

Supporting Large Scale Scientific and Engineering Applications Using Database Technology

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Setting Expectations

- Most computational science involving “big data” is still managed by file systems
- Programming is mainly procedural using scripting languages
- There is little data sharing independent of the programs – no data independence
- MapReduce approaches perceived as effective and easier to use
- Thus, database technology has a high-hill to climb to become the de-facto platform for engineering and scientific apps

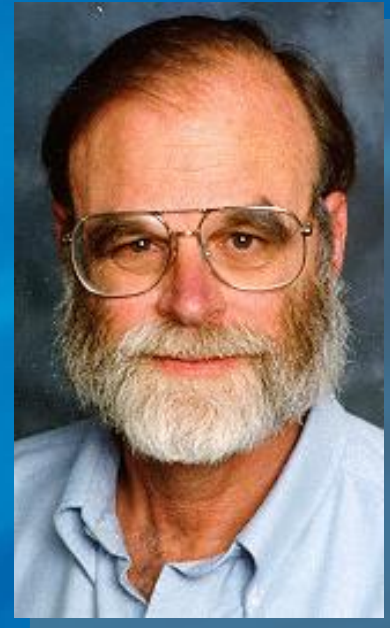
Some perceived problems

- Databases are hard to use
- Database are not sufficiently scalable
- Tools of the database field such as data modeling not widely understood by scientists
- Fear of vendor “lock-in”
- Hard to break away from established practices in a science
-

Our Experience

- Microsoft has been learning about scientific and engineering apps for the last 10 years
- Have had good successes working side-by-side with scientists
 - Astronomy, genomics, comparative analysis for RNA sequences, protein folding, carbon climate analysis
- Every success has been transformational to the way science is performed in each science
- We believe there is a great opportunity for databases to significantly impact the sciences

Gray's Laws for Data Engineering



- Large-scale scientific computing is data intensive
 - Database management systems can help
- The solution is in “scale-out” architectures
 - Both functional and data scale-out
- Move analysis to the data!
 - Increasingly true with larger data set sizes
- Start the design with “20 queries”
 - Engages domain and computer scientists in data modeling design on the most important queries
- Go from “working to working”
 - “Don’t let the best get on the way of the better”
 - Iterative improvement works

A Data Platform for Science

Visualization &
Reporting Svcs

Libraries
(MATLAB,...)

Web Services
(XML, REST, RSS)

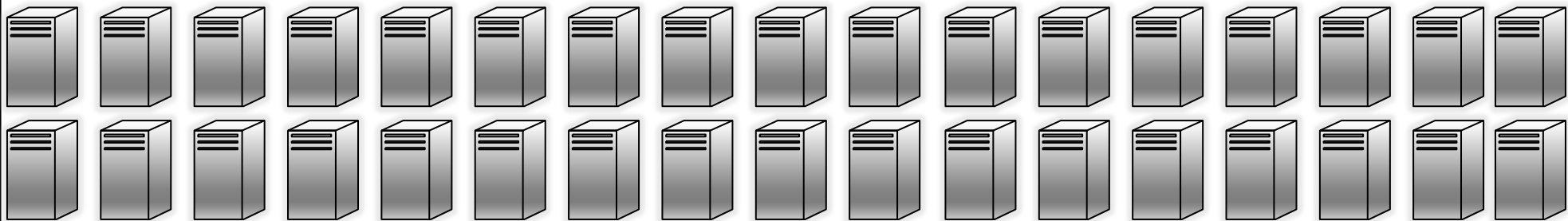
OLAP, Data
Mining, Excel

Streaming
Complex Events

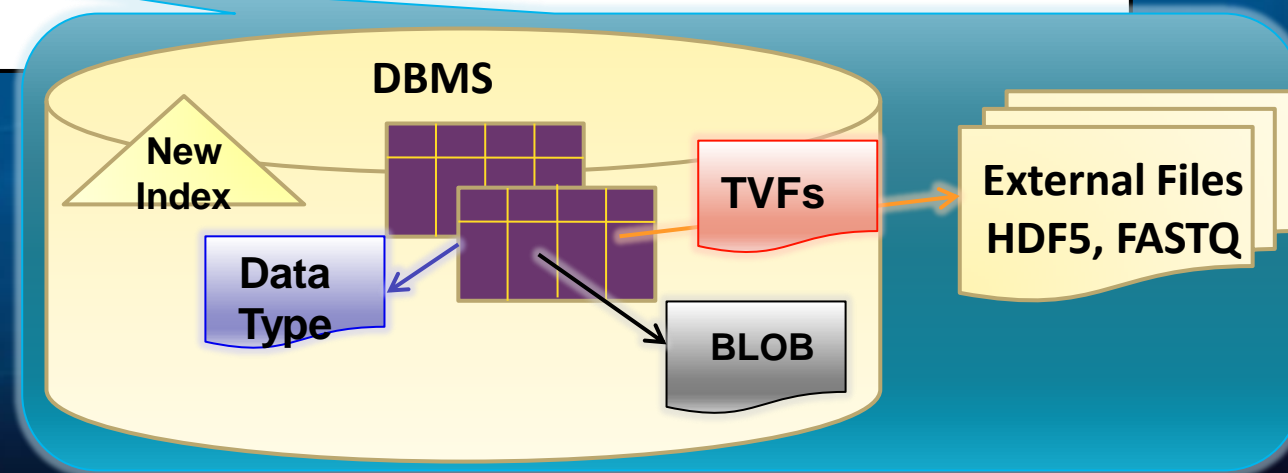
.NET Languages with Language Integrated Query

Entity Framework (EDM, Entity SQL, O-R mapping)

Science models (e.g., HDF5, FASTQ, RDF)



Parallel DBMS cluster



Some Case Studies

- Astronomy: SkyServer, Pan-STARRS
- Global scale carbon flux – FLUXNET
- Predictive medicine – Clalit Health Services
- High-throughput genomics – 1000 genome
 - Massive sequence alignment (UT Austin)
 - Microsoft Life Sciences
- Integrated Comparative Analysis System for RNA Sequences – The Gutell's Lab @ UTA
- ... many more

