

Galaxy Overview
The Basics

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UF Research Computing
Information Technology
Home of High-Performance Computing and **HiPerGator**

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UF Research Computing

UF Research Computing
Information Technology
Home of High-Performance Computing and **HiPerGator**

- Mission
 - Improve opportunities for research and scholarship
 - Improve competitiveness in securing external funding
 - Provide high-performance computing resources **and support** to UF researchers

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HiPerGator

The University of Florida Supercomputer for Research

- 16,384 cores—**total of about 19,000 cores today**
- Infiniband interconnect
- >3PB fast, high-availability, storage
- **GPGPUs**—90+, Kepler-class
- Large memory (**512GB to 1TB of RAM**) nodes

Approaches

UNIVERSITY OF FLORIDA | High-Performance Computing

HiPerGator

The University of Florida Supercomputer for Research

Cluster basics

User interaction
Scheduler
Compute resources

Login node (Head node)
Tell the scheduler what you want to do
Your job runs on the cluster

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What is Galaxy?

BioIT World BONUS EDITION: Open Source

Galaxy Provides Life Support for NGS Exploration

powered by Galaxy

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Galaxy: Data intensive biology for everyone

- Accessible, reproducible, transparent computational biology
- galaxy.hpc.ufl.edu
 - Local instance of Galaxy
 - Faster access to storage, easier upload
 - Local compute resources
 - Local control

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Galaxy Analysis Workspace

Galaxy / UF HPC Analyze Data Workflow Shared Data Admin Help User

History

Tools

MACS

Treatment file: 3 hg19.chr10.bam
Input file: Selection is Optional
Format: Auto
Effective Genome Size: Human (hg18)
Tag size (Optional): 25
P-value: 1e-05
Keep duplicate tags at the exact same location? Keep ALL Auto by Binomial Keep Single
Use Model: True
Use Model: small fold enrichment for model building: 10
large fold: 30
Advanced Options:

History

0915 Macs Exercise 5.3 Gb
data.2B
31:Summary Statistics on hg19chr10bam
31:MACS.log on hg19chr10bam
30:MACS.wiggle.on hg19chr10bam
29:MACS.xls on hg19chr10bam
28:MACS.summits.on hg19chr10bam
27:MACS.peaks.on hg19chr10bam
26:RAM-to-SAM on data
25:converted SAM
25:hg19chr5bam
26:hg19chr7bam
23:hg19chr7bam

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Advanced Options:

History

0915 Macs Exercise 5.3 Gb
data.2B
31:Summary Statistics on hg19chr10bam
31:UCSC Main on Human: hg19Track.3451 (chr19:6900:-6859) 3553
31:MACS.log on hg19chr10bam
30:MACS.wiggle.on hg19chr10bam
29:MACS.xls on hg19chr10bam
28:MACS.summits.on hg19chr10bam
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MACS

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Input file: Selection is Optional
Format: Auto
Effective Genome Size: Human (hg18)
Tag size (Optional): 25
P-value: 1e-05
Keep duplicate tags at the exact same location? Keep ALL Auto by Binomial Keep Single
Use Model: True
Use Model: small fold enrichment for model building: 10
large fold: 30
Advanced Options:
• MACS: Model-based Analysis for ChIP-Seq
• CCAT Control-based ChIP-seq Analysis Tool
• GeneTrack indexer on a BED file
• Peak predictor on GeneTrack index
• NGSC Peaking
• NGSC Summarization
• SAMtools Data Filter
Diagnosis Report: No
Execute

History

0915 Macs Exercise 5.3 Gb
data.2B
31:Summary Statistics on hg19chr10bam
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27:MACS.peaks.on hg19chr10bam
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25:hg19chr5bam
26:hg19chr7bam
23:hg19chr7bam

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Left Screenshot (Step 0915 Macs Exercise):

- Treatment file: 3: hg19.chr10.bam
- Input file: 0915 Macs Exercise 5.3 Gb
- Format: Auto
- Effective Genome Size: Human (hg18) 25
- Tag size (Optional): 1e-05
- P-Value:
- Keep duplicate tags at the exact same location? (radio buttons: Keep All, Keep First, Binomial, Keep Single)
- Use Model? (radio buttons: True, False)
- small fold enrichment for model building: 10
- large fold: 30
- Advanced Options: No (+)
- Diagnosis Report: No (+)

