MG-RAST: A Case Study in Large Scale Metagenomics Analysis

Narayan Desai
desai@mcs.anl.gov
Mathematics and Computer Science Division
Argonne National Laboratory

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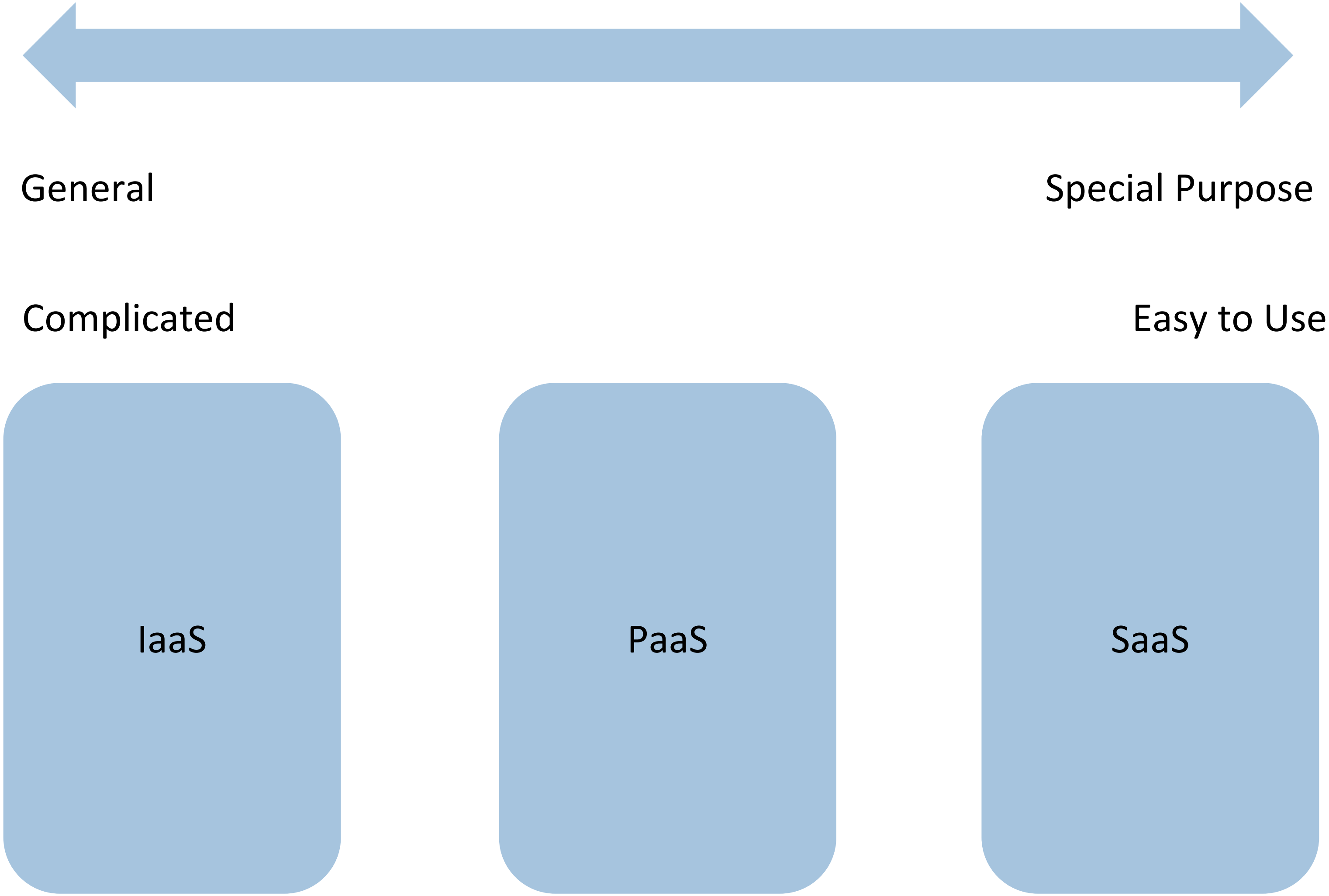
Talk Overview

- Definition of terms
- MG-RAST overview
- Our cloud adoption process
- Strategies for cloud adoption

