



# UF Research Computing

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## Introduction to Galaxy at UF HPC

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Biological Applications Support

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Assoc Sci., Biology / HPC Training

Fall 2011 UFGI Training Session

UF Research Computing/HPC Center



# Today's "desktop"

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# Tools of trade

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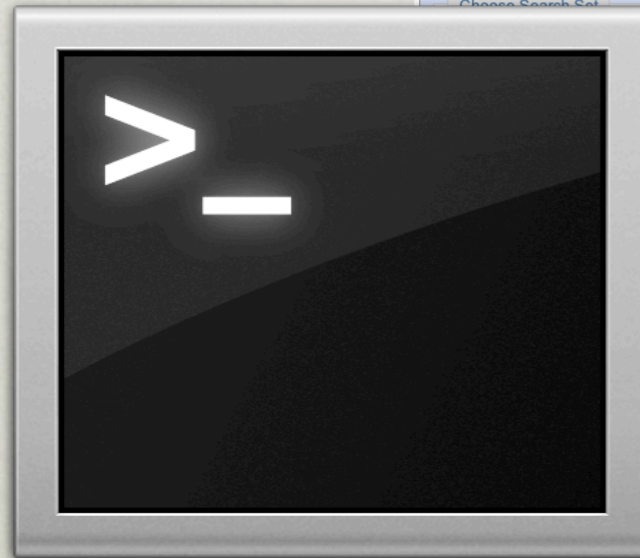
the way they should be...

---





# Two sides of a coin



**BLAST®** Basic Local Alignment Search Tool

Home Recent Results Saved Strategies Help

NCBI/BLAST/blastn suite

blastn blastp blastx tblastn tblastx

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s)  Clear

Or, upload file  No file chosen

Job Title

Enter a descriptive title for your BLAST search

Align two or more sequences

Choose Search Set

Genomic + transcript  Mouse genomic + transcript  Others (non-mammalian)  Genomic plus transcript (Human G+T)  Mammalian (M/XP)  Uncultured/environmental sample sequences

Restrict query to limit search

Similar sequences (megablast)

Similar sequences (discontiguous megablast)

Fast similar sequences (blastn)

FAST algorithm

Database Human G+T using Megablast (Optimize for highly similar sequences)

## GARLI Web Service – create job

GARLI – Genetic Algorithm for Rapid Likelihood Inference

Version 2.0 – Author(s): Derrick J. Zwickl (zwickl@ku.edu) – Category: Phylogenetics

### Job Information

#### Current user:

Anonymous

#### \* E-mail Address:

#### \* Job name (use only a-z A-Z 0-9 . \_):

### General Settings

#### \* Analysis type

ML search

#### \* Number of replicates (1 – 2000)

1

#### \* Sequence data file

PCR Session FAQ Help

ay

The UCSC Genome Browser was created by the [Genome Bioinformatics Group of UC Santa Cruz](#).  
Software Copyright (c) The Regents of the University of California. All rights reserved.

clade genome assembly position or search term [gene](#)

Mammal Human Feb. 2009 (GRCh37/hg19) chr21:33,031,597-33,041,570  submit

[Click here to reset](#) the browser user interface settings to their defaults.

## About the Human Feb. 2009 (GRCh37/hg19) assembly [\(sequences\)](#)

The February 2009 human reference sequence (GRCh37) was produced by the [Genome Reference Consortium](#).

### Sample position queries

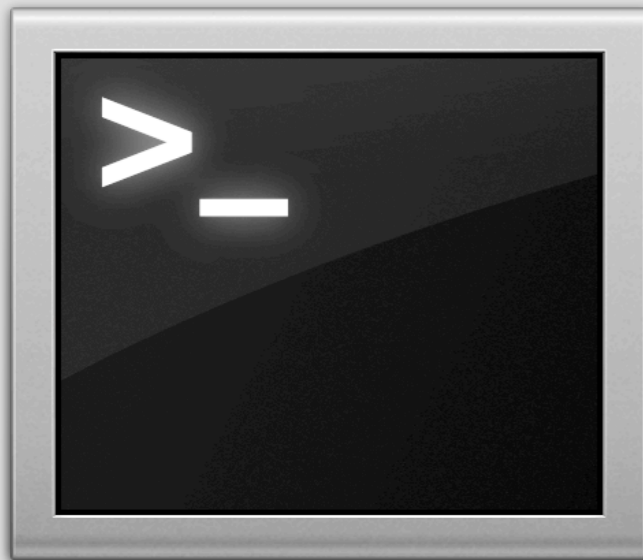
A genome position can be specified by the accession number of a sequenced genomic clone, an mRNA or EST or STS marker, a chromosomal coordinate range, or keywords from the GenBank description of an mRNA. The following list shows examples of valid position queries for the human genome. See the [User's Guide](#) for more information.

Request:	Genome Browser Response:
chr7	Displays all of chromosome 7
chrUn_gI000212	Displays all of the unplaced contig gI000212
chr3:1-1000000	Displays first million bases of chr 3, counting from p-arm telomere
chr3:1000000+2000	Displays a region of chr3 that spans 2000 bases, starting with position 1000000



# In the beginning was CLI

Head node



Login to  
head  
node

Scheduler



Interactive  
session or batch  
submission

Computing  
resources



Your job  
runs on the  
cluster



# The avalanche

**Bio-ITWorld.com**  
Indispensable Technologies Driving Discovery, Development, and Clinical Trials

Drug Discovery | eClinical Trials | IT & Informatics | Publications | Resource Center | Advertise

September 28

Subs | Podc | Web | Web | Life S | White Spec | Publi eNev | RSS | Abou

Galaxy / UF HPC

Analyze Data | Workflow | Shared Data | Admin | 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 Genomic Scores
- Operate on Genomic Intervals
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- Regional Variation
- Multiple regression
- Multivariate Analysis
- Evolution
- Motif Tools
- Multiple Alignments
- Metagenomic analyses
- FASTA manipulation
- NCBI BLAST+
  - NCBI BLAST+ **blastn** Search nucleotide database with nucleotide query sequence(s)
  - NCBI BLAST+ **blastp** Search protein database with protein query sequence(s)
  - NCBI BLAST+ **blastx** Search protein database with translated nucleotide query sequence(s)
  - NCBI BLAST+ **tblastn** Search translated nucleotide database with protein query sequence(s)
  - NCBI BLAST+ **tblastx** Search translated nucleotide database with translated nucleotide query sequence(s)
  - BLAST XML to tabular Convert BLAST XML output to tabular
- NGS: QC and manipulation

BLASTN 2.2.25+

**Reference:**  
Stephen F. Altschul, Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)  
14,487,257 sequences; 37,277,922,133 total letters

Query= gi|344217682|dbj|AB665989.1| Dendropanax trividus rbcL gene for ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit, partial cds

Length=744

Sequences producing significant alignments:

- dbj|AB665989.1| Dendropanax trividus rbcL gene for ribulose-1,5-... 1.0e-100
- dbj|D44571.1|KPUCPRC20 Kalopanax pictus chloroplast gene for Rib... 1.0e-100
- gb|U50246.1|KPUS0246 Kalopanax pictus ribulose-1,5-bisphosphate ... 1.0e-100
- gb|DQ133807.1| Eleutherococcus setchuenensis ribulose-1,5-bispho... 1.0e-100
- gb|DQ133796.1| Eleutherococcus sessiliflorus ribulose-1,5-bispho... 1.0e-100
- gb|FJ470119.1| Fatsia japonica voucher WELT SP86502 ribulose-1,5-... 1.0e-100
- dbj|D44552.1|AC3CPRC01 Chengiopanax sciadophylloides chloroplast... 1.0e-100
- gb|U50258.1|TPU50258 Trevesia palmata ribulose-1,5-bisphosphate ... 1.0e-100
- gb|FJ976155.1| Osmoxylon sessiliflorum ribulose-1,5-bisphosphate... 1.0e-100
- gb|FJ470121.1| Schefflera digitata voucher WELT SP86504 ribulose... 1.0e-100
- gb|U50239.1|ATU50239 Acanthopanax trifoliatum ribulose-1,5-bisph... 1.0e-100
- gb|HM850396.1| Tetrapanax papyrifer ribulose-1,5-bisphosphate ca... 1.0e-100
- gb|FJ470120.1| Raukaura anomala voucher WELT SP86505 ribulose-1,... 1.0e-100
- gb|AF307932.1| Pseudopanax laetevirens ribulose-1,5-bisphosphate... 1.0e-100
- gb|U50251.1|PGU50251 Polyscias guilfoylei ribulose-1,5-bisphosph... 1.0e-100
- gb|FJ470122.1| Raukaura simplex voucher WELT SP86665 ribulose-1,5-... 1.0e-100
- gb|U50256.1|TPU50256 Tetrapanax papyriferus ribulose-1,5-bisphos... 1.0e-100
- gb|U50242.1|CSU50242 Cussonia spicata ribulose-1,5-bisphosphate ... 1.0e-100
- gb|L01924.2|HEDCPRBCL Hedera helix ribulose 1,5-bisphosphate car... 1.0e-100
- gb|FJ470150.1| Pseudopanax ferox voucher WELT SP86492 ribulose-1... 1.0e-100
- gb|FJ470149.1| Pseudopanax ferox voucher WELT SP86476 ribulose-1... 1.0e-100
- gb|FJ470146.1| Pseudopanax linearis voucher WELT SP86482 ribulos... 1.0e-100
- gb|FJ470145.1| Pseudopanax discolor voucher WELT SP86435 ribulos... 1.0e-100
- gb|FJ470133.1| Pseudopanax chathamicus voucher WELT SP86425 ribu... 1.0e-100
- gb|FJ470132.1| Pseudopanax linearis voucher WELT SP86465 ribulos... 1.0e-100
- gb|FJ470131.1| Pseudopanax linearis voucher WELT SP86434 ribulos... 1.0e-100
- gb|FJ470130.1| Pseudopanax ferox voucher WELT SP86430 ribulose-1... 1.0e-100
- gb|FJ470129.1| Pseudopanax gilliesii voucher WELT SP86456 ribulo... 1.0e-100

