



SCIENCE-AS-A-SERVICE WITH THE AGAVE PLATFORM

Rion Dooley @deardooley
dooley@tacc.utexas.edu

TACC AT A GLANCE



Personnel

160 Full time staff (~70 PhD)

Facilities

10 MW Data center capacity

New office facility to be completed
by start of 2016

Systems and Services

A Billion compute hours per year

5 Billion files, 50 Petabytes of Data,
Hundreds of Public Datasets

Capacity & Services

HPC, HTC, Visualization, Large scale
data storage, Cloud computing
Consulting, Curation and analysis,
Code optimization, Portals and
Gateways, Web service APIs, Training
and Outreach



EXTREME SCALE SUPERCOMPUTING



Stampede

- #7 HPC system in the world for computation 500k CPU core 9.7 PF

Lonestar 5

- Texas-focused Cray XC40 30,000 Intel Haswell cores 1.25 PF

Wrangler

- 0.6 PB usable DSSD flash storage w 1 TB/s read rate + 10 PB Lustre

Maverick

- 132 Fat nodes w dual 10 core Ivy Bridge + NVIDIA Kepler K40 GPGPU

Chameleon & Jetstream Cloud

- 1400 nodes OpenStack

Disk and Tape Storage

- 100+ PB storage in HIPAA-aligned data center



Coming Soon: Hikari

- Green computing system partnership with NEDO and NTT. 10k Haswell cores. HVDC and Solar (partial)
- Support for container ecosystem

TACC SUPPORTS AN INCREDIBLE AMOUNT & DIVERSITY OF RESEARCH

- Since 2013...
 - Over *2 Billion* processor hours delivered to end users
 - 6+ **million** successful jobs
 - About 10,000 students, faculty, and staff use our Stampede directly
 - Over 30,000 more use it indirectly via portals and services
 - Peer-reviewed requests for time (via XSEDE) run ~500% available hours
- **Stampede alone** supports nearly 2,500 funded projects across the United States and abroad

THE EVOLUTION OF A CYBERINFRASTRUCTURE



Once upon a time, most of us built garage-style clusters...



HPC systems have grown up since then and become much more powerful and sophisticated