Right Screenshot (History View):

- 35: Summary Statistics on data 28
- 33: UCSC Main on Human man: 0 chr1:156690:-165971
- 31: MACS job log on hg19.chr9.bam
- 30: MACS wiggle on hg19.chr9.bam
- 29: MACS xls on hg19.chr9.bam
- 28: MACS summits on hg19.chr9.bam
- 27: MACS peaks on hg19.chr9.bam
- 26: BAM-to-SAM on data
- 25: converted SAM index
- 25: hg19.chr9.bam

Metadata Step (27: MACS peaks on hg19.chr9.bam):

- Tags: LANA x chip x hg19 x peaks x chr9 x
- Annotation / Notes: Peak calling on LANA ChIP-Seq data using Human chromosome 9 from hg19 build

1.Chrom	2.Start	3.End	4.Name
chr9	176690	179457	MACS_pea
chr9	502364	506252	MACS_pea
chr9	763181	765291	MACS_pea
chr9	2241428	2243431	MACS_pea
chr9	3161298	3162300	MACS_pea
chr9	3467312	3468066	MACS_pea

Getting Data into Galaxy:

- Upload a file from your computer
 - Direct upload (<2GB)
 - For large files: scp or copy files to HPC
 - Load from within Galaxy
 - http://wiki.hpc.ufl.edu/index.php/Galaxy_Data_Import
- External data
 - UCSC table browser
 - Biomart
 - interMine / modMine
 - EuPathDB
 - EncodedB
 - EpiGRAPH
 - FlyMine
 - GrameneMart...

Data Libraries Step (Data Library "GMS 6001 MACS Exercise"):

Name	Message	Uploaded By	Date	File Size
2011-09-14 7 hg19.acs.sorted.bam		om@hpc.ufl.edu	2011-09-14	1.6 Gb
2011-09-14 7 hg19.acs.sorted.bam +		om@hpc.ufl.edu	2011-09-14	1.6 Gb
hg19.chr10.bam		om@hpc.ufl.edu	2011-09-14	80.5 Mb
hg19.chr11.bam		om@hpc.ufl.edu	2011-09-14	82.5 Mb
hg19.chr12.bam		om@hpc.ufl.edu	2011-09-14	74.9 Mb
hg19.chr13.bam		om@hpc.ufl.edu	2011-09-14	79.9 Mb
hg19.chr14.bam		om@hpc.ufl.edu	2011-09-14	80.9 Mb
hg19.chr15.bam		om@hpc.ufl.edu	2011-09-14	86.1 Mb
hg19.chr16.bam		om@hpc.ufl.edu	2011-09-14	48.1 Mb
hg19.chr17.bam		om@hpc.ufl.edu	2011-09-14	55.9 Mb
hg19.chr18.bam		om@hpc.ufl.edu	2011-09-14	48.1 Mb
hg19.chr19.bam		om@hpc.ufl.edu	2011-09-14	33.1 Mb
hg19.chr20.bam		om@hpc.ufl.edu	2011-09-14	39.6 Mb
hg19.chr21.bam		om@hpc.ufl.edu	2011-09-14	143.5 Mb
hg19.chr22.bam		om@hpc.ufl.edu	2011-09-14	181.9 Mb
hg19.chr23.bam		om@hpc.ufl.edu	2011-09-14	134.9 Mb
hg19.chr24.bam		om@hpc.ufl.edu	2011-09-14	16.9 Mb
hg19.chr25.bam		om@hpc.ufl.edu	2011-09-14	126.3 Mb
hg19.chr26.bam		om@hpc.ufl.edu	2011-09-14	448.0 Mb
hg19.chr27.bam		om@hpc.ufl.edu	2011-09-14	131.3 Mb
hg19.chr28.bam		om@hpc.ufl.edu	2011-09-14	85.7 Mb
hg19.chr29.bam		om@hpc.ufl.edu	2011-09-14	107.7 Mb
hg19.chr30.bam		om@hpc.ufl.edu	2011-09-14	65.7 Mb
hg19.chr31.bam		om@hpc.ufl.edu	2011-09-14	85.9 Mb
hg19.chr32.bam		om@hpc.ufl.edu	2011-09-14	64.8 Mb

Data Access Control:

Groups:

Name	Users	Roles
HPC	0	2
HPC_Lab	2	1

Users:

User Name	Groups	Roles	External	Last Login
ajelison	0	1	yes	Sep 15, 2011
bazwick	0	1	yes	Sep 15, 2011
cgraves3	0	1	yes	Sep 15, 2011
jeffrey	0	1	yes	Sep 15, 2011
coitisi	0	1	yes	Sep 15, 2011

Galaxy Tool Suites

- ▶ Text Manipulation
- ▶ Format Converters
- ▶ Filtering and Sorting
- ▶ Join, Subtract, Group
- ▶ Sequence Tools
- ▶ Multi-species Alignment Tools
- ▶ Genomic Interval Operation
- ▶ Summary Statistics, graphing
- ▶ Regional Variation
- ▶ EMBOSS
- ▶ Evolution
- ▶ RNA-Seq
- ▶ ChIP-Seq
- ▶ GATK
- ▶ Phylogenetics

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A galaxy of tools

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Galaxy Workflows

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Sharing and publishing

Share or Publish History 'LANA ChIP peaks on hg19'

Making History Accessible via Link and Publishing

This history is currently restricted so that only you and the users listed below can access it. You can:

- Make History Accessible via Link**
- Generates a web link that you can share with other people so that they can view and import the history.
- Make History Accessible and Publish**
- Makes the history accessible via link (see above) and publishes the history to Galaxy's [Published Histories](#) section, where it is publicly listed and searchable.

Sharing History with Specific Users

You have not shared this history with any users.

Share with a user

Back to Histories List

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Sharing and publishing

Share or Publish History 'LANA ChIP peaks on hg19'

Making History Accessible via Link and Publishing It
This history is currently accessible via link and published.
Anyone can view and import this history by visiting the following URL:
<http://galaxy.hpc.ufl.edu/u/moskalenko/h/lana-chip-peaks-on-hg19/>

This history is publicly listed and searchable in Galaxy's Published Histories section.

You can:

- Unpublish History**
Removes this history from Galaxy's Published Histories section so that it is not publicly listed or searchable.
- Disable Access to History via Link and Unpublish**
Disables this history's link so that it is not accessible and removes history from Galaxy's Published Histories section so that it is not publicly listed or searchable.

Sharing History with Specific Users
The following users will see this history in their history list and will be able to view, import, and run it.

Email	magitz@ufl.edu ▾
Share with another user	

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Summary

- Analyze data without the CLI
- Visualize the results
- Publish histories, workflows, and annotated pages
- Add new tools, get support @ HPC
- Focus on your science, not minutiae
- UF Galaxy** – coming to a browser near you!

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Demo

Galaxy / UF HPC / Analyze Data Workflow Shared Data Help User

Tools Options ▾

- Get Data
- Send Data
- ENCODE Tools
- Lift-Over
- Text Manipulation
- Filter and Sort
- Join, Subtract and Group
- Convert Formats
- Extract Features
- Fetch Sequences
- Fetch Alignments
- Get Generic Scores
- Observe on Genomic Intervals
- Statistics
- Graph/Display Data
- Regional Variation
- Multiple regression
- Manhattan Analysis
- Evolution
- Modif Tools
- Multiple Alignments
- Metagenomic analysis
- FASTA manipulation
- NCB BLAST +
- NCSS, NCBI and manipulation
- NGS Bioinformatics

History Options ▾

MACS hg19 0 bytes

Your history is empty. Click 'Get Data' on the left pane to start

UF HPC Galaxy News:

- 2001-09-09: Prototype Galaxy Instance

An instance of Galaxy Platform for Biological Research has been installed at the University of Florida High-Performance Computing Center for research and education purposes. This instance is not available for public use, yet. However, you can email HPC or the instance administrator (galaxy@ufl.edu) to request to be notified of its general availability.

The Galaxy project is supported in part by NSF, NIH(R), and the Huck Institutes of the Life Sciences.

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Galaxy demo

<http://galaxy.hpc.ufl.edu>

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User Name: magitz
Password:

Forgot my password

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- Help and Support**
 - Help Request Tickets
 - <https://support.hpc.ufl.edu>
 - For any kind of question or help requests
 - <http://wiki.hpc.ufl.edu>
 - Documents on hardware and software resources
 - Various user guides
 - Many sample submission scripts
 - <http://hpc.ufl.edu>
 - Frequently Asked Questions
 - Account set up and maintenance

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