Terms

- Clouds are computational utilities
  - Provide metered access to processors, storage, networking
  - Access to all resources via APIs
    - Disintermediated access
  - Enables specialization and competition
- Three basic models
  - IaaS
    - Rental access to hardware
  - PaaS
    - Framework for performing a particular set of tasks
  - SaaS
    - Remotely deployed and managed software

Range of Cloud Options



General

Special Purpose

Complicated

Easy to Use

IaaS

PaaS

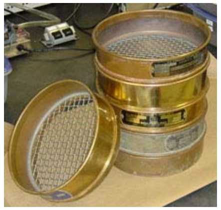
SaaS

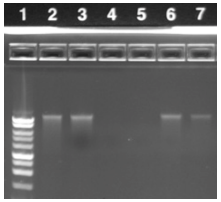
Metagenomics …

Definition::

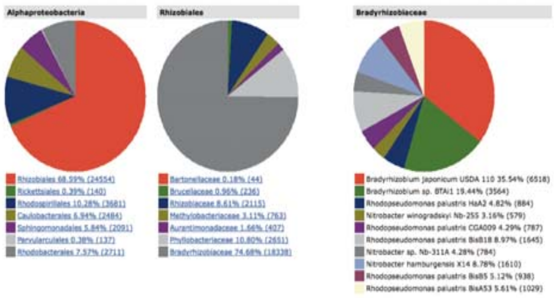
“random shotgun DNA sequencing applied directly to environmental samples”

- **whole shotgun metagenomics**
- Result is a combination of short reads of DNA from all organisms in sampled community
    - Mixed together

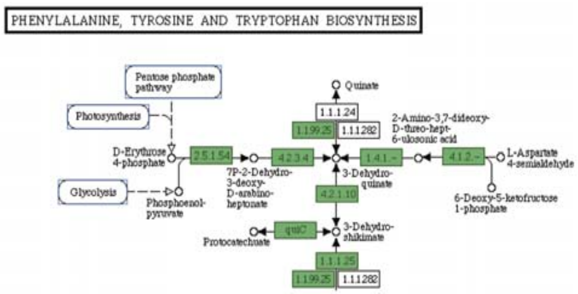




Who are they?



What are they doing?