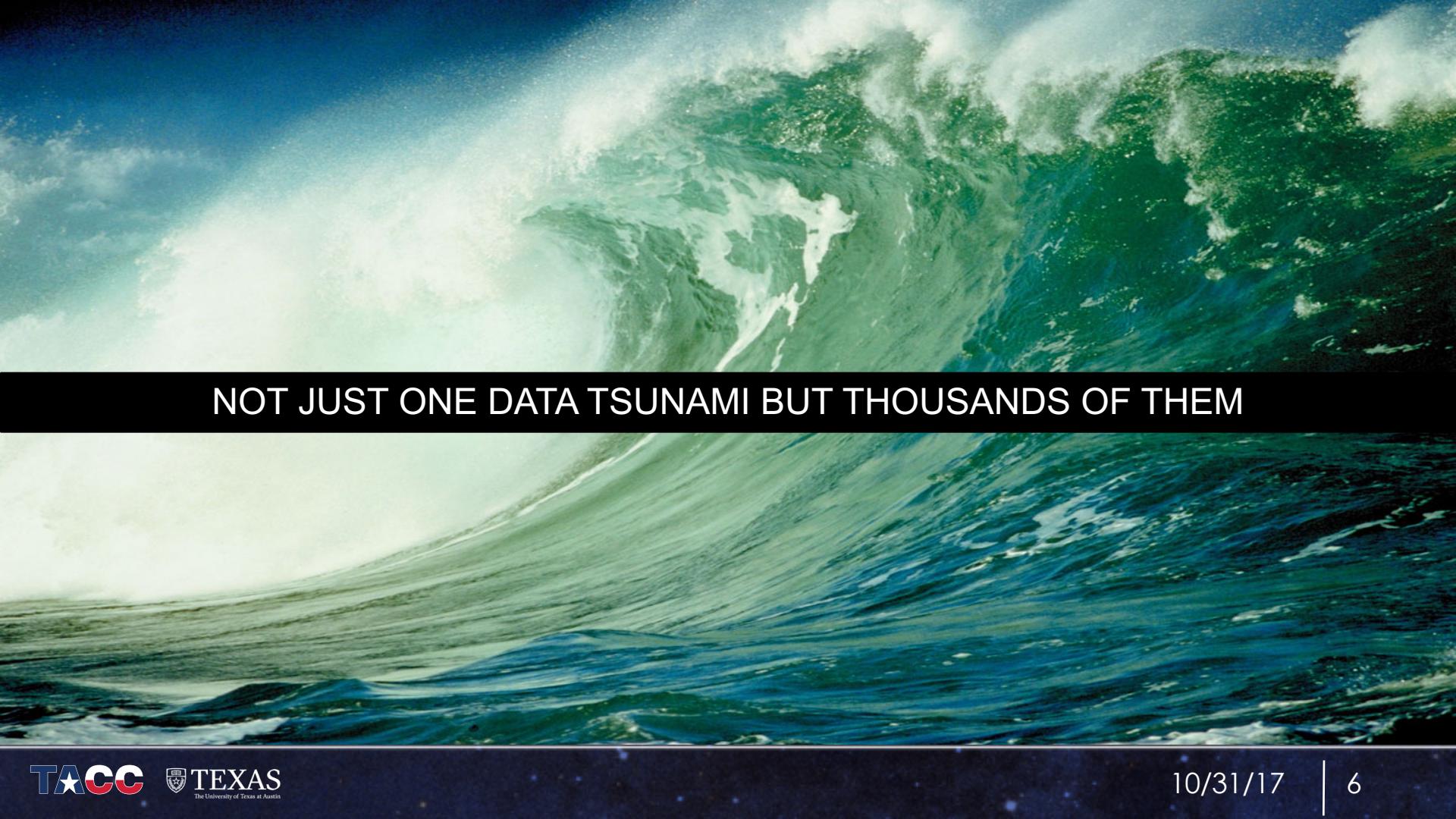


But a curious thing happened while HPC was running its victory lap...

We built a very successful center based on 3 pillars in our first 7 years

- *Simulation & HPC*
- *Visualization*
- *People (Consulting & Algorithms)*





NOT JUST ONE DATA TSUNAMI BUT THOUSANDS OF THEM

CAMBRIAN EXPLOSION OF LANGUAGE, TECHNOLOGY, AND HARDWARE

CATALYSTS

- Triumph of Linux and FOSS
- Rise of collaborative massive scale
- Emergence of Internet-scale technologies
- Rapid innovation to solve IO bound problems
- Repeal of Moore's Law

WORKFLOWS NOW TECHNICALLY COMPLICATED

LANGUAGES

- Python 2 & 3
- R
- Julia
- Perl
- Matlab
- Java
- Scala, Clojure, etc
- .NET
- C++
- Swift
- Haskell
- Go
- Javascript

FRAMEWORKS

- MapReduce: Hadoop, Storm, Pachyderm
- Event & Streaming: Kinesis, Azure Stream Analytics, Camel, Streambase
- Deep/Machine Learning: Watson, Azure BI, Tensorflow
- In-memory parsing: Kognito, Apache Spark
- New data warehouse: Snowflake
- Containers: Docker, Rocket, MESOS, Kubernetes
- Cloud: AWS, GCE, OpenStack, VMWare

HARDWARE

- Rise of many-core computing means 50-100 threads/node*
- Xeon / Xeon Phi
- GPU
- OpenPower
- ARM
- Multi-level memory architectures
- Hierarchical storage architectures
- FPGAs

DIVERSE DISTRIBUTED RESEARCH TEAMS



Mike

- Computing novice
- Works remotely at partner site



Eliza

- Masters specific analysis skills
- Readily adopts new tech



Paulo

- Staff computational expert
- Supports multiple projects



Nikolaidas Group

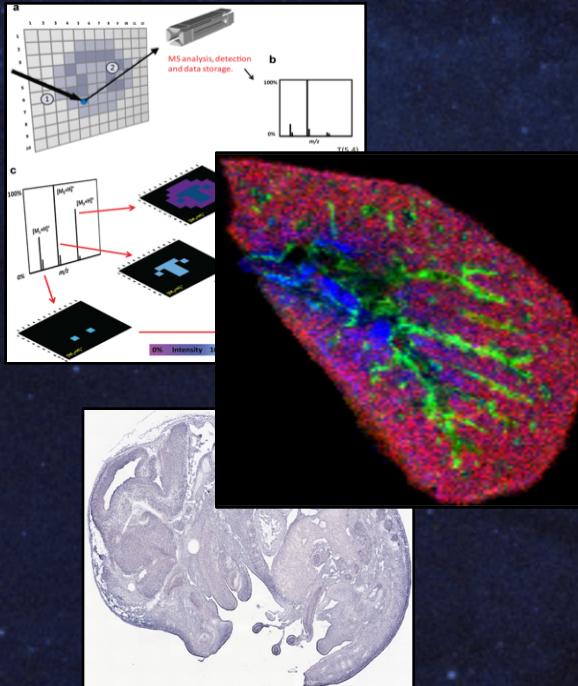
- Mostly experimentalists
- Strict data sharing & access



