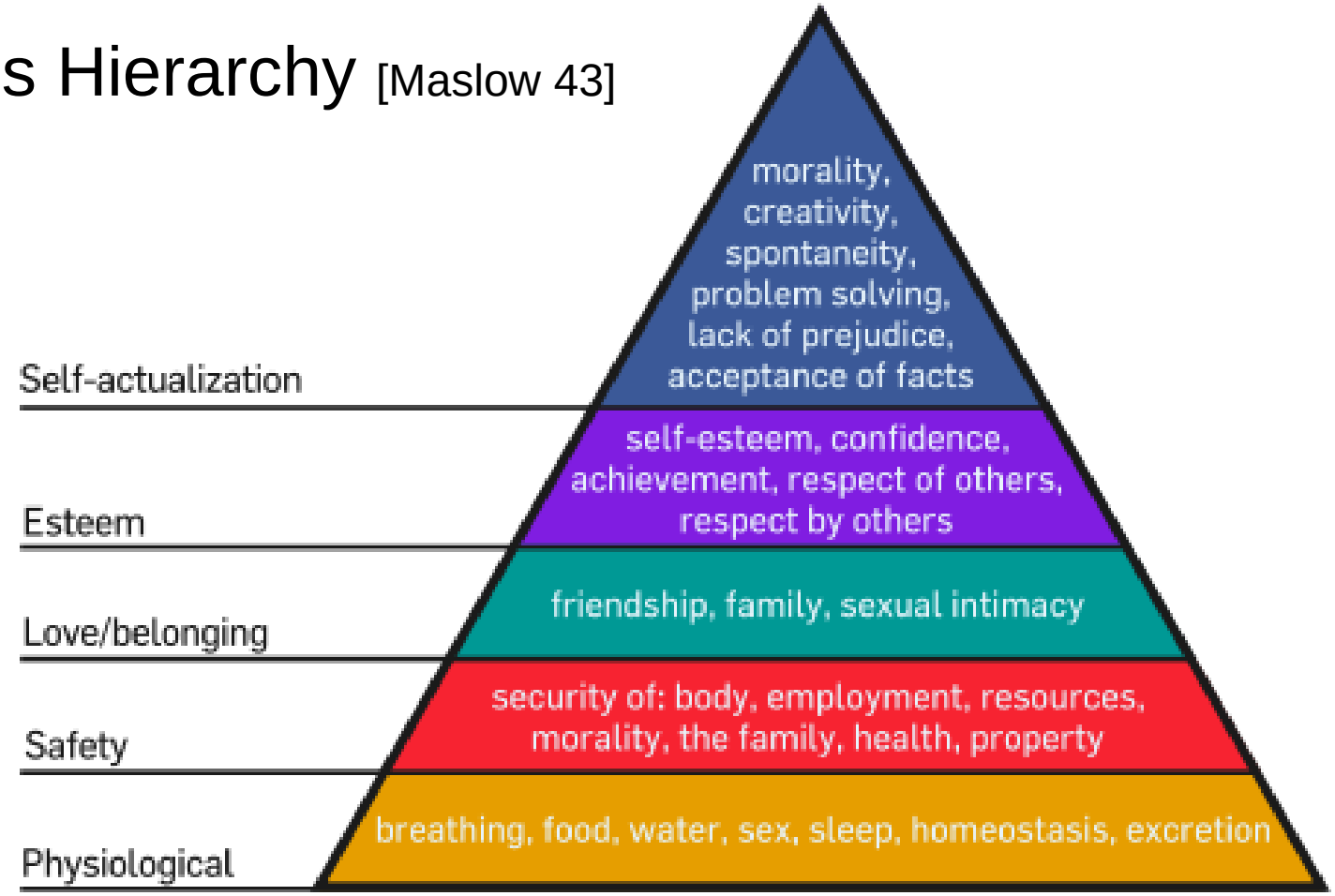
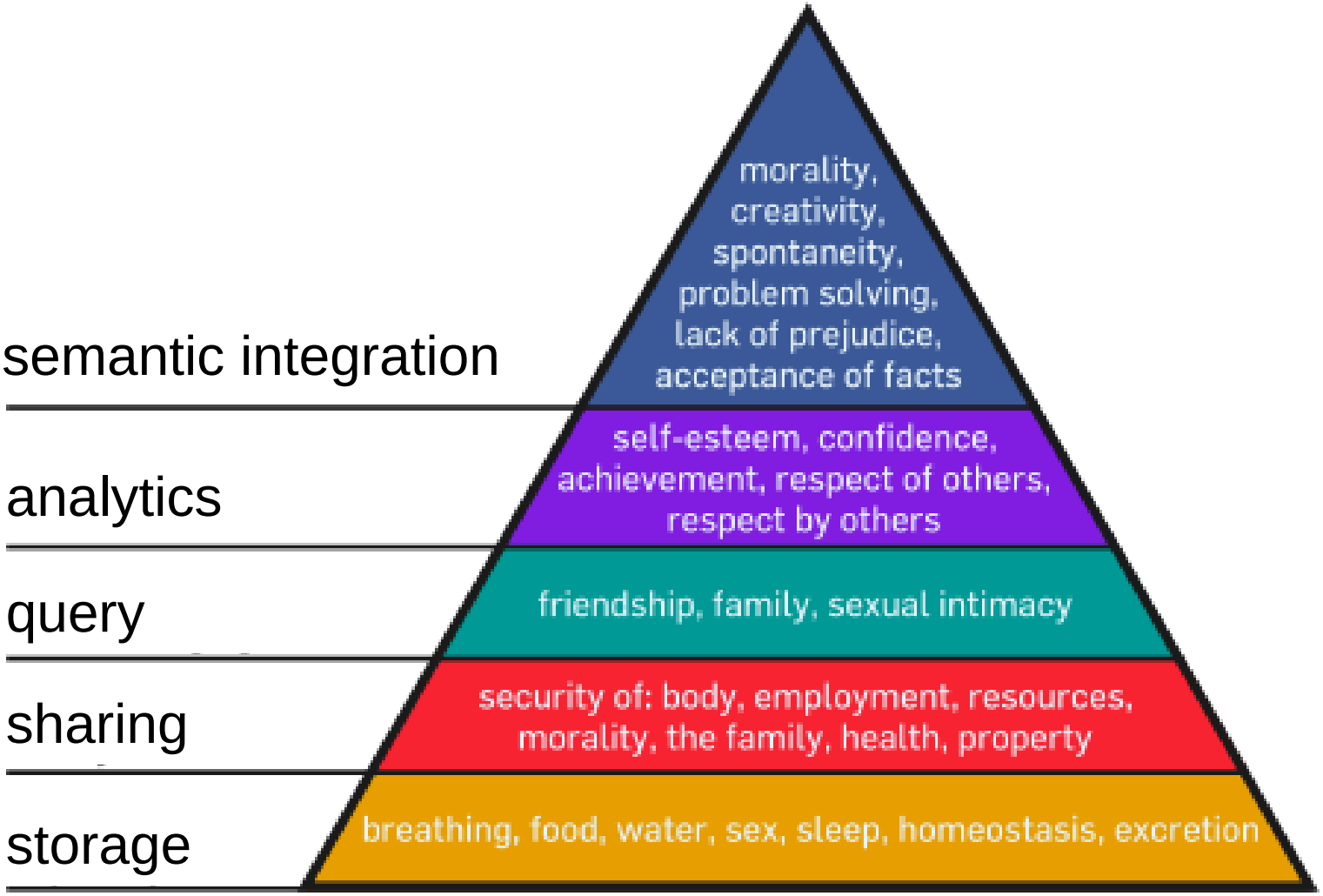
Needs Hierarchy [Maslow 43]

