

Tutorials List

About the Tutorials List page

This page lists all current tutorials for all platforms. **Note: A few YouTube videos are listed in the table below. For the full list, see the [CyVerse YouTube channel](#).**

- **Global search:** To search on a word or phrase in the table, click in the **Global Filter** field and begin entering the query.
- **Sorting:** To sort on a column, hover over the column header and click the arrow.
- **To open the tutorial,** click the link in the Tutorial Name column.
- **To email the tutorial's author,** email the author using the link in the tutorial.

Tutorial Name <i>Also check CyVerse YouTube channel</i>	Author	Platform	Type	Category	Goals, Steps, Apps Used <input type="text"/>
Annotating genomes with MAKER-P**	Subramaniam	DE	App		Highlights from some iPlant session presentations at the International Plant and Animal Genome Meeting XXIII (January 2015, San Diego). YouTube, pub 2/2015.
Applied Concepts in Cyberinfrastructure: Exoplanets video**	Lyons, Merchant	DE	YouTube		The Applied Concepts in Cyberinfrastructure course tackles new problems by collaborating with researchers across the University of Arizona. This video features Dr. Jared Males, Department of Astronomy and Steward Observatory and NASA Sagan Fellow, whose big data challenge was how to process tens of thousands of images in order to find the small cluster of pixels that represents a real exoplanet. (If the link no longer works, go to CyVerse YouTube channel and search on Transcriptomes.)
Assemble a Genome Using SOAPdenovo*	Barthelson	DE	Workflow	NGS	Commonly used procedure for <i>de novo</i> whole genome assembly of Illumina reads using the DE: Assemble reads, Assess assembly More... Apps used: <ul style="list-style-type: none"> • SOAPdenovo 2.0.4 • Assess assembly vs. whole genome
Assemble and Annotate Brassica Rapa Transcriptome in the Cloud through the iPlant Collaborative and XSEDE**	Devisetty	DE	App	RNA-Seq	Report a hybrid approach that combines the transcripts generated from de novo and reference-based strategies to generate a transcriptome assembly and subsequently annotating them.
Atmosphere Cloud -- Data transfer, Volumes, and Imaging**	Williams	Atmo	App	Images	YouTube, pub 2/2014.
Atmosphere: Launching, connecting, suspending, terminating instances**	Williams	Atmo	App	Images	YouTube, pub 2/2014.

Basic Stacks*	Noutsos	Atmo	App	Images	<p>Use next generation sequence data produced from Reduced Representation Libraries (RRL) such as Restriction site associated (RAD) tags.</p> <p>▼ More...</p> <p>All necessary Python modules are already installed on instance.</p> <p>Prepare raw RAD Illumina data for analysis by removing low quality reads and demultiplexing a set of barcoded samples. Use Stacks to assemble RAD tags de novo from parents and progeny of an F1 mapping cross. Call SNPs, genotypes, and haplotypes of these individuals within Stacks.</p>
BATools 0.0.1*	Kling	Atmo	App	Images	<p>Introduce new users to BATools and the BATools Wrapper Script.</p> <p>▼ More...</p> <p>BATools 0.0.1 is an Atmosphere image that has R version 3.0.1 installed. BATools, an R package for Whole Genome Prediction, is also installed on this image.</p>
Bisque Analysis Module: NuclearDetector3D**	Narro	Bisque	YouTube	Image Analysis	<p>Demo of using the NuclearDetector3D analysis module to detect and quantify nuclei. September 2016. (If the link no longer works, go to CyVerse YouTube channel and search on Transcriptomes.)</p>
Bisque bioimaging platform**	Merchant	Bisque	YouTube	Image Data	<p>7 minute Flash talk that provides overview of key Bisque features. iPlant presentation at the International Plant and Animal Genome Meeting XXIII (January 2015, San Diego). YouTube, pub 2/2015.</p>
Bisque Features**	Narro	Bisque	YouTube	Image Data and Analysis	<p>Video describes the major features of the Bisque Image Analysis Environment. September 2016. (If the link no longer works, go to CyVerse YouTube channel and search on Transcriptomes.)</p>
Bisque Overload and Upload**	iPlant	Bisque	App	Image Data	<p>Video tutorial. (If the link no longer works, go to CyVerse YouTube channel and search on Transcriptomes.)</p>
Bisque Overview and Upload Tutorial**	CyVerse	Bisque	App	Image Data	<p>(If the link no longer works, go to CyVerse YouTube channel and search on Transcriptomes.)</p>
Bisque Overview Modules** (CLICK TO DOWNLOAD PDF)	Predoehl	Bisque	App	Image Data	<p>High-level overview of the Bisque system, from the perspective of a module developer.</p> <p>▼ More...</p> <p>Key concepts involved in the process of integrating a new image analysis module into the Bisque platform. The scope of this document is restricted to batch-mode binary image analysis programs running in a Unix-style environment. Bisque offers a robust way to augment such a program with a graphical user interface, and share it with others. The present document focuses on an approach to such an augmentation using Python, a popular scripting language. Python offers many facilities that support this task, and the Bisque developers have created a convenient Python API wrapping the REST interface of Bisque.</p>