Roshan

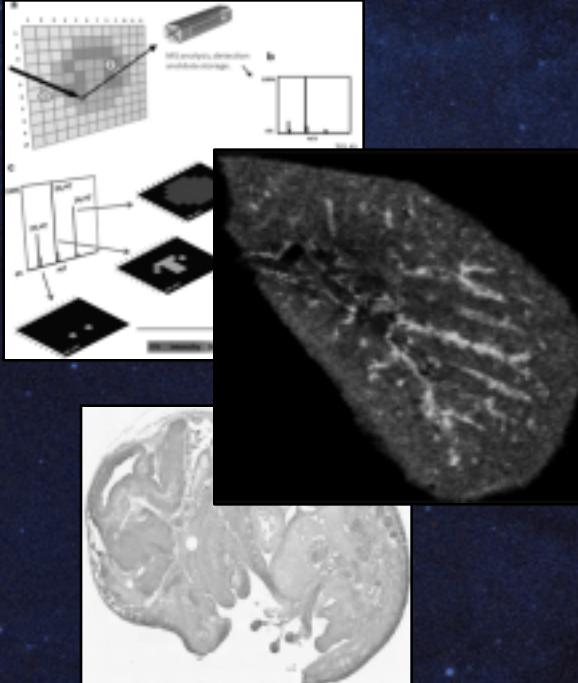
- Computationally experienced
- Focused on interpretation

THEIR NEEDS (30,000 FT. VIEW)



- ▶ Store, organize, share *primary data*
- ▶ Iteratively perform 1' analyses
- ▶ Store, organize, share *derived data products*
- ▶ Iteratively generate and explore hypotheses
- ▶ Share analytical code with the scientific public
- ▶ Integrate results from new experiments
- ▶ Publish data alongside plots, visualizations and analytical tools

THEIR NEEDS (500 FT. VIEW)



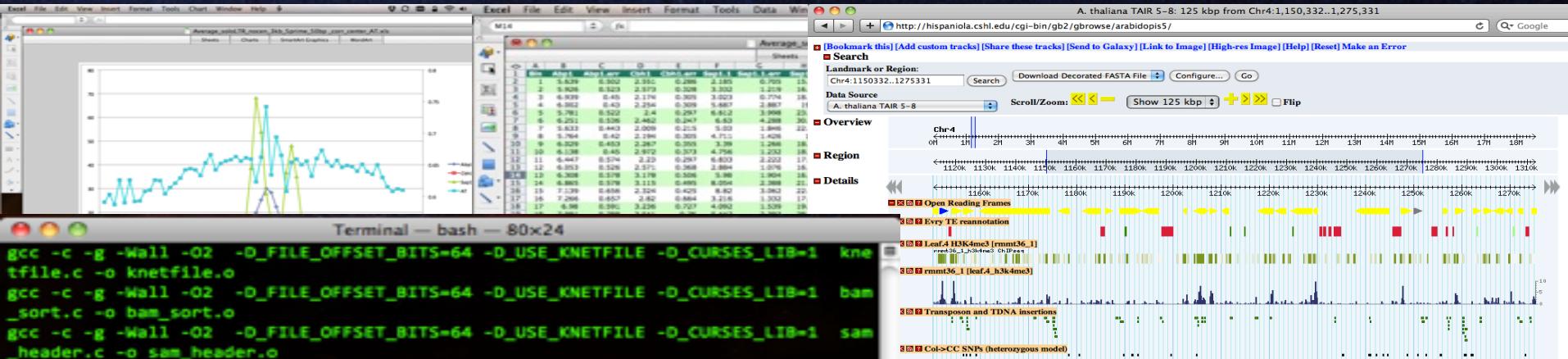
- ▶ Data lifecycle management
 - ▶ Fine-grained permission management
 - ▶ Discoverability
 - ▶ Version control
 - ▶ Domesticating promising new analysis codes based on often immature technology
 - ▶ Doing reproducible computational science
 - ▶ Adopting efficient analytical methods

HOW DO WE HELP RESEARCHERS WITH SUCH
DIVERSE NEEDS AND BACKGROUNDS?



BUILD A MASSIVE STORAGE CLOUD NEXT TO INNOVATIVE, POWERFUL, USABLE COMPUTERS AT THE END OF FAST INTERNET PIPES





MANY DOMAIN SCIENTISTS ARE NOT EXPERTS AT COMPUTING TECHNOLOGY.
CREATE PURPOSE-BUILT, HIGHLY INTUITIVE INTERFACES



Point-and-click interfaces

- Data management, sharing, and analysis
- Publishing reproducible analysis workflows
- Discovery of new or updated tools and data
- Interactive visualization of results

Backed by world-class computing and data capacity

R version 3.0.3 (2014-03-06) -- "Warm Puppy"
Copyright (C) 2014 The R Foundation for Statistical Computing
Platform: x86_64-unknown-linux-gnu (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

Natural language support but running in an English environment

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help,
'start()' for an HTML browser interface to R, or
Type 'q()' to quit R.