History Options

- UFGI Grad Demo 2.5 Mb
- 7: UCSC Main on Human: snp125 (chr16:135000-175000)
- 6: megablast on db
- 5: blastn on db
- 4: blastn on db
- 3: blastn on db
- 2: RBCL blastn on nt
- 1: RBCL



# The stars of the Galaxy

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## ◆ Computational biology platform

- Open and Web-based
- Accessible
- Reproducible
- Transparent





# Analysis Workspace

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

**Tools** Options ▾

- Get Data
- Send Data
- ENCODE Tools
- Lift-Over
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- Metagenomic analyses
- FASTA manipulation
- NCBI BLAST+
- NGS: QC and manipulation
- NGS: Picard (beta)
- NGS: Mapping
- NGS: Indel Analysis
- NGS: RNA Analysis
- NGS: SAM 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

small fold enrichment for model building:  
10

large fold:  
30

Advanced Options:

**History** Options ▾

0915 Macs Exercise 5.3 Gb

- 35: Summary Statistics on data 28
- 33: UCSC Main on Human: ct UserTrack 3545 (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
- 25: hg19.chr9.bam
- 24: hg19.chr8.bam
- 23: hg19.chr7.bam



# Analysis Workspace

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**NGS: Peak Calling**

- 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

**NGS: Simulation**

**SNP/WGA: Data; Filters**

**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 ▾

small fold enrichment for model building: 10

large fold: 30

Advanced Options:

**History** Options ▾

0915 Macs Exercise 5.3 Gb

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# space

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Selection is Optional

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25

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1e-05

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 Keep Single

Use Model?:  
True

small fold enrichment for model building:  
10

large fold:  
30

Advanced Options:  
No

Diagnosis Report:  
No

Execute

- 35: Summary Statistics on data 28
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NGS: Simulation

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True

small fold enrichment for model building:

10

large fold:

30

Advanced Options:

No

Diagnosis Report:

No

Execute

History

Options

0915 Macs Exercise 5.3 Gb

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# Galaxy

## Tools

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## NGS: Peak Calling

- MACS Model-based A  
ChIP-Seq
- CCAT Control-based  
Analysis Tool
- GeneTrack indexer or
- Peak predictor on Gen  
index

## NGS: Simulation

## SNP/WGA: Data; Filters

### MACS

chr9	179077	179078	MACS_peak_1	14.00
chr9	503365	503366	MACS_peak_2	17.00
chr9	764211	764212	MACS_peak_3	20.00
chr9	2241905	2241906	MACS_peak_4	15.00
chr9	3161806	3161807	MACS_peak_5	10.00
chr9	3467733	3467734	MACS_peak_6	14.00
chr9	3526275	3526276	MACS_peak_7	19.00
chr9	3809982	3809983	MACS_peak_8	17.00
chr9	3907058	3907059	MACS_peak_9	15.00
chr9	4315804	4315805	MACS_peak_10	17.00
chr9	4887865	4887866	MACS_peak_11	11.00
chr9	5186618	5186619	MACS_peak_12	13.00
chr9	5439013	5439014	MACS_peak_13	14.00
chr9	5510340	5510341	MACS_peak_14	13.00
chr9	5566231	5566232	MACS_peak_15	11.00
chr9	5609455	5609456	MACS_peak_16	9.00
chr9	5832438	5832439	MACS_peak_17	12.00
chr9	6015764	6015765	MACS_peak_18	17.00
chr9	6038019	6038020	MACS_peak_19	16.00
chr9	6681231	6681232	MACS_peak_20	29.00
chr9	6757871	6757872	MACS_peak_21	12.00
chr9	7028374	7028375	MACS_peak_22	11.00
chr9	9428809	9428810	MACS_peak_23	8.00
chr9	9442235	9442236	MACS_peak_24	5.00
chr9	9487422	9487423	MACS_peak_25	3.00
chr9	9524985	9524986	MACS_peak_26	5.00
chr9	9677411	9677412	MACS_peak_27	7.00
chr9	12776446	12776447	MACS_peak_28	14.00
chr9	13034378	13034379	MACS_peak_29	12.00
chr9	14201262	14201263	MACS_peak_30	12.00
chr9	15038466	15038467	MACS_peak_31	7.00
chr9	16371450	16371451	MACS_peak_32	12.00
chr9	16704876	16704877	MACS_peak_33	10.00
chr9	16964119	16964120	MACS_peak_34	11.00
chr9	17005070	17005071	MACS_peak_35	11.00
chr9	17063745	17063746	MACS_peak_36	10.00
chr9	18168582	18168583	MACS_peak_37	9.00
chr9	19050354	19050355	MACS_peak_38	13.00
chr9	21085741	21085742	MACS_peak_39	47.00
chr9	21591829	21591830	MACS_peak_40	16.00
chr9	22016338	22016339	MACS_peak_41	7.00

Execute

25: nq19:chr9.Dam

Options



5.3 Gb

cs on

man:





chr1:156690-

data



# Data - metadata


**History** Options ▾




LANA ChIP peaks on hg19 5.3 Gb

**Tags:**






LANA × chip × hg19 ×

peaks × chr9 × 

**Annotation / Notes:**  
Peak calling on LANA ChIP-Seq data using Human chromosome 9 from hg19 build


**27: MACS peaks on hg19.chr9.bam**   

236 regions  
format: bed, database: ?

**Tags:**

LANA × chip × hg19 ×

chr9 × MACS × 

view in [GeneTrack](#)

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



# Threading the needle

---

## ◆ Upload a file from your computer

- Scp or copy files to HPC using Samba
- Load from within Galaxy

- [http://wiki.hpc.ufl.edu/index.php/Galaxy\\_Data\\_Import](http://wiki.hpc.ufl.edu/index.php/Galaxy_Data_Import)

## ◆ External data

- UCSC table browser
- Biomart
- interMine / modMine
- EuPathDB
- EncodeDB
- EpiGRAPH
- FlyMine
- GrameneMart...



# Libraries for inquiring minds

## Data Library "GMS 6001 MACS Exercise"

MACS test data

<input type="checkbox"/> Name	Message	Uploaded By	Date	File Size
<input type="checkbox"/> <a href="#">2010-12-14 7 hg19 aln sorted.bam</a> ▾		om@hpc.ufl.edu	2011-09-13	1.6 Gb
<input type="checkbox"/> <a href="#">2010-12-14 7 hhv8 aln sorted.bam</a> ▾		om@hpc.ufl.edu	2011-09-13	1.4 Gb
<input type="checkbox"/> <a href="#">hg19.chr10.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	80.8 Mb
<input type="checkbox"/> <a href="#">hg19.chr11.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	82.5 Mb
<input type="checkbox"/> <a href="#">hg19.chr12.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	74.9 Mb
<input type="checkbox"/> <a href="#">hg19.chr13.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	50.9 Mb
<input type="checkbox"/> <a href="#">hg19.chr14.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	36.1 Mb
<input type="checkbox"/> <a href="#">hg19.chr15.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	48.1 Mb
<input type="checkbox"/> <a href="#">hg19.chr16.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	55.9 Mb
<input type="checkbox"/> <a href="#">hg19.chr17.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	64.5 Mb
<input type="checkbox"/> <a href="#">hg19.chr18.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	33.5 Mb
<input type="checkbox"/> <a href="#">hg19.chr19.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	39.6 Mb
<input type="checkbox"/> <a href="#">hg19.chr1.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	148.5 Mb
<input type="checkbox"/> <a href="#">hg19.chr20.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	38.5 Mb
<input type="checkbox"/> <a href="#">hg19.chr21.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	17.5 Mb
<input type="checkbox"/> <a href="#">hg19.chr22.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	16.9 Mb
<input type="checkbox"/> <a href="#">hg19.chr2.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	126.3 Mb
<input type="checkbox"/> <a href="#">hg19.chr2.sam</a> ▾		om@hpc.ufl.edu	2011-09-14	488.0 Mb
<input type="checkbox"/> <a href="#">hg19.chr3.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	118.0 Mb
<input type="checkbox"/> <a href="#">hg19.chr4.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	85.7 Mb
<input type="checkbox"/> <a href="#">hg19.chr5.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	102.7 Mb
<input type="checkbox"/> <a href="#">hg19.chr6.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	65.7 Mb
<input type="checkbox"/> <a href="#">hg19.chr7.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	89.9 Mb
<input type="checkbox"/> <a href="#">hg19.chr8.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	85.9 Mb
<input type="checkbox"/> <a href="#">hg19.chr9.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	64.8 Mb