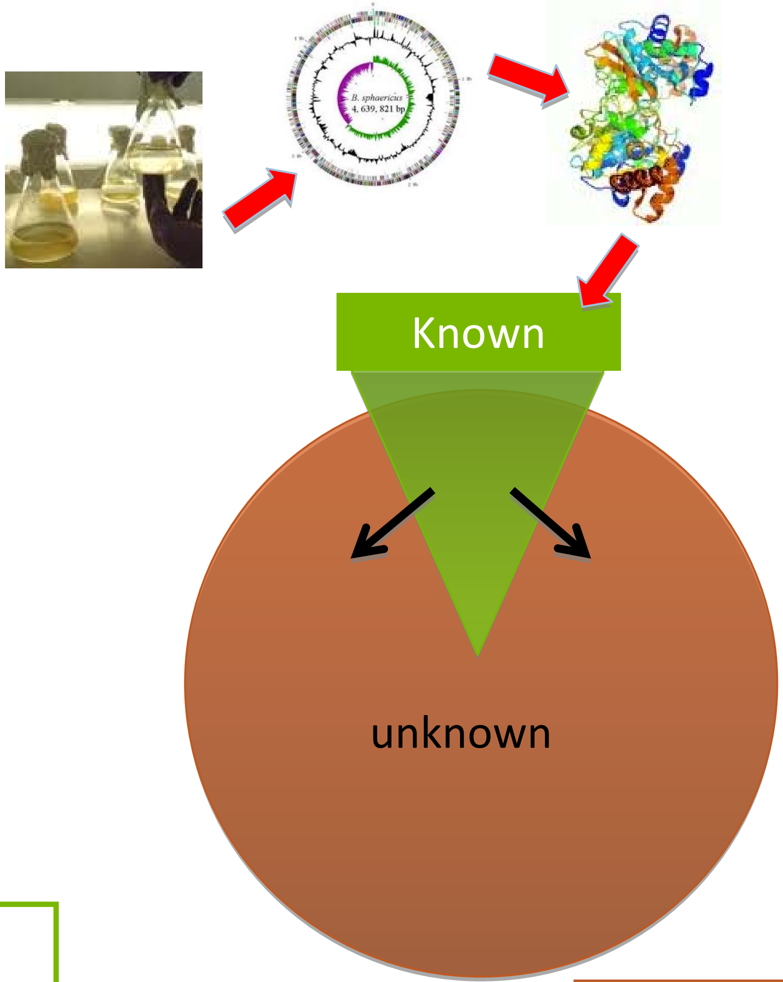


Metagenomics and Discovery

Today:
Mapping our knowledge to help understand microbial ecology

→ **using existing knowledge**

Via:
Mapping to curated databases



Known

unknown

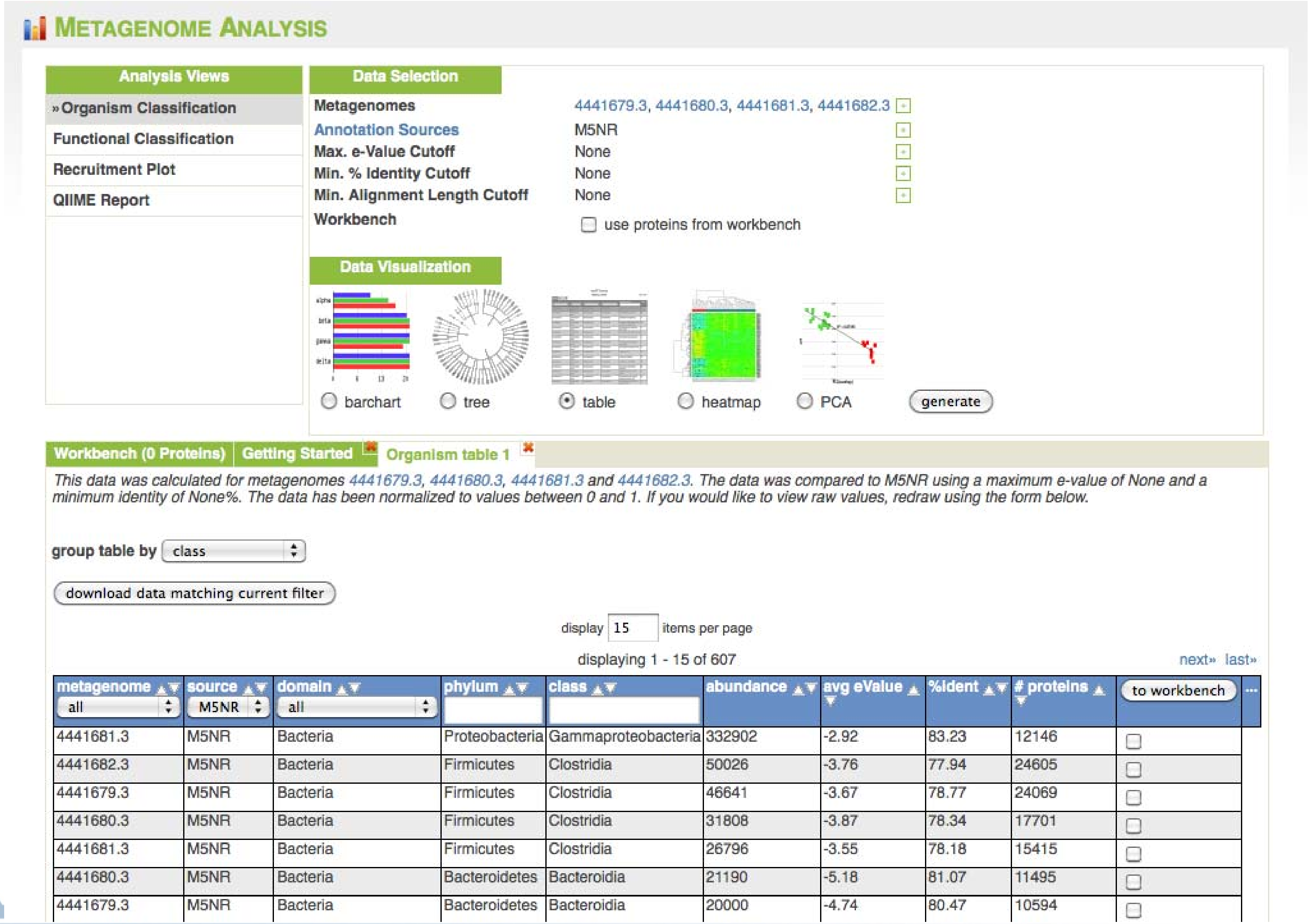
Future:
Discover new biology from computationally mining the unknowns

→Patterns
→co-occurrence
→Exclusion
→..

