

## **SQLSHARE**

## Results from a Multi-Year SQLas-a-Service Experiment

SHRAINIK JAIN

DB DAY 2015

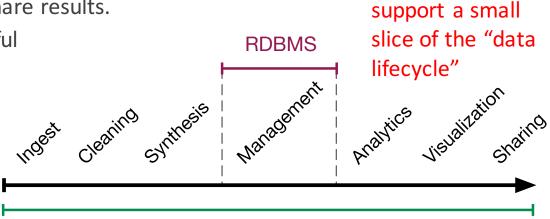
S Jain, D Moritz, B Howe, et al. SQLShare: Results from a Multi-Year SQL-as-a-Service Experiment, SIGMOD16.

## Part 1: SQLShare, DBaaS for Scientists

## Databases are great, but....

They are underused in science workloads (physical, life and social sciences)

- Why?
  - Is there a fundamental mismatch in Data Model?
  - "Scientists can't write SQL"?
  - Other barriers to adoption?
    - Pre-engineered Schemas: Don't usually exist, given the ad-hoc nature of research.
    - Clean data a pre-condition: But real data is messy!
    - A database can make it harder rather than easier to share results.
    - Provenance: Tracking the history of operations is painful
    - Low data lifetime.



Databases only

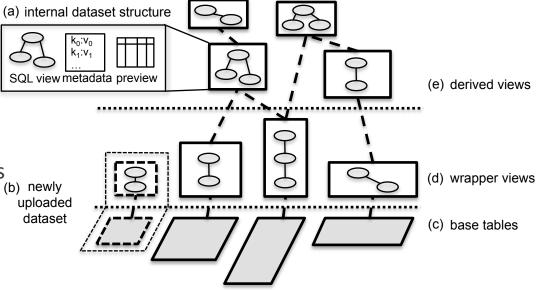
## SQLShare: Making databases easier to use

#### **Relaxed Schemas**

- Infer data types automatically.
- Tolerate errors. For example:
  - use NULLs for the case of variable number of columns per row.
  - No column names
  - 0

#### Provenance and Sharing

- Views as first class citizens
- Checkpoint operations as derived datasets or views





#### 3) Share the results

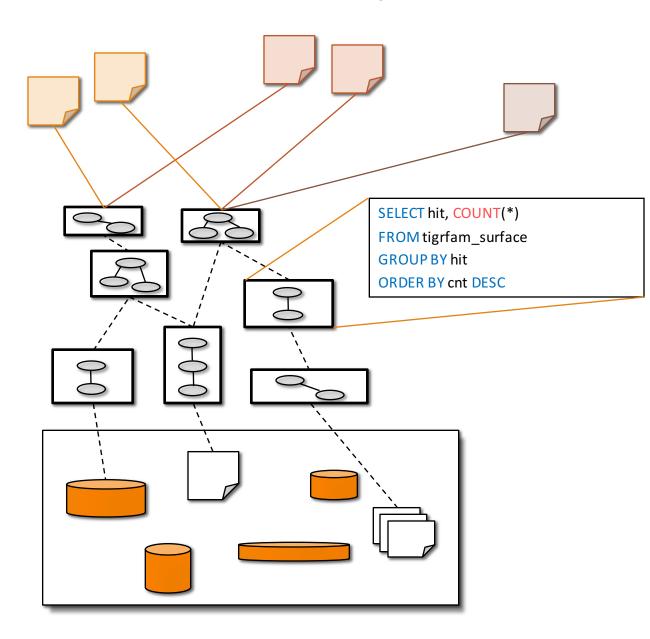
Make them public, tag them, share with specific colleagues – anyone with access can query

