



THE AGAVE PLATFORM

SCIENCE AS A SERVICE FOR THE OPEN SCIENCE COMMUNITY

Rion Dooley @deardooley
deardooley@gmail.com

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)*





WORKFLOWS NOW TECHNICALLY COMPLICATED

LANGUAGES	FRAMEWORKS	HARDWARE
<ul style="list-style-type: none">• Python 2 & 3• R• Julia• Perl• Matlab• Java• Scala, Clojure, etc• .NET• C++• Swift• Haskell• Go• Javascript	<ul style="list-style-type: none">• <u>MapReduce</u>: Hadoop, Storm, Pachyderm• <u>Event & Streaming</u>: Kinesis, Azure Stream Analytics, Camel, Streambase• <u>Deep/Machine Learning</u>: Watson, Azure BI, Tensorflow• <u>In-memory parsing</u>: Kognito, Apache Spark• <u>New data warehouse</u>: Snowflake• <u>Containers</u>: Docker, Rocket, MESOS, Kubernetes• <u>Cloud</u>: AWS, GCE, OpenStack, VMWare	<ul style="list-style-type: none">• Rise of many-core computing means 50-100 threads/node*• Xeon / Xeon Phi• GPU• OpenPower• ARM• Multi-level memory architectures• Hierarchical storage architectures• FPGAs

BIG DATA...

SO HOT RIGHT NOW

memegenerator.net

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

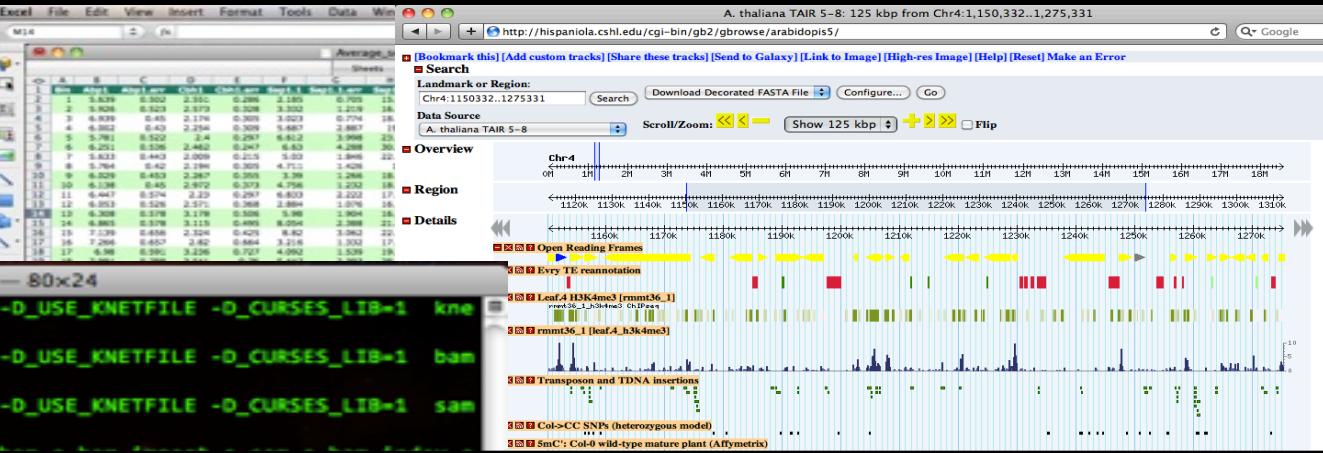
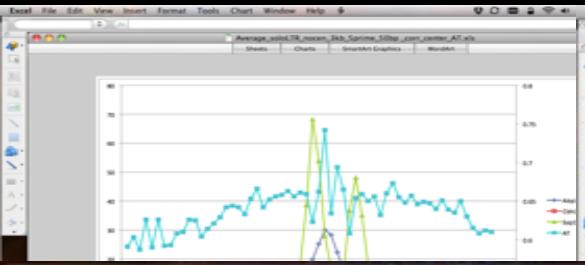
- Mostly experimentalists
- Strict data sharing & access



Roshan

- Computationally experienced
- Focused on interpretation

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



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



DESIGNSAFE.CI
A NATURAL HAZARDS
ENGINEERING COMMUNITY

Steve-TACC

Home Data Jobs Welcome, mock Logout

Data on Stampede

12 Files in...

Return Home Drop here Import from Dropbox

File Name File Size Actions

- alarm 4.0 kB
- viminfo 809 B
- telnet.tcl 12.5 kB
- 2d_redo.tcl 132.2 kB
- bin 4.0 kB
- Intel 4.0 kB
- ib 4.0 kB
- mattab_inputs 4.0 kB
- mock 4.0 kB
- RLH_Telem_Set.jm 9.4 kB
- SAcheck 4.0 kB

Successfully uploaded Telnet.tcl Getting listing...