In [1]:

```
import string, os
import matplotlib
import matplotlib.pyplot as plt
%matplotlib inline
from IPython.display import Image, display, Math, Latex, SVG, HTML
import numpy as np
from scipy.cluster.hierarchy import linkage,dendrogram
from scipy.spatial.distance import pdist
# from urllib2 import urlopen
from urllib.request import urlopen
import pyspark
sc = pyspark.SparkContext('local[*]')
```

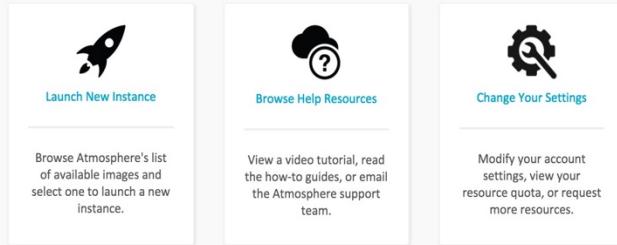
Pathogens

Hosted SaaS

- JupyterHub notebooks
- Rstudio
- Web-based VNC

Also, backed by world-class computing and data capacity

Getting Started



Resources in Use [Need more?](#)



Instance History (5 instances launched)



Updated a few seconds ago

Easy to use Cloud Computing

- Atmosphere (Cyverse)
- Jetstream (IU,UA,TACC)
- Chameleon (UC,TACC)

Cloud consoles are aimed at sysadmins and unintuitive.

We're changing that with improved UX and support

- APIs are still available
- No cost to end user



GIVE EXPERTS ACCESS TO EVERY SINGLE ONE OF YOUR BUILDING BLOCKS.
WEB SERVICE APIs EVERYWHERE. AUGMENT WITH PROFESSIONAL TOOLING.

MIKE: LEARNING COMPUTATIONAL SKILLS



Mike generates mass-spec data from his samples, which are used to decide on future experiments

- ▶ Eliza and Paulo have published analytical scripts for his data as 'apps' into a project web portal
- ▶ Paulo has wired up the lab's equipment to send data directly to remote storage
- ▶ Mike can perform basic analysis and reporting on his data from the web interface
- ▶ Roshan can see Mike's results in the project portal and discuss them with him
- ▶ Mike collaborates with Eliza to improve the results of their analytical scripts

ELIZA: AUGMENTING HER RESEARCH CAPABILITY



Eliza collects and analyzes *in situ* hybridization imagery as a major part of her inquiry

- ▶ She uses code developed by Paulo and others to perform feature detection
- ▶ She helps Paulo develop code for Mike to use in his proteomics work
- ▶ She has developed scripted workflows that run locally on her laptop to complete her analyses
- ▶ She writes her own code in Python and R for aggregate analysis and shares it via the Docker Hub and the project portal
- ▶ She presents her data viz via interactive Rshiny apps that she deploys to the project portal

PAULO: CONCENTRATING ON COMPUTATIONAL RESEARCH



Paulo likes to solve hard computational problems but is also responsible for lab research infrastructure

- ▶ He has automated data movement from instruments to remote storage, including duplication to AWS Glacier. Roshan gets the bill ☺
- ▶ He builds and maintains the project web portal. He didn't have much experience with such technology when the project started
- ▶ Paulo has used Spark to developed new software for feature extraction from *in situ* hybridization images – he can automatically deploy it to the portal, powered by TACC Wrangler, as part of his build process
- ▶ He is working on a paper describing his software and is getting valuable feedback from other folks he has shared it with via the project portal and public source repositories

ROSHAN: FOCUSING ON THE BIG PICTURE



- ▶ Roshan has deep experience in gene expression analysis - Paulo has populated the project portal with many of the tools she needs to accomplish her goals
- ▶ She collaborates with Mike and Eliza on interpreting their experimental results
- ▶ Because Eliza has included a custom notification in her scripting workflow, Roshan knows when new image analyses have been completed and can schedule time to look at them
- ▶ She can work with Paulo to enable the project web portal to make use of her newly-awarded XSEDE computing and storage allocation
- ▶ She routinely shares results with experimentalist colleagues and reviewers via a simple Dropbox-like interface



Agave Platform

<https://github.com/agaveplatform/nectar-2017-workshop>

AGAVE IS A MULTI-TENANT PAAS
DELIVERING SCIENCE-AS-A-SERVICE SOLUTIONS
IN HYBRID CLOUD ENVIRONMENTS

-

Think of it like



salesforce

for Science

WHAT IS AGAVE?