#### 2) Write Queries

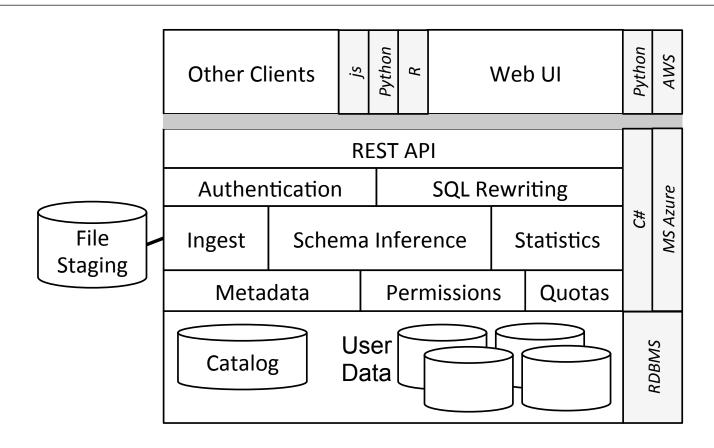
Right in your browser, writing views on top of views on top of views ...

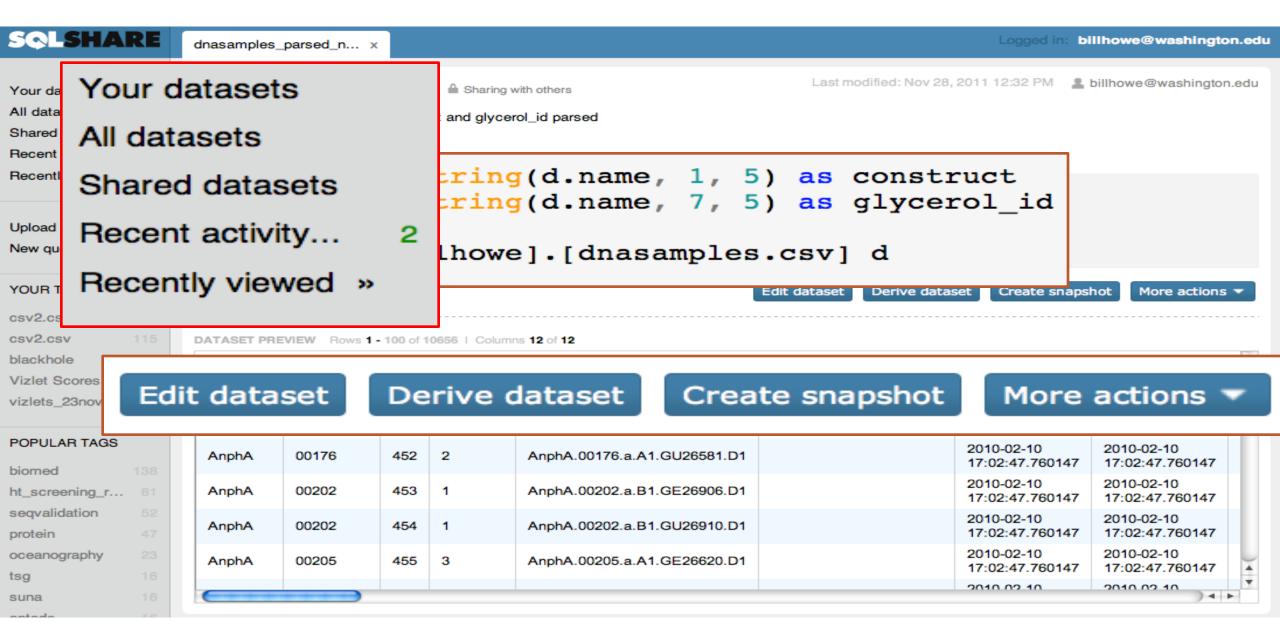
#### 1) <u>Upload data "as is"</u>

Cloud-hosted, secure; no need to install or design a database; no pre-defined schema; schema inference; some itegration