2012-2015 Texas Advanced Computing Center, University of Texas at Austin

Welcome, Stampede

Stampede.tacc.org

System status:

Utilization

89% Queued 6 Other 56

DATA UTILIZATION REPORT

App Analytics

Displaying 1 - 1 of 1 1 items(s)

Texas Pandemic Flu Simulator

API Explorer

Community Data Agave Core Thalassine API

API is built exclusively on our open-access web service Application Programming Interfaces, or APIs. This means that you have programmatic access to everything you see at our site. Want to annotate a gene with its ortholog from within a script? Find the API and make a request! To publish your own data to Agave? Learn to use our Community Data APIs to do just that. This page provides an interactive console where you can explore various using Agave API without having to master some of the more complicated aspects of using web services.

Filter APIs... You can filter APIs by namespace, service, description, tags, etc. Filter with the free text or target specific code, for example, with `namespace:org1` or `tags:expression`.

APIs

- agv! airport_to_json version 0.1 Given a valid AGI locus return it's alignment from the Agave11 annotation
- agv! airport_generator_alignmentbag version 0.1 Given a valid AGI locus return it's alignment from the Agave11 annotation
- agv! airport_generator_checklist version 0.1.0 Check whether AGI/Alas exists in the BAR databases
- agv! airport_generator_getalias version 0.1.0 Returns AGI/Alas data for Generator autocomplete function
- at! atm version 0.1
- atted+! atted_compressed_by_locus version 0.0.6 Given a valid AGI locus, fetch
- IntAct IntAct
- IntAct IntAct
- IntAct IntAct

Public Apps >> BIRTHouse 3.1.0.0

Integrated by Zhenyu Lu Rating (2)

Public Apps (2) My public apps (2) My public Apps (199)

Public Apps (2) My public Apps (199)

Projects

Name: Job Output Project Date: 13-Nov-2015 Members: 1

Title	Last Modified	Size	File Origin	Type	Tags	Read Direction
mc1.fasta	13-Jun-2015 03:38	60 B	Uploaded File	Barcode Sequences		
mc2.fasta	13-Jun-2015 03:38	76 B	Uploaded File	Barcode Sequences		
sample_01.fasta	13-Jun-2015 03:38	2.01 kB	Uploaded File	Barcode Sequences		
sample_01.fasta	13-Jun-2015 03:42	4.63 kB	Uploaded File	Single End Read Level Data	read-data	
mc1.fasta	13-Jun-2015 03:42	60 B	Job: vdplice test job	job		
sample_01.fasta	13-Jun-2015 03:42	2.01 kB	Job: vdplice test job	job		
sample_01.fasta	13-Jun-2015 03:42	349 B	Job: vdplice test job	job		
sample_01.fasta	13-Jun-2015 03:42	349 B	Job: vdplice test job	job		
sample_01.fasta	13-Jun-2015 03:46	2.01 kB	Job: igblast test	job		
sample_01.fasta	14-Jun-2015 03:46	2.01 kB	Job: test	job		

VDJ SERVER

CREATE NEW +

- unshared project
- test project
- demultiplex project
- filetype project
- test project HA
- Job Output Project

Settings

Manage Users

Uploaded Data

Jarfile/Jar Associations

Paired Read Associations

Analyses

BugForVideos

LSC Group Meeting Demo

PROJECTS

Name: Job Output Project Date: 13-Nov-2015 Members: 1

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sample_01.fasta	13-Jun-2015 03:42	349 B	Job: vdplice test job	job		
sample_01.fasta	13-Jun-2015 03:42	349 B	Job: vdplice test job	job		
sample_01.fasta	13-Jun-2015 03:46	2.01 kB	Job: igblast test	job		
sample_01.fasta	14-Jun-2015 03:46	2.01 kB	Job: test	job		

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
'q()' to quit R.

> |

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-mers, 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 below.