BLAST a Transcriptome*	Hilgert	DE	Workflow	NGS	<p>Reduce number of transcripts and level of redundancy in an assembled transcriptome, and identify coding sequences that can be submitted to BLASTP searches.</p> <p>▼ More...</p> <p>Eliminate small transcripts, Reduce transcript redundancy, Identify and translate coding sequences, Submit translated transcriptome to BLASTP or Submit translated transcriptome to Delta-BLAST</p> <p>Apps used:</p> <ul style="list-style-type: none"> • Select contigs • CD-HIT-est 4.6.1 • Transcript decoder 1.0 • Blastp-2.2.29 or DeltaBLAST-2.2.29
Bringing Authentic Genomics Research into the Classroom: Analysis of Maize Stress Response (Green Line)**	Makarevitch	DE, DNA Subway	App	RNA-Seq	<p>Analysis of plant response to abiotic stress. YouTube, pub 2/2015. (If the link no longer works, go to CyVerse YouTube channel and search on Transcriptomes.)</p> <p>▼ More...</p> <p>Create a large RNA-seq dataset that includes several maize inbreds subjected to various environmental stresses that can be interrogated to answer a variety of questions. Investigating maize global genome expression in response to abiotic stress provides students with opportunities to ask interesting, novel, and relevant questions, while developing their skills in big data analysis.</p>
Bulk metadata upload video tutorials (DE)**	Walls	DE		Metadata	<p>Watch this video tutorial to see how to apply metadata in bulk to one or more files in the CyVerse Data Store, using a specially designed tool in the DE. This process is useful if your metadata is already entered into a spreadsheet. It is particularly helpful if you have many files that have the same attributes but the same or different values for each attribute. (If the link no longer works, go to CyVerse YouTube channel and search on Transcriptomes.)</p>

