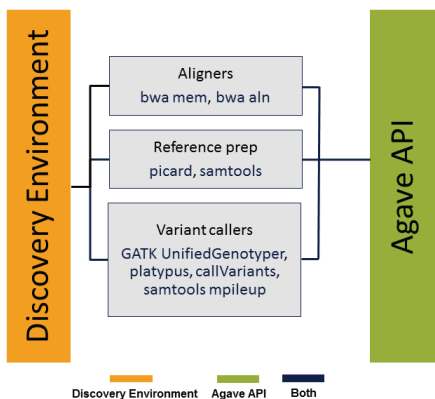
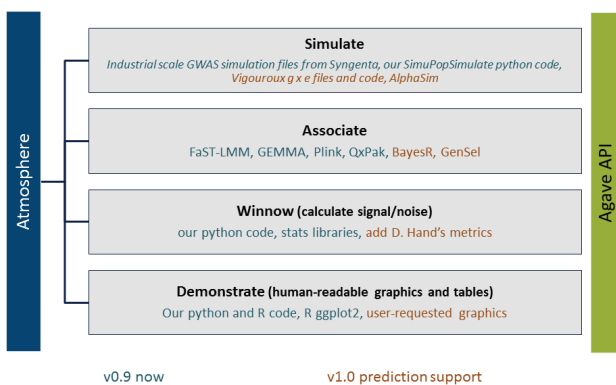


## Variant Caller Pipeline



## Validate Pipeline

-extensible, scalable testing of tool accuracy and precision



## Genomics Workflows

### Quick Reference Guide

Workflow	Platform	Limits
Genome Assembly	DE, Agave	--
Transcriptome Assembly	DE, Agave	48 hrs run time max
Genome Annotation WQ-MAKER	Atmo	--
RNA Seq	DE, Atmo	--
HT Process	DE, Agave	150 GB input data max
Methylation Analysis	DE, Agave	--
Association Analysis	DE, Agave	--
Variant Caller	DE, Agave	48 hrs run time max
Validate	Atmo, Agave	--
SRA Submission	DE	--

DE - Discovery Environment  
Atmo - Atmosphere  
Agave - Agave API



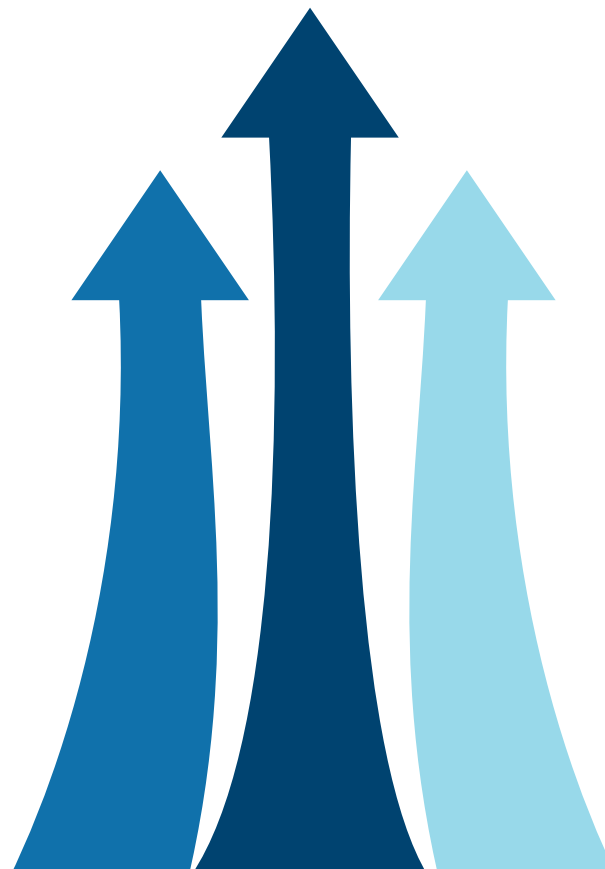
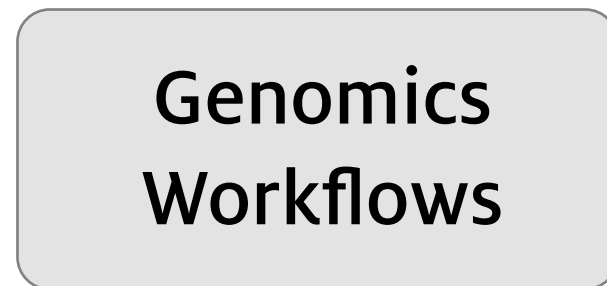
Transforming SCIENCE  
through DATA-DRIVEN  
DISCOVERY