Example
Systematic discovery of patterns
e.g. CRSPR by Jill Banfield

MG-RAST

metagenomics analysis server



METAGENOME ANALYSIS

Analysis Views

- » Organism Classification
- Functional Classification
- Recruitment Plot
- QIIME Report

Data Selection

Metagenomes	4441679.3, 4441680.3, 4441681.3, 4441682.3
Annotation Sources	M5NR
Max. e-Value Cutoff	None
Min. % Identity Cutoff	None
Min. Alignment Length Cutoff	None
Workbench	☐ use proteins from workbench

Data Visualization

○ barchart ○ tree ● table ○ heatmap ○ PCA

This data was calculated for metagenomes 4441679.3, 4441680.3, 4441681.3 and 4441682.3. The data was compared to M5NR using a maximum e-value of None and a minimum identity of None%. The data has been normalized to values between 0 and 1. If you would like to view raw values, redraw using the form below.

group table by: class

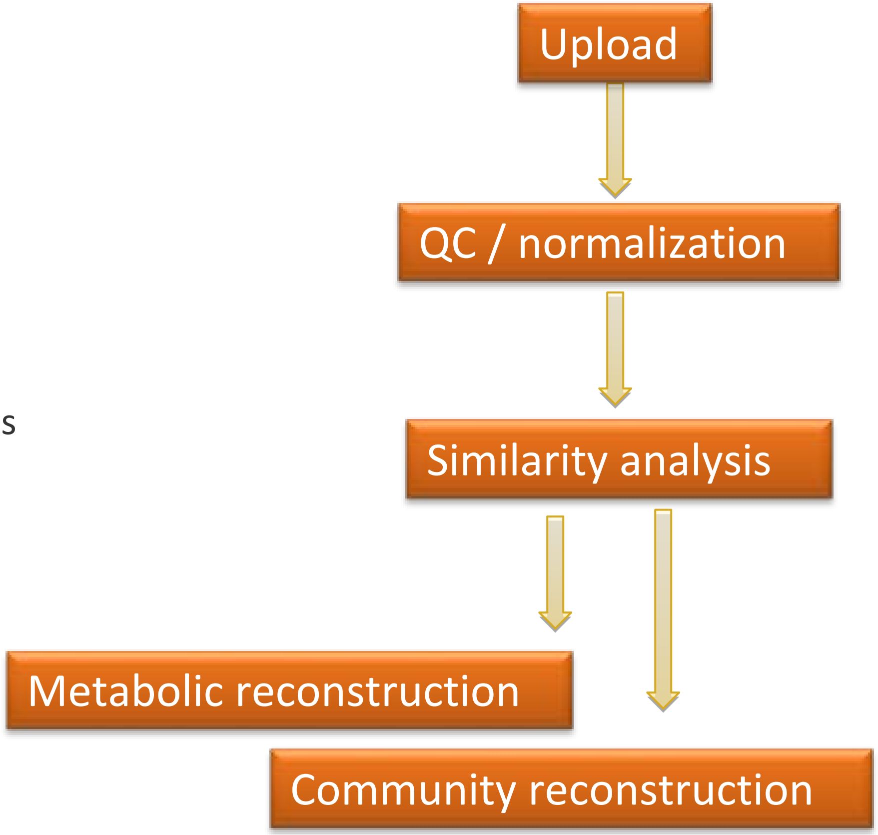
display 15 items per page

displaying 1 - 15 of 607

metagenome all	source M5NR	domain all	phylum	class	abundance	avg eValue	%ident	# proteins	to workbench
4441681.3	M5NR	Bacteria	Proteobacteria	Gammaproteobacteria	332902	-2.92	83.23	12146	☐
4441682.3	M5NR	Bacteria	Firmicutes	Clostridia	50026	-3.76	77.94	24605	☐
4441679.3	M5NR	Bacteria	Firmicutes	Clostridia	46641	-3.67	78.77	24069	☐
4441680.3	M5NR	Bacteria	Firmicutes	Clostridia	31808	-3.87	78.34	17701	☐
4441681.3	M5NR	Bacteria	Firmicutes	Clostridia	26796	-3.55	78.18	15415	☐
4441680.3	M5NR	Bacteria	Bacteroidetes	Bacteroidia	21190	-5.18	81.07	11495	☐
4441679.3	M5NR	Bacteria	Bacteroidetes	Bacteroidia	20000	-4.74	80.47	10594	☐

Brief history of MG-RAST

- December 2007 (v1)
  - 100+ groups and ~250 data submitters
  - 100+ data sets, ~10+ GBp total size
- October 2009 (v2)
  - **Pre-publication sharing available**
  - ~1500 data submitters, ~300 public data sets
  - 6000+ data sets
  - 200+ GBp total data sets
  - About ~30 GBp/month throughput
- March 2011 (release v3)
  - 2500+ data submitters
  - ~2000 public data sets
  - 25,000 data sets total
  - Throughput:
    - 47GBp in 24h
    - 3000 submissions in 24h
- January 2012 (v3.1.2)
  - 36,139 data sets
  - 9.31 TBp analyzed
  - 500 users / day
  - 7500+ users total