We note that this is a python3 notebook. At the moment, python3 is required to use the pyspark library.

```
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[*]')
```

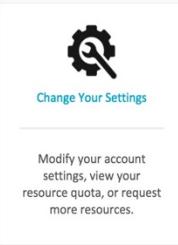
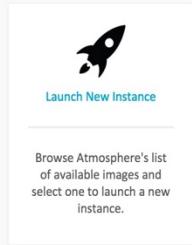
Pathogens

Hosted SaaS

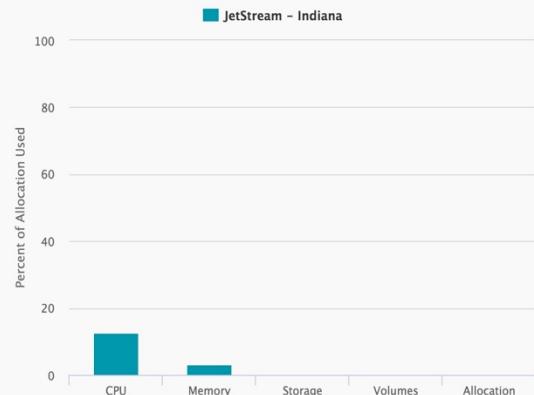
- JupyterHub notebooks
- Rstudio
- Web-based VNC

Also, backed by world-class computing and data capacity

Getting Started



Resources in Use Need more?



1 Instances

active - deploy_error



0 Volumes

Community Activity

edwintest3 created an image Nov 16, 2015 02:31 am MAKER-P 2.28 with CCTools 5

edwintest3 created an image Nov 16, 2015 02:31 am TSW Workshop Williams 1.2

atmoadmin created an image Oct 23, 2015 12:06 am Trusty Tahr (x64)

atmoadmin created an image Oct 23, 2015 12:06 am cirros-0.3.4-x86_64

atmoadmin created an image Oct 23, 2015 12:06 am CentOS-7-x86_64-GenericCloud-20150628_01

atmoadmin created an image Oct 23, 2015 12:06 am CentOS-6-x86_64-GenericCloud-1508

atmoadmin created an image Oct 23, 2015 12:06 am CentOS-7-x86_64-GenericCloud-1508

Instance History (5 instances launched)



Updated a few seconds ago

<https://use.jetstream-cloud.org/application/images/5>

©2016 Jetstream

[Feedback & Support](#)

Easy to use Cloud Computing

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

Cloud consoles are aimed at sysadmins and unintuitive.

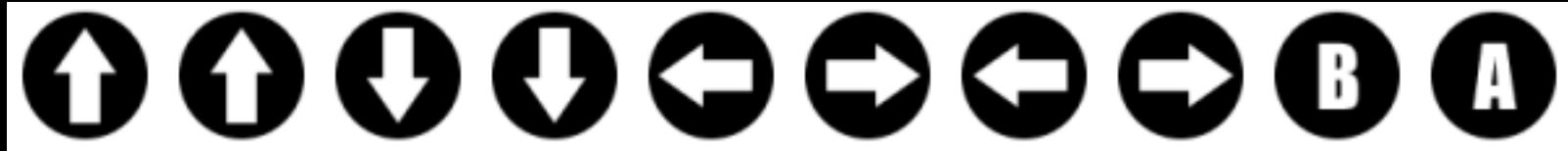
We're changing that with improved UX and support

- APIs are still available
- No cost to end user

WHAT DO THESE HAVE IN COMMON?