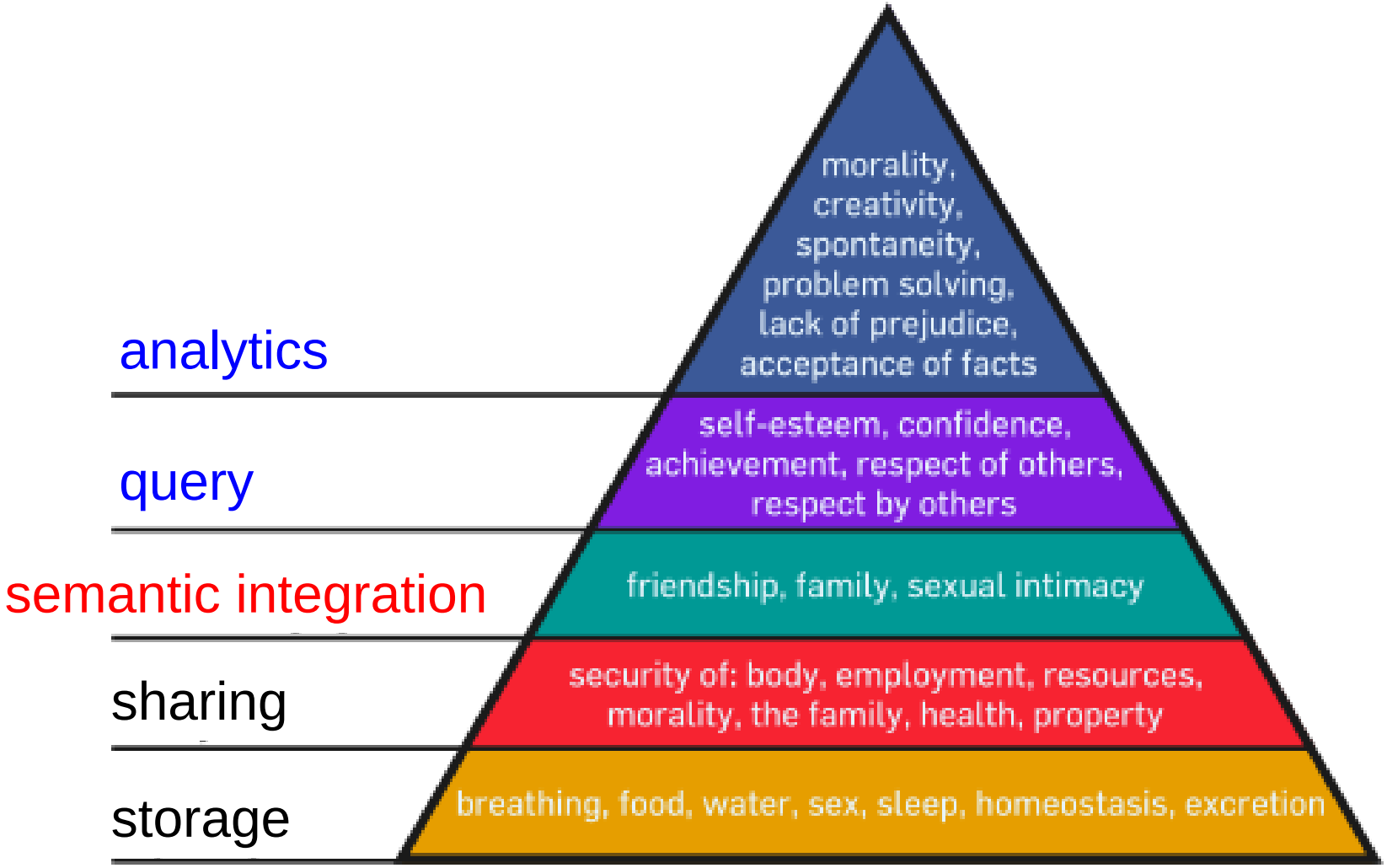


"As each need is satisfied, the next higher level in the hierarchy dominates conscious functioning."