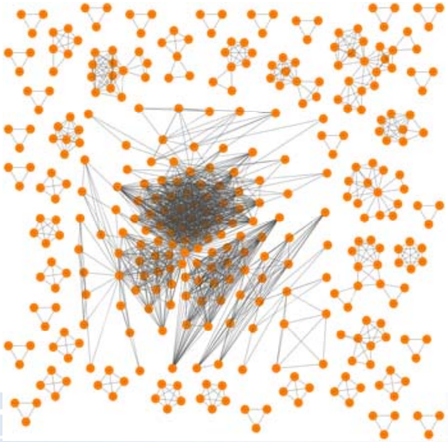

Upload

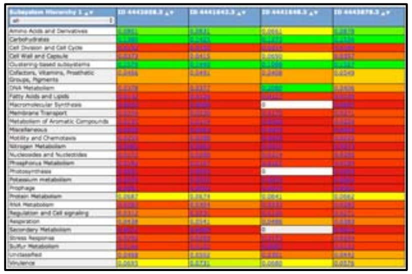
QC / normalization

Similarity analysis

Metabolic reconstruction

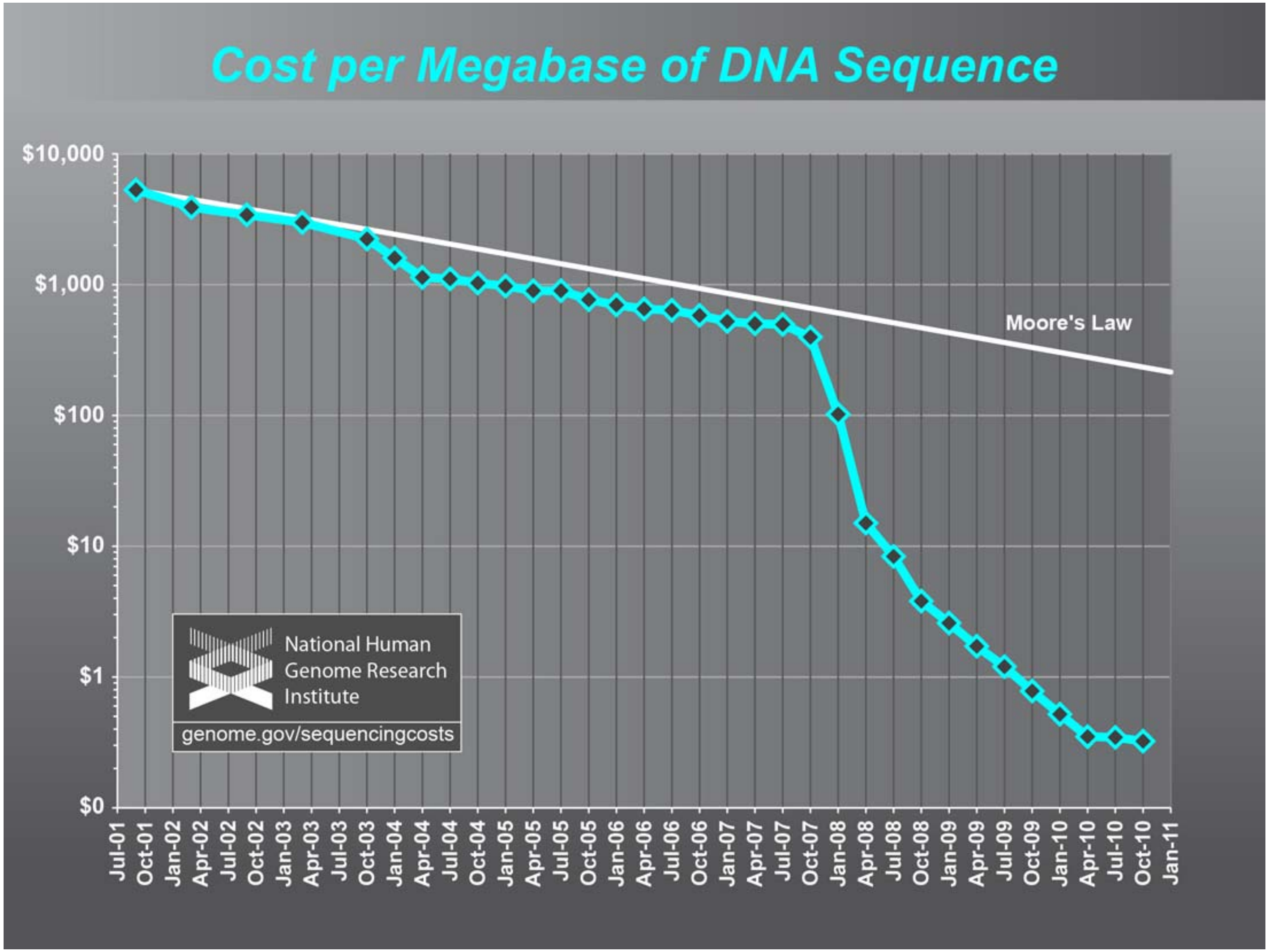
Community reconstruction





simplified

The Most Overused Slide in Genomics

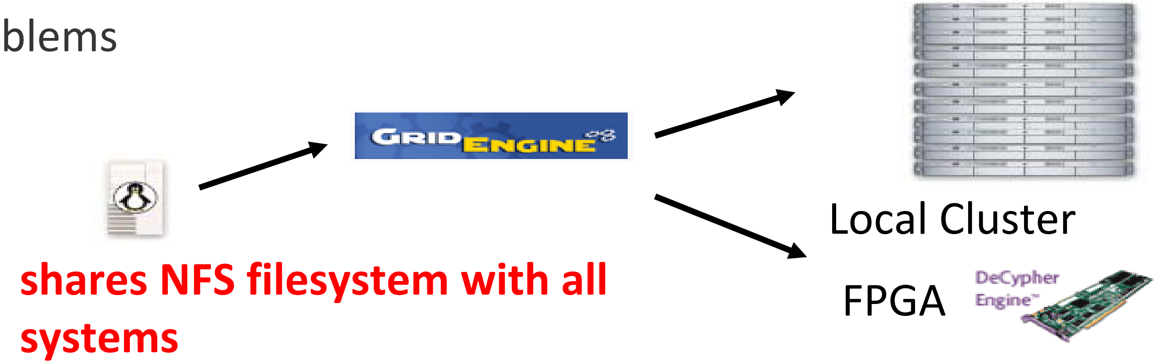


Observations (circa 2009)

- We’re in trouble
  - Data set size is outpacing our throughput
  - The pipeline is getting further and further behind
- Gap between sequencing costs and computation costs is growing
  - We’re in a hole, and it is getting deeper
- Computational capacity is a serious concern
  - Computing is growing its share of the budget
  - But the scaling curves suggest we won’t be able to keep up solely with hardware additions
- Any sustainable solution will require algorithm changes
  - What is the most relevant/useful analysis we can afford to compute?
- Public portals have a complicated resource consumption dynamic
  - Users abstracted from resource costs