Case study

Sky-Server, PAN-STARRS

*Distributed, scale-out database system,
moving analysis to the data*

Dr. Alex Szalay, JHU

PAN-STARRS

- Sky survey to detect 'killer asteroids'
- Two phases
 - PS1: single telescope prototype now
 - PS4: 4 telescope array in 4 years
- Hawaii + JHU + Harvard + Edinburgh + Max Planck Society
- High data rate: 2.5 Petabytes/year
- 5B celestial objects/250B detections
- 100TB prototype database built at JHU with Microsoft help



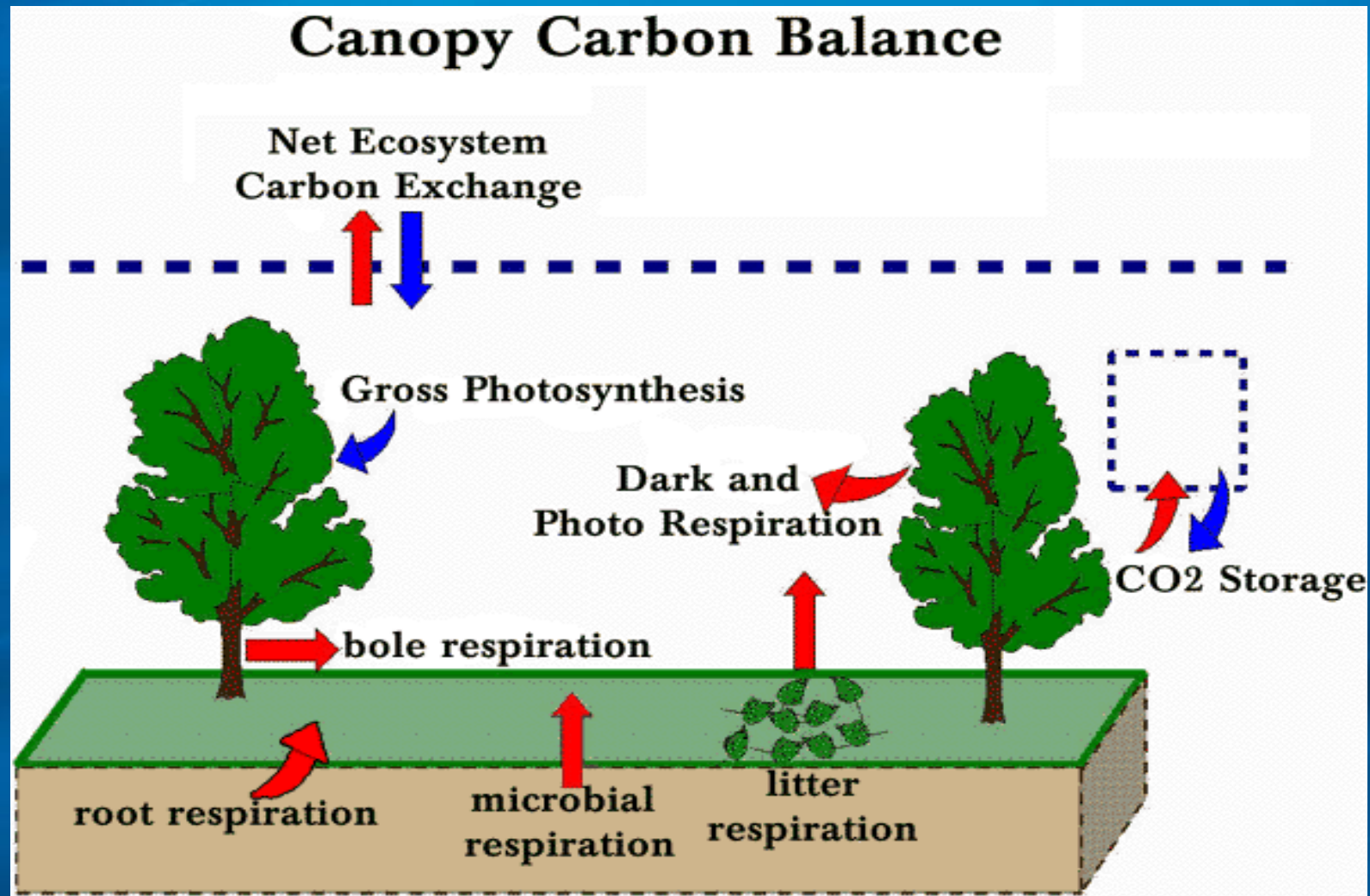
Case study

Global Scale Carbon Flux Research @
Berkeley Water Center

*Leveraging Reporting and Data Analysis to
increase quality of data*

Dr. Deborah Agarwal and BWC tech team

Carbon Climate Analysis



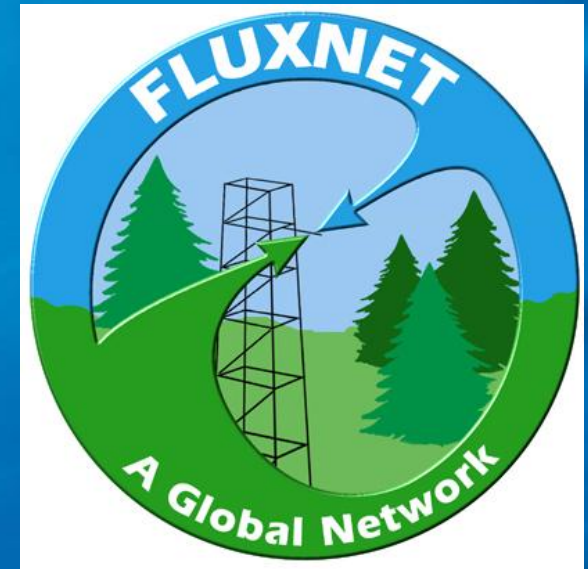
$$F_c + F_{\text{storage}} = -\text{NEE} = P_{\text{new}} + R_{\text{leaf}} + R_{\text{wood}} + R_{\text{roots}} + R_{\text{microbes}}$$

Applications of eddy covariance measurements, Part 1: Lecture on Analyzing and Interpreting CO₂ Flux Measurements, Dennis Baldocchi, CarboEurope Summer Course, 2006, Namur, Belgium (<http://nature.berkeley.edu/biometlab/lectures/>)