## SQLShare





http://sqlshare.escience.washington.edu

12/2/15 BILL HOWE, UW 7

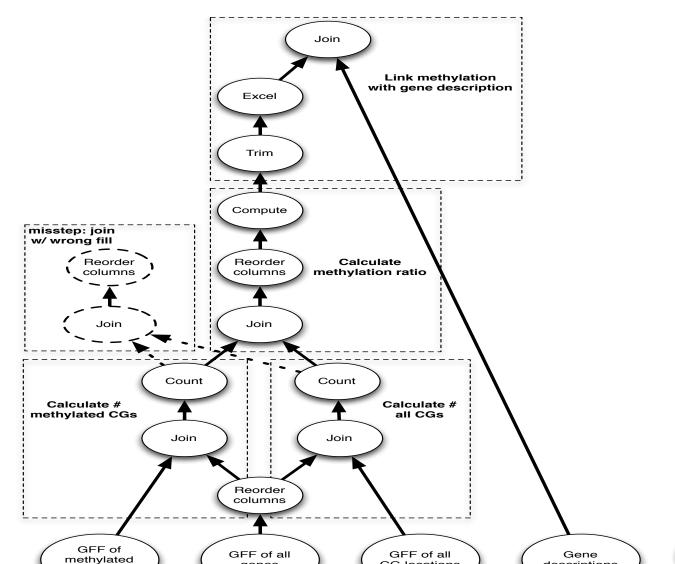


#### Example: Computing the overlaps of two sets of blast results

```
SELECT x.strain, x.chr, x.region as snp region, x.start bp as snp start bp
  , x.end bp as snp end bp, w.start bp as nc start bp, w.end bp as nc end bp
  , w. category as nc category
  , CASE WHEN (x.start bp >= w.start bp AND x.end bp <= w.end bp)
 THEN x.end bp - x.start bp + 1
 WHEN (x.start bp <= w.start bp AND w.start bp <= x.end bp)
 THEN x.end bp - w.start bp + 1
 WHEN (x.start bp <= w.end bp AND w.end bp <= x.end bp)
 THEN w.end bp - x.start bp + 1
END AS len overlap
FROM [koesterj@washington.edu].[hotspots deserts.tab] x
INNER JOIN [koesterj@washington.edu].[table_noncoding_positions.tab] w
ON x.chr = w.chr
WHERE (x.start_bp >= w.start_bp AND x.end_bp <= w.end_bp)
OR (x.start bp <= w.start bp AND w.start bp <= x.end bp)
OR (x.start bp <= w.end bp AND w.end bp <= x.end bp)
ORDER BY x.strain, x.chr ASC, x.start bp ASC
```

We see thousands of queries written by non-programmers

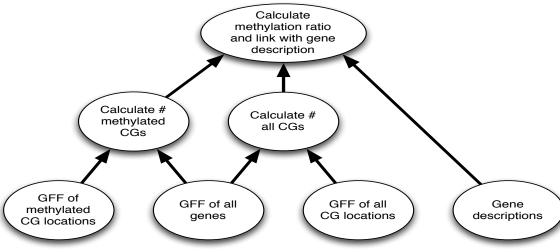
```
1 table <- read.csv(''table.csv'')</pre>
                                               1 WITH data AS
                                                    (SELECT * FROM [table.csv]),
2 # define 3 min time intervals
3 breaks <- seq(</pre>
                                                       — compute the minimum timestamp
            min(table$time),
                                                       bounds AS
           max(table$time),
                                                    (SELECT min(time) AS mintime FROM data),
                                                       — assign each timestamp a bin
             \mathbf{b}\mathbf{y}=3)
                                                       binned AS
7 # bin the table according to the breaks
                                                7
8 b <- cut(table$time, breaks=breaks)
                                                    (SELECT bounds.mintime +
                                                            floor ((data.time - bounds.mintime)/3.0) *
                                                9
                                                            3.0 as binid
10 # calculate the mean of each variable
                                               10
11 b.time <- tapply(table$time, b, mean))
                                                      FROM data, bounds)
12 b. Fluo <- tapply (table $Fluo, b, mean))
                                               12 — compute the average of each bin
13 b. Temp <- tapply (table $Temp, b, mean))
                                               13 SELECT binid
14 b.Oxyg <- tapply(table$Oxyg, b, mean))
                                                    , avg(Fluo) as Fluo
15 b. Nitr <- tapply(table$Nitr, b, mean))
                                                    , avg(Temp) as Temp
16 b.Lat <- tapply(table$Lat, b, mean))
                                                    , avg(Oxyg) as Oxyg
17 b.Lon <- tapply(table$Lon, b, mean))
                                                    , avg(Nitr) as Nitr
                                               18
                                                    , avg(Lon) as Lon
18
19 binned. table <- data.frame(
                                                    , avg(Lat) as Lat
                                               19
            cbind (b. time, b. Fluo, b. Temp,
                                                    , avg(time) as time
                  b.Oxyg, b.Nitr,
                                               21 FROM binned
21
                  b.Lat, b.Lon))
                                               22 GROUP BY binid
23 write.csv(binned.table, 'binned.csv')
                                               23 ORDER BY binid asc
```