MG-RAST v2 Computational Architecture
=> Purpose built dedicated system

- Standard bioinformatics pipeline design
- Dedicated compute resources
  - ~64 nodes
- Tightly integrated system/runtime environment
  - Global filesystems
  - Single resource manager (SGE)
- Shared with another project
  - Configuration/change difficulties
  - Capacity problems



shares NFS filesystem with all systems

MG-RAST Cloud Adoption Strategy

Goals: Scale the MG-RAST pipeline to work across distributed and shared resources
Get the most work done with the resources we can access

- Pursue shared computing resources
  - Dedicated resources are a luxury we can’t afford
- Perform detailed performance analysis
  - Where are our bottlenecks?
- Redesign analysis workflow
  - Negotiate tradeoffs between performance and sensitivity
  - Continuous refinement
- Use resources efficiently
  - Nebulous concept; varies between resource types
  - Minimize computational (and financial) costs
- Move the most expensive computational stages to the cheapest resources
  - Sequence similarity search

Software requirements

- Portability of analysis was the key problem to solve
  - Analysis orchestration
  - Data mobility
  - Tool execution portability
- Replaced system resource manager with a distributed workload management system
  - Argonne/Another Workflow Engine (AWE)
  - Data portability layer (Shock)
- AWE provides encapsulation for analysis work flows
  - Analysis environment and package prerequisites sent to compute elements on the fly
  - Minimal requirements on host environment
  - Can be run under system resource manager
- Enabled execution of the sims calculation across a range on shared systems
  - HPC clusters
  - Cloud resources

Our new architecture

- Centralized web portal
  - Database server
  - Archival dataset access
- Centralized orchestration of computation
  - Workload management
  - Storage services
- Small dedicated cluster
  - For data intensive operations only
  - Moving these tasks towards the data archival infrastructure
- Dynamic cloud resources (IaaS)
  - Large scale similarity searches
  - Clustering
  - QC
- Focusing on driving more systems into the cloud
  - Let our sysadmin focus on running the software, not the hardware
  - Need to address performance issues for specialized systems on the way

How did this work?

- Enabled MG-RAST to use any resources we could get access to
  - Regardless of geographic location (ANL or NERSC)
  - For any available duration (workunits run for 10-30 minutes each)
  - With any kind of system environment
- This expansion helped, but not a panacea
  - Access to more capacity with growth helps, but we can’t expect an ever increasing slice of the pie
- Overall impact was about a 10X improvement in throughput
  - More or less a one trick pony, aside from Moore’s Law improvements
- Initially targeting a single work type (similarity search) proved to be a long term liability
  - Should have pushed more of our system into the cloud initially
- Infrastructure flexibility enabled easy experimentation with new analysis approaches
  - Biggest overall payoff for our group

Lessons Learned

- Access to large shared resources wins
  - Better than dedicated access to small resources
- Cloud APIs and sandboxing enable rapid improvement of computing architecture
- Clouds simplify experimentation
  - Lets you focus on the hard thinking
    - In our case, analysis/algorithm development
  - Isn't this why we are all here?
- These factors have caused us to start moving most of our development activities towards clouds
  - Moving emphasis away from dedicated resources, even for ad hoc development

Three Architectures for Cloud Adoption

- Pile of instances
  - Everybody builds their own
  - Maximum flexibility, maximum complexity
  - Who wants to be a sysadmin!
- Curated set of images
  - Small set of image maintainers
  - Large set of image instantiators
  - Limits administration/maintenance costs
- Persistent, managed group infrastructure
  - Sysadmin runs resources inside the cloud
  - More flexible and dynamic than dedicated hardware
  - Less flexible than previous two
  - Most similar to the status quo

Cloud Adoption Architectures (cont)

- No right answer
- Many tradeoffs between approaches
  - Flexibility versus Cost
- Some require particular resources
  - System administration effort
  - Technical expertise
- Options vary with group size
  - DIY is popular for small groups, but gets costly in large groups

Contributors

- Folker Meyer
- Andreas Wilke
- Elizabeth Marland
- Jared Wilkening
- Travis Harrison
- Mark D’Souza
- Tobias Paczian
- Kevin Keegan
- Will Trimble
- Hunter Matthews
- Jason Hedden

Questions?