Carbon-Climate Analysis Goals

Get a handle on data collection

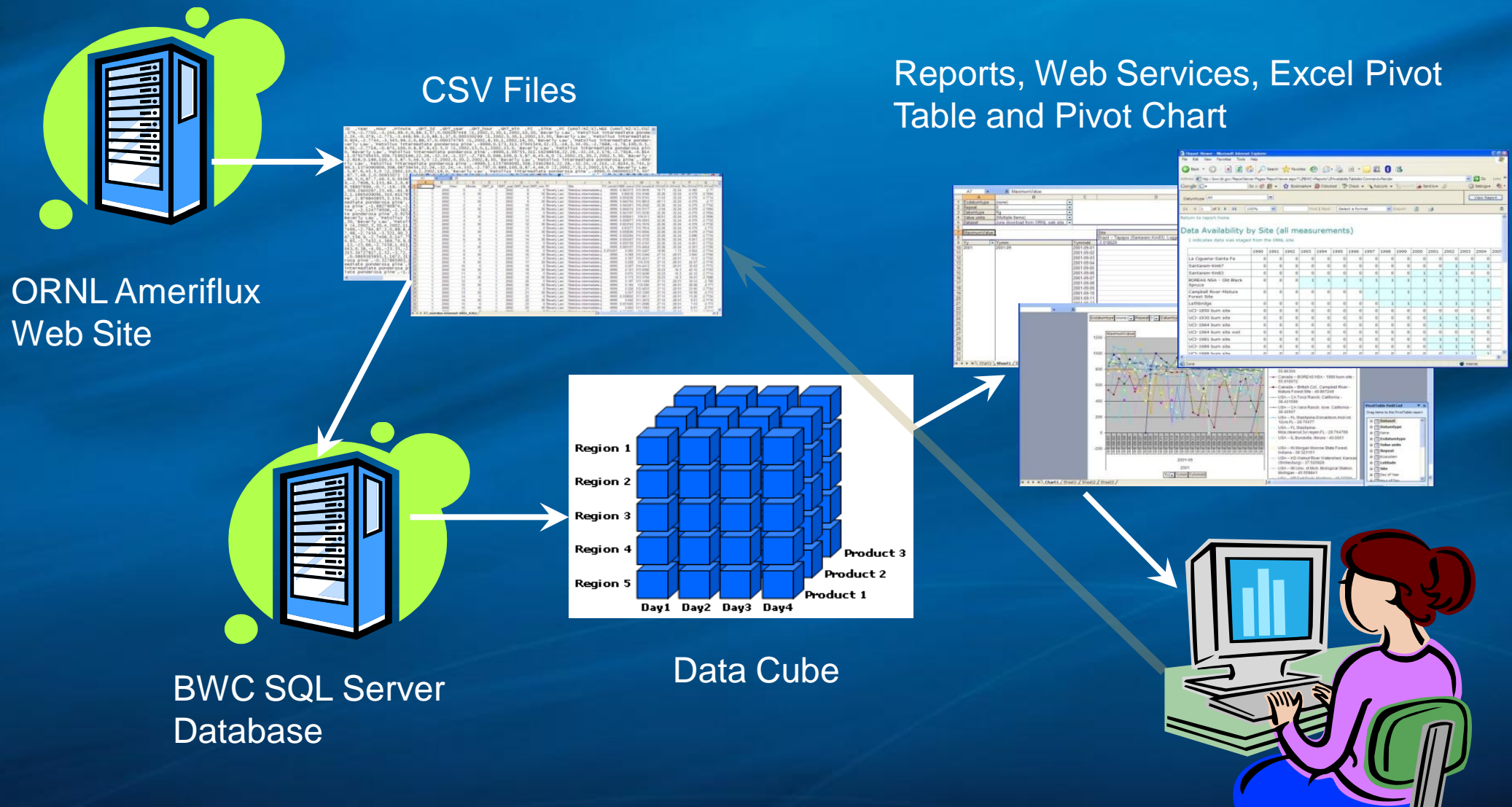
- Towers measure consistent carbon flux and micrometeorological parameters
- Tower researchers quality check data and then provide the data to regional archives.
- Regional and global carbon-climate analysis activities rely on data from regional archives
- Recent La Thuile workshop is gathering over 900 site-years of data available from over 200 sites around the world.



Measurements Are Often Not Simple or Complete

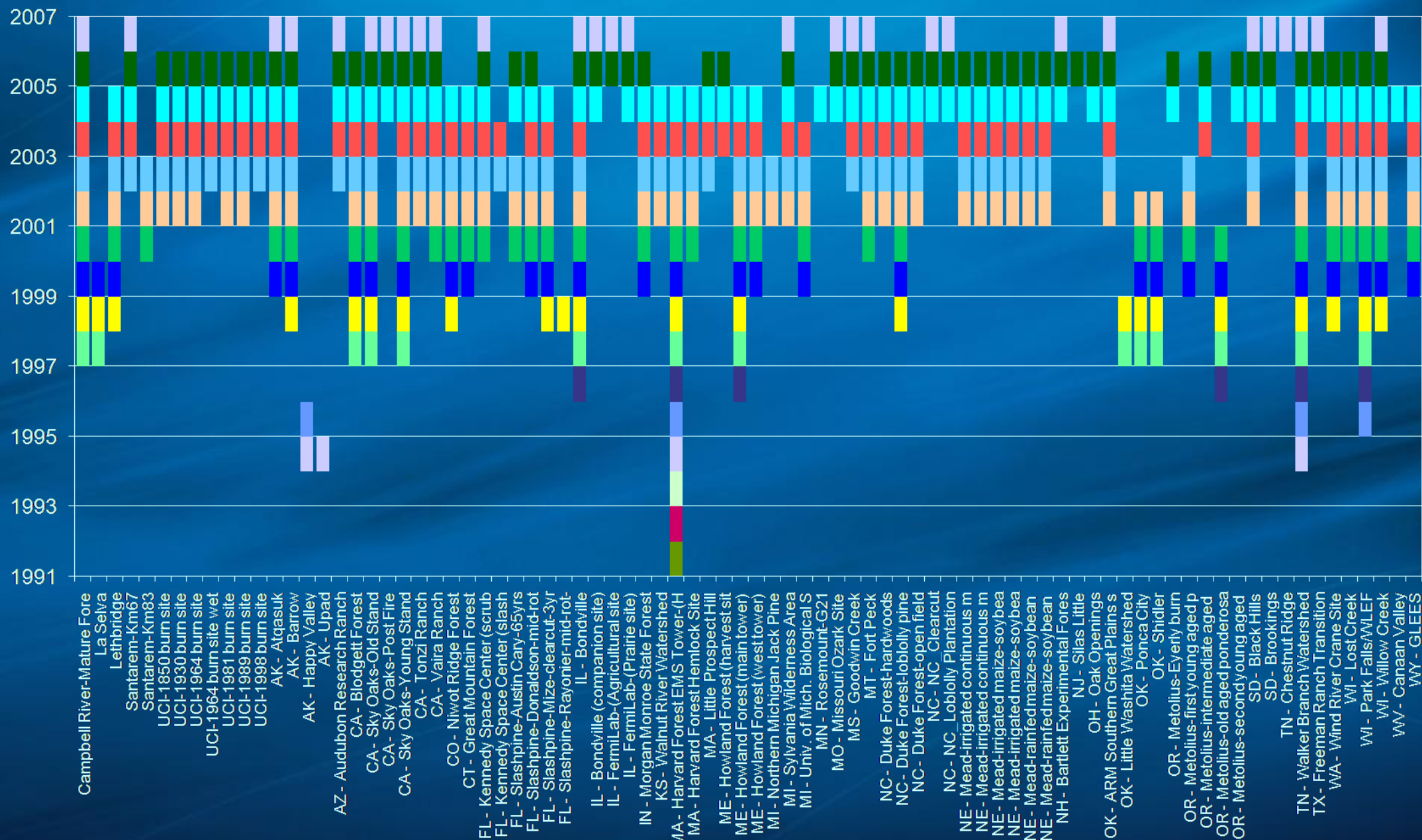
- Gaps in the data
 - E.g., quiet nights, bird poop, high winds
- Discrepancies in units of measure
- Difficult to make measurements
 - Leaf area index
 - Wood respiration
 - Soil respiration
- Localized measurements – tower footprint
- Local investigator knowledge important
- Pls' science goals are not uniform across the towers