KONAMI CODE





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



Agave

Platform

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

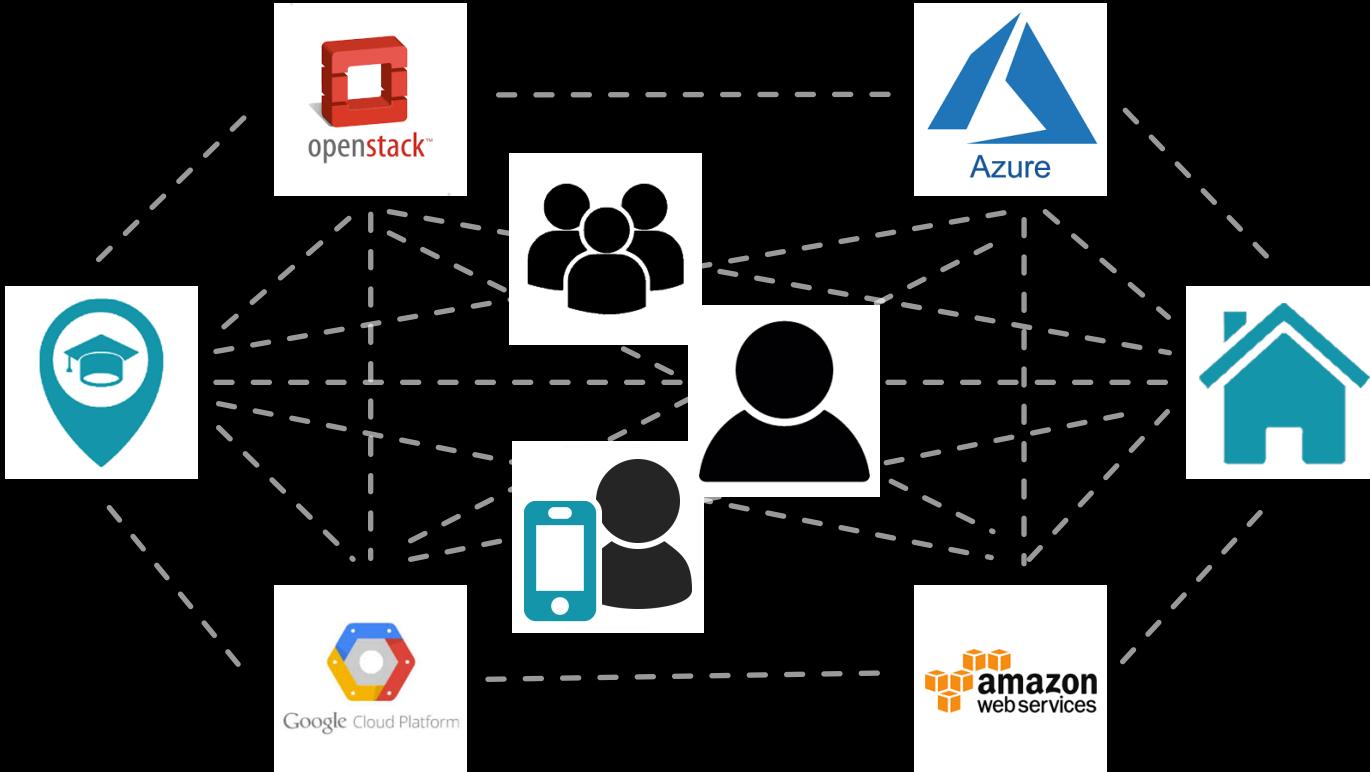
-

Think of it like

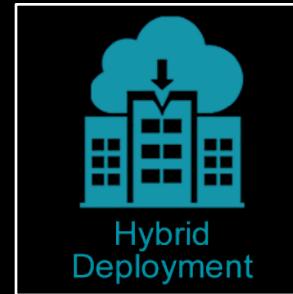


for Science

BRIDGE BUILDING



OPEN SOURCE WITH FLEXIBLE DEPLOYMENT



- Use your existing IdP
 - White-label docs & tools
 - Ansible for automation
 - Pluggable logging
 - Pluggable monitoring
 - Managed or self-hosted
 - Consulting available
- Use your existing IdP
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 - Ansible for automation
 - Pluggable logging
 - Pluggable monitoring
 - Managed or self-hosted
 - Consulting available

WHAT DOES IT DO?

MANAGE
DATA

RUN
CODE

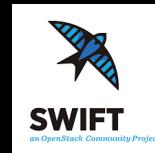
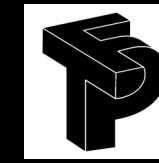
COLLABORATE
ANYWHERE

CONNECT
ANYTHING



AGAVE HELPS YOU 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



AGAVE HELPS YOU 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



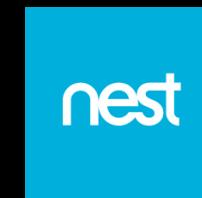
AGAVE HELPS YOU COLLABORATE MEANINFULLY

- ▶ Fine-grained access control
- ▶ Deep link to any resource in the API
- ▶ Pre-authenticated disposable links
- ▶ Alerts and notifications into existing apps
- ▶ Web standards come standard
- ▶ Integrations with popular frameworks and cloud services



AGAVE HELPS YOU INTEGRATE ANYWHERE

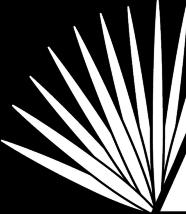
- ▶ Events, crons, monitors, and polling to stay informed
- ▶ Webhooks, web sockets, and custom vendor integrations to integrate with the world around you
- ▶ OAuth2, OIDC, and service accounts
- ▶ Self-service API Management
- ▶ Data mediation as a service
- ▶ Support for enterprise IoT solutions