Characterizing Differential Expression With RNA-Seq (Without Reference Genome)*	Barthelson	DE	Workflow	NGS	<p>Identify changes in gene expression levels between at least two sequenced transcriptome samples (18 separate tutorials).</p> <p>▼ More...</p> <p>Tutorials: Eliminate small transcripts, Reduce transcript redundancy, Identify coding sequences, Rename transcripts, Split RefSeq file, Map transcripts, Combine mapping outputs, Identify best matches, Reformat Blat results, Annotate transcripts, Map RNA-Seq reads to transcripts, Reformat mapping output, Count mapped reads, Trim count tables, Combine counts, Determine differential expression, Separate transcripts by type, Generate transcript lists.</p> <p>Apps used:</p> <ul style="list-style-type: none"> • Select contigs, CD-HIT-est 4.6.1, Transcript decoder 1.0, Linux stream editor, Split FASTA file, Blat (with options), Concatenate Multiple Files, Best Hit for Blat Output, Cut Columns, Rename contigs 2.0, Bowtie-2.2.1--Build-and-Map, SAM to sorted BAM, Index BAM and get stats, Join multiple tab-delimited files, DESeq, Numeric Evaluation of a Data Column, Cut Columns
Cluster Orthologs and Paralogs and Assemble Custom Gene Sets*	DeBarry	DE	Workflow		<p>Input entire protein-encoding gene or transcript repertoires from genomes of interest, and cluster homologs (orthologs and paralogs), then query clusters to assemble gene sets based on presence/absence and copy number</p> <p>▼ More...</p> <p>Apps used:</p> <ul style="list-style-type: none"> • Translation of CDS from Transcript Data (app: Transcript Decoder 1.0) • Rename Sequences and Prepare Input Files (app: fastaRename) • All-by-All BLASTp and Parse • Cluster Homologs, optionally, add unclustered sequences to OrthoMCL output, generate reports on the number of clusters in and between species • Query Clusters and Assemble Custom Gene Sets with queryOrthoMCL Map Fasta Headers to clusterReport and/or queryOrthoMCL output with flattenClusters
CoGe1**	Lyons	CoGe	App		<p>Intro to CoGe, a Powered by iPlant platform for comparative genomics (genomes of plants and animals). YouTube, pub 10/2014. (If the link no longer works, go to CyVerse YouTube channel and search on Transcriptomes.)</p>
CoGe2**	Lyons	CoGe			<p>Intro to CoGe, a Powered by iPlant platform for comparative genomics (genomes of plants and animals). YouTube, pub 10/2014. (If the link no longer works, go to CyVerse YouTube channel and search on Transcriptomes.)</p>

Collaborating with Image Data in Bisque**	Fedorov, Kviekval, Walls	Bisque	Webinar	Image Data	Overview of how to manage data and metadata, share data, annotate data and search it in BisQue. Webinar on April 22, 2016. (If the link no longer works, go to CyVerse YouTube channel and search on Transcriptomes.)
Data Store Intro 1 – Mod 1**	Lyons	DE, Data Store	App		Intro to iPlant and Data Store for BIO5 researchers, Part 1. YouTube, pub 9/2014.
Data Store Intro 2 – Mod 1**	Lyons	DE, Data Store	App		Intro to iPlant and Data Store for BIO5 researchers, Part 2. YouTube, pub 9/2014.
Data Store Intro 3 – Mod 1**	Lyons	DE, Data Store	App		Intro to iPlant and Data Store for BIO5 researchers, Part 3. YouTube, pub 9/2014.
Data Store Intro 4 – Mod 1**	Lyons	DE, Data Store	App		Intro to iPlant and Data Store for BIO5 researchers, Part 4. YouTube, pub 9/2014.
DE Quick Start**	Williams	DE	DE	Manual	Become familiar with the Discovery Environment by learning how to create a multiple sequence alignment.
Discover Variants Using SAM Tools*	Lu	DE	Workflow	NGS	Detect and call variants from sequence reads using Bowtie and SAM Tools. v More... Align reads, Reformat file, Identify variants, Verify variants. Apps used: <ul style="list-style-type: none"> • Bowtie-2.2.1--Build-and-Map • SAM to sorted BAM • Calling SNPs INDELS with SAMtools BCFtools • SAMTOOLS-0.1.19 VCF-Utilities varFilter
Characterizing Differential Expression with RNA-Seq (Tuxedo Method)**	McKay	DE	Workflow	RNA-Seq	Learn to identify all changes in gene expression levels between at two or more sequenced transcriptome samples.
Epigenetics Part I – Bisulfite Sequence Analysis and Adenosine to Inosine Modifications**	Song, Lu, Barthelson	DE	Workflow		This CyVerse Focus Forum webinar is the first of two webinars on epigenetics analysis in CyVerse. It will provide biologists with an overview of how to use applications available in the Discovery Environment to carry out epigenetics analyses on their datasets. Published 7/22/16. v More... The webinar will include mapping bisulfite sequencing reads using Bismark and ZED-align, and getting methylation ratios of individual cytosines across the genome. We will also discuss getting Differentially Methylated Regions (DMRs) using aligned reads from the outputs of popular bisulfite sequence aligners, Bismark as well as ZED-align. Finally, we will briefly describe a third aligner, GSNAP, which is useful for bisulfite sequencing and for adenosine to inosine modification.