Scientific Data Server – User Interface



Visualizing Data Availability

Ameriflux Sites Reporting Data Colored by Year



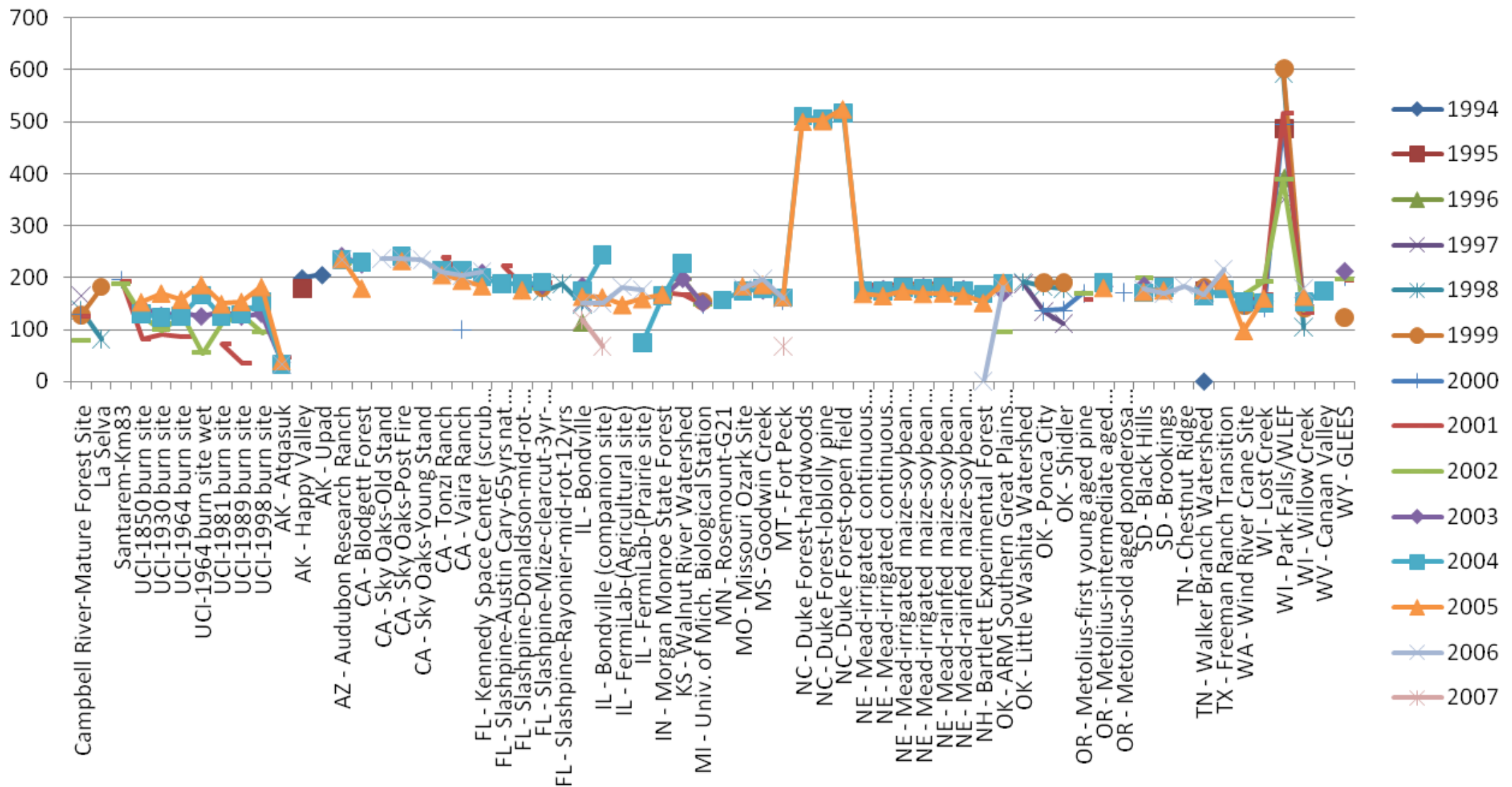
Required Variable Reporting by Site by Year

- Each row corresponds to one site-year
- Each cell corresponds to one site year of (FC, CO₂ or SCO₂, UST, PAR or Rg, TA, and Rh or H₂O).
- Color indicates:
 - Red – likely not enough for processing - % < .3 reported (roughly less than 5K of 17.5K)
 - Green – likely enough for processing .3 < % < .999
 - Yellow – may not be good for processing due to gap-filling - % > .999
- Red CO₂ (second column) can be ignored for cropland/grassland sites
- Sites shown are just a sample

[illegible]

Of the 285 site years with good FC, 50 site years are missing one of (UST, PAR/Rg, and TA) and 79 sites have likely gap-filled data.