GROCERY STORE APPROACH

- Take what you want
- Leave the rest
- Self-paced
- No lock-in





Agave

Tooling

TOOLS THAT FIT YOUR TOOLBELT

- 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)

DEVELOPER FRIENDLY DOCUMENTATION

Introduction

The Agave Platform (<http://agaveapi.co>) is an open source, science-as-a-service API platform for powering your digital lab. Agave allows you to bring together your public, private, and shared high performance computing (HPC), high throughput computing (HTC), Cloud, and Big Data resources under a single, web-friendly REST API.

- Run code
- Manage data
- Collaborate meaningfully
- Integrate anywhere

The Agave documentation site contains documentation, guides, tutorials, and lots of examples to help you build your own digital lab.

If you came here looking for a UI to interact with the platform and kick the tires, please see our reference web application, Agave ToGo, at <http://togo.agaveapi.co>.

Conventions

Throughout the documentation you will regularly encounter the following variables. These represent user-specific values that should be replaced when attempting any of the calls using your account. Once you log into this site, these values will be replaced with values appropriate for you to use when copying and pasting the examples on your own.

Variable	Description	Example
<code>\$(API_HOST)</code>	Base hostname of the API.	<code>public.agaveapi.co</code>
<code>\$(API_VERSION)</code>	Version of the API.	<code>v2</code>

Developer guides

The screenshot shows the Agave API Explorer interface. On the left, a sidebar lists various service categories: Clients, Apps, Jobs, Files, Meta, Monitors, Notifications, Positis, and Profiles. The 'Apps' category is currently selected, indicated by a blue background. In the main content area, the title 'List apps' is displayed above a search bar containing the URL 'http://docs.agaveplatform.org/live-dc'. Below the search bar is a token input field labeled 'TOKEN' with the value 'ed62565f4a038d30fc434c'. A large blue button labeled 'GET /apps/v2/' is centered at the top. To its right, a 'Show samples' button is followed by a circular arrow icon. The main body of the page is titled 'Get a list of available applications.' It contains several parameter fields:

- public**: A dropdown menu set to 'false' with a 'boolean' type label below it. A note states: "Whether to return only public apps. (Acceptable values are: 'true', 'false')."
- name**: An input field with a placeholder 'name' and a 'string' type label below it.
- executionSystem**: An input field with a placeholder 'executionSystem' and a 'string' type label below it.
- tags**: An input field with a placeholder 'tags' and a 'string' type label below it.
- filter**: An input field with a placeholder 'filter' and a 'string' type label below it. A note explains: "A comma-separated list of fields in the response objects to return. This allows developers to create their own response objects."

On the right side of the page, there are two sections: 'RESPONSE SAMPLE' and 'RESPONSE SCHEMA'. The 'RESPONSE SAMPLE' section shows a JSON object representing an application record. The 'RESPONSE SCHEMA' section describes the schema for the response objects.

```
RESPONSE SAMPLE
{
  {
    "id": "string",
    "executionSystem": "string",
    "lastModified": "2017-11-04T19:02:58.543Z",
    "name": "string",
    "isPublic": true,
    "revision": 0,
    "shortDescription": "string",
    "version": "string"
  }
}

RESPONSE SCHEMA
```

Interactive API browser



COPY AND PASTE OR GIT CLONE

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-mers, 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 below.