Steven Roberts



SQL as a lab notebook: <a href="http://bit.ly/16Xj2JP">http://bit.ly/16Xj2JP</a>





CG locations

genes

Popular service for Bioinformatics Workflows

descriptions

CG locations



### Did it work?

#### SQLShare used for real life work:

- Multiple labs used it and liked it.
- And wrote increasingly complex queries.
- And wrote queries on dirty data.
  - And even used SQL to cleanup data!

SQLShare Queries were diverse.

Attracted new kinds of ad-hoc queries

That were written to replace files and scripts

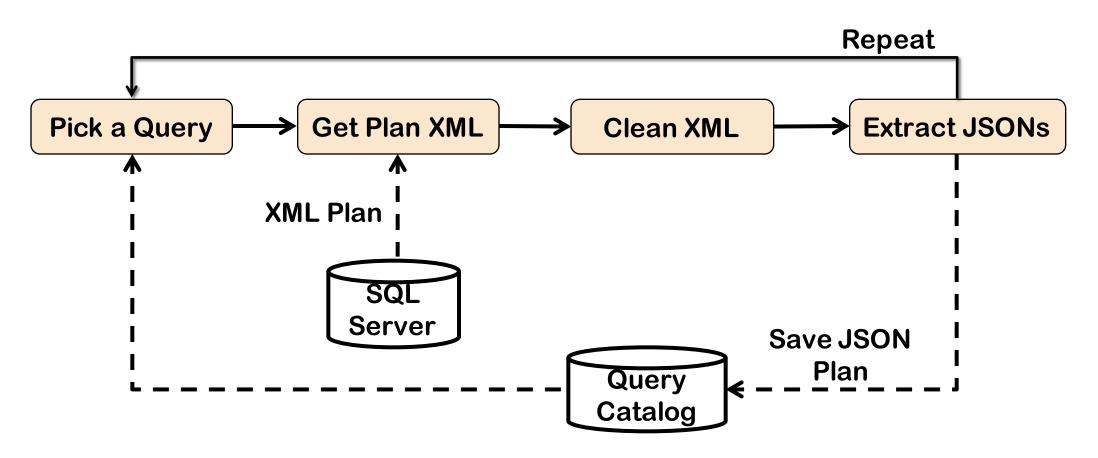
#### SQLShare Attracted High-Churn Work

- Varying data lifecycle.
- Quick insights from dirty data

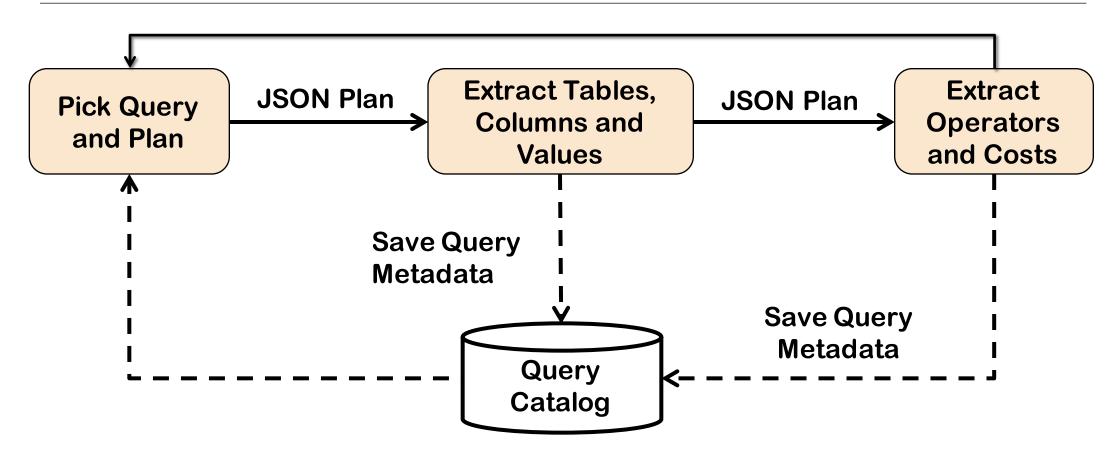
## Part 2: SQLShare Workload Analysis

... Or reasons why this is potential benchmark dataset.

## Analyzing the corpus: Methodology



## Analyzing the corpus: Methodology



## SQLShare query corpus

#### Workload Metadata

Measure	Value
Users	591
Tables	3891
Columns	73070
Views	7958
Non-trivial Views	4535
Queries	25052

#### Query Metadata

Feature	Average Value
Length	217.32
Runtime	3175.38 s
# of operators	18.12
# of Distinct Operators	2.71
# of Tables accessed	2.31
# of Columns accessed	16.22
# of Queries per Table	12

## Results from SQLShare Workload analysis

SQLShare Queries are *Complex* 

SQLShare Queries are *Diverse* 