Obviously bad annual averages



Data cube used to browse average yearly Rg values across all site-years
16 additional likely problematic site-years at 5 sites

Case study

Clalit Health Services

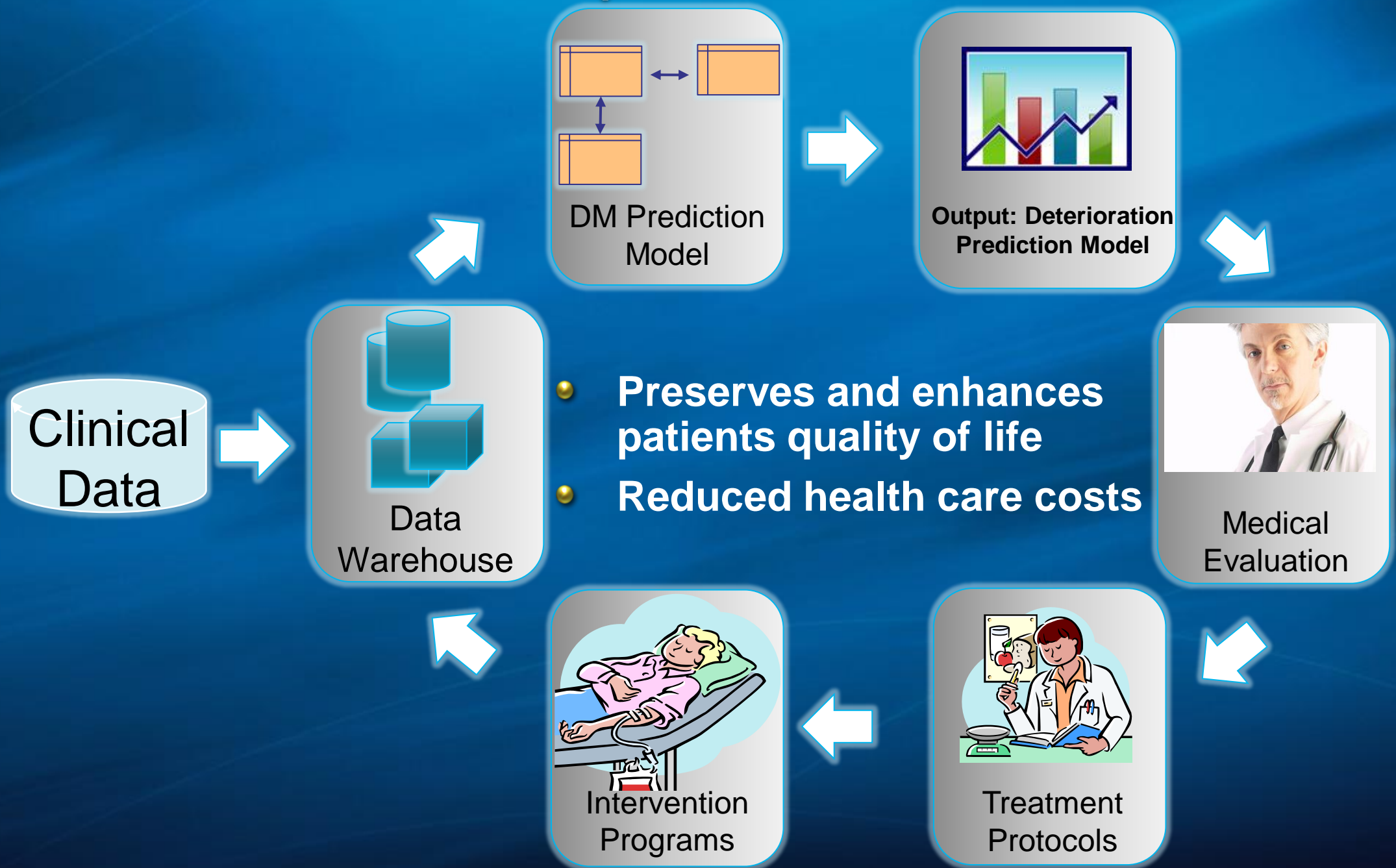
*Business intelligence moves medicine
from reactive to proactive*

Clalit Health Services

- Largest provider of medical care in Israel
 - 3.7 million patients
 - 14 hospitals
 - 1400 clinics
- Needed to identify which members would most benefit from proactive intervention to prevent health deterioration
- Developed an integrated 1.5 TB relational database plus data mining service

Solution

A shift from reactive to proactive medicine

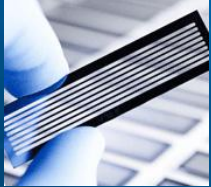


Case study

High-Throughput Genomics

*Data Modeling, In-situ Data
Management, Aggregation in database*

1000 Genome Pipeline



Wet Lab:
Sample
Preparation



1 flowcell



Illumina
Sequencer

1 image per tile / base / cycle



Level 0 Data:
TIF Images

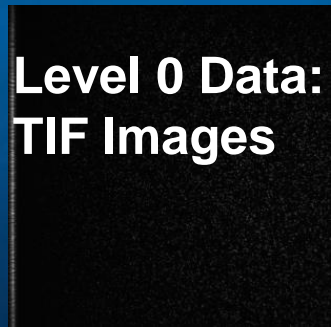
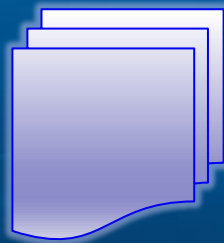


Image analysis



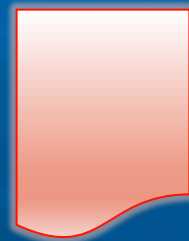
Level 1 Data:
Short Reads



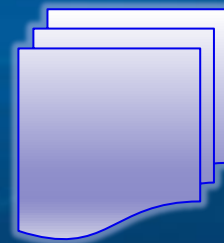
Alignment



Reference Seq.