We note that this is a python3 notebook. At the moment, python3 is required to use the pyspark library.

```
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

Jupyter integration

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

Run a Job

This will run a Docker container on Agave's Docker compute cluster. Note, you may have to wait a moment for your container to launch if there is heavy usage right now.

Name: Test job 1457014283

Image: SciPy-3

Command:

Job Status
All Submitted Queued Running Completed

Demos & samples

WEBAPPS TOSTUDY AND TOGO

The screenshot shows the Agave ToGo Admin Dashboard. On the left, a sidebar lists categories like Apps, Projects, Data, Jobs, Lambdas, Webhooks, Systems, Monitors, Community, Feedback, and Support. The main dashboard area features several cards: '1349 Jobs' (blue), '12,5TB Data Moved' (red), '549 App Users' (teal), and '+25% Activity Increase' (purple). Below these are two charts: 'PROJECT ACTIVITY' showing a bar chart for 'Total' (3756) across categories USER, COMMENTS, JOBS, DOCS, and KARMA; and 'ACTIVITY FEEDS' showing a bar chart for 'New' activity across the same categories.

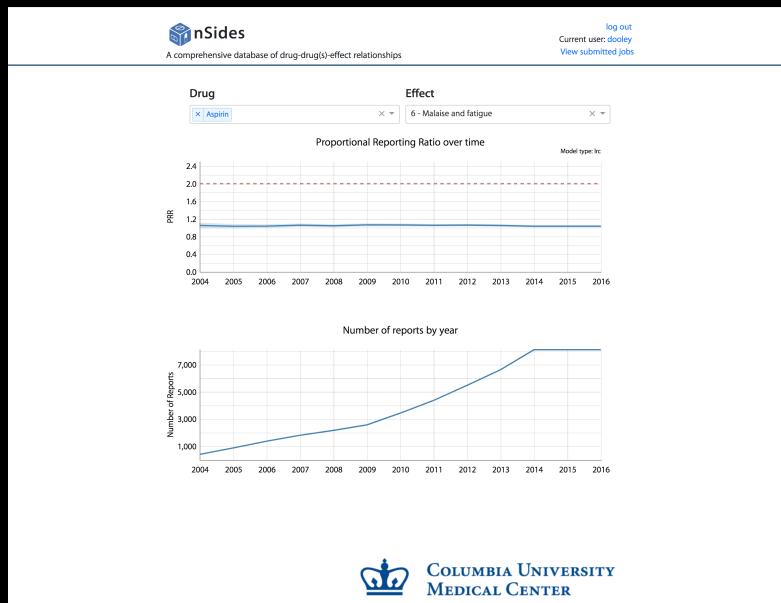
<http://togo.agaveplatform.org/app>

The screenshot shows the Agave ToGo MicroSites application homepage. The header includes the Agave logo and navigation links for Home, Compute, Data, Remote Sessions, About, and Support. The main content area has a 'Welcome' message and a section titled 'Agave ToGo MicroSites' with a date 'October 31st, 2017'. Below this are two paragraphs of placeholder text. At the bottom, there are sections for 'ABOUT', 'FOLLOW US ON' (with social media icons), and 'CONTACTS' (listing Community Slack channel, Agave Help Desk, and Developer Documentation).

<http://agaveplatform.github.io/microsites/app>



WHO'S USING THIS STUFF?

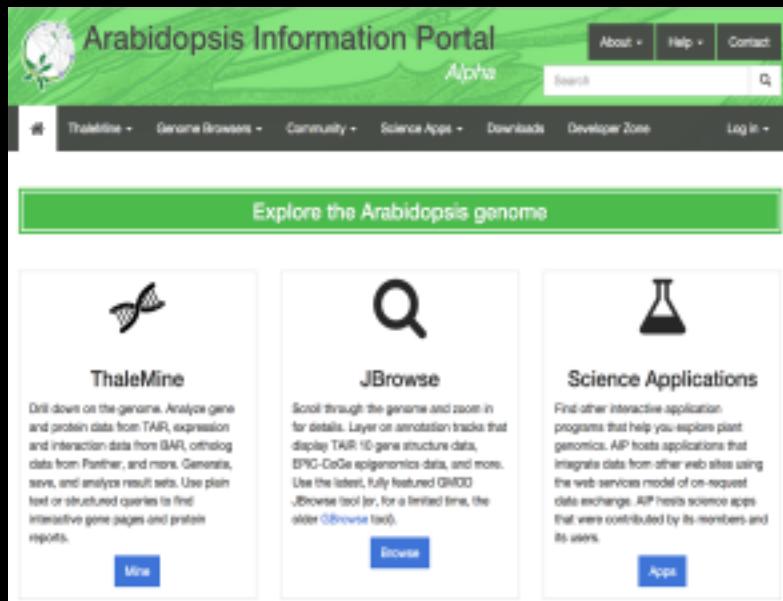


<http://nsides.io>

The screenshot shows the IKE Annotated Repository interface. It includes a search bar for 'Search Ike Annotated Repository Files', a map view of Hawaii with location markers, a sidebar with search and filter options, and a table titled 'Matching Files: 23' with download links for various files. The table lists files such as /new_data/DS_Store, /new_data/01-07.pdf, and /new_data/3-1642-001.pdf.

<https://ikewai.its.uhawaii.edu>

WHO'S USING THIS STUFF?



The screenshot shows the homepage of the Arabidopsis Information Portal (Alpha). At the top, there's a navigation bar with links for About, Help, Contact, Search, and Log In. Below the header, a green banner says "Explore the Arabidopsis genome". There are three main sections: "ThaleMine" (with a magnifying glass icon), "JBrowse" (with a magnifying glass icon), and "Science Applications" (with a flask icon). Each section has a brief description and a "More" or "Browse" button.

<http://araport.org>



The screenshot shows the homepage of the DESIGNSAFE-CI NHERI Community. The top features the DESIGNSAFE-CI logo and a banner for "A CLOUD-BASED ENVIRONMENT FOR RESEARCH IN NATURAL HAZARDS ENGINEERING". Below the banner, there are links for NHERI Community, Research Workbench, Experimental Facilities, Learning Center, About, and Contact. A large image of a coastal area with waves crashing against a rocky shore is on the right. The central part of the page has a green header "NHERI COMMUNITY" and a paragraph about news and highlights. Below this is a "News & Features" section with a link to register for experimental facilities workshops.