For selected datasets:





# The Sandbox effect

## Roles associated with new group

HPC test CHIP-seq analyses

## Groups

search

[Advanced Search](#)

<input type="checkbox"/> <u>Name</u> ↓	Users	Roles
<input type="checkbox"/> <u>HPC</u> ▼	0	2
<input type="checkbox"/> <u>Taylor HPC Lab</u> ▼	2	1

For 0 selected groups: [Delete](#) [Undelete](#) [Purge](#)

## Roles

search

[Advanced Search](#)

<input type="checkbox"/> <u>Name</u> ↓	<u>Description</u>	<u>Type</u>	<u>Groups</u>
<input type="checkbox"/> <u>HPC</u> ▼	Role for group HPC	system	1
<input type="checkbox"/> <u>HPC test CHIP-seq analyses</u> ▼	Test analyses of CHIP-seq data	admin	1

## Users associated with new group

om@hpc.ufl.edu  
magitz@ufl.edu

## Users

search

[Advanced Search](#)

<input type="checkbox"/> <u>Email</u> ↓	<u>User Name</u>	<u>Groups</u>	<u>Roles</u>	<u>External</u>	<u>Last Login</u>
<input type="checkbox"/> <u>aedison@ufl.edu</u> ▼	aedison	0	1	yes	Sep 15, 2011
<input type="checkbox"/> <u>bostwick@ufl.edu</u> ▼	bostwick	0	1	yes	Sep 15, 2011
<input type="checkbox"/> <u>cgraves3@ufl.edu</u> ▼	cgraves3	0	1	yes	Sep 15, 2011
<input type="checkbox"/> <u>cjeffrey@ufl.edu</u> ▼	cjeffrey	0	1	yes	Sep 15, 2011
<input type="checkbox"/> <u>colltd3@ufl.edu</u> ▼	colltd3	0	1	yes	Sep 15, 2011



# The Toolimia

---

- ◆ 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 ???



# A galaxy of tools

## NGS: QC and manipulation

### ILLUMINA DATA

[FASTQ Groomer](#) convert between various FASTQ quality formats

[FASTQ splitter](#) on joined paired end reads

[FASTQ joiner](#) on paired end reads

[FASTQ Summary Statistics](#) by column

### ROCHE-454 DATA

[Build base quality distribution](#)

[Select high quality segments](#)

[Combine FASTA and QUAL](#) into FASTQ

### AB-SOLID DATA

[Convert SOLID output to fastq](#)

[Compute quality statistics](#) for SOLID data

[Draw quality score boxplot](#) for SOLID data

### GENERIC FASTQ MANIPULATION

[Filter FASTQ reads](#) by quality score and length

[FASTQ Trimmer](#) by column

[FASTQ Quality Trimmer](#) by sliding window

## EVOLUTION

### Metagenomic analyses

### Human Genome Variation

### EMBOSS

## NGS TOOLBOX BETA

### NGS: QC and manipulation

### NGS: Mapping

#### ILLUMINA

- [Map with Bowtie](#) for Illumina

- [Map with BWA](#) for Illumina

#### ROCHE-454

- [Lastz](#) map short reads against reference sequence

- [Megablast](#) compare short reads against htgs, nt, and wgs databases

- [Parse blast XML output](#)

#### AB-SOLID

- [Map with Bowtie](#) for SOLID

### NGS: SAM Tools

### NGS: Indel Analysis

### NGS: Peak Calling

### NGS: RNA Analysis

## RGENETICS

### SNP/WGA: Data; Filters

### SNP/WGA: QC; LD; Plots

### SNP/WGA: Statistical Models

## NGS TOOLBOX BETA

### NGS: QC and manipulation

### NGS: Mapping

### NGS: SAM Tools

- [Filter SAM](#) on bitwise flag values

- [Convert SAM](#) to interval

- [SAM-to-BAM](#) converts SAM format to BAM format

- [BAM-to-SAM](#) converts BAM format to SAM format

- [Merge BAM Files](#) merges BAM files together

- [Generate pileup](#) from BAM dataset

- [Filter pileup](#) on coverage and SNPs

- [Pileup-to-Interval](#) condenses pileup format into ranges of bases

- [flagstat](#) provides simple stats on BAM files

### NGS: Indel Analysis

### NGS: Peak Calling

### NGS: RNA Analysis

## RGENETICS

### SNP/WGA: Data; Filters

### SNP/WGA: QC; LD; Plots

### SNP/WGA: Statistical Models

## NGS: SAM Tools

### NGS: Indel Analysis

- [Filter Indels](#) for SAM

- [Extract indels](#) from SAM

- [Indel Analysis](#)

### NGS: Peak Calling

- [MACS](#) Model-based Analysis of ChIP-Seq

- [GeneTrack indexer](#) on a BED file

- [Peak predictor](#) on GeneTrack index

### NGS: RNA Analysis

#### RNA-SEQ

- [Tophat](#) Find splice junctions using RNA-seq data

- [Cufflinks](#) transcript assembly and FPKM (RPKM) estimates for RNA-Seq data

- [Cuffcompare](#) compare assembled transcripts to a reference annotation and track Cufflinks transcripts across multiple experiments

- [Cuffdiff](#) find significant changes in transcript expression, splicing, and promoter use

#### FILTERING

- [Filter Combined Transcripts](#) using tracking file



# As the river workflows

Workflow configuration and execution details:

- Unknown**  
*This tool cannot be used in workflows*
- BAM-to-SAM**  
 Include "BAM-to-SAM" in workflow
- Convert Genomic Intervals To Strict BED6**  
 Include "Convert Genomic Intervals To Strict BED6" in workflow
- MACS**  
 Include "MACS" in workflow
- Convert BED to GeneTrack Index**  
 Include "Convert BED to GeneTrack Index" in workflow

Workflow Steps:

- 25: hg19.chr9.bam  
 Treat as input dataset
- 26: BAM-to-SAM on data 25: converted SAM
- 27: MACS peaks on hg19.chr9.bam
- 27: MACS peaks on hg19.chr9.bam
- 28: MACS submits on hg19.chr9.bam
- 29: MACS xls on hg19.chr9.bam
- 30: MACS wiggle on hg19.chr9.bam
- 31: MACS job log on hg19.chr9.bam
- 27: MACS peaks on hg19.chr9.bam

Dataset List (Right Panel):