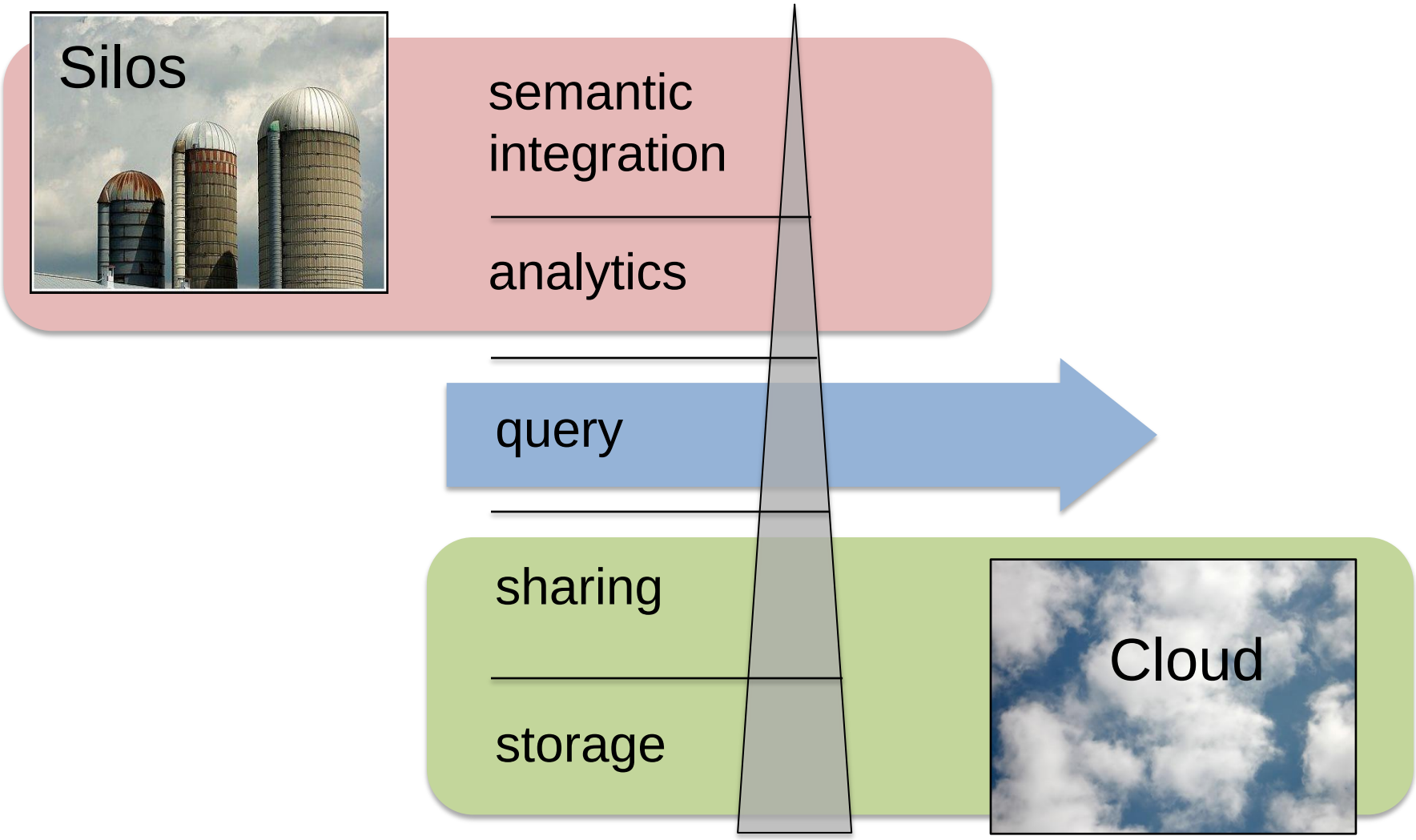
A “Needs Hierarchy” of Science Data Management



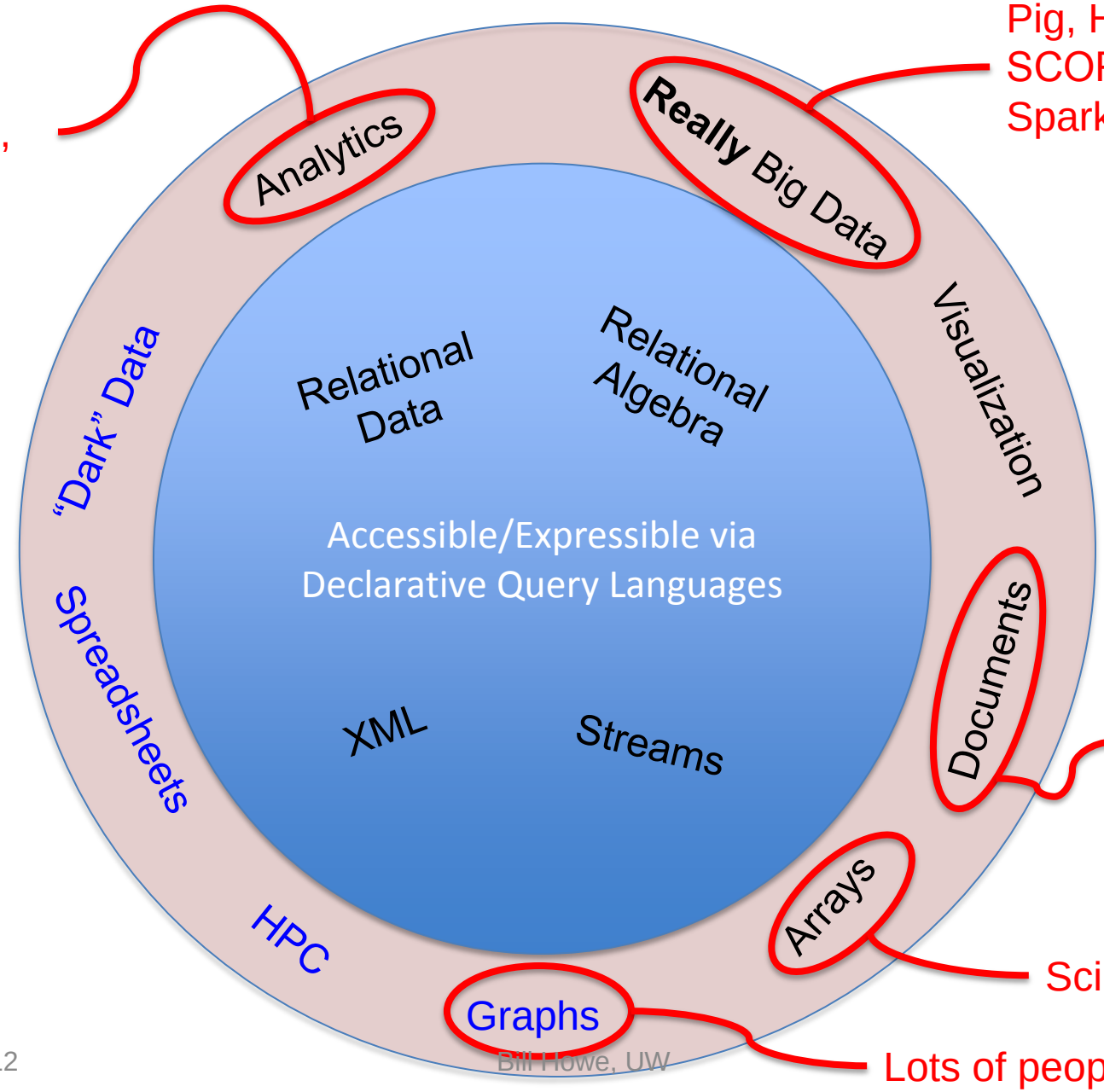
A "Needs Hierarchy" of Science Data Management