Level 2 Data:
Alignments



Consensus



Level 3 Data:
Sequences



380,160 images
750 GB / run

8 SRF files (1 per lane)
10-15 GB / run

1 file per lane
0.5 GB / run

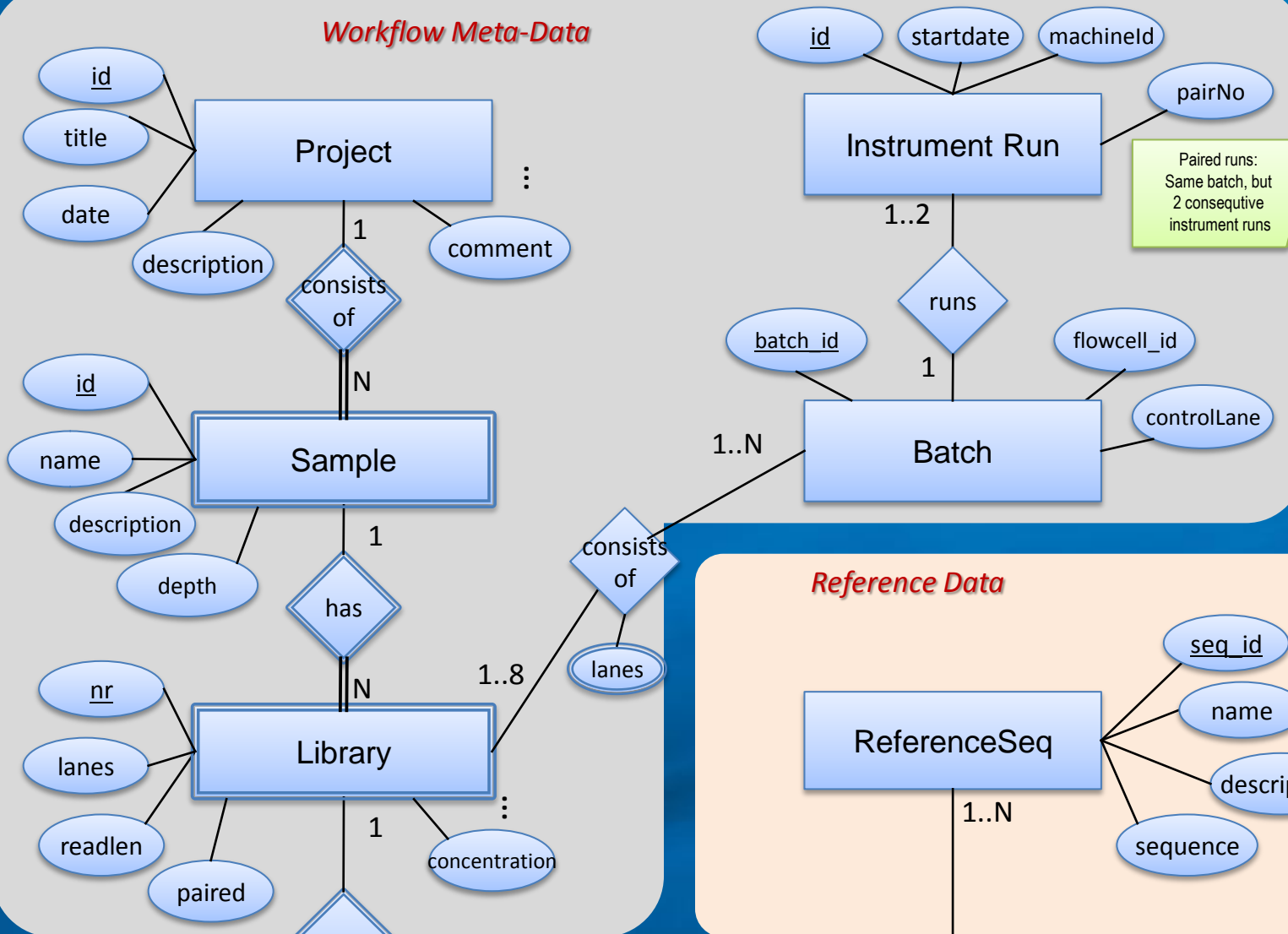
1 file per sample
~3 GB

About the Scale of the Problem

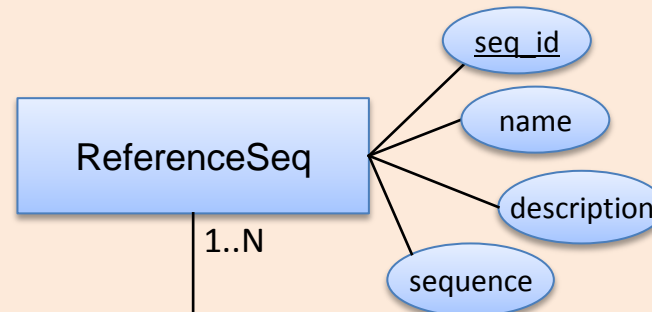
- Sanger Institute has currently 28 instruments
- 24 x 7 (in avg 20 in use at any given time)
- => per week:
 - ~75 TB Level 0 data (images)
 - 0.5 TB Level 1 data (short-reads)
- Plan for another 10 Solexas by end of year
- Only one of 3 labs worldwide
- Technology constantly improving