Evaluate and Pre-Process Sequencing Reads*	Barthelson	DE	Workflow	NGS	<p>Clean and filter Illumina reads using DE apps.</p> <p>▼ More...</p> <p>Evaluate the quality of reads in a set of sequence files, Remove adapter sequences, Filter the sequences by their quality, Reevaluate the cleaned reads, Evaluate the cleaned reads using a different method</p> <p>Apps used:</p> <ul style="list-style-type: none"> • FastQC 0.10.1 (multi-file) • Scythe-adapter-trimming • Sickle-quality-based-trimming • FastQC 0.10.1 (multi-file) • Prinseq-Graph-noPCA evaluate reads
Evolinc*	Devisetty, Nelson	Atmo	Workflow	NGS	<p>Evolinc is a two-part pipeline to identify lincRNAs from an assembled transcriptome file (.gtf output from cufflinks) and then determine the extent to which those lincRNAs are conserved in the genome and transcriptome of other species.</p> <p>▼ More...</p> <p>The first part of the pipeline is the lincRNA identification. Note, currently Evolinc only identifies <i>intergenic</i> non-coding RNAs. We will incorporate identification of all lincRNAs (including natural antisense, overlapping, and those of <i>intra-genic/intronic</i> origins) in a later version. The second part is the comparative genomics and transcriptomics analysis. You feed the output from first part to second part. The pipelines were kept separate in case users did not want to perform an evolutionary analysis on the identified lincRNAs.</p>
External Scripting for BisQue Workflows**	Fedorov, Kviekval	BisQue	Webinar	Image Analysis	<p>Provides software developers with an overview of how to use the BisQue API to script processing tools for BisQue data including uploading images and datasets with external metadata in CSV and other sources, analyzing and annotating images with external tools, and collecting and summarizing information stored in BisQue. Webinar on May 25, 2016.</p>
FaST-LMM.Py v2.02*	Talley	Atmo	App	Images	<p>Introduce new users to the FaST-LMM software for GWAS analysis.</p>
fastStructure*	Devisetty	Atmo	App	Images	<p>fastStructure is a fast algorithm for inferring population structure from large SNP genotype data. It is based on a variational Bayesian framework for posterior inference and is written in Python2.x (Anil Raj et al., <i>Genetics</i> Jan 2014).</p>