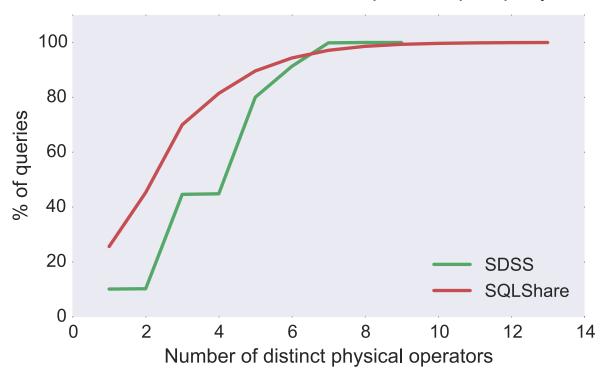
Views Afford Controlled Data Sharing

Dataset Permanence Varies by User: Ad hoc data analytics often deals with low lifetime datasets

SQLShare Attracts High-Churn Work

## Results: SQLShare Queries are Complex





Lots of simple queries, but huge complexity in the tail!

### Results: SQLShare Queries are Diverse

#### Diversity:

Percentage of 'unique' queries.

#### How do we define Uniqueness?

- Naïve measure:
  - ASCII string uniqueness
- If two queries reference different sets of attributes?
- Query plan template uniqueness?

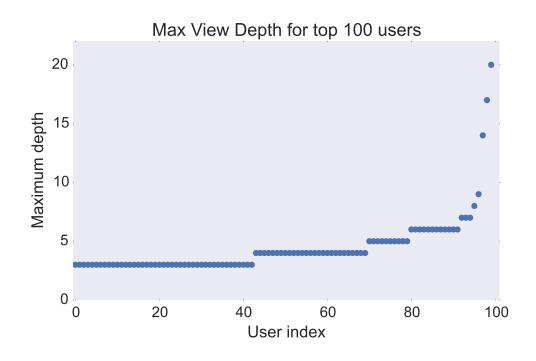
### Results: SQLShare Queries are Diverse

<b>Diversity Metric</b>	SDSS	SQLShare
Total Queries	7M	25052
String distinct queries	200K	24096
Column distinct queries	467	10928
Distinct query template	686	15199

SQLShare queries are more diverse and have 63% distinct query templates. In contrast, SDSS has only 0.3% distinct query templates

# Results: Views Afford Controlled Data Sharing & Provenance

- The view-centric data model also affords collaboration: users can share the derived dataset (and its provenance)
- About 56% of the datasets in the system are derived from other datasets using views.
- 37% of the datasets in SQLShare are public.
- 10% of the queries logged in the system access datasets that the query author does not own.