Data Model

Workflow Meta-Data

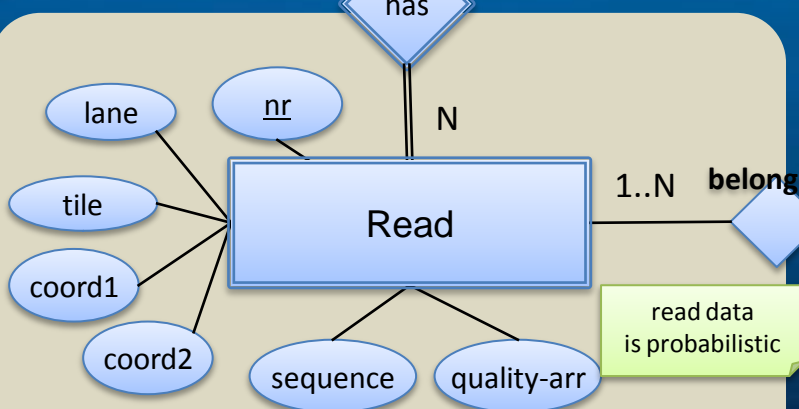


Reference Data



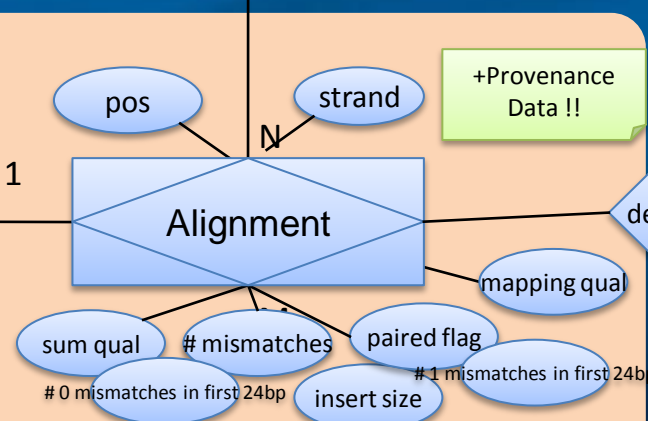
+more data
abt. refseqs

Level 1 Data



read data
is probabilistic

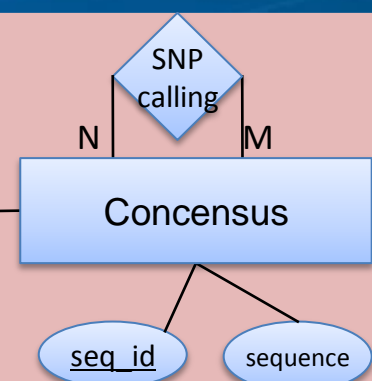
Level 2 Data



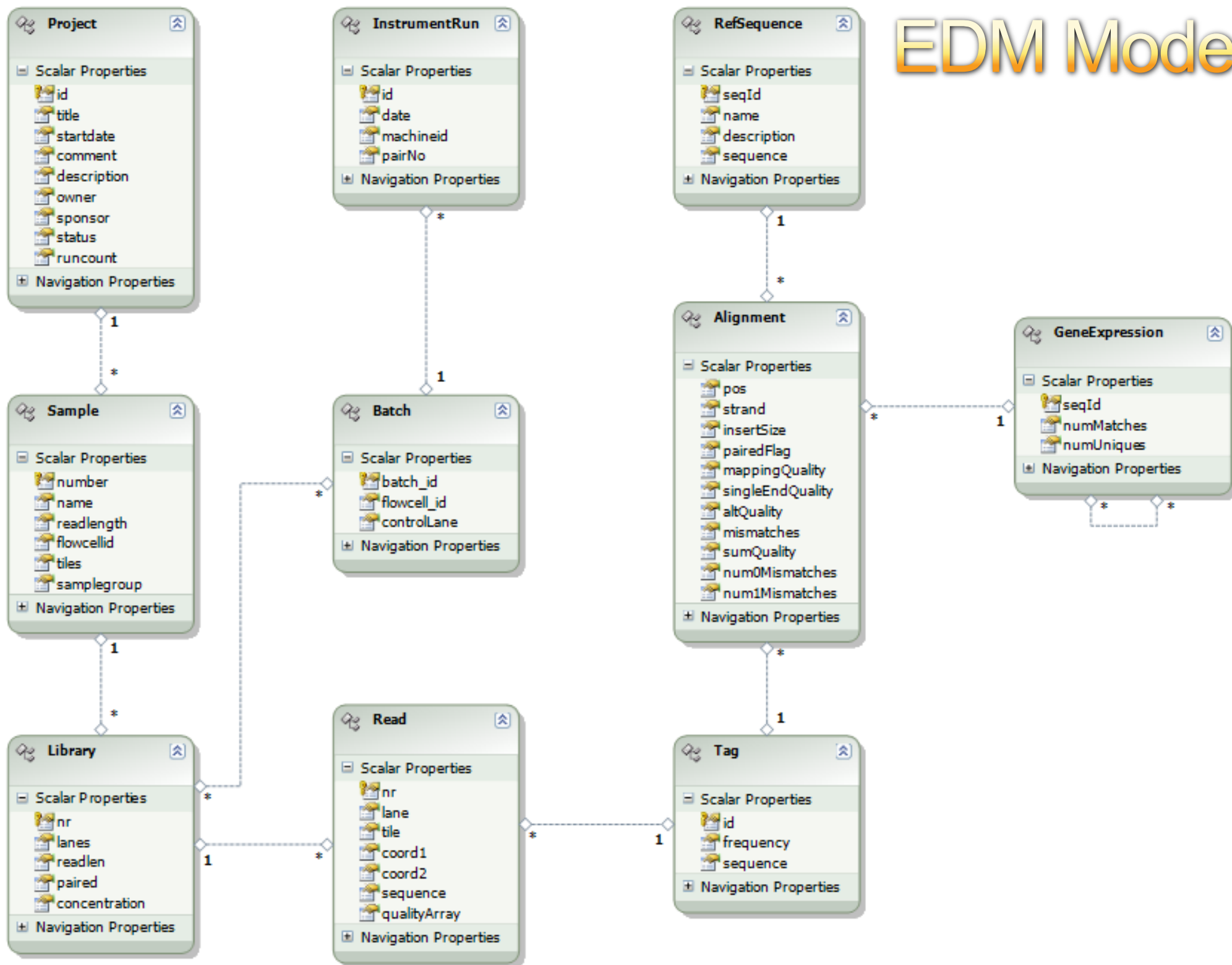
+Provenance
Data !!

0 mismatches in first 24bp
1 mismatches in first 24bp

Level 3 Data

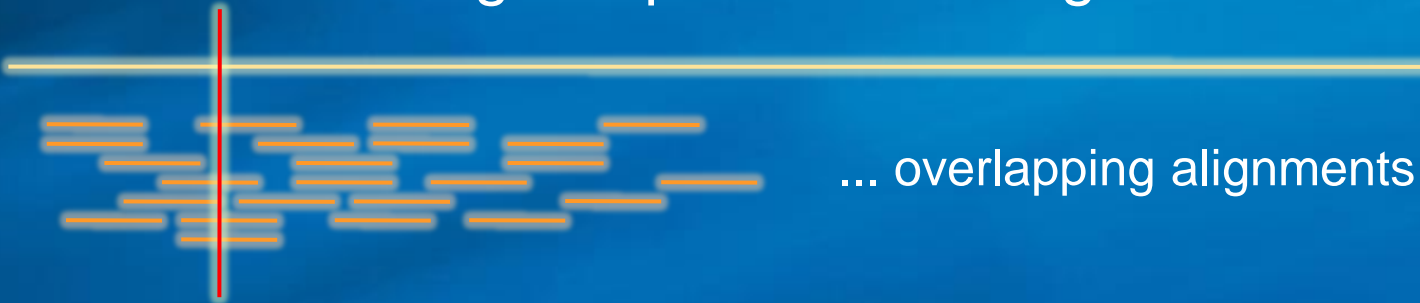


EDM Model



Consensus Calling

Consensus at a given position of the genome?