A "Needs Hierarchy" of Science Data Management



Goal: Expose all the world's science data through declarative query interfaces


MADLib, Chris Re, etc.
Analytics
Really Big Data
Pig, HIVE, SCOPE, …, Spark, etc.
Visualization
Documents
AI, IR folks
Arrays
SciDB
Graphs
Lots of people
HPC
Spreadsheets
"Dark" Data
Relational Data
Relational Algebra
Accessible/Expressible via Declarative Query Languages
XML
Streams

Microsoft Research

Projects in this Space

- Database-as-a-Service for the 99%
  http://sqlshare.escience.washington.edu
- Parallel Datalog for Declarative, Scalable Analytics for the 1%
  http://clue.cs.washington.edu
- Exploratory Visual Analytics
  http://vizdeck.com
- Data Pricing: Incentives for Data Sharing
  (lead: Magda Balazinska)

NSF

Gordon and Betty MOORE FOUNDATION

eScience Institute

DATABASE-AS-A-SERVICE FOR THE 99%

Problem

How much time do you spend "handling data" as opposed to "doing science"?

Mode answer: "90%"

ANNOTATIONSUMMARY-COMBINEDORFANNOTATION16_Phaeo_genome

###query	length	COG hit #1	e-value #1	identity #1	score #1	hit length #1	description #1
chr_4[480001-580000].287	4500						
chr_4[560001-660000].1	3556						
chr_9[400001-500000].503	4211	COG4547	2.00E-04	19	44.6	620	Cobalamin biosynthesis protein
chr_9[320001-420000].548	2833	COG5406	2.00E-04	38	43.9	1001	Nucleosome binding factor SPN
chr_27[320001-404298].20	3991	COG4547	5.00E-05	18	46.2	620	Cobalamin biosynthesis protein
chr_26[320001-420000].378	3963	COG5099	5.00E-05	17	46.2	777	RNA-binding protein of the Puf
chr_26[400001-441226].196	2949	COG5099	2.00E-04	17	43.9	777	RNA-binding protein of the Puf
chr_24[160001-260000].65	3542						
chr_5[720001-820000].339	3141	COG5099	4.00E-09	20	59.3	777	RNA-binding protein of the Puf
chr_9[160001-260000].243	3002	COG5077	1.00E-25	26	114	1089	Ubiquitin carboxyl-terminal hyd
chr_12[720001-820000].86	2895	COG5032	2.00E-09	30	60.5	2105	Phosphatidylinositol kinase and
chr_12[800001-900000].109	1463	COG5032	1.00E-09	30	60.1	2105	Phosphatidylinositol kinase and
chr_11[1-100000].70	2886						
chr_11[80001-180000].100	1523						

COGAnnotation_coastal_sample.txt

id	query	hit	e_value	identity_	score	query_start	query_end	hit_start	hit_end	hit_length
1	FHJ7DRN01A0TND.1	COG0414	1.00E-08	28	51	1	74	180	257	285
2	FHJ7DRN01A1AD2.2	COG0092	3.00E-20	47	89.9	6	85	41	120	233
3	FHJ7DRN01A2HWZ.4	COG3889	0.0006	26	35.8	9	94	758	845	872
…										
2853	FHJ7DRN02HXTBY.5	COG5077	7.00E-09	37	52.3	3	77	313	388	1089
2854	FHJ7DRN02HZO4J.2	COG0444	2.00E-31	67	127	1	73	135	207	316
…										
3566	FHJ7DRN02FUJW3.1	COG5032	1.00E-09	32	54.7	1	75	1965	2038	2105
…										

SELECT * FROM Phaeo_genome p, coastal_sample c WHERE p.COG_hit = c.hit

Find all TIGRFam ids (proteins) that are missing from at least one of three samples (relations)

```
SELECT col0 FROM [refseq_hma_fasta_TGIRfam_refs]
UNION
SELECT col0 FROM [est_hma_fasta_TGIRfam_refs]
UNION
SELECT col0 FROM [combo_hma_fasta_TGIRfam_refs]

EXCEPT

SELECT col0 FROM [refseq_hma_fasta_TGIRfam_refs]
INTERSECT
SELECT col0 FROM [est_hma_fasta_TGIRfam_refs]
INTERSECT
SELECT col0 FROM [combo_hma_fasta_TGIRfam_refs]
```