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

WHO'S USING THIS STUFF?

The screenshot displays the CyVerse Discovery Environment interface. The left sidebar contains navigation links for Data, Apps, and Analyses. The main area is divided into three sections: Data, Apps, and Analyses.

Data Section:

- Upload
- File
- Edit
- Download
- Share
- Metadata
- Refresh

Navigation:

- bigfiles
- bigsignatures
- bisulfite_data
- cage_data
- delsome
- diffpress_output
- example_data
- fastq
- fastq
- food
- gatesdryad
- import-tests
- iplant_org
- mascourt_output
- pint
- posts
- presentations
- public
- remix
- respect_20
- rx3d
- scratches
- somes
- stackengines

Viewing: /platen/home/dooley/bigfiles

Name	Last Modified	Size
Sgb.dat	2016 Nov 17 22:29:03	5.54 GB
b	2016 Nov 17 22:31:32	2.61 GB
c	2016 Nov 17 22:31:22	2.61 GB

Displaying 1 - 3 of 3 1 item(s)

Apps Section:

Sort By: Name

App	Description	Status	Rating	Action
agave	UNKNOWN	(0)	★ ★ ★ ★	Manage Tools
baypass 2.0	CyVerseUK 1.0.0	Best 2.4.3 (with Beagle) on CyVerseUK 1.0.0	★★★★★ (0)	Switch View
agave	UNKNOWN	(0)	★ ★ ★ ★	Manage Tools
Bismark (genome preparation)	0.14.4	UNKNOWN	(0)	Manage Tools
Bismark (methylation extractor)	0.18.0	UNKNOWN	(0)	Manage Tools
Blatmark 0.14.4	UNKNOWN	(0)	★ ★ ★ ★	Manage Tools
bismark_genome_preparation	0.18.1	UNKNOWN	(0)	Manage Tools
blatkt 0.1.2	UNKNOWN	(0)	★ ★ ★ ★	Manage Tools
blatkt 0.1.2	UNKNOWN	(0)	★ ★ ★ ★	Manage Tools
Blast 0.0.0	UNKNOWN	(0)	★ ★ ★ ★	Manage Tools
Blast 0.0.0	UNKNOWN	(0)	★ ★ ★ ★	Manage Tools
Blast 0.0.0	UNKNOWN	(0)	★ ★ ★ ★	Manage Tools
Blast 0.0.0	UNKNOWN	(0)	★ ★ ★ ★	Manage Tools
bowtie2 2.2.6	UNKNOWN	(0)	★ ★ ★ ★	Manage Tools

Analyses Section:

Analyses

Analyses

Name	Owner	App	Start Date	End Date	Status
Gofes v2.analysis	dooley@pcmcslab.org	GoSeq v2	2014 Nov 15 06:07:41	2014 Nov 15 06:09:07	Failed
Gofes v2.analysis	dooley@pcmcslab.org	GoSeq v2	2014 Nov 15 06:07:41	2014 Nov 15 06:09:07	Failed
MergGP 0.0.1.analysis	dooley@pcmcslab.org	HergeGP 0.0.1	2013 Dec 7 21:09:44	2013 Dec 7 21:11:29	Complete
MergGP 0.0.1.analysis	dooley@pcmcslab.org	HergeGP 0.0.1	2013 Dec 7 19:57:18	2013 Dec 7 19:58:12	Complete

Displaying 1 - 4 of 7 0 item(s)

The screenshot shows the VDJ SERVER homepage. At the top left is the logo 'VDJ SERVER'. To its right is a circular graphic containing various scientific icons like a DNA helix, test tubes, a microscope, and a computer monitor. The main area has a light blue background with the word 'WELCOME!' in large orange letters at the top right. Below it is a paragraph of text about the service. Further down are four large buttons with red outlines: 'LOGIN' (with a 'Forgot password?' link), 'Create Account', and 'Send Us Feedback'. At the bottom are four cards with red headers: 'UPLOAD' (with an icon of a blue up arrow), 'ANALYZE' (with an icon of a magnifying glass over a DNA helix), 'PUBLISH' (with an icon of a blue up arrow inside a box), and 'SHARE' (with an icon of a person sharing a document). Each card has descriptive text below its header.

<http://de.cyverse.org>

<https://vdjserver.org>

WHO'S USING THIS STUFF?

The DNA Subway interface features a "SUBWAY" map with four tracks:

- Associate & Economic Sequence**: Red track.
- Predict Consensus Using TAKIET**: Orange track.
- Estimate Sequence Relationships**: Blue track.
- Next Generation Sequencing**: Green track.

Nodes along the tracks include: Alignment, Phylogenetic Tree, and Phylogenetic Tree Viewer. A central node labeled "Browsers & Transfer" connects all tracks. A "Click to watch" button is located near the bottom right. A note at the top right says "Note for PLANTS & ANIMALS". A "DNA SUBWAY" logo is at the bottom left. The URL <http://cyverse.org> is overlaid in yellow.