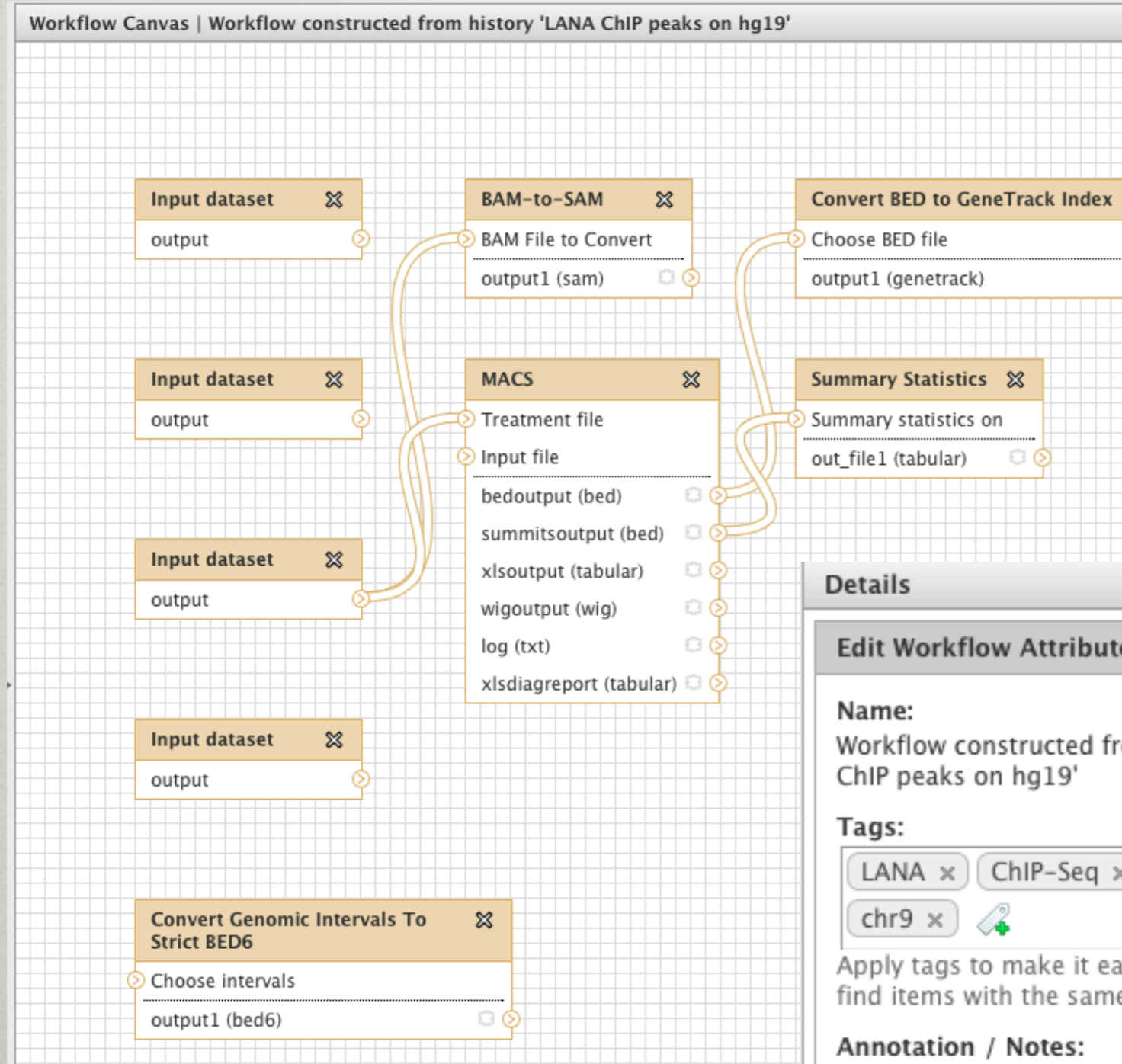
- 31: M hg19. [Actions]
- 30: M hg19. [Actions]
- 29: M hg19. [Actions]
- 28: M hg19. [Actions]
- 27: MACS peaks on hg19.chr9.bam [Actions]
- 26: BAM-to-SAM on data 25: converted SAM [Actions]
- 25: hg19.chr9.bam [Actions]
- 24: hg19.chr8.bam [Actions]
- 23: hg19.chr7.bam [Actions]
- 22: hg19.chr6.bam [Actions]
- 21: hg19.chr5.bam [Actions]
- 20: hg19.chr4.bam [Actions]
- 19: hg19.chr3.bam [Actions]

Context Menu (Right Panel):

- Extract Workflow
- Dataset Security
- Show Deleted Datasets
- Show Hidden Datasets
- Show Structure
- Export to File
- Delete
- Other Actions
- Import from File



# And flows



### Details

**Tool: MACS**

**Treatment file**  
Data input 'tfile' (interval or sam or bam or eland or elandmulti or bed)

**Input file**  
Data input 'cfile' (interval or sam or bam or eland or elandmulti or bed)

**Format:** ▼  
Auto

**Effective Genome Size:**  
Human (hg19)

**Tag size (Optional):** ▼  
25

---

### Details

#### Edit Workflow Attributes

**Name:**  
Workflow constructed from history 'LANA ChIP peaks on hg19'

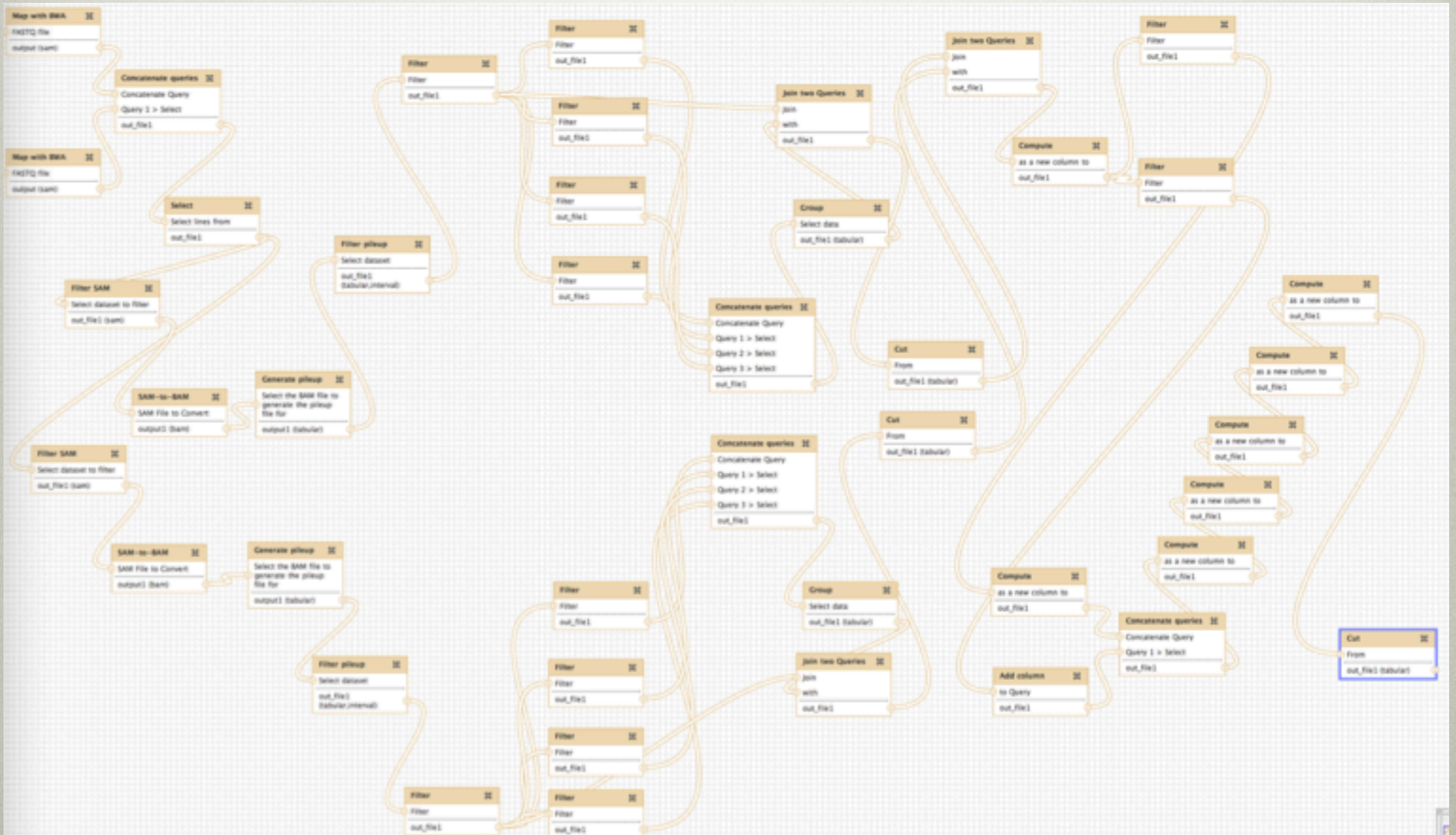
**Tags:**  
LANA x ChIP-Seq x hg19 x chr9 x

Apply tags to make it easy to search for and find items with the same tag.

**Annotation / Notes:**  
This is a partial peak calling with MACS using hg19 and chr9 data



# And flows again





# Seeing is believing

Home Genomes Blat Tables Gene Sorter PCR DNA Convert Ensembl

## UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x

position/search chr10:1-135,534,747 [gene](#) jump clear size 135,534,747 bp. configure

chr10 (p15.3-q26.3) p14 p13 q21.1

Scale chr10: 50 Mb | 50000000 | 100000000

move start < 2.0 > move end < 2.0 >

Click on a feature for details. Click or drag in the base position track to zoom in. Click side bars for track options. Drag side bars or labels up or down to reorder tracks. Drag tracks left or right to new position.

track search default tracks default order hide all add custom tracks track hubs configure reverse resize refresh

collapse all Use drop-down controls below and press refresh to alter tracks displayed. Tracks with lots of items will automatically be displayed in more compact modes. expand all

**Mapping and Sequencing Tracks** refresh

[Base Position](#) [Chromosome Band](#) [STS Markers](#) **18** [FISH Clones](#) [Recomb Rate](#) [Map Contigs](#)

dense ↑ hide ↑ hide ↑ hide ↑



# Sharing is caring

---

## Share or Publish History 'LANA ChIP peaks on hg19'

### Making History Accessible via Link and Publishing It

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](#)





# Publish or perish

## 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



# To share or not to share

## Share or Publish Workflow 'LANA CHIP peaks on hg19'

### Making Workflow Accessible via Link and Publishing It

This workflow is currently accessible via link and published.