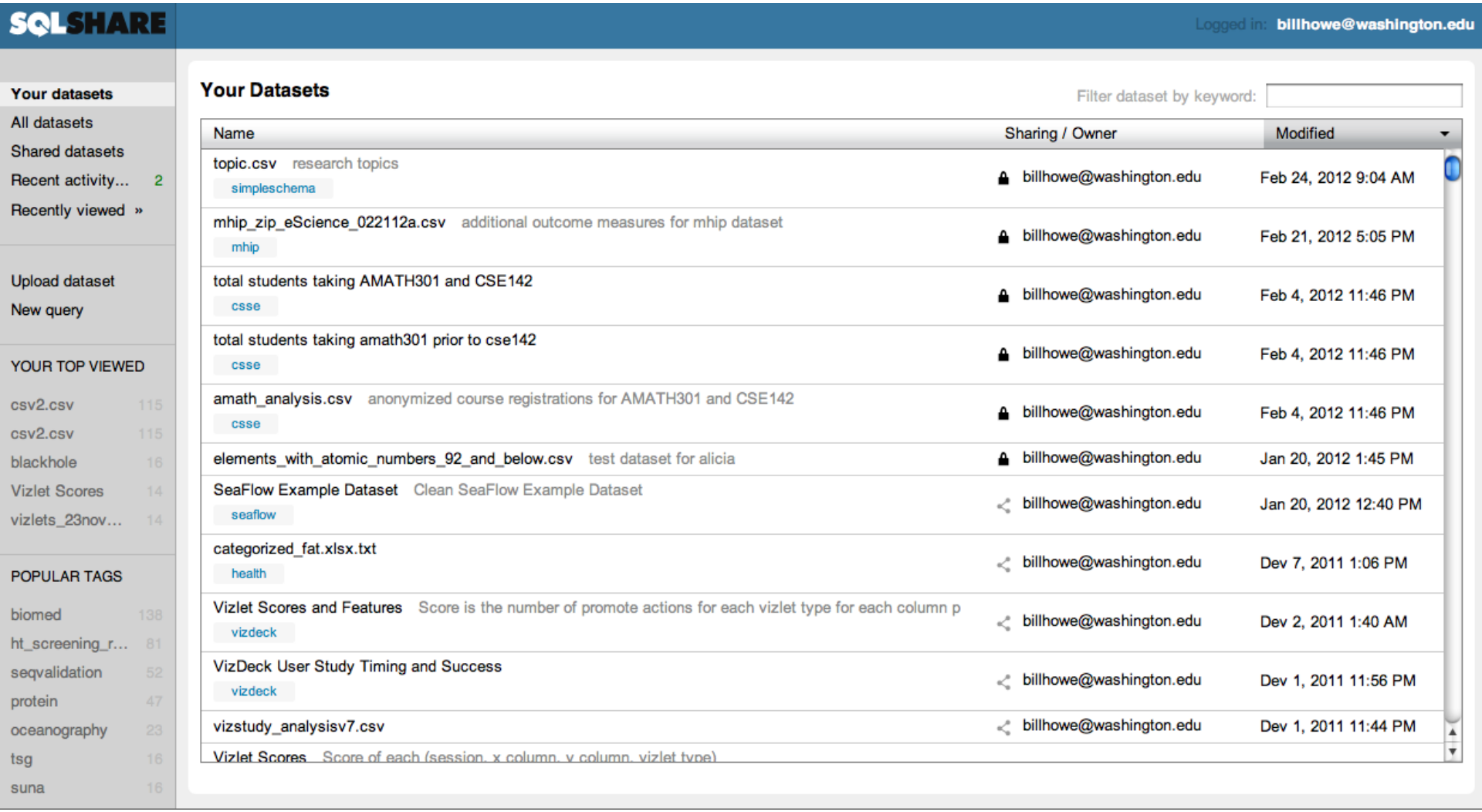
Saved Queries = Views

- Integrate data from multiple sources?
  - *joins and unions with views*
- Standardize on units, apply naming conventions?
  - rename columns, apply functions with views
- Attach metadata?
  - add new tables, add new columns with views
- Data cleaning, quality control?
  - hide bad values with views
- Maintain provenance?
  - inspect view dependencies
- Propagate updates?
  - view maintenance
- Protect sensitive data?
  - expose subsets with views (assuming views carry permissions)

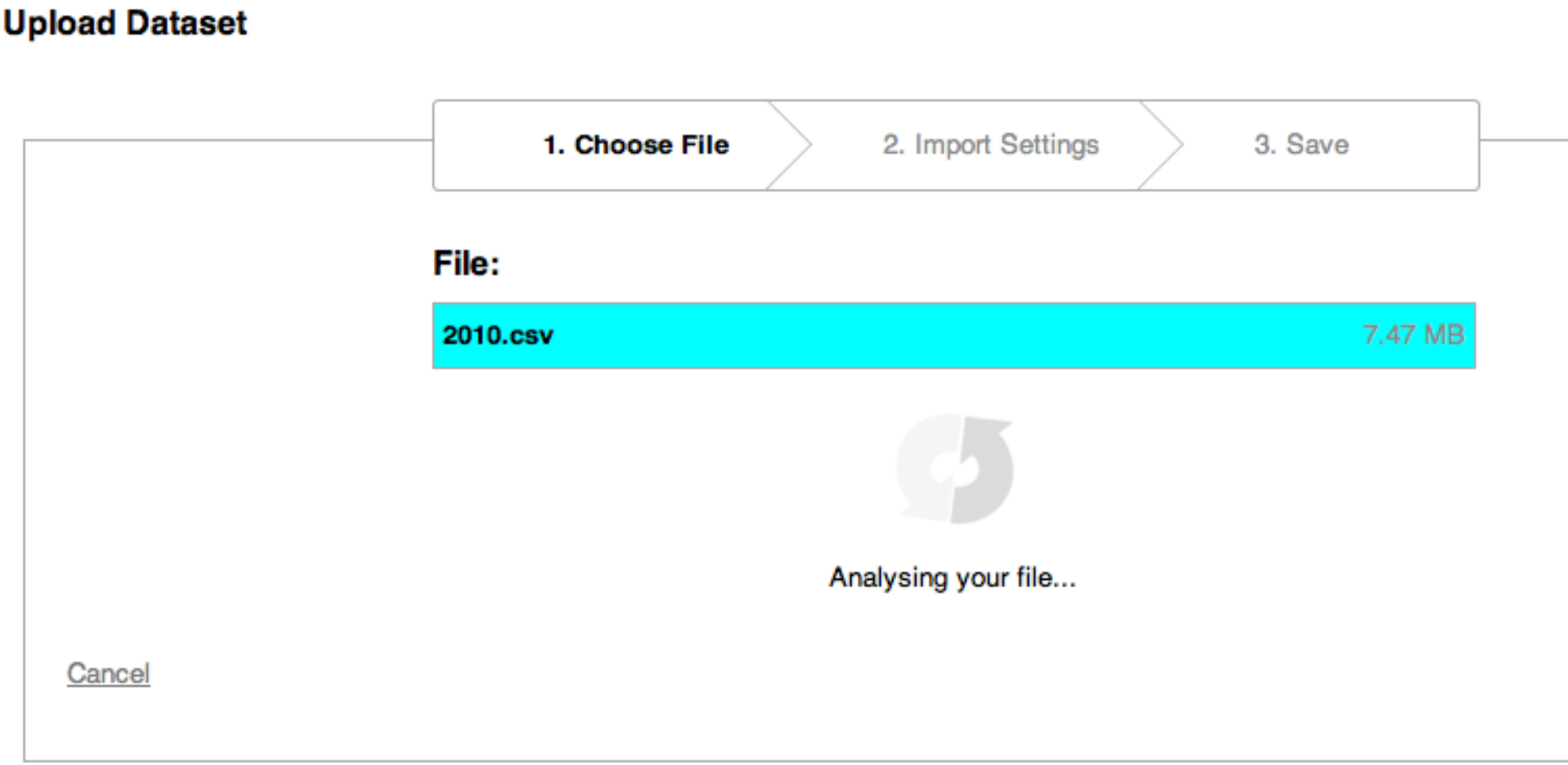
What's the point?

- Databases are underused by the 99%
- Conventional wisdom says "Scientists won't write SQL"
  - This is nonsense
  - We corroborate findings by SDSS, etc.
- Instead, we implicate difficulty in
  - installation
  - configuration
  - **schema design**
  - performance tuning
  - **data loading**
  - app-building

We ask instead, "How can we deliver declarative query in support of ad hoc scientific Q&A?"



http://sqlshare.escience.washington.edu



http://sqlshare.escience.washington.edu

Upload Dataset

1. Choose File | **2. Import Settings** | 3. Save

Dataset was imported with the following settings:

You can change the parser options if your data was not properly imported.