Genomics Workflows slides  
are available for download at:  
[www.cyverse.org/learning-center](http://www.cyverse.org/learning-center)



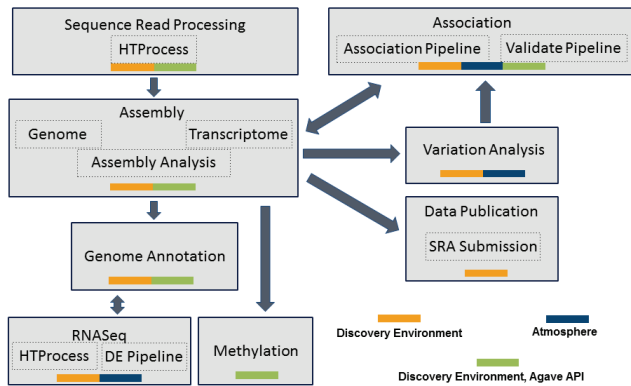
While you are there...

- Explore our tutorials
- See the science we enable

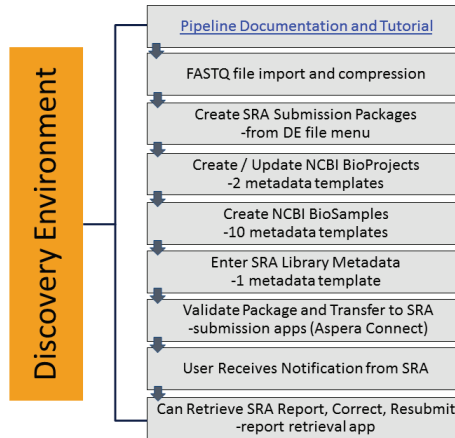


Funded by National  
Science Foundation award  
numbers DBI-0735191  
and DBI-1265383