- ▶ Works with your new and legacy inf
- ▶ On premise, hybrid, or hosted deployment
- ▶ Multi-tenant
- ▶ Secure by default

WHAT KICKING THE TIRES LOOKS LIKE

MONTHLY USAGE

30 compute sites
100 clients
1,000 apps
6,000 simulations
1,000,000 transfers
2,500,000 GB data moved

AVG. MONTHLY GROWTH

45 new systems
30 new clients
50 new apps
2000 docs shared
100,000 new transfers
250,000 GB data moved

WORLDWIDE PLATFORM USAGE

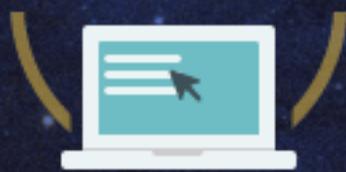


WHAT DOES IT DO?

MANAGE
DATA



RUN
CODE



COLLABORATE
ANYWHERE

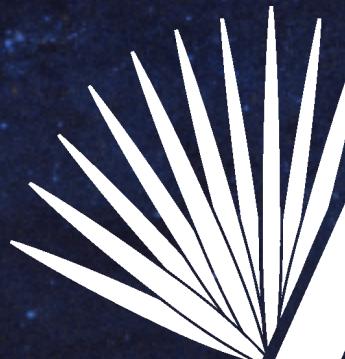


CONNECT
ANYTHING



WHAT CAN AGAVE DO FOR ME?



The Agave logo graphic features a stylized cluster of white, fan-like leaves or petals radiating from the left side of the word "Agave".

Agave

Platform

PLATFORM : 30,000 FOOT VIEW

- ▶ Expand the reach of your infrastructure
- ▶ Enable new channels of collaboration
- ▶ Increase your research velocity



PLATFORM : KEYBOARD VIEW

1. Identity-as-a-Service
2. Flexible Authentication
3. API Management
4. Admin Services



PLATFORM : KEYBOARD VIEW

Identity-as-a-Service

- ▶ Integrated with, or supplement your existing IaaS solutions
- ▶ OpenID Connect compliant
- ▶ Extensible user profiles.
- ▶ REST profile management API (OpenID, Schema.org, SCIM, OIDC Federation, vCard,...)
- ▶ REST group management API (SCIM)
- ▶ Fine grained user and group RBAC



PLATFORM : KEYBOARD VIEW

Flexible Authentication

- ▶ OAuth2 - Full implementation
- ▶ Federated login
- ▶ SSO
- ▶ MFA
- ▶ Custom flows



PLATFORM : KEYBOARD VIEW

API Management

- ▶ SSL termination
- ▶ Gateway proxy
- ▶ Load balancing
- ▶ JWT generation
- ▶ Lifecycle management
- ▶ Swagger 2 API support
- ▶ Metrics
- ▶ Self-service client registration
- ▶ Self-service api registration
- ▶ Developer documentation



PLATFORM : KEYBOARD VIEW

Admin Services

- ▶ Service accounts
- ▶ Admin roles and role mapping
- ▶ Client management
- ▶ Provisioning and publishing
- ▶ Credential generation & impersonation
- ▶ Token validation
- ▶ Header inspection
- ▶ On-demand log streams
- ▶ Self-service API registration and management





Agave

Science APIs

SCIENCE APIS: 30,000 FOOT VIEW

- ▶ Science as a Service
- ▶ Reproducibility
- ▶ Provenance
- ▶ Scalability
- ▶ Advanced access control and collaboration
- ▶ Bring your own data, code, systems, and services
- ▶ Mix and match technologies, services, languages, and env
- ▶ Collaborate across groups and organizations



SCIENCE APIS : KEYBOARD VIEW

1. Conventions
2. Manage data
3. Run code
4. Collaborate meaningfully
5. Integrate anything



SCIENCE APIs : KEYBOARD VIEW

Conventions

- ▶ REST API
- ▶ Sync and Async
- ▶ Event driven
- ▶ JSON in/out
- ▶ Search, response customization, pagination, formatting



SCIENCE APIS : KEYBOARD VIEW

Manage Data

- ▶ Single, consistent interface to access distributed data
- ▶ Managed, tenacious data movement
- ▶ Opinion-free metadata management
- ▶ Full provenance and searchable audit trail.
- ▶ Events, alerts, and notifications
- ▶ Horizontal scaling



