# New Tools, New Datasources

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# Overview

- Tools
- Datasources
- External Display Applications

# The Difference?

- Tools
  - Any command-line executable
- Datasources
  - Getting Data from an external source
- External Display Applications
  - Sending Data to an external web application

# Overview

- Tools
- Datasources
- External Display Applications

# Recent Additions


- Status: Stable (pretty well tested) --> Alpha

# Recent Additions

**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

**VCF Tools**

- Intersect Generate the intersection of two VCF files
- Annotate a VCF file (dbSNP, hapmap)
- Filter a VCF file
- Extract reads from a specified region

**NGS: Picard (beta)**

QC/METRICS FOR SAM/BAM

- BAM Index Statistics
- Sam/bam Alignment Summary Metrics
- Sam/bam GC Bias Metrics
- Estimate Library Complexity
- Insertion size metrics for PAIRED data
- Sam/bam Hybrid Selection Metrics For (eg exome) targeted data

BAM/SAM CLEANING

- Add or Replace Groups
- Reorder SAM
- Replace Sam Header
- Paired Read Mate Fixer for paired data
- Mark Duplicate reads

FASTQC: FASTQ/SAM/BAM

- Fastqc: Fastqc QC using FastQC from Babraham

**NGS: GATK Tools** Alpha

REALIGNMENT

- Realigner Target Creator for use in local realignment
- Indel Realigner – perform local realignment

BASE RECALIBRATION

- Count Covariates on BAM files
- Table Recalibration on BAM files
- Analyze Covariates – perform local realignment

GENOTYPING

- Unified Genotyper SNP and indel caller

Report Bugs, please

# Adding your Own

- Write or download a command-line executable
- Determine number and kind of
  - Input and Output Datasets
  - Input Parameters
- Construct a descriptive tool configuration XML file
  - Write a wrapper script, only if required

# Tool Configuration

- Tool Action - Default tool action should be adequate (Upload tool uses custom tool action)
- Tool Command
- Inputs
  - Action - Used by datasource tools
  - Parameters
- Outputs
- Help
- Tests

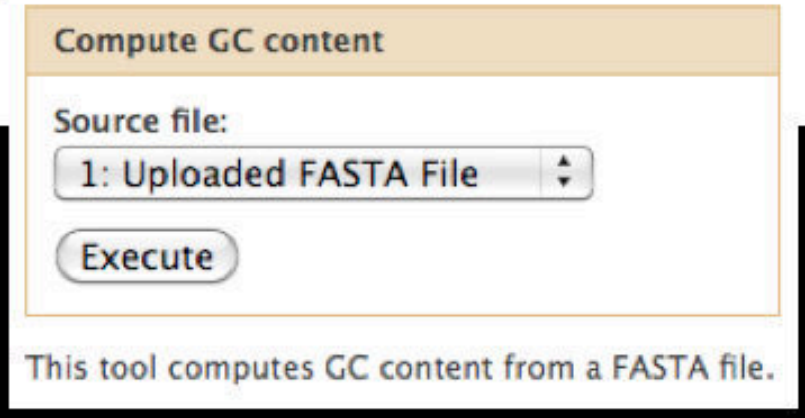
# A Basic Tool

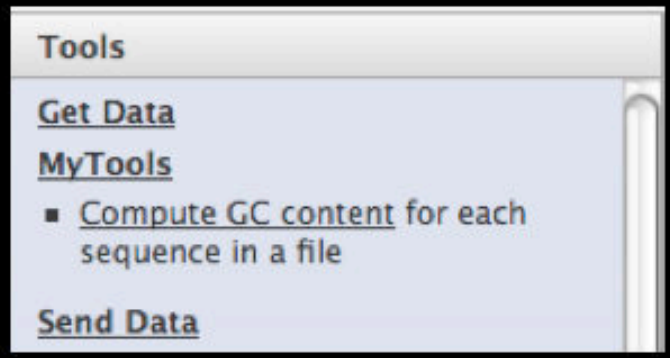
```
<tool id="fa_gc_content_1" name="Compute GC content">
  <description>for each sequence in a file</description>
  <command interpreter="perl">toolExample.pl $input $output</command>
  <inputs>
    <param format="fasta" name="input" type="data" label="Source file"
  </inputs>
  <outputs>
    <data format="tabular" name="output" />
  </outputs>

  <tests>
    <test>
      <param name="input" value="fa_gc_content_input.fa"/>
      <output name="out_file1" file="fa_gc_content_output.txt"/>
    </test>
  </tests>

  <help>
This tool computes GC content from a FASTA file.
  </help>

</tool>
```




```
<section name="MyTools" id="mTools">
    <tool file="myTools/toolExample.xml" />
</section>
```

**tool_conf.xml**

## Cluster

Cluster intervals of: 6: UCSC Main on Human: knownGene

max distance between intervals: 1 (bp)

min number of intervals per cluster: 2

Return type: Merge clusters into single intervals

Execute

**TIP:** If your query does not appear in the pulldown menu -> it is not in interval format. Use "edit attributes" to set chromosome, start, end, and strand columns

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**Screencasts!**

See Galaxy Interval Operation Screencasts (right click to open this link in another window).

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**Syntax**

- **Maximum distance** is greatest distance in base pairs allowed between intervals that will be considered "clustered". **Negative** values for distance are allowed, and are useful for clustering intervals that overla
- **Minimum intervals per cluster** allow a threshold to be set on the minimum number of intervals to be considered a cluster. Any area with less than this minimum will not be included in the ouput.
- **Merge clusters into single intervals** outputs intervals that span the entire cluster.
- **Find cluster intervals; preserve comments and order** filters out non-cluster intervals while maintaining the original ordering and comments in the file.
- **Find cluster intervals; output grouped by clusters** filters out non-cluster intervals, but outputs the cluster intervals so that they are grouped together. Comments and original ordering in the file are lost.

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**Example**


cluster.xml

```
<tool id="gops_cluster_1" name="Cluster">
  <description>[[Cluster]] the intervals of a query</description>
  <command interpreter="python2.4">
    gops_cluster.py $input1 $output -1 $input1_chromCol,$input1_startC
                   -d $distance -m $minregions -o $returntype
  </command>
  <inputs>
    <param format="interval" name="input1" type="data">
      <label>Cluster intervals of</label>
    </param>
    <param name="distance" size="5" type="integer" value="1" help="(bp
      <label>max distance between intervals</label>
    </param>
    <param name="minregions" size="5" type="integer" value="2">
      <label>min number of intervals per cluster</label>
    </param>
    <param name="returntype" type="select" label="Return type">
      <option value="1">Merge clusters into single intervals</option>
      <option value="2">Find cluster intervals; preserve comments and
      <option value="3">Find cluster intervals; output grouped by clus
      <option value="4">Find the smallest interval in each cluster</op
      <option value="5">Find the largest interval in each cluster</opt
    </param>
   </inputs>
   <help>

.. class:: infomark

**TIP:** If your query does not appear in the pulldown menu -> it is n

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**Screencasts!**

See Galaxy Interval Operation Screencasts_ (right click to open this l

.. _Screencasts: http://www.bx.psu.edu/cgi-bin/trac.cgi/wiki/GopsDesc

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**Syntax**

- **Maximum distance** is greatest distance in base pairs allowed betw
- **Minimum intervals per cluster** allow a threshold to be set on the
- **Merge clusters into single intervals** outputs intervals that span
- **Find cluster intervals; preserve comments and order** filters out
- **Find cluster intervals; output grouped by clusters** filters out n
```

Line: 87 Column: 8 XML Soft Tabs: 2

# Input Parameter types

## Basic

- Text
- Integer
- Float
- Select
  - Static
  - Dynamic
- Boolean
- Genome build
- Data column
- Data
- Hidden
- Base URL
- File
- Drill down
- Grouping
  - Conditional
  - Repeat
- Config Files

# Configfile Inputs

- Temporary file is available as input to the tool
- Cheetah templating language is used to define the contents of a temporary file
- Examples
  - Formatted list of input values
  - R (statistics package) scripts
  - Gnuplot Commands
  - Dynamically generated python scripts

# Advanced Topics

- Datasets and Datatypes
- Metadata
- Dynamic Select lists
- Tool Output actions
  - changing formats, setting metadata based upon user inputs
- Filtering outputs
- Parameter Validation

# Datasets and Datatypes

- All datasets are associated with a Datatype
  - File format
  - Type of Data: genomic intervals, sequence, alignment
    - Hierarchical structure allows accepting more specific datatypes without conversion (tabular <- interval <- bed)
    - Datatype Converters allow use of non-subclassed datatypes as direct input for tools (MAF to FASTA converter allows selection of MAF file as input when FASTA is required)
  - Metadata
- datatypes_conf.xml and lib/galaxy/datatypes

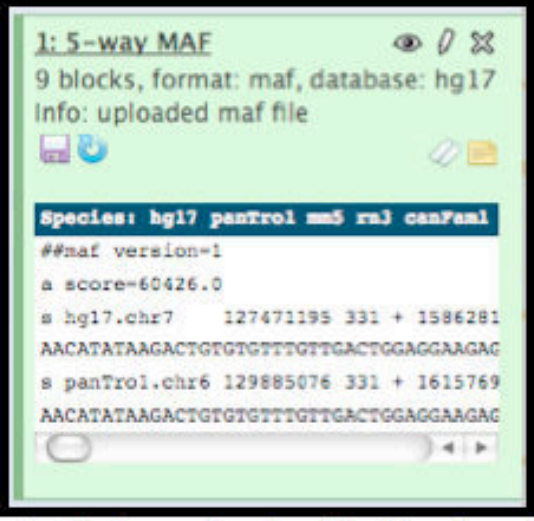
https://bitbucket.org/galaxy/galaxy-central/wiki/AddingDatatypes

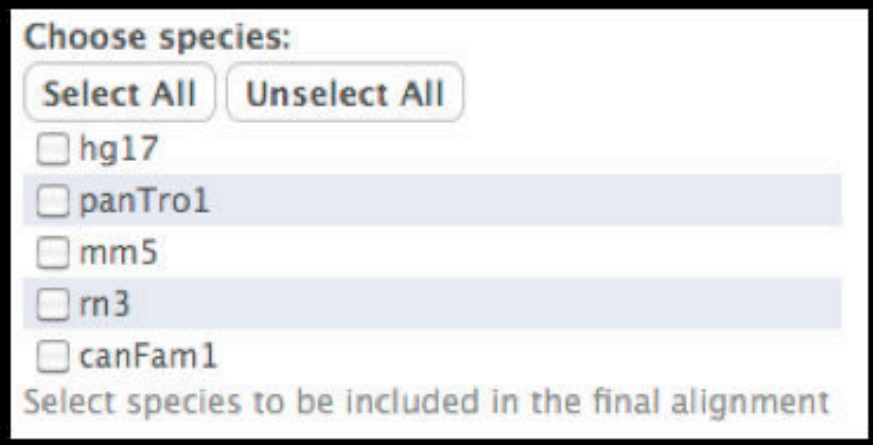
# Datatype Metadata

- Information that describes the contents of the Dataset
  - Line / Sequence Counts
  - Count and type of tabular columns
  - Column assignments: start, stop, strand
    Genome build(s): dbkey, species
  - Files: indexes
- Used by tools to customize interface and results

# Dynamic Select Lists

- Use species metadata value from MAF file to dynamically generate a list of checkboxes

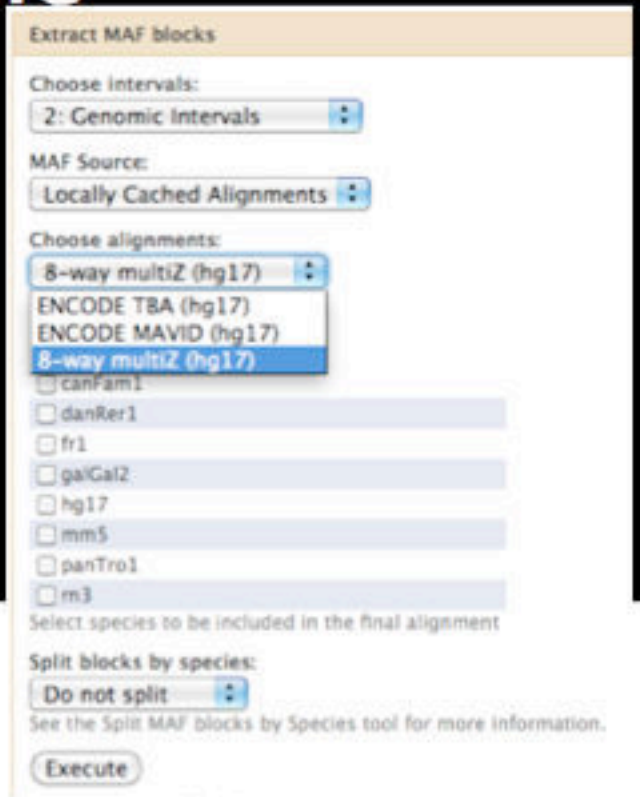



```
<param name="species" type="select" display="checkboxes" multiple="true" label="Choose species" help="Select s
  <options>
    <filter type="data_meta" ref="mafFile" key="species" />
  </options>
</param>
```

# List of available alignments should be filtered based upon the dbkey of the input interval file

- Locally cached MAFs
- Don't want to modify the tool each time a new MAF set is added to the cache
- Dynamic Select: Use a separate file to describe available cached MAFs




```
<param name="mafType" type="select" label="Choose alignments">
  <options from_file="maf_index.loc">
    <column name="name" index="0"/>
    <column name="value" index="1"/>
    <column name="dbkey" index="2"/>
    <column name="species" index="3"/>
    <filter type="data_meta" ref="input1" key="dbkey" column="2" multiple="True" separator=","/>
    <validator type="no_options" message="No alignments are available for the build associated with the selected inter
  </options>
</param>
```

```
$ cat maf_index.loc
#Display_name UID       indexed_for:build1,build2,build3        exists_in_maf:build1,build2,build3      Comma_Separated_Full_Paths_To_Files
ENCODE TBA (hg17)       ENCODE_TBA_hg17 armadillo,baboon,galGal2,panTro1,colobus_monkey,cow,canFam1,dusky_titi,elephant,fr1,galago,hedgehog,hg
ENCODE MAVID (hg17)     ENCODE_MAVID_hg17       armadillo,baboon,galGal2,panTro1,colobus_monkey,cow,canFam1,dusky_titi,elephant,fr1,galago,hed
ENCODE TBA (hg16)       ENCODE_TBA_hg16 armadillo,baboon,galGal2,panTro1,colobus_monkey,cow,canFam1,dusky_titi,elephant=elephant,fr1,galago,he
8-way multiZ (hg17)     8_WAY_MULTIZ_hg17       canFam1,danRer1,fr1,galGal2,hg17,mm5,panTro1,rn3        canFam1,danRer1,fr1,galGal2,hg17,mm5,p
17-way multiZ (hg18)    17_WAY_MULTIZ_hg18      hg18,panTro1,bosTau2,rheMac2,mm8,rn4,canFam2,echTel1,loxAfr1,oryCun1,danRer3,monDom4,dasNov1,g
3-way multiZ (hg18,panTro2,rheMac2)     3_WAY_MULTIZ_hg18       hg18,panTro2,rheMac2    hg18,panTro2,rheMac2    /depot/data2/galaxy/hg18/align
```

# Tool Output Actions

- Allow run-time attributes (parameter settings, input metadata, datatype) to change attributes of a created output file
- Examples:
  - Cut tool
    - Default output is tabular
    - What if input was BED and all required interval columns are kept?
  - NGS mappers (e.g. bowtie)
    - Set dbkey of output when using pre-built indices

# Cut Tool

```
<outputs>
  <data format="tabular" name="out_file1" >
    <actions>
      <conditional name="delimiter">
        <when value="T">
          <conditional name="input">
            <when datatype_isinstance="interval">
              <action type="format" default="tabular">
                <option type="from_param" name="columnList" column="0" offset="0"> <!-- chromCol is 1-->

                  <filter type="insert_column" column="0" value="interval"/>

                  <filter type="insert_column" ref="columnList" /> <!-- startCol -->

                  <filter type="insert_column" ref="columnList" /> <!-- endCol -->

                  <filter type="multiple_splitter" column="1" separator=","/>
                  <filter type="column_strip" column="1"/> <!-- get rid of all external whitespace -->
                  <filter type="string_function" column="1" name="lower" />
                  <filter type="param_value" column="1" value="^c\d{1,}$" compare="re_search" keep="True"/>
                  <filter type="column_strip" column="1" strip="c"/> <!-- get rid of c's  -->
                  <filter type="boolean" column="1" cast="int" />

                  <filter type="multiple_splitter" column="2" separator=","/>
                  <filter type="column_strip" column="2"/> <!-- get rid of all external whitespace -->
                  <filter type="string_function" column="2" name="lower" />
                  <filter type="param_value" column="2" value="^c\d{1,}$" compare="re_search" keep="True"/>
                  <filter type="column_strip" column="2" strip="c"/> <!-- get rid of c's  -->
                  <filter type="boolean" column="2" cast="int" />

                  <filter type="multiple_splitter" column="3" separator=","/>
                  <filter type="column_strip" column="3"/> <!-- get rid of all external whitespace -->
                  <filter type="string_function" column="3" name="lower" />
                  <filter type="param_value" column="3" value="^c\d{1,}$" compare="re_search" keep="True"/>
                  <filter type="column_strip" column="3" strip="c"/> <!-- get rid of c's  -->
                  <filter type="boolean" column="3" cast="int" />

                  <filter type="metadata_value" ref="input" name="chromCol" column="1" />
                  <filter type="metadata_value" ref="input" name="startCol" column="2" />
                  <filter type="metadata_value" ref="input" name="endCol" column="3" />

                </option>
              </action>
```

```
<conditional name="out_file1">
  <when datatype_isinstance="interval">
    <action type="metadata" name="chromCol">
      <option type="from_param" name="columnList" column="0" offset="0"> <!-- chromCol is 0-->
        <filter type="multiple_splitter" column="0" separator=","/>
        <filter type="column_strip" column="0"/> <!-- get rid of all external whitespace -->
        <filter type="string_function" column="0" name="lower" />
        <filter type="param_value" column="0" value="^c\d{1,}$" compare="re_search" keep="True"/>
        <filter type="column_strip" column="0" strip="c"/> <!-- get rid of c's  -->
        <filter type="insert_column" value="1" iterate="True" column="0"/>
        <filter type="boolean" column="1" cast="int" />
        <filter type="metadata_value" ref="input" name="chromCol" column="1" />
      </option>
    </action>

    <action type="metadata" name="startCol">
      <option type="from_param" name="columnList" column="0" offset="0"> <!-- startCol is 0-->
        <filter type="multiple_splitter" column="0" separator=","/>
        <filter type="column_strip" column="0"/> <!-- get rid of all external whitespace -->
        <filter type="string_function" column="0" name="lower" />
        <filter type="param_value" column="0" value="^c\d{1,}$" compare="re_search" keep="True"/>
        <filter type="column_strip" column="0" strip="c"/> <!-- get rid of c's  -->
        <filter type="insert_column" value="1" iterate="True" column="0"/>
        <filter type="boolean" column="1" cast="int" />
        <filter type="metadata_value" ref="input" name="startCol" column="1" />
      </option>
    </action>

    <action type="metadata" name="endCol">
      <option type="from_param" name="columnList" column="0" offset="0"> <!-- endCol is 0-->
        <filter type="multiple_splitter" column="0" separator=","/>
        <filter type="column_strip" column="0"/> <!-- get rid of all external whitespace -->
        <filter type="string_function" column="0" name="lower" />
        <filter type="param_value" column="0" value="^c\d{1,}$" compare="re_search" keep="True"/>
        <filter type="column_strip" column="0" strip="c"/> <!-- get rid of c's  -->
        <filter type="insert_column" value="1" iterate="True" column="0"/>
        <filter type="boolean" column="1" cast="int" />
        <filter type="metadata_value" ref="input" name="endCol" column="1" />
      </option>
    </action>

    <action type="metadata" name="nameCol" default="0">
      <option type="from_param" name="columnList" column="0" offset="0"> <!-- nameCol is 0-->
        <filter type="multiple_splitter" column="0" separator=","/>
        <filter type="column_strip" column="0"/> <!-- get rid of all external whitespace -->
        <filter type="string_function" column="0" name="lower" />
        <filter type="param_value" column="0" value="^c\d{1,}$" compare="re_search" keep="True"/>
        <filter type="column_strip" column="0" strip="c"/> <!-- get rid of c's  -->
        <filter type="insert_column" value="1" iterate="True" column="0"/>
        <filter type="boolean" column="1" cast="int" />
        <filter type="metadata_value" ref="input" name="nameCol" column="1" />
      </option>
    </action>
```

# Cut Tool

```
            <action type="metadata" name="strandCol" default="0">
              <option type="from_param" name="columnList" column="0" offset="0"> <!-- strandCol is 0-->
                <filter type="multiple_splitter" column="0" separator=","/>
                <filter type="column_strip" column="0"/> <!-- get rid of all external whitespace -->
                <filter type="string_function" column="0" name="lower" />
                <filter type="param_value" column="0" value="^c\d{1,}$" compare="re_search" keep="True"/>
                <filter type="column_strip" column="0" strip="c"/> <!-- get rid of c's  -->
                <filter type="insert_column" value="1" iterate="True" column="0"/>
                <filter type="boolean" column="1" cast="int" />
                <filter type="metadata_value" ref="input" name="strandCol" column="1" />
              </option>
            </action>
          </when>
        </conditional>

      </when>
    </conditional>
  </when>
</conditional>
</actions>
</data>
```

tools/filters/cutWrapper.xml

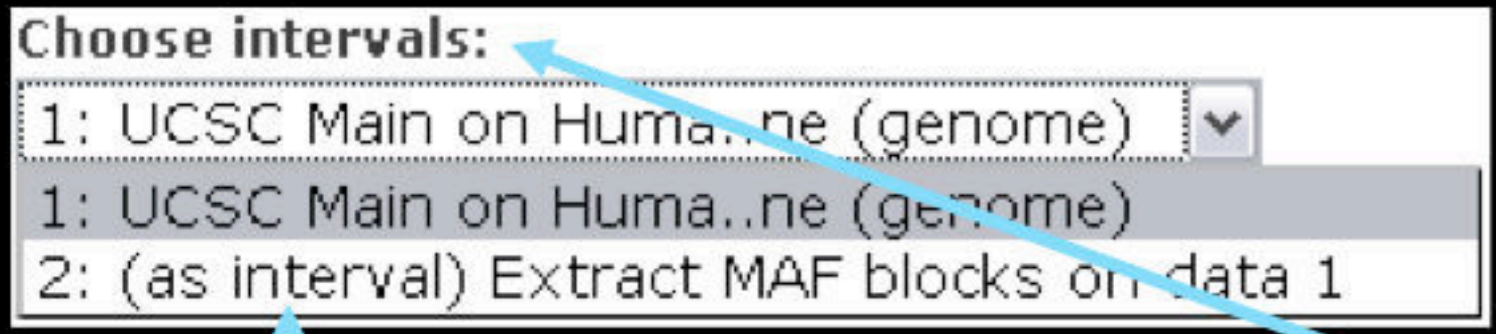
# Filtering Outputs

- Parameter settings can be used to change the outputs that are created

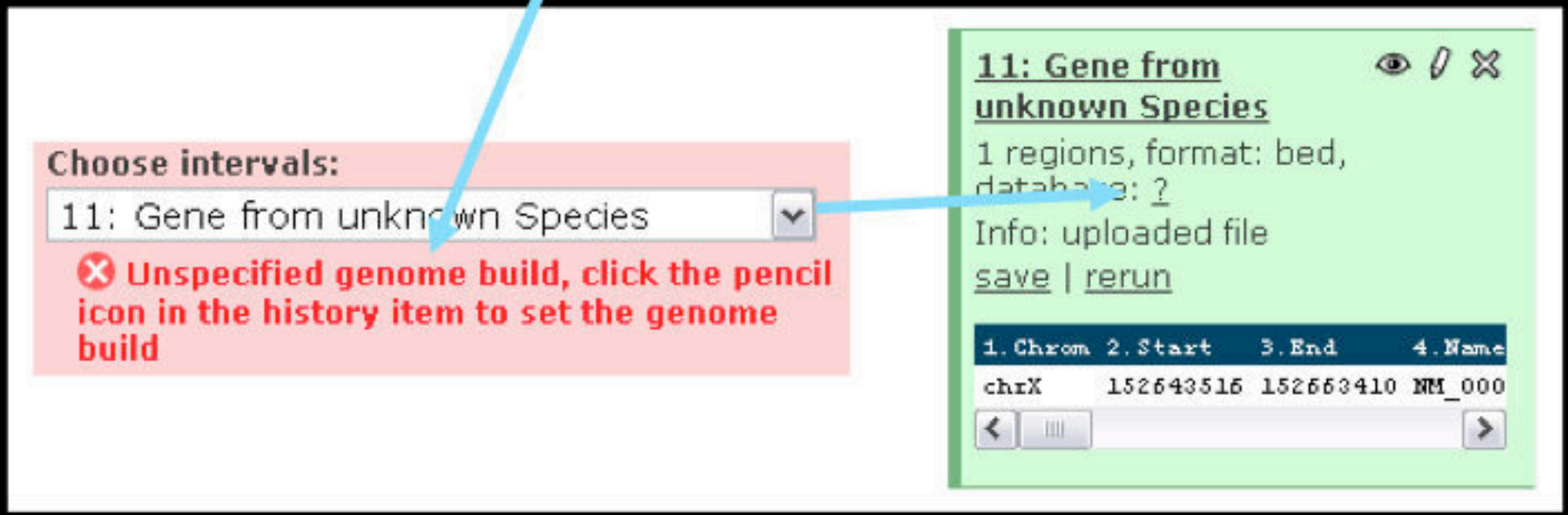
```
  <outputs>
    <data name="output_bed_file" format="bed" label="${tool.name} on ${on_string} (peaks: bed)"/>
    <data name="output_xls_to_interval_peaks_file" format="interval" label="${tool.name} on ${on_string}
(peaks: interval)">
      <filter>xls_to_interval is True</filter>
    </data>
    <data name="output_xls_to_interval_negative_peaks_file" format="interval" label="${tool.name} on $
{on_string} (negative peaks: interval)">
      <filter>xls_to_interval is True</filter>
      <filter>input_type['input_control_file1'] is not None</filter>
    </data>
    <data name="output_treatment_wig_file" format="wig" label="${tool.name} on ${on_string} (treatment:
wig)">
      <filter>wig_type['wig_type_selector']=='wig'</filter>
    </data>
    <data name="output_control_wig_file" format="wig" label="${tool.name} on ${on_string} (control: wig)">
      <filter>wig_type['wig_type_selector'] == 'wig'</filter>
      <filter>input_type['input_control_file1'] is not None</filter>
    </data>
    <data name="output_extra_files" format="html" label="${tool.name} on ${on_string} (html report)"/>
  </outputs>
```

tools/peak_calling/macs_wrapper.xml

# Parameter Validation




```
<param format="interval" name="input1" type="data" label="Choose intervals">↓
  <validator type="unspecified_build" />↓
</param>↓
```




tools/maf/interval2maf.xml

# Available Validators

| Validator | Use |
|---|---|
| expression | Evaluates a python expression using the parameter value |
| regex | Checks if parameter value matches the specified regular expression |
| in_range | Ensures a numerical parameter value falls between a min and max |
| length | Ensures the length of a text parameter value falls between a min and max |
| metadata | Checks if specified metadata is missing for a dataset |
| unspecified_build | Checks if the dbkey for a dataset has been set |
| no_options | Ensures at least one option has been set for select parameters |
| empty_field | Ensures a text field has not been left empty |
| dataset_metadata_in_file | Checks if a particular metadata value for a dataset exists in a File |
| dataset_ok | Ensures an input dataset is in the OK state |

# I created a tool...now what

- Share it!
- Galaxy Tool Shed
  - coming up next
  - Talk by Greg Von Kuster

# Overview

- Tools
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# Recent Additions

# Adding your Own

- Synchronous
  - data ready immediately
- Asynchronous
  - data needs to be generated by external source first