fRNAkenseq (HTseq-with-BAM-input) Manual*	Hubbard	CoGe	App		Utilize fRNAkenseq, affectionately abbreviated as fRNAk. v More... To complete the first two steps of RNA seq analysis- mapping and transcript quantification - simply navigate from the main page to MapCount. Select the libraries for which you want to quantify gene expression. Choose the genome representing the organism your samples are from. This genome will be pulled from the databank of over 20,000 fasta and annotation pairs available to fRNAk. These genomes will be processed by fRNAk using BowTie2 in order to enable use of the TopHat2 mapping algorithm which requires index FASTA files (Langmead <i>et al.</i> , 2012). Also, choose the number of processors to devote to the mapping algorithms in order to parallelize their operations.
Functional Analysis of Your RNAseq Data**	McCarthy	DE	App	NGS	Describe set of tools for functional modeling of RNA-Seq data, including Gene Ontology and pathways enrichment. YouTube, pub 2/2015. v More... Describe how researchers can use iPlant tools to rapidly add functional information to their own transcript data, providing an initial set of annotations that can subsequently be used for functional modeling; utilize "real-life", publicly available RNA-Seq data sets to demonstrate the applicability of these functional modeling tools and attendees are encouraged to bring their own data sets; discuss future plans for improving functional modeling tools on iPlant and community feedback is welcome.
Genome Annotation using MAKER**	Subramaniam		App		YouTube, pub 10/2015.
Genome-wide Association Study (GWAS) Using a Genotyping-by-sequencing Approach*	Wang, Noutsos	DE	Workflow	GWAS	Learn to identify genetic variants that are associated with a trait.
Get Started with CyVerse webinar **	Williams	DE	App	Overview	YouTube, pub 8/2016.
GWAS / GTL Apps Overview**	Stapleton	DE	App		Available tools for GWAS within the iPlant cyberinfrastructure as of July 2014. YouTube, pub 7/2014.
iCommands**	Lyons	Data Store			
Installing R packages on Atmosphere*	Kling	Atmo	App	Images	Install R packages on Atmosphere: Launch instance, transfer files to instance, install R package, request imaging.
Integrating an Analysis Module into Bisque-1** (CLICK TO DOWNLOAD PDF)	Kharitonovam, Predoehl	BisQue	App		Specifics of using Bisque to run and share an analysis module. Extends and builds on the material of a related document, "Bisque module integration." Intended for users who would like to integrate their analysis code into the Bisque system. Assuming that you already have that code and the input required to run it (files and parameters), this overview outlines steps needed to get started with Bisque.

Kallisto-0.42.3-INDEX-QUANT-PE	Devisetty	DE	App	RNA-Seq	Kallisto is a program for quantifying abundances of transcripts from RNA-Seq data, or more generally of target sequences using high-throughput sequencing reads. It is based on the novel idea of <i>pseudoalignment</i> for rapidly determining the compatibility of reads with targets, without the need for alignment.
KOBAS 2.0-09052014*	Hopkins	Atmo	App	Images	Learn how to annotate and identify using KOBAS 2.0. ▼ More... Image is a build of KOBAS 2.0. Identify statistically enriched pathways, diseases, and GO terms for set of genes or proteins, using pathway, disease, and GO knowledge from multiple famous databases.
MAKER-P Genome Annotation using Atmosphere**	Stein	DE	App	Images	Learn how to run MAKER-P on an Atmosphere image using example small genome assembly. ▼ More... Launch MAKER-P Atmosphere image, Run MAKER-P on example small genome assembly.
MAKER-P Genome Annotation using cc-tools and Atmosphere**	Subramaniam	Atmo	App	Images	Learn how to run MAKER-P with cctools on an Atmosphere image using example genome assembly. ▼ More... Launch MAKER-P Atmosphere image, Run MAKER-P with cctools on example genome assembly.
Metadata in BisQue**	Narro	BisQue	YouTube	Image Data	Series of videos describing BisQue's support for metadata. Demos the basics of creating a metadata template, applying it to an image, annotating the image using the metadata template, searching and browsing a dataset of images that have been annotated using a metadata template. September 2016.
mini SOAPdenovo*	Williams	DE	App		Gain familiarity with a commonly used procedure for <i>de novo</i> whole genome assembly of Illumina reads using the DE. ▼ More... Assembly of paired and unpaired Illumina reads (app: Soapdenovo2) Analysis of assembly quality for comparison to what was accomplished in one of the Assemblathon procedures that used Soapdenovo1
NCBI Sequence Read Archive (SRA) Submission*	DeBarry	DE	Workflow		Make submissions to the NCBI Sequence Read Archive (SRA), including compressed FASTQ and an XML metadata file, organized into a submission package. ▼ More... Upload compressed sequence files into DE; Create submission package folders and add compressed sequence files; Add metadata to every folder in submission package; Validate submission package and submit to SRA; Submission of package and validation; If necessary, correct errors and resubmit.
Next Generation Sequencing: Getting Started, Read Evaluation, and Cleanup**	Barthelson	DE	App	NGS	Webinar on next-gen sequencing read cleanup (the most important thing of all!). YouTube, pub 4/2015.