## Results: Dataset Permanence Varies by User

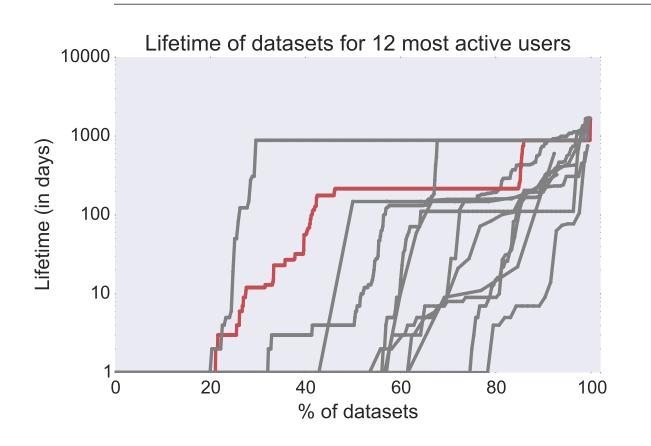
Many users are operating in short-duration analysis loops, where they upload some data, write a few queries, and then move on to another task.

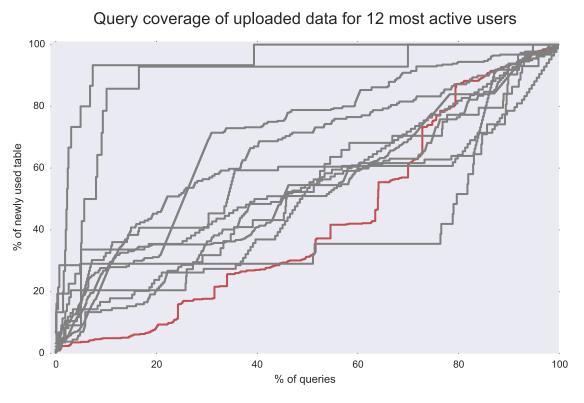
• How do we measure this?

#### Dataset Lifetime:

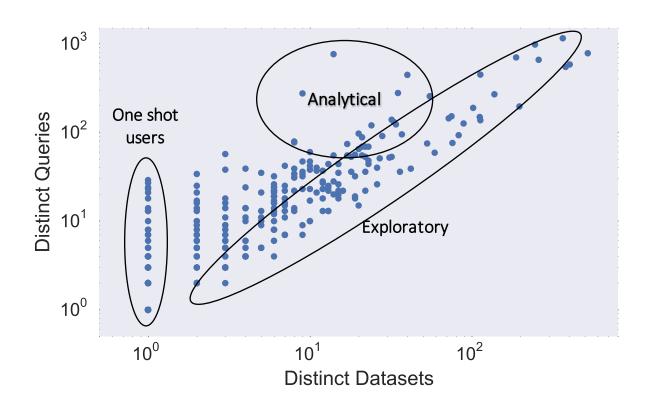
 The difference in days between the first and the last time that dataset was accessed in a query

## Results: Dataset Permanence Varies by User





## Results: SQLShare Attracts High-Churn Work



### Towards a Benchmark Dataset

We're releasing the data, queries, and views as a research corpus

https://uwescience.github.io/sqlshare/data\_release.html

### Future work

#### Identify query idioms:

- Cleanup tasks.
- Binning.

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#### Publish the SQLShare dataset.

- A benchmark of 'real' queries.
  - Captures complex data & complex tasks.

#### Enable more real-life science operations:

- Write SQL to do more.
  - Matrix multiplication?
  - Automatic conversion from RA to SCIDB AFL.

## Thanks!