Anyone can view and import this workflow by visiting the following URL:

<http://galaxy.hpc.ufl.edu/u/moskalenko/w/lana-chip-peaks-on-hg19>

This workflow is publicly listed and searchable in Galaxy's [Published Workflows](#) section.

You can:

**Unpublish Workflow**

Removes this workflow from Galaxy's [Published Workflows](#) section so that it is not publicly listed or searchable.

**Disable Access to Workflow via Link and Unpublish**

## Published Workflows

[Advanced Search](#)

Name	Annotation	Owner	Community Rating	Community Tags	Last Updated ↓
<a href="#">LANA CHIP peaks on hg19</a>		moskalenko	★★★★★		2 minutes ago

## Published Histories

[Advanced Search](#)

Name	Annotation	Owner	Community Rating	Community Tags	Last Updated ↓
<a href="#">LANA CHIP peaks on hg19</a>	Peak calling on LANA CHIP-Seq data using Human chromosome 9 from hg19 build	moskalenko	★★★★★	<a href="#">chr9</a> <a href="#">hg19</a> <a href="#">peaks</a> <a href="#">lana</a> <a href="#">chip</a>	4 minutes ago



# The white pages

Published Pages | [aun1](#) | Windshield Splatter

## Windshield splatter analysis with the Galaxy metagenomic pipeline: A live supplement

SERGEI KOSAKOVSKY POND<sup>1,2,\*</sup>, SAMIR WADHAWAN<sup>3,6\*</sup>, FRANCESCA CHIAROMONTE<sup>4</sup>, GURUPRASAD ANANDA<sup>1,3</sup>, WEN-YU CHUNG<sup>1,3,7</sup>, JAMES TAYLOR<sup>1,5</sup>, ANTON NEKRUTENKO<sup>1,3</sup> and THE GALAXY TEAM<sup>1\*</sup>

Correspondence should addressed to [SKP](#), [JT](#), or [AN](#).

### How to use this document

This document is a live copy of supplementary materials for [the manuscript](#). It provides access to the **exact** analyses and workflows discussed in the paper, so you can play with them by re-running, changing parameters, or even applying them to your own data. Specifically, we provide the two histories and one workflow found below. You can view these items by clicking on their name to expand them. You can also import these items into your Galaxy workspace and start using them; click on the green plus to import an item. To import workflows you must [create a Galaxy account](#) (unless you already have one) – a hassle-free procedure where you are only asked for a username and password.

This is the Galaxy history detailing the comparison of our pipeline to MEGAN:

[+](#) **Galaxy History | Galaxy vs MEGAN** Comparison of Galaxy vs. MEGAN pipeline. [+](#) [↗](#)

This is the Galaxy history showing a generic analysis of metagenomic data. (This corresponds to the "A complete metagenomic pipeline" section of the manuscript and **Figure 3A**):

[+](#) **Galaxy History | metagenomic analysis** [+](#) [↗](#)

This is the Galaxy workflow for generic analysis of metagenomic data. (This corresponds to the "A complete metagenomic pipeline" section of the manuscript and **Figure 3B**):

[+](#) **Galaxy Workflow | metagenomic analysis** Generic workflow for performing a metagenomic analysis on NGS data. [+](#) [↗](#)

### Accessing the Data


Windshield Splatter datasets analyzed in this manuscript can be accessed through this [Galaxy Library](#). From there they can be re-analyzed through Galaxy using the above workflows or downloaded.

### Supplemental Analysis


#### Comparison between Galaxy pipeline and Megan

(Use [this link](#) to see Galaxy history representing this analysis. Individual elements of this history are referred to as **History Item1, 2 and so on using bold typeface**)

### About this Page

**Author**  
aun1 

**Related Pages**  
[All published pages](#)  
[Published pages by aun1](#)

**Rating**  
Community (6 ratings, 5.0 average) 

**Tags**  
Community:  
[megan](#) [galaxy](#) [paper](#)



# The Road Ahead

---

- ◆ Local UCSC Genome Browser
- ◆ Additional tools
- ◆ More hardware to support Galaxy
- ◆ Reference genomes – tell us!!!
- ◆ Your feedback and sense of direction are most important



# Biocomputing ML

---



Have you  
signed up for the  
UF Biocomputing  
Discussion List?

[http://hpc.ufl.edu/cgi-bin/mailman/  
listinfo/biocomputing](http://hpc.ufl.edu/cgi-bin/mailman/listinfo/biocomputing)



# BioC Requirements

[http://wiki.hpc.ufl.edu/index.php/BioC\\_Requirements\\_Information\\_Gathering](http://wiki.hpc.ufl.edu/index.php/BioC_Requirements_Information_Gathering)



- [+] Docs
- [+] Infrastructure
- [+] Research
- [+] Software
- [x] Training

#### Navigation

- [Main Page](#)
- [Current events](#)
- [Recent changes](#)
- [Random page](#)
- [Help](#)

#### Toolbox

- [What links here](#)
- [Related changes](#)
- [Upload file](#)
- [Special pages](#)
- [Printable version](#)
- [Permanent link](#)

Page [Discussion](#)

Read [Edit](#) [View history](#)

## BioC Requirements Information Gathering

*This is an area for gathering usage scenarios and requirements from the UF Biological Research Community to enable a more focused discussion during face-to-face meetings leading to the determination of the hardware specifications for the BioC cluster*

### General requirements [\[edit\]](#)

- The perceived direction of the discussions at the BioC Investor meetings as of now - early November - seems to give more and more priority to the storage as the primary need and the raw computing capacity and the memory configuration as a somewhat secondary although not unimportant consideration. So, we should split the gathering of usage information between these two large areas to be able to distil the most important conclusions more easily.

**Note:** Please use ~~~~ - 4 tildas to mark your username and the date of the comment to allow some tracking of information, ideas and proposals. You don't have to fill out every section - just the ones you feel strongly about, those you would like to influence. Click on the "Edit" link above your lab name and start writing. Use the [\[Page\]](#) for threaded discussions as you would have in an email conversation. Thank you!

### Storage [\[edit\]](#)

**List your estimates of your storage needs for the next 6, 12 and 18 months below. All labs investing into BioC cluster are listed below alphabetically.**

### General Information [\[edit\]](#)



# 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!



# 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 Genomic Scores](#)
- [Operate on Genomic Intervals](#)
- [Statistics](#)
- [Graph/Display Data](#)
- [Regional Variation](#)
- [Multiple regression](#)
- [Multivariate Analysis](#)
- [Evolution](#)
- [Motif Tools](#)
- [Multiple Alignments](#)
- [Metagenomic analyses](#)
- [FASTA manipulation](#)
- [NCBI BLAST+](#)
- [NGS: QC and manipulation](#)
- [NGS: Picard \(beta\)](#)

**History** Options ▾

MACS hg19 0 bytes

**UFL HPC Galaxy News:**

- 2001-08-09: Prototype Galaxy Instance**  
An instance of [Galaxy Platform](#) for Biological Research Computing was brought online at the University of Florida [High-Performance Computing Center](#) for testing and demonstration purposes. This instance is not available for public use, yet. However, you can email [HPC](#) or the [biological applications support](#) directly to request to be notified of its general availability.

The Galaxy project is supported in part by [NSF](#), [NHGRI](#), and the [Huck Institutes of the Life Sciences](#).





# MACS demo

---

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



# MACS demo

---

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

## UF HPC Center Login

Username:

Password:

Login

[Request an account](#)

[Reset my password](#)



# History/Shared Data

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 Genomic Scores
- Operate on Genomic Intervals
- Statistics
- Graph/Display Data
- Regional Variation
- Multiple regression
- Multivariate Analysis
- Evolution
- Motif Tools
- Multiple Alignments
- Meta
- FAST
- NCBI
- NGS:
- NGS:

History Options

Unnamed history 0 bytes

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

**UF**  
UNIVERSITY of  
FLORIDA

UF HPC center

UFL HPC Galaxy News:

- 2001-08-09: Prototype Galaxy Instance

An instance of Galaxy Platform for Biological Research Computing was brought online at the University of Florida High-Performance Computing Center for testing and demonstration purposes. This instance is not available for public use, yet. However, you can email HPC or the biological applications support directly to request

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



# Shared Data

Galaxy / UF HPC / Analyze Data Workflow **Shared Data** Help Use

## Data Libraries

[Advanced Search](#)

<u>Data library name</u> ↓	<u>Data library description</u>
<b>GMS 6001 MACS Exercise</b>	HPC Intro and MACS exercise on 9/15/11
<a href="#">OM Testing</a>	Test data for Galaxy development