☑ Contains column header | Values are separated by ,

DATASET PREVIEW (Imported table with **3 columns**)

activity	thrust	time in past 12 months
SQLShare Engineering	long-tail	1
SQLShare research	long-tail	1
Client+Cloud	long-tail	1
HaLoop	scalable analytics	1.5
Cloud Vis	scalable analytics	1

Cancel

Back Next

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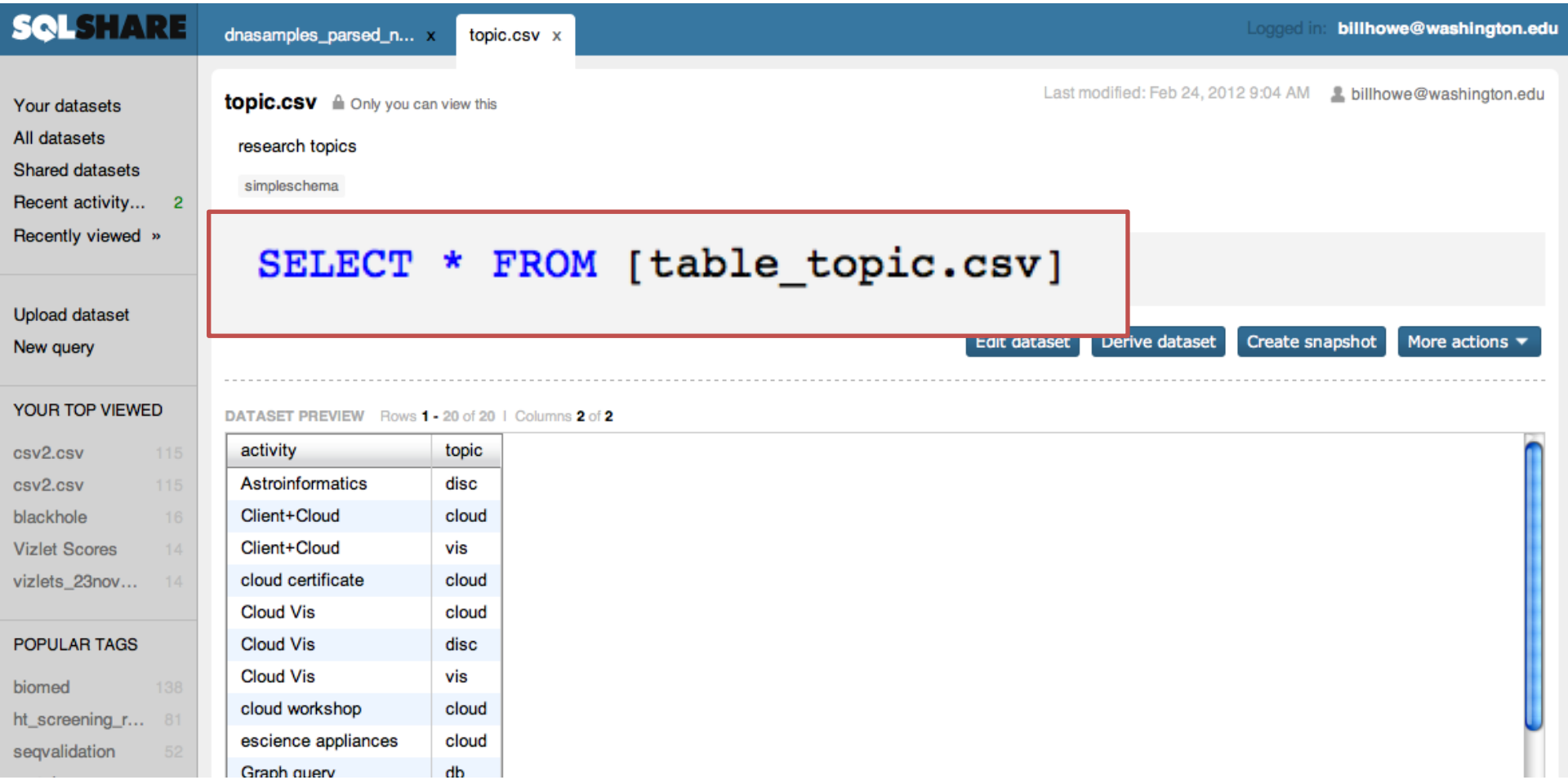

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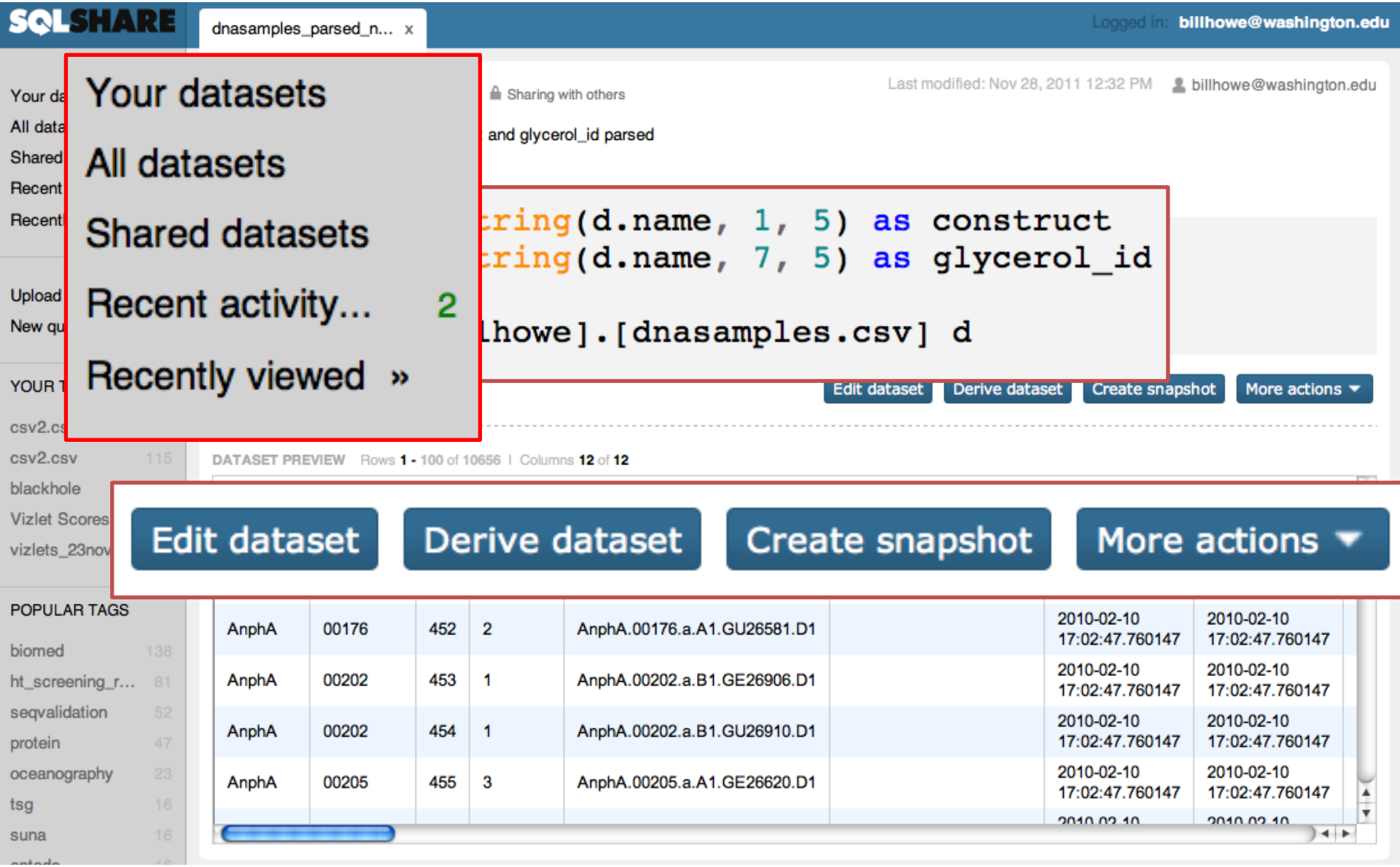