- 40x coverage of an individual genome: 120B bp
- Each has an alignment position, a base and a quality (error probability)
 - Consensus: aggregation function per position
 - Take base with largest support (qualities currently not used?)
 - Seq = Concat (all consensi per position)

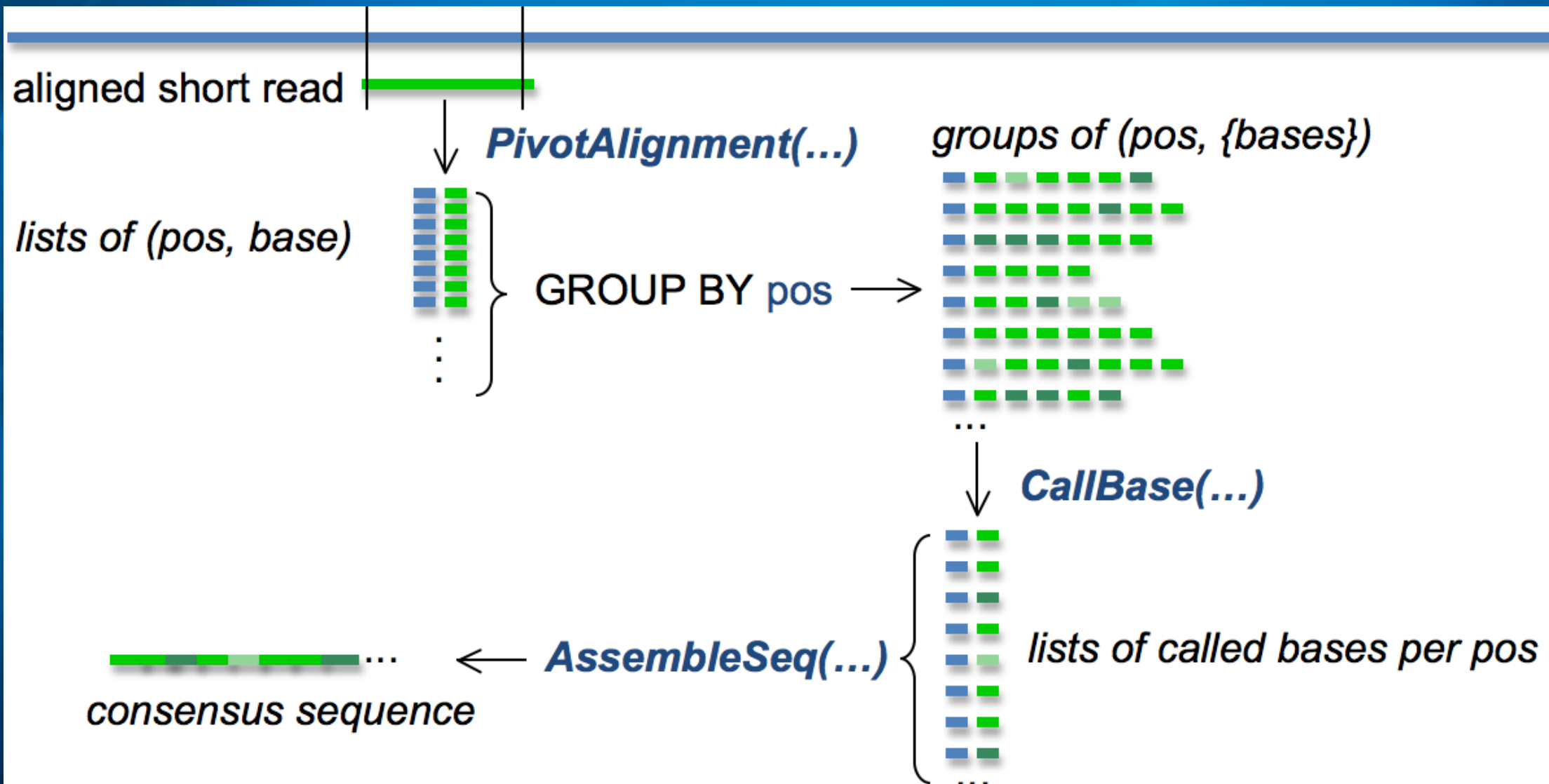
Aggregation to the Extreme

- Imagine, we could assemble a whole genome inside the database:

```
SELECT chromosome, AssembleSequence(position,base)
  FROM ( SELECT chromosome,position, CallBase(base,qual)
        FROM Alignments CROSS APPLY
              PivotAlignment(position,strand,seq,quals)
        WHERE a_e_id=...
        GROUP BY chromosome, position )
GROUP BY chromosome
```

- Shows benefits of SQL-CLR integration

Consensus calling



Consensus calling

```
SELECT chromosome, position, CallBase(base, qual)
FROM Alignments CROSS APPLY
    PivotAlignment(position, strand, seq, quals)
WHERE a_e_id=...
GROUP BY chromosome, position
```

- PivotAlignment(...)
 - Table-valued function that pivots a short-read (with quality values) into table of the form:
(position, base, quality)
- CallBase(b,q)
 - aggregate function that decides which base is the consensus among all alignments on a pos.

Lessons Learned

- Data modeling is key
 - Great way for learn the vocabulary of the science
 - Enables formulation of the “20 queries”
 - Separates semantics from representation
 - Enables provenance, time varying
- Extended relational DBMS solve a large portion of the problem
 - Structured, semi-structured, and “in-situ” file data
 - Powerful analysis tools (UDFs, UDTs, UDAggs)
 - Automatic parallelism
 - In-database map-reduce
- Data services important
 - Streaming, Reporting, OLAP, Data mining
 - Semantic modeling and mapping
 - Integration with scientists tools (Matlab, Lapack, R)

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