# MACS – Load data

## Data Library “GMS 6001 MACS Exercise”

MACS test data

<input type="checkbox"/> Name	Message	Uploaded By	Date	File Size
<input type="checkbox"/> <a href="#">2010-12-14 7 hg19 aln sorted.bam</a> ▾		om@hpc.ufl.edu	2011-09-13	1.6 Gb
<input type="checkbox"/> <a href="#">2010-12-14 7 hhv8 aln sorted.bam</a> ▾		om@hpc.ufl.edu	2011-09-13	1.4 Gb
<input checked="" type="checkbox"/> <a href="#">hg19.chr10.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	80.8 Mb
<input type="checkbox"/> <a href="#">hg19.chr11.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	82.5 Mb
<input type="checkbox"/> <a href="#">hg19.chr12.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	74.9 Mb
<input type="checkbox"/> <a href="#">hg19.chr13.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	50.9 Mb
<input type="checkbox"/> <a href="#">hg19.chr14.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	36.1 Mb
<input type="checkbox"/> <a href="#">hg19.chr15.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	48.1 Mb
<input type="checkbox"/> <a href="#">hg19.chr16.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	55.9 Mb
<input type="checkbox"/> <a href="#">hg19.chr17.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	64.5 Mb
<input type="checkbox"/> <a href="#">hg19.chr18.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	33.5 Mb
<input type="checkbox"/> <a href="#">hg19.chr19.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	39.6 Mb
<input type="checkbox"/> <a href="#">hg19.chr1.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	148.5 Mb
<input type="checkbox"/> <a href="#">hg19.chr20.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	38.5 Mb
<input type="checkbox"/> <a href="#">hg19.chr21.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	17.5 Mb
<input type="checkbox"/> <a href="#">hg19.chr22.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	16.9 Mb
<input type="checkbox"/> <a href="#">hg19.chr2.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	126.3 Mb
<input type="checkbox"/> <a href="#">hg19.chr2.sam</a> ▾		om@hpc.ufl.edu	2011-09-14	488.0 Mb
<input type="checkbox"/> <a href="#">hg19.chr3.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	118.0 Mb
<input type="checkbox"/> <a href="#">hg19.chr4.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	85.7 Mb
<input type="checkbox"/> <a href="#">hg19.chr5.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	102.7 Mb
<input type="checkbox"/> <a href="#">hg19.chr6.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	65.7 Mb
<input type="checkbox"/> <a href="#">hg19.chr7.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	89.9 Mb
<input type="checkbox"/> <a href="#">hg19.chr8.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	85.9 Mb
<input type="checkbox"/> <a href="#">hg19.chr9.bam</a> ▾		om@hpc.ufl.edu	2011-09-14	64.8 Mb

For selected datasets:



# What's inside

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](#)
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- [FASTA manipulation](#)
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- [NGS: QC and manipulation](#)
- [NGS: Picard \(beta\)](#)
- [NGS: Mapping](#)
- [NGS: Indel Analysis](#)
- [NGS: RNA Analysis](#)
- [NGS: SAM Tools](#)
  - [Filter SAM on bitwise flag values](#)
  - [Convert SAM to interval](#)
  - [SAM-to-BAM](#) converts SAM format to BAM format
  - [BAM-to-SAM](#) converts BAM format to SAM format

✔ The following job has been successfully added to the queue:

**2: BAM-to-SAM on data 1: converted SAM**

You can check the status of queued jobs and view the resulting data by refreshing the **History** pane. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.

```

@SQ      SN:chrUn_g1000248      LN:39786
@SQ      SN:chrUn_g1000249      LN:38502
@SQ      SN:chrX      LN:155270560
@SQ      SN:chrY      LN:59373566
@PG      ID:Bowtie      VN:0.12.5      CL:"bowtie --chunkmbs 1024 --sam --solexa1.3-quals -e 70 -M 1 -n 2 -l 28 --tryhard
HWUSI-EAS1654_0011:7:101:15569:18265#0/1      16      chr10      60132      0      40M      *      0      0      0      TTAATTGACG
HWUSI-EAS1654_0011:7:70:15927:14469#0/1      16      chr10      60156      0      40M      *      0      0      0      TTGAGTTCGGTTGAGTTT
HWUSI-EAS1654_0011:7:77:2963:15680#0/1      16      chr10      60189      0      40M      *      0      0      0      TCTTCCACAAGGGATTGT
HWUSI-EAS1654_0011:7:56:13734:7224#0/1      0      chr10      60478      0      40M      *      0      0      0      CGCCTTTGGAAGGAGCAT
HWUSI-EAS1654_0011:7:27:17072:12387#0/1      0      chr10      60491      255      40M      *      0      0      0      AGCATTATCCCCAGCAF
HWUSI-EAS1654_0011:7:41:17138:6404#0/1      0      chr10      60491      255      40M      *      0      0      0      AGCATATATCCCCAGCAF
HWUSI-EAS1654_0011:7:82:1846:20862#0/1      0      chr10      60491      255      40M      *      0      0      0      AGCATATATCCCCAGCAF
HWUSI-EAS1654_0011:7:96:15342:7286#0/1      16      chr10      60513      0      40M      *      0      0      0      TCCGGTTTTTTGAAGTCT
HWUSI-EAS1654_0011:7:91:12232:19734#0/1      0      chr10      60618      0      40M      *      0      0      0      AATCTTTGTGTATACAT
HWUSI-EAS1654_0011:7:4:3181:2553#0/1      0      chr10      60918      0      40M      *      0      0      0      GAAGTATCAATATGCCTI
HWUSI-EAS1654_0011:7:43:15903:1917#0/1      16      chr10      61129      0      40M      *      0      0      0      TTTGTATTGGTAGGATAA
HWUSI-EAS1654_0011:7:11:8621:5776#0/1      16      chr10      61203      0      40M      *      0      0      0      ATGAGGCCCTACTCTGTG
HWUSI-EAS1654_0011:7:44:10220:2559#0/1      0      chr10      62846      0      40M      *      0      0      0      ATACTGGGGAGGAGCTGT
HWUSI-EAS1654_0011:7:95:15568:1582#0/1      16      chr10      63074      0      40M      *      0      0      0      TGAAAGCCAATGGCTGG
HWUSI-EAS1654_0011:7:32:3459:2766#0/1      0      chr10      63307      0      40M      *      0      0      0      AAAGGACATATAATCTTG
HWUSI-EAS1654_0011:7:89:18639:10678#0/1      0      chr10      63307      0      40M      *      0      0      0      AAAGGACATATAATCTTG
HWUSI-EAS1654_0011:7:109:19350:5114#0/1      16      chr10      63367      0      40M      *      0      0      0      TCCAGCTGATGCTTTCTG
HWUSI-EAS1654_0011:7:68:3139:9708#0/1      16      chr10      63523      0      40M      *      0      0      0      CCCAAAGATGTTACAA
HWUSI-EAS1654_0011:7:27:15884:16777#0/1      0      chr10      63723      0      40M      *      0      0      0      CAGTCTTCAGCCCTAGAC
HWUSI-EAS1654_0011:7:64:1626:5553#0/1      0      chr10      63915      0      40M      *      0      0      0      AGCTAATCAGGGAGGGGC
HWUSI-EAS1654_0011:7:21:7450:15409#0/1      0      chr10      64133      0      40M      *      0      0      0      GACAAGGCTTTGATTTA
HWUSI-EAS1654_0011:7:67:16528:10957#0/1      0      chr10      64143      0      40M      *      0      0      0      TTGATTTAACCCAATCCA
HWUSI-EAS1654_0011:7:61:13906:4548#0/1      0      chr10      64190      0      40M      *      0      0      0      TATGAGCAAAGTCTCCA
HWUSI-EAS1654_0011:7:42:8178:16716#0/1      16      chr10      64272      0      40M      *      0      0      0      ATTCTAAAAGCCAGGAAP
HWUSI-EAS1654_0011:7:64:10597:5725#0/1      16      chr10      64305      0      40M      *      0      0      0      TAATCTAGGAAAACCTCC
HWUSI-EAS1654_0011:7:50:6555:17127#0/1      16      chr10      64375      0      40M      *      0      0      0      TGGGAAATTCATCACAAP
HWUSI-EAS1654_0011:7:119:10260:12806#0/1      0      chr10      64633      0      40M      *      0      0      0      0      TGAAAGAAAG
HWUSI-EAS1654_0011:7:117:5789:14945#0/1      0      chr10      64648      0      40M      *      0      0      0      GTCATTTTCAGACAAAAC
HWUSI-EAS1654_0011:7:49:10018:10089#0/1      0      chr10      64844      0      40M      *      0      0      0      AAAGGACATGATGAAAGC
HWUSI-EAS1654_0011:7:81:5640:15183#0/1      0      chr10      65212      0      40M      *      0      0      0      ACTGGAGCTCCCAATTT
HWUSI-EAS1654_0011:7:67:19633:13182#0/1      0      chr10      65483      0      40M      *      0      0      0      GCCATAAAATGAGTCTCA
HWUSI-EAS1654_0011:7:77:17790:3617#0/1      0      chr10      65626      0      40M      *      0      0      0      CTGAATGAGCATTGGGCC
HWUSI-EAS1654_0011:7:60:8645:3117#0/1      16      chr10      65700      0      40M      *      0      0      0      TATCGAAACCTCTGGGAT
HWUSI-EAS1654_0011:7:60:6931:13228#0/1      0      chr10      66024      0      40M      *      0      0      0      TCACTAAGAAATGAAACF
HWUSI-EAS1654_0011:7:76:1871:15186#0/1      0      chr10      66045      0      40M      *      0      0      0      GATATTACAACTGACACC
HWUSI-EAS1654_0011:7:114:9163:3182#0/1      0      chr10      66273      0      40M      *      0      0      0      CGGATTCACAGCAGAAAT