NGS Eclipse Plugin**	Duitama	DE	App	NGS	YouTube, pub 2/2014.
Overview of GWAS Theory**	Lorenz	DE	App		Basic science of GWAS. YouTube, pub 7/2014.
Overview of the iPlant Collaborative**	Vaughn	All			Highlights from some iPlant session presentations at the International Plant and Animal Genome Meeting XXIII (January 2015, San Diego). YouTube, pub 2/2015.
Power and Limitations of GWAS**	Lorenz	DE	App		Power and limitation of a GWAS approach to understanding genetics and breeding potential. YouTube, pub 7/2014.
QIIME-1.9.1 for Atmosphere*	Devisetty	Atmo	Images	Metagenomics	QIIME is an open-source bioinformatics pipeline for performing microbiome analysis from raw DNA sequencing data. QIIME is designed to take users from raw sequencing data generated on the Illumina or other platforms through publication quality graphics and statistics. QIIME has been applied to studies based on billions of sequences from tens of thousands of samples.
QIIME-1.9.1 for the DE* (6 apps)	Devisetty	DE	App	Metagenomics	<p>QIIME is an open-source bioinformatics pipeline for performing microbiome analysis from raw DNA sequencing data. QIIME is designed to take users from raw sequencing data generated on the Illumina or other platforms through publication quality graphics and statistics. This includes demultiplexing and quality filtering, OTU picking, taxonomic assignment, and phylogenetic reconstruction, and diversity analyses and visualizations. QIIME has been applied to studies based on billions of sequences from tens of thousands of samples.</p> <p> Click to see apps Apps used: <ul style="list-style-type: none"> • qiime1.9.1-validate_mapping_file • qiime1.9.1-split_libraries_fastq • qiime1.9.1-count_seqs • qiime1.9.1-pick_open_reference_otus • qiime1.9.1-core_diversity_analyses • qiime1.9.1-make_emperor </p>
QUAST 4.0*	Devisetty	Atmo	Image	NGS	<p>QUAST is a tool for evaluating genome assemblies by computing various metrics.</p> <p>Gurevich, A., Saveliev, V., Vyahhi, N., and Tesler, G. (2013) QUAST: quality assessment tool for genome assemblies. <i>Bioinformatics</i> 29, 1072-1075</p>
RNA-Seq 1**	Barthelson	DE	App	RNA-Seq	Basic steps to RNA-seq analyses using iPlant. YouTube, pub 10/2014.
RNA-Seq 2**	Barthelson	DE	App	RNA-Seq	Review steps in RNA-seq analysis using iPlant. YouTube, pub 10/2014.
RNA-Seq 3**	Barthelson	DE	App	RNA-Seq	Step-by-step instructions on how to do RNA-Seq analysis using iPlant. YouTube, pub 10/2014.
RNA-Seq Methods and Algorithms (Part I)**	Pimentel	DE	App	NGS	Part I (Intro and Overview of RNA-Seq) webinar on Kallisto and Sleuth ; new tools for working with RNA-Seq datasets. YouTube, pub 10/2015.
RNA-Seq Methods and Algorithms (Part II)**	Pimentel	DE	App	NGS	Part II (Alignment Algorithms) of webinar on Kallisto and Sleuth ; new tools for working with RNA-Seq datasets. YouTube, pub 10/2015.
RNA-Seq Methods and Algorithms (Part III)**	Pimentel	DE	App	NGS	Part III of webinar (Quantification) on Kallisto and Sleuth ; new tools for working with RNA-Seq datasets. YouTube, pub 10/2015.