SCIENCE APIS : KEYBOARD VIEW

Run code

- ▶ Bring your own code and/or leverage our catalog
- ▶ Run your apps as interactive, batch, or event driven processes
- ▶ Full lifecycle management
- ▶ Full provenance and searchable audit trail
- ▶ Reproducibility as a feature
- ▶ Publish entire experimental runs



SCIENCE APIS : KEYBOARD VIEW

Collaborate meaningfully

- ▶ Secure by default, share as desired
- ▶ Deep link to any resource in the API
- ▶ Generate disposable links to securely share with others
- ▶ Events, webhooks, and web sockets to integrate circa 2016
- ▶ Web standards come standard

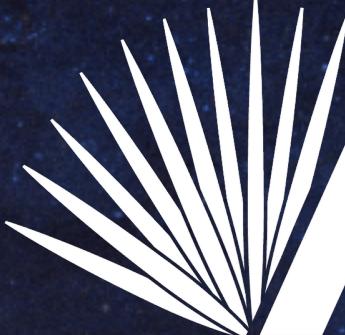


SCIENCE APIS : KEYBOARD VIEW

Integrate anywhere

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Agave

Tooling

TOOLING: 30,000 FOOT VIEW

- ▶ Accelerate your development
- ▶ Better utilize the strengths of your dev and tech teams
- ▶ Identify, meet, and mitigate disruptive technology changes before they disrupt you
- ▶ Leverage white label solutions
- ▶ Shrink wrapped integrations with popular technologies
- ▶ `git clone ...` && `docker run...` && PROFIT



TOOLING : KEYBOARD VIEW

- ▶ Building blocks
 - ▶ SDK (python2/3, java, node, angularjs1/2, perl, R, php, ...)
 - ▶ CLI
 - ▶ Modules, plugins, and code samples



TOOLING : KEYBOARD VIEW

- ▶ Kitchen sinks & coffee mugs
 - ▶ Agave ToGo
 - ▶ Microsites





Agave

To Go

AGAVE TOGO

- Client SDK: Python, JavaScript, Java, PHP, *Perl*, *R*
- Command Line Interface
- Plugins: AngularJS, Wordpress, Drupal, Tomcat
- Web applications (ToGo)
- Integrated environments (Jupyter Hub)
- Workflow management (End of Day)

AGAVE TOGO

A Genomics Example Using the pyspark Library

In this example, we make use of the `pyspark` library to determine if any pathogens are present in a sample. The basic idea is to make use of `k-means`, a biological analog of `n`-grams, to compute the "distance" from a known pathogen genome to the DNA in our sample. We can use different metrics for the distance, as will be shown.

```
In [1]: import string, os  
import numpy as np  
from collections import defaultdict  
from scipy.spatial.distance import pdist, squareform  
from urllib.request import urlopen  
import pyspark  
sc = pyspark.SparkContext()
```

We note that this is a python library.

Agave ToGo Admin Dashboard

Dashboard

Introducing the new Agave ToGo!

This application is meant to serve as a reference from which you can build your own application. Feel free to fork this repository and edit as needed. To contribute back enhancement and bug fixes, please fork the repository and submit a pull request.

1349 Jobs 12.5TB Data Moved 549 App Users +25% Activity Increase

PROJECT ACTIVITY ACTIVITY FEEDS

Total: 3756 Comments: 1 Jobs: 1 Docs: 1 Karma: 1

Agave Docker Runner Demo

This is a simple front-end webapp demonstrating Agave's support for running Docker containers. Click the "Start Tutorial" button to begin the guided tour.

Start Tutorial

localhost:8080/app#/

AGAVE TOGO

Welcome Agave ToGo Microsite - Compute Edition

Home > Welcome

Agave ToGo MicroSites

October 31, 2017

Agave ToGo Microsites are a great way to bring together small groups of users needing to automate and collaborate around specific tasks.

FOLLOW US ON

ABOUT

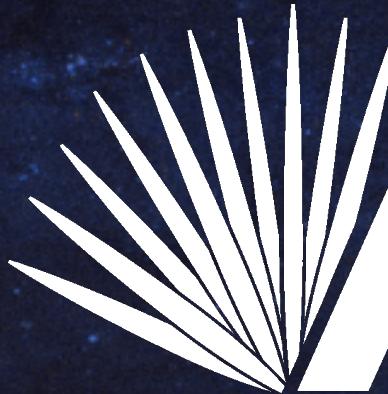
CONTACTS

Community Slack channel
Agave Help Desk
Developer Documentation

TOOLING : KEYBOARD VIEW

- ▶ Cool kid friendly
 - ▶ Jupyter notebooks
 - ▶ Wordpress, Drupal, Django CMS, AngularJS, Node,...