<http://dnasubway.org>

The BioExtract Server interface has a "Dense Workflow" header. It includes a sidebar with "Available Data Sources" (checkboxes for All, Macerelous, Nucleotide Sequences, Protein Sequences, Viridiplantae, and Viridiplantae Protein) and a "Fetch Sequence(s)" section. The main area contains a "Query Form" with "Search Field" and "Search Term(s)" fields, and a "Current Query" section with "Submit Query" and "Clear" buttons. A note at the bottom left says "About BioExtract harnesses the power of online informatics tools for creating and customizing workflows. Users can query online sequence data, analyze it using an informatics tools (web service and desktop), create and share custom workflows for repeated analysis, and save the resulting data and workflows in standardized report work was initially supported by NSF grant DBI-0350330. Current work is being supported by NSF 0931135468". The URL <https://www.bioextract.org> is overlaid in yellow.

<https://www.bioextract.org>

WHO'S USING THIS STUFF?

The screenshot shows the homepage of the iReceptor website. At the top is a green logo featuring a stylized Y-shaped receptor molecule. To its right, the word "iReceptor" is written in a lowercase, sans-serif font. Below the logo is a navigation bar with links for "ABOUT", "NEWS", "ARCHITECTURE", and "CONTACT". A large 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." Below this is another section titled "LATEST NEWS" which lists an "iCANARIE Workshop" held on Oct 30-31, 2014, from 10/30/2014 - 08:59. Further down are sections for "Antibody & T-cell Receptor Data Integration Planning Meeting" (09/10/2014 - 15:57) and "iReceptor iCANARIE announcement" (06/23/2014 - 11:31). At the bottom, it says "iReceptor is live!!" (06/22/2014 - 09:45).

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

The screenshot shows the homepage of the iMicrobe website. The header includes the iMicrobe logo, a search bar, and links for "Browse", "Tools", "Download", and "Login". A note at the top states: "Note: This is a new beta version and not currently under development. Please let us know of any issues or suggestions!" Below the header is a large banner with the text "iMicrobe Enables Science" and "Search, analyze, compare, and visualize your data!". Two orange buttons are visible: "GET STARTED" and "LOGIN". The main content area is titled "Use cases" and lists five categories: "Browse" (described as a "window shop" for datasets by ecosystem, project, principal investigator, and more), "Search" (described as how-in-on datasets based on environmental factors using our powerful search tool), "Discover" (described as using our analytics to find datasets like yours based on sequence composition and shared functional or taxonomic annotations), "Recommendations" (described as joining the Microbe community and get personalized recommendations on recent articles in microbial ecology), and "Learn" (described as tapping into an ecosystem of solutions for analyzing large-scale meta-omics datasets at protocols using Microbe tools, joining the community and share your protocols using Microbe Apps). A "Developers" section is also present, describing it as a hub for open-source developers who are creating tools for microbial ecology.

<https://www.imicrobe.us>





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