RNA-Seq Methods and Algorithms (Part IV)**	Pimentel	DE	App	NGS	Part IV (Differential Expression) of webinar on Kallisto and Sleuth ; new tools for working with RNA-Seq datasets. YouTube, pub 10/2015.
RNA-Seq Methods and Algorithms (Part V)**	Pimentel	DE	App	NGS	Part V (Live Kallisto Shell demo) of webinar on Kallisto and Sleuth ; new tools for working with RNA-Seq datasets. YouTube, pub 10/2015.
RNA-Seq Methods and Algorithms (Part VI)**	Pimentel	DE	App	NGS	Part VI (Live Sleuth Demo in R) of webinar on Kallisto and Sleuth ; new tools for working with RNA-Seq datasets. YouTube, pub 10/2015.
maQUAST 1.1.0*	Devisetty	Atmo	Image	RNA-Seq	maQUAST is a tool for evaluating RNA-Seq assemblies using reference genome and gene data database. In addition, maQUAST is also capable of estimating gene database coverage by raw reads and <i>de novo</i> quality assessment using third-party software (STAR, TopHat, GMAP etc.).
maQUAST 1.2.0*	Devisetty	Atmo	Image	RNA-Seq	maQUAST is a tool for evaluating RNA-Seq assemblies using reference genome and gene data database. In addition, maQUAST is also capable of estimating gene database coverage by raw reads and <i>de novo</i> quality assessment using third-party software (STAR, TopHat, GMAP etc.).
Taxonomic Name Resolution Service (TNRS)*	Hilgert	TNRS	App	App	Become familiar with TNRS to identify, correct, and update scientific names of plants. Compile and submit a list of names, process names, download, and examine results.
Transcriptome Assemblies: Approaches**	Barthelson	DE	App	Transcriptomes	YouTube, pub 4/2015. (If the link no longer works, go to CyVerse YouTube channel and search on Transcriptomes.)
Transcriptome Assembly (De Novo)**	Barthelson	DE	Workflow	Transcriptomes	Learn to assemble a transcriptome without a reference genome and to evaluate the assembly.
Transposable Elements, Gene Discovery, and DNA Barcoding (Yellow and Blue Lines)**	Burnette	DE, DNA Subway	App		Identify a TE family in the genome of an organism. YouTube, pub 2/2015.
Using iPlant Tools and Plastome Sequencing As a Springboard into Comparative Genomics**	Bailey	DE	App		Use iPlant Tools and Plastome Sequencing As a Springboard into Comparative Genomics. YouTube, pub 2/2015. More... Plastome Organization and Sequence for the Mimosoid Legume <i>Leucaena Trichandra</i> : Sequenced the plastome of <i>L. trichandra</i> , one of the first plastome sequences from the diverse Mimosoideae and a species involved in the origin of four tetraploid species of <i>Leucaena</i> . <i>De novo</i> assembly of a 300bp insert paired-end Illumina HiSeq library generated a 164,692bp plastome containing 112 unique genes arranged in the typical large single copy (LSC), inverted repeat, and small single copy regions.

Utilizing iPlant to Unearth Long Non-Coding RNAs**	Nelson	DE, CoGe	App	RNA-Seq	<p>Utilize iPlant to Unearth Long Non-Coding RNAs and Characterize Their Evolution in the Plant Family Brassicaceae. YouTube, pub 2/2015.</p> <p>▼ More...</p> <p>Address issues in identification of biologically relevant lncRNAs by using comparative genomics and transcriptomics to recover and curate lncRNAs in the plant family Brassicaceae, using CyVerse resources and CoGe.</p>
Validate Workflow v0.9*	Carpenter	Atmo	App	Images	<p>Learn to navigate the Validate Workflow.</p> <p>▼ More...</p> <p>Apps used:</p> <ul style="list-style-type: none"> • GWAS • FaST-LMM • GEMMA • QxPak • PLINK • Winnow • Simulate Demonstrate

Assemble a transcriptome without a reference genome and evaluate the assembly