The Agave logo graphic consists of a cluster of white, fan-like lines radiating from the left side of the word "Agave".

Agave

App Exchange

APP EXCHANGE: 30,000 FOOT VIEW

- ▶ Library of existing scientific codes
- ▶ Portability across HPC, HTC, Cloud, container, and native environments -- TRUE HYBRID PORTABILITY
- ▶ Write once, run virtually anywhere
- ▶ Social tagging and commentary
- ▶ Benchmarking
- ▶ Based on (~250) existing HPC and HTC apps at TACC



APP EXCHANGE: KEYBOARD VIEW

- ▶ Automated builds to multiple formats
- ▶ Multiple SCM integration
- ▶ Apps built for Docker, Singularity, VM, native runtimes.
- ▶ Automation to run acceptance tests and. Performance benchmarks against known datasets.
- ▶ Consistent execution and monitoring API
- ▶ Form and UI generation
- ▶ Provenance, attribution, fully reproducible runs





OPERATIONAL COSTS

- ▶ License
 - ▶ BSD 2-Clause
- ▶ Services:
 - ▶ monitoring, automation, updates, SLA, backups, security scans, logging, etc
- ▶ Hosting:
 - ▶ db, nosql, cloud storage, app catalog, image registry, public assets, api definitions, service/asset hosting

PEOPLE COSTS

- ▶ Admins:
 - ▶ sql, nosql, tenant, systems, scaling
- ▶ User support:
 - ▶ developer on-boarding
 - ▶ Trainings
 - ▶ docs
 - ▶ workshop design
 - ▶ tech audits
 - ▶ solutions arch.

SUPPORT COSTS

- ▶ Platform
 - ▶ change management
 - ▶ Devops
 - ▶ Scaling
- ▶ Integration
 - ▶ boutique services
 - ▶ custom integrations
 - ▶ custom IAM
 - ▶ tech evaluations

WHO'S USING THIS STUFF?

This screenshot shows the iPlant Collaborative's Discovery Environment. The top navigation bar includes links for Home, Help, Log In, and Sign Up. The main area features a search bar with placeholder text "Search iPlant DE" and a dropdown menu showing results for "BENEFIT OF THE SOIL". On the left, there's a sidebar with categories like "iPlant DE Home", "iPlant DE Development", "iPlant DE Tools", "iPlant DE Data", "iPlant DE Apps", "iPlant DE Services", "iPlant DE Resources", "iPlant DE Forms", and "iPlant DE Commerce". A central panel displays a list of items under "BENEFIT OF THE SOIL", including "Soil Health", "Soil Management", "Soil Health Monitoring", "Soil Health Monitoring", "Soil Health Monitoring", "Soil Health Monitoring", and "Soil Health Monitoring". At the bottom, there are buttons for "Launch Analytics" and "Feedback".

<http://iplantcollaborative.org>

This screenshot shows the DNA Subway interface. The top header includes "DNA SUBWAY", "LOG IN", "LOG OUT", and "Help". Below the header is a search bar with placeholder text "Search DNA Subway". The main content area features a "DNA Subway" logo with a red "D", yellow "N", and blue "A", followed by the word "SUBWAY". It displays a network diagram where four colored lines (red, orange, blue, green) represent different pathways or databases. Arrows indicate connections between nodes, such as "Annotations", "Proteins", "Transcripts", "Genes", "Phenotypes", and "Variants". A callout box says "Annotations to Transfer". At the bottom, there are buttons for "DNA Subway Training", "DNA Subway Help", "Background", "About Us", and "Logout".

<http://dnasubway.org>

This screenshot shows the BioExtract interface. The top header includes "BioExtract", "LOG IN", "LOG OUT", and "Help". Below the header is a search bar with placeholder text "Search BioExtract". The main content area features a "BioExtract Brief View" section with a "Data access, analysis, storage, and workflow creation" link. It also includes sections for "Annotations/Data Resources", "Search BioExtract", and "Batch Requests". A sidebar on the right lists "Batch Requests" and "Where to Next". At the bottom, there are buttons for "Search Field", "Search Term(s)", and "Search Query".

<https://www.bioextract.org>

WHO'S USING THIS STUFF?

 **Arabidopsis Information Portal**
Alpha

About | Help | Contact | Search | Log in |

ThaleMine | Genome Browsers | Community | Science Apps | Downloads | Developer Zone | Log in |

Explore the Arabidopsis genome

 **ThaleMine**
Drill down on the genome. Analyze gene and protein data from TAIR, expression and interaction data from BAR, ortholog data from Panther, and more. Generata, save, and analyze result sets. Use plain text or structured queries to find interactive gene pages and protein reports.