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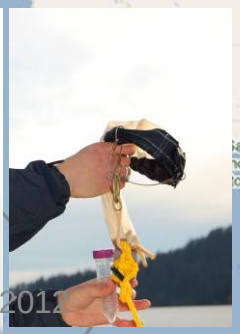
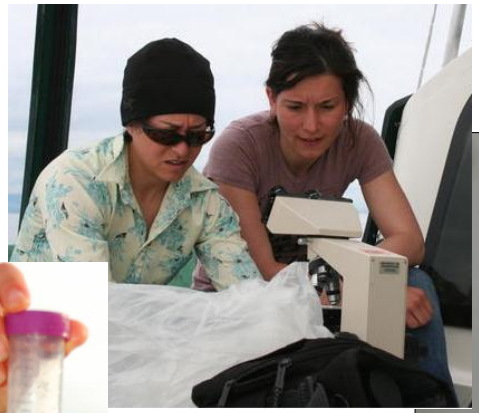
2010 Pilot- Outreach and Education-based sampling: Schooner Adventuress

Robin Kodner



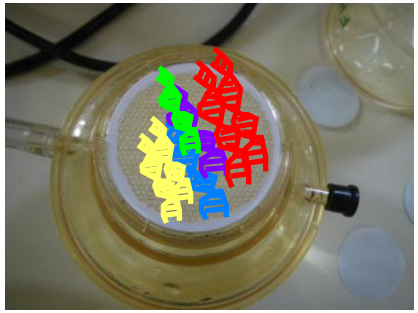
plankton tows

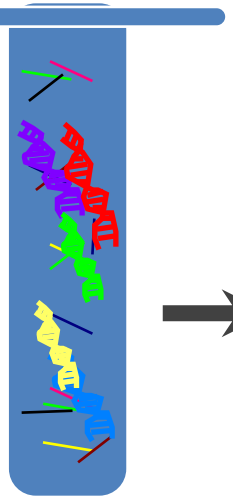


	A	B	C	D	E	F	G	H	I	J	K
1	Sample: 13 - Stuart Island										
2	Date: 1 Sep 2010, counted on 21 Sep 2010										
3	Dilution Factor:	1									
4	Notes: 55 mL of sample										
5	Total volume counted (uL):										10
6	*Chaetosceros*	35	34	20	28	67	20	47	13	10	16
7	*Asterionellopsis*	19	21	5	15	1	14	6		1	4
8	*Thalassiosira*	6			4	6	1	1		4	2
9	*Ditylum*	2	1	1	2	2	2	1	1	6	3
10	*Cylindrotheca*	2			1		1				1
11	*Dictyocha*	2									1
12	*Pseudo-nitzschia*	2	6		2	3			5	4	2
13	*Odontella*	1	2	2				2	3		
14	*Leptocylindrus*	1			4		5	1	14	5	1
15	*Skeletonema*		17		13	10	2		22		
16	*Rhizosolenia*		2	2	4	1		1	2	1	2
17	*Tropidoneis*		1	1	1				1		1
18	*Pyrophacus*					2					
19	*Protoperidinium*							1	1		
20	*Ceratium*								1		
21											
22											
23											
24											
25											
26											
27											
28	Total Cell Count:		84	31	74	92	45	60	63	31	33
29	Total Cells:										513
30	Cells/mL										51300