```

**History** Options ▾

MACS hg19 80.8 Mb

**2: BAM-to-SAM on data 1: converted SAM** 👁️ ✂️ 🗑️

**1: hg19.chr10.bam** 👁️ ✂️ 🗑️



# MACS (Peak Calling)

**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 Genomic Scores
- Operate on Genomic Intervals
- Statistics
- Graph/Display Data
- Regional Variation
- Multiple regression
- Multivariate Analysis
- Evolution
- Motif Tools
- Multiple Alignments
- Metagenomic analyses
- FASTA manipulation
- NCBI BLAST+
- NGS: QC and manipulation
- NGS: Picard (beta)
- NGS: Mapping
- NGS: Indel Analysis
- NGS: RNA Analysis
- NGS: SAM Tools
- NGS: GATK Tools
- NGS: Peak Calling**
- NGS: Simulation
- SNP/WGA: Data; Filters

**UF**  
UNIVERSITY of  
FLORIDA

UF HPC center

**UFL HPC Galaxy News:**

- [2011-08-09: Prototype Galaxy Instance](#)  
An instance of [Galaxy Platform](#) for Biological Research Computing was brought online at the University of Florida [High-Performance Computing Center](#) for testing and demonstration purposes. This instance is not available for public use, yet. However, you can email [HPC](#) or the [biological applications support](#) directly to request to be notified of its general availability.

The Galaxy project is supported in part by [NSF](#), [NHGRI](#), and the [Huck Institutes of the Life Sciences](#).

**History** Options ▾

- MACS hg19 80.8 Mb
- 1: hg19.chr10.bam**

**NGS: Peak Calling**

- **MACS Model-based Analysis for ChIP-Seq**



# Submission form

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 Genomic Scores](#)
- [Operate on Genomic Intervals](#)
- [Statistics](#)
- [Graph/Display Data](#)
- [Regional Variation](#)
- [Multiple regression](#)
- [Multivariate Analysis](#)
- [Evolution](#)
- [Motif Tools](#)
- [Multiple Alignments](#)
- [Metagenomic analyses](#)
- [FASTA manipulation](#)
- [NCBI BLAST+](#)
- [NGS: QC and manipulation](#)
- [NGS: Picard \(beta\)](#)
- [NGS: Mapping](#)
- [NGS: Indel Analysis](#)
- [NGS: RNA Analysis](#)
- [NGS: SAM Tools](#)
- [NGS: GATK Tools](#)
- [NGS: Peak Calling](#)
  - MACS Model-based Analysis for CHIP-Seq
  - CCAT Control-based CHIP-seq Analysis Tool

**MACS**

Treatment file:  
1: hg19.chr10.bam

Input file:  
Selection is Optional

Format:  
Auto

Effective Genome Size:  
Human (hg19)

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

small fold enrichment for model building:  
10

large fold:  
30

Advanced Options:  
No

Diagnosis Report:  
No

Execute

History Options ▾

- MACS hg19 400.5 MB
- 2: BAM-to-SAM on data 1: converted SAM
- 1: hg19.chr10.bam





# MACS options

---

- **Basic:**
  - Treatment file: **Your alignment file – choose BAM file**
  - Effective genome size: **Human (hg19) – must set once**
- **Advanced:**
  - Use model or shift size
  - Model - fold enrichment (small and large): 10:30
  - Bandwidth – scan bandwidth size for model or  $\frac{1}{2}$  window size without the model: default is 300



# Submit the job to cluster

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

**Parameters:**

300

**Use Lambda?:**  
 True  
 False

**Small Lambda:**  
1000

**Large Lambda:**  
10000

**Generate a wig file?:**  
 Yes  
 No

**Diagnosis Report:**  
No ▾

**Execute**



# Cluster job run

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 Genomic Scores
- Operate on Genomic Intervals
- Statistics
- Graph/Display Data
- Regional Variation
- Multiple regression
- Multivariate Analysis
- Evolution
- Motif Tools

Options

MACS 400.5 Mb hg19

8: [MACS diagnosis report on hg19.chr10.bam](#)

7: [MACS job log on hg19.chr10.bam](#)

6: [MACS wiggle on hg19.chr10.bam](#)

5: [MACS xls on hg19.chr10.bam](#)

4: [MACS summits on hg19.chr10.bam](#)

3: [MACS peaks on hg19.chr10.bam](#)

The following job has been successfully added to the queue:

- 3: MACS peaks on hg19.chr10.bam
- 4: MACS summits on hg19.chr10.bam
- 5: MACS xls on hg19.chr10.bam
- 6: MACS wiggle on hg19.chr10.bam
- 7: MACS job log on hg19.chr10.bam
- 8: MACS diagnosis report on hg19.chr10.bam

You can check the status of queued jobs and view the resulting data by refreshing the **History** pane. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.



# Job completion

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 Genomic Scores
- Operate on Genomic Intervals
- Statistics
- Graph/Display Data
- Regional Variation
- Multiple regression
- Multivariate Analysis
- Evolution

Options

MACS 498.3 Mb hg19

8: MACS diagnosis report on hg19.chr10.bam


7: MACS job log on hg19.chr10.bam

6: MACS wiggle on hg19.chr10.bam

5: MACS xls on hg19.chr10.bam

4: MACS summits on hg19.chr10.bam

3: MACS peaks on hg19.chr10.bam

 The following job has been successfully added to the queue:

- 3: MACS peaks on hg19.chr10.bam
- 4: MACS summits on hg19.chr10.bam
- 5: MACS xls on hg19.chr10.bam
- 6: MACS wiggle on hg19.chr10.bam
- 7: MACS job log on hg19.chr10.bam
- 8: MACS diagnosis report on hg19.chr10.bam

You can check the status of queued jobs and view the resulting data by refreshing the **History** pane. When the job has been run the status will change from 'running' to 'finished' if completed successfully or 'error' if problems were encountered.



# Build a browser track

The screenshot displays the UCSC Genome Browser interface. On the left, the 'Tools' panel lists various utilities, with 'Build custom track for UCSC genome browser' circled in red. The central panel, titled 'Build custom track', features a 'Tracks' section with an 'Add new Track' button also circled in red, and an 'Execute' button below it. An information icon (i) provides instructions on how to view custom tracks, while a warning icon (⚠) notes that all input datasets must share the same genome build. On the right, the 'History' panel shows a list of tracks, including 'MACS hg19' (498.3 Mb) and several tracks numbered 1 through 8, each with visibility, edit, and delete icons.

**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 Genomic Scores
- Operate on Genomic Intervals
- Statistics
- Graph/Display Data
  - Build custom track for UCSC genome browser
  - Histogram of a numeric column
  - Scatterplot of two numeric columns
  - Bar chart for multiple columns
  - Plotting tool for multiple series and graph types
  - Boxplot of quality statistics
  - GMAJ Multiple Alignment Viewer
  - LAJ Pairwise Alignment Viewer

**Build custom track**

Tracks

Add new Track

Execute

**i** This tool allows you to build custom tracks using datasets in your history for the UCSC genome browser. You can view these custom tracks on the UCSC genome browser by clicking on **display** at **UCSC main/test** link in the history panel of the output dataset.

**⚠** Please note that this tool requires **all input datasets(tracks) to have the same genome build**. The tool throws an error when this requirement is not met. You may then have to choose a valid dataset or remove invalid tracks.

**History** Options ▾

MACS hg19 498.3 Mb

- 8: MACS diagnosis report on hg19.chr10.bam
- 7: MACS job log on hg19.chr10.bam
- 6: MACS wiggle on hg19.chr10.bam
- 5: MACS xls on hg19.chr10.bam
- 4: MACS summits on hg19.chr10.bam
- 3: MACS peaks on hg19.chr10.bam
- 2: BAM-to-SAM on data 1: converted SAM
- 1: hg19.chr10.bam



# Submit a track build job

### Build custom track

**Tracks**

**Track 1**

**Dataset:**  
4: MACS summits on hg19.chr10.bam ↕

**name:**  
Chr10LANA

**description:**

**Color:**  
Black ↕

**Visibility:**  
Dense ↕

**i** This tool allows you to build custom tracks using datasets in your history for the UCSC genome browser. You can view these custom tracks on the UCSC genome browser by clicking on **display at UCSC main/test** link in the history panel of the output dataset.

---

**!** Please note that this tool requires **all input datasets(tracks) to have the same genome build**. The tool throws an error when this requirement is not met. You may then have to choose a valid dataset or remove invalid tracks.