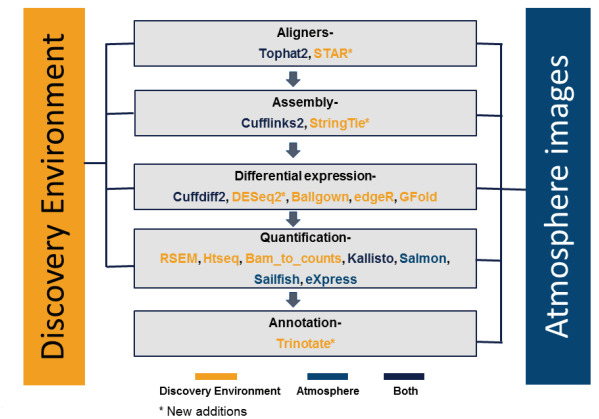
## Overview of Genomics Workflows



## Data Dissemination: NCBI SRA Submission Pipeline

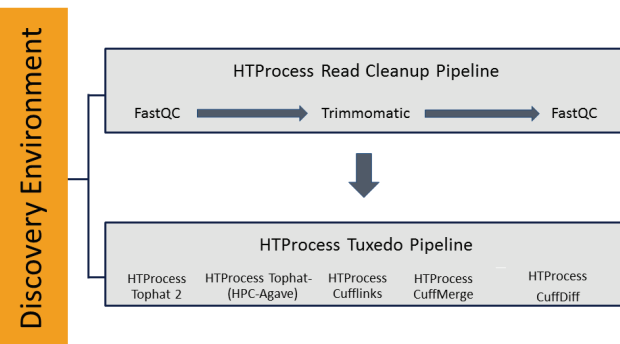


## RNA Seq 1 for Differential Expression

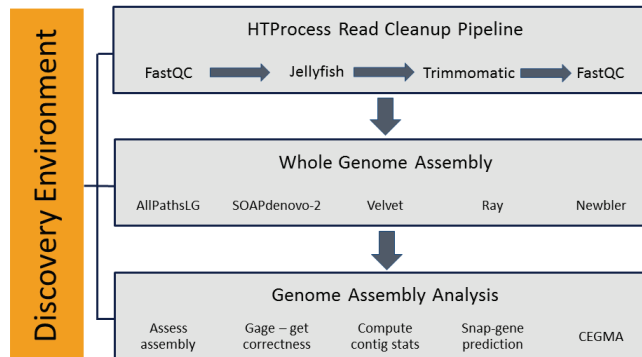


## RNA seq 2: High Throughput Process Apps

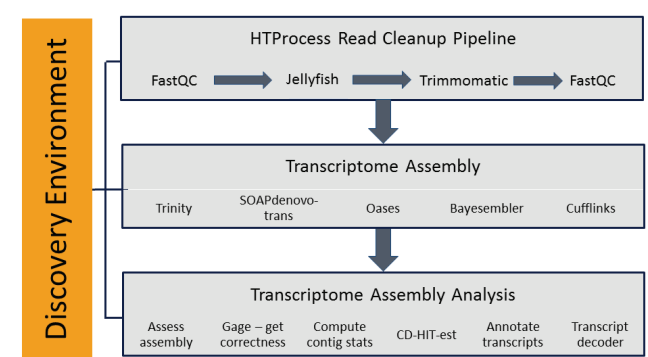
For handling large groups of data and easier workflow management. Files are managed as a group or library contained in a single directory.



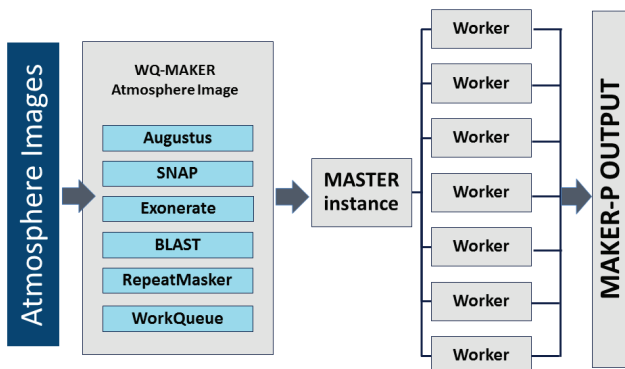
## Genome Assembly



## Transcriptome Assembly

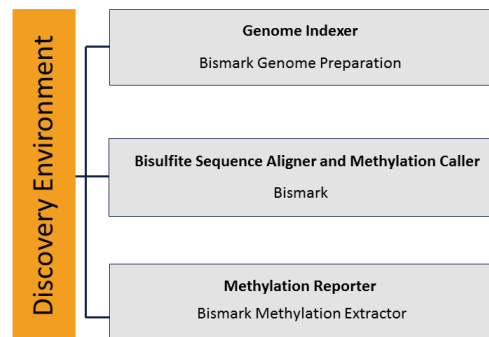


## Genome Annotation: WQ-MAKER in Atmosphere

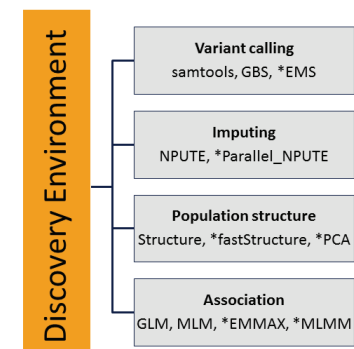


In collaboration with the Douglas Thain lab (<http://www3.nd.edu/~dthain/>)

## All New Methylation Analysis



## Association Analysis



\* New additions