taxa counts

whole water



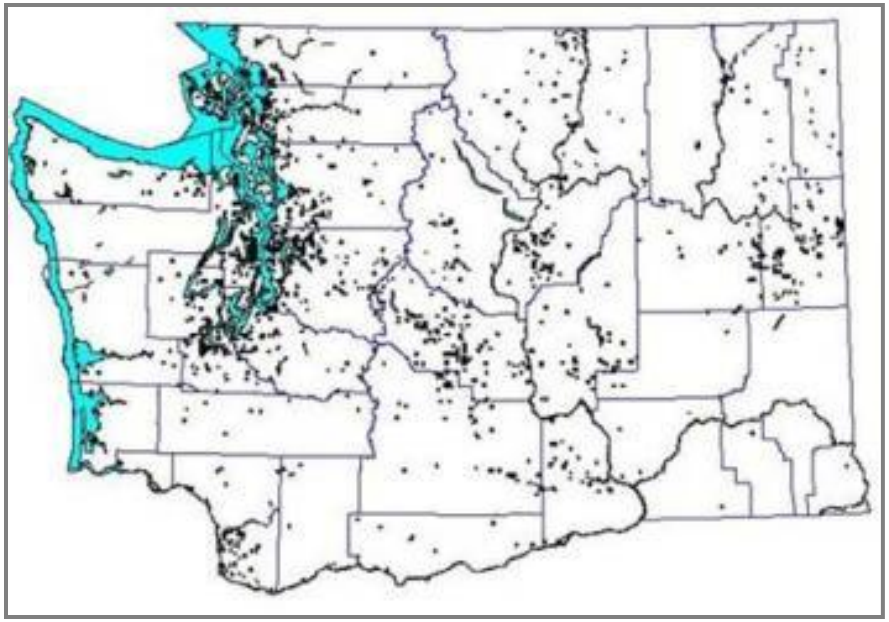


nutrient analysis + toxin analysis

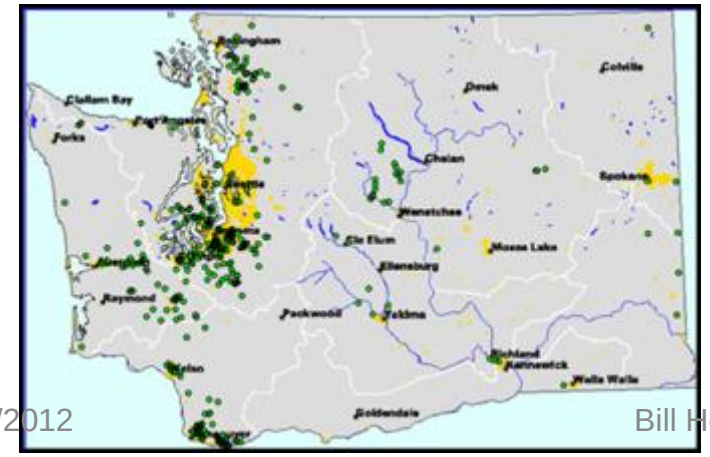
NatureMapping Program

Karen Dvornich

Wildlife Observations (1902-)

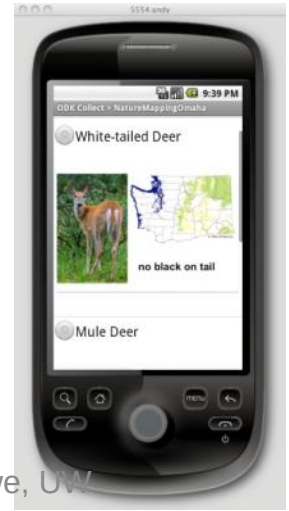


Water Quality Monitoring Sites (2003 -)

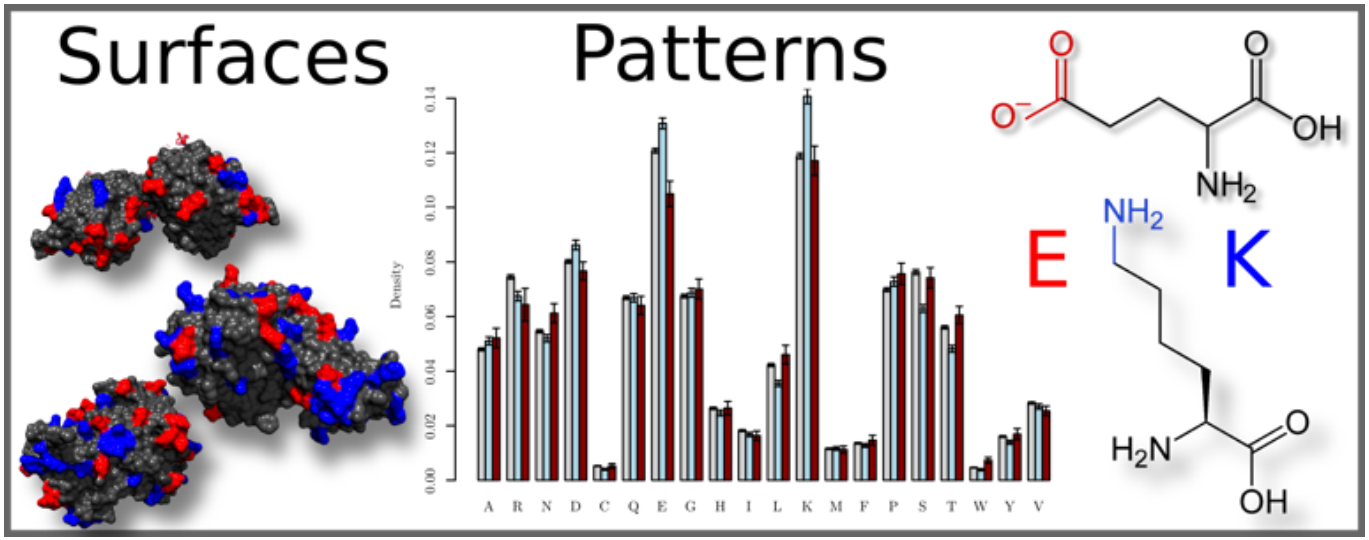


Data collection and submission options:

1. **Download/upload spreadsheet**
2. **Online data entry**
3. **NatureTracker on handheld/GPS**
4. **Android ODK (Open Data Kit)**



Andrew White,
UW Chemistry



"An undergraduate student and I are working with gigabytes of tabular data derived from analysis of protein surfaces.

Previously, we were using huge directory trees and plain text files.

Now we can accomplish a 10 minute 100 line script in 1 line of SQL."

-- Andrew D White

SQLShare as a CS Research Platform

- SQL Autocomplete
  - (Nodira Khoussainova, YongChul Kwon, Magda Balazinska)
- English to SQL
  - (Bill Howe, Luke Zettlemoyer, Emad Soroush, Paras Koutris)
- Automatic "Starter" Queries
  - (Bill Howe, Garret Cole, Nodira Khoussainova, Leilani Battle)
- VizDeck: Automatic Mashups and Visualization
  - (Bill Howe, Alicia Key)
- Personalized Query Recommendation
  - (Yuan Zhou, Bill Howe)
- Info Extraction from Spreadsheets
  - (Mike Cafarella, Dave Maier, Bill Howe)
- Differential Privacy in Multi-tenant DBs
  - (Dan Suciu, Bill Howe)

SSDBM 2011
SIGMOD 2011 (demo)

SSDBM 2011
CHI 2012
SIGMOD 2012 (demo)

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Four Conjectures about Declarative Query for Science

- Most science data manipulation tasks can be expressed in relational algebra
- Most science analytics task can be expressed in relational algebra + recursion

  Hellerstein 09, Re 12
- These expressions can be efficiently and scalably executed in the cloud
- Researchers are willing and able to program using relational algebra languages

  c.f. SDSS