 **JBrowse**
Scroll through the genome and zoom in for details. Layer on annotation tracks that display TAIR 10-gene structure data, EPIC-CoGe epigenetics data, and more. Use the latest, fully featured GRCh38 JBrowse tool (or, for a limited time, the older GRCh37 tool).

 **Science Applications**
Find other interactive application programs that help you explore plant genomics. AIP hosts applications that integrate data from other web sites using the web services model of on-request data exchange. AIP hosts science apps that were contributed by its members and its users.

 **DESIGN SAFE-CI**
A NATIONAL HAZARDS
ENGINEERING RESEARCH CENTER

A CLOUD-BASED ENVIRONMENT FOR RESEARCH IN NATURAL HAZARDS ENGINEERING

Home | NHERI Community | Research Workbench | Experimental Facilities | Learning Center | About | Contact

NHERI COMMUNITY

Find here the latest news and highlights on important natural hazards research discoveries and NHERI program announcements including upcoming meetings. Resources and collaboration tools for the NHERI community will also be provided here.

News & Features

Register for NHERI Experimental Facilities Workshop
10-19-15
NHERI Experimental Facilities are hosting



<http://araport.org>

<https://www.designsafe-ci.org>

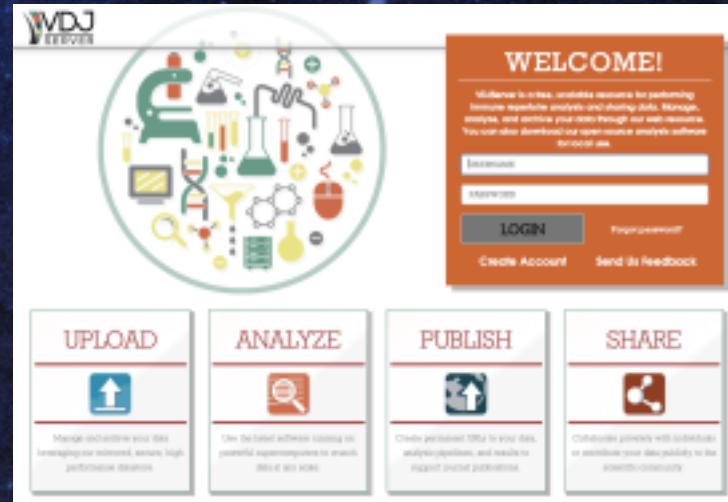
WHO'S USING THIS STUFF?



The screenshot shows the iReceptor website homepage. At the top is a green header bar with the iReceptor logo (a stylized green Y-shape) and the word "iReceptor". Below the header are navigation links: ABOUT, NEWS, ARCHITECTURE, and CONTACT. The main content area has a white background. On the left, a section titled "What is iReceptor?" contains a brief description of the project's goal: "iReceptor is a distributed data management system and scientific gateway for mining 'Next Generation' sequence data from immune responses. The goal of the project is to improve the design of vaccines and therapeutic antibodies by integrating Canadian and international data repositories of antibody and T-cell receptor gene sequences." To the right of this is a "LATEST NEWS" sidebar with several news items:

- CAMERRI Workshop Oct 29-31, 2014 11/03/2014 - 06:58
- Antibody & T-Cell Receptor Data Integration Planning Meeting 08/10/2014 - 18:07
- iReceptor CANARIO announcement 08/03/2014 - 11:31
- iReceptor is live!! 08/02/2014 - 08:44

<https://ireceptorgw.irmacs.sfu.ca/>



The screenshot shows the VDJ Server website homepage. It features a large orange "WELCOME!" banner at the top right. Below the banner is a circular graphic containing various scientific icons related to immunology and genetics. To the right of the graphic is a login form with fields for "Email Address" and "Password", and buttons for "LOGIN", "Create Account", and "Send us Feedback". To the left of the graphic is a news item about the CAMERRI Workshop. Below the graphic are four large buttons with red headers: "UPLOAD", "ANALYZE", "PUBLISH", and "SHARE". Each button has a corresponding icon and a brief description.

- UPLOAD**
Manage individual viral data samples or our integrated, access, logic performance database.
- ANALYZE**
Our detailed software running on powerful supercomputers to analyze your data.
- PUBLISH**
Create permanent URLs to your data, analysis pipelines, and results in instant online publication.
- SHARE**
Collaborate privately with individuals or maximize your data visibility to the research community.

<https://vdjserver.org>



THANK YOU!

FOLLOW US

@agaveapi

<https://agaveapi.co>