# Open the track

**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 Genomic Scores](#)
- [Operate on Genomic Intervals](#)
- [Statistics](#)
- [Graph/Display Data](#)
  - [Histogram](#) of a numeric column
  - [Scatterplot](#) of two numeric columns

```
track name="Chr10LANA" description="User Supplied Track (from Galaxy)"
color=0,0,255 visibility=1
chr10 309835 311665 MACS_peak_1 134.30
chr10 374946 376165 MACS_peak_2 87.06
chr10 382566 385025 MACS_peak_3 54.46
chr10 439141 440977 MACS_peak_4 53.43
chr10 1030693 1036216 MACS_peak_5 68.77
chr10 1093464 1096423 MACS_peak_6 126.75
chr10 1196247 1198127 MACS_peak_7 68.34
chr10 3237793 3240452 MACS_peak_8 62.17
chr10 3268557 3270788 MACS_peak_9 56.84
chr10 3355912 3357691 MACS_peak_10 98.16
chr10 3371713 3374115 MACS_peak_11
```

**History** Options ▾

MACS hg19 498.3 Mb

**9: Build custom track on data 4 and data 3** 👁️ ✎ ✕

995 lines, 3 comments  
format: customtrack, database: ?  
Info: Generated a custom track containing 2 subtracks.

📄 ⓘ ↻ 📌 📄

1	2
track name="Chr10LANA" description="User Supplied Track (from Galaxy)"	
chr10	309835
chr10	374946
chr10	382566
chr10	439141
chr10	1030693



# Genome Browser

Tools Options ▾

**Get Data**

- Upload File from your computer
- UCSC Main table browser**
- UCSC Archaea table browser
- BX main browser
- BioMart Central server
- GrameneMart Central server
- Flymine server
- modENCODE fly server
- modENCODE modMine server
- Ratmine server
- YeastMine server
- modENCODE worm server
- Wormbase server
- EuPathDB server
- EncodeDB at NHGRI
- EpiGRAPH server

Send Data

[ENCODE Tools](#)

[Lift-Over](#)

[Text Manipulation](#)

[Filter and Sort](#)

[Join, Subtract and Group](#)

[Convert Formats](#)

[Extract Features](#)

[Fetch Sequences](#)

[Fetch Alignments](#)

Home Genomes **Genome Browser** Blat Tables Gene Sorter PCR Session FAQ

## Table Browser

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, to retrieve DNA sequence covered by a track. For help in using this application see [Using the Table Browser](#) for a description of the controls in this form, the [User's Guide](#) for general information and sample queries, and the OpenHelix Table Browser [tutorial](#) for a narrated presentation of the software features and usage. For more complex queries, you may use [Galaxy](#) or our [public MySQL server](#). To examine the biological function of your set through annotation enrichment, send the data to [GREAT](#). Refer to the [Credits](#) page for the list of contributors and usage restrictions associated with this data.

**clade:** Mammal ▾ **genome:** Human ▾ **assembly:** Feb. 2009 (GRCh37/hg19) ▾

**group:** Custom Tracks ▾ **track:** Chr9 hg19 LANA MACS peaks ▾ [manage custom tracks](#)

[track hubs](#)

**table:** ct\_Chr9hg19LANAMACSpeaks\_3943 ▾ [describe table schema](#)

**region:**  genome  position chr9:1-140127172 [lookup](#) [define regions](#)

**identifiers (names/accessions):** [paste list](#) [upload list](#)

**filter:** [create](#)

**intersection:** [create](#)

**correlation:** [create](#)

**output format:** BED - browser extensible data ▾ Send output to  [Galaxy](#)  [GREAT](#)

**output file:**  (leave blank to keep output in browser)

**file type returned:**  plain text  gzip compressed

[get output](#) [summary/statistics](#)

To reset **all** user cart settings (including custom tracks), [click here](#).





# Add a custom track

Home Genomes Blat Tables Gene Sorter PCR DNA Convert Ensembl

## UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

move <<<< << < > >> >>>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x

position/search chr10:1-135,534,747 [gene](#) jump clear size 135,534,747 bp. configure

chr10 (p15.3-q26.3) p14 p13 q21.1

Scale chr10: 50 Mb | 50000000 | 100000000

move start < 2.0 > move end < 2.0 >

Click on a feature for details. Click or drag in the base position track to zoom in. Click side bars for track options. Drag side bars or labels up or down to reorder tracks. Drag tracks left or right to new position.

track search default tracks default order hide all **add custom tracks** track hubs configure reverse resize refresh

collapse all Use drop-down controls below and press refresh to alter tracks displayed. Tracks with lots of items will automatically be displayed in more compact modes. expand all

**Mapping and Sequencing Tracks** refresh

[Base Position](#) [Chromosome Band](#) [STS Markers](#) **18** [FISH Clones](#) [Recomb Rate](#) [Map Contigs](#)

dense ↑ hide ↑ hide ↑ hide ↑



# Paste track data

Home Genomes Genome Browser Blat Tables Gene Sorter PCR Se

## Add Custom Tracks

clade  genome  assembly

Display your own data as custom annotation tracks in the browser. Data must be formatted in [GFF](#), [GTF](#), [WIG](#), [bigWig](#), [MAF](#), [BAM](#), [BED detail](#), [Personal Genome SNP](#), or [PSL](#) formats. To [track](#) and [browser](#) line attributes as described in the [User's Guide](#). URLs for data in the bigBed and embedded in a track line in the box below. Publicly available custom tracks are listed [here](#). Examp

Paste URLs or data: Or upload:  no file selected

```
track name="Chr10LANA" description="User Supplied Track (from Galaxy)"
color=0,0,255 visibility=1
chr10 309835 311665 MACS_peak_1 134.30
chr10 374946 376165 MACS_peak_2 87.06
chr10 382566 385025 MACS_peak_3 54.46
chr10 439141 440977 MACS_peak_4 53.43
chr10 1030693 1036216 MACS_peak_5 68.77
```

Optional track documentation: Or upload:  no file selected



# View track

Genomes Blat Tables Gene Sorter PCR DNA Convert Ensembl NCBI PDF/P

## UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x

position/search chr10:310,802-310,803 [gene](#)  jump clear size 2 bp. [configure](#)

chr10 (p15.3) p14 p13 q21.1 21.3 23.1 25.1

Scale chr10: 1 bases | 310802 | T

Chr10LANA My Custom Track

move start < 2.0 > move end < 2.0 >

track search default tracks default order hide all manage custom tracks track hubs configure reverse resize refresh

collapse all Use drop-down controls below and press refresh to alter tracks displayed. expand all  
Tracks with lots of items will automatically be displayed in more compact modes.

My Custom Track drag to reorder Custom Tracks refresh

[Chr10LANA](#)

dense ⇅





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Help!!!



# How to get help

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## ◆ Asking for help

- Support Request Tickets

- <http://support.hpc.ufl.edu>

- Use for everything - not just software bugs but for any questions or help requests

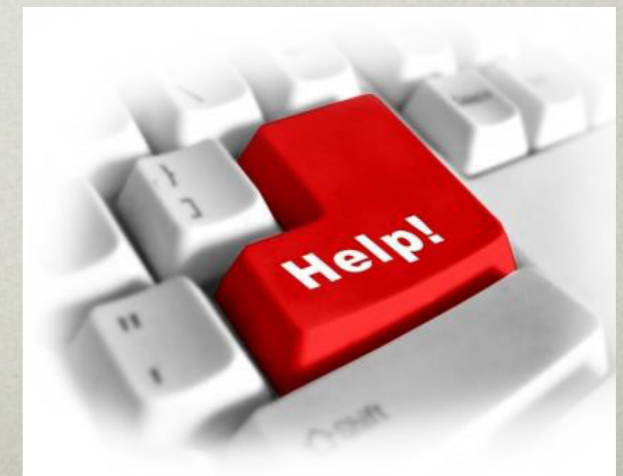
- Searchable database of solutions

- When you don't have access to web

- [support@hpc.ufl.edu](mailto:support@hpc.ufl.edu)

- [om@hpc.ufl.edu](mailto:om@hpc.ufl.edu) (Biological Support)

- [magitz@ufl.edu](mailto:magitz@ufl.edu) (Bio training and Q/A)





# Documentation

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## ◆ UF HPC Encyclopedia

- <http://wiki.hpc.ufl.edu>
  - Documents on hardware and software resources
  - User guides
  - Sample submission scripts
  - Research-specific sections
- <http://hpc.ufl.edu/support>
  - Frequently Asked Questions
  - Account set up and maintenance





# Training Schedule

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- ✓ October 20th: Intro to UFHPC, getting started
- ✓ October 27th: Modules and basic submission scripts
- ✓ November 3rd: Galaxy overview
- ◆ November 10th: No session - Florida Genetics 2011
- ◆ November 17th: Introduction to working in Linux shell environment
- ◆ November 24th: No session – Thanksgiving
- ◆ December 1st: Working with NGS data (quality filtering, format conversion, etc.)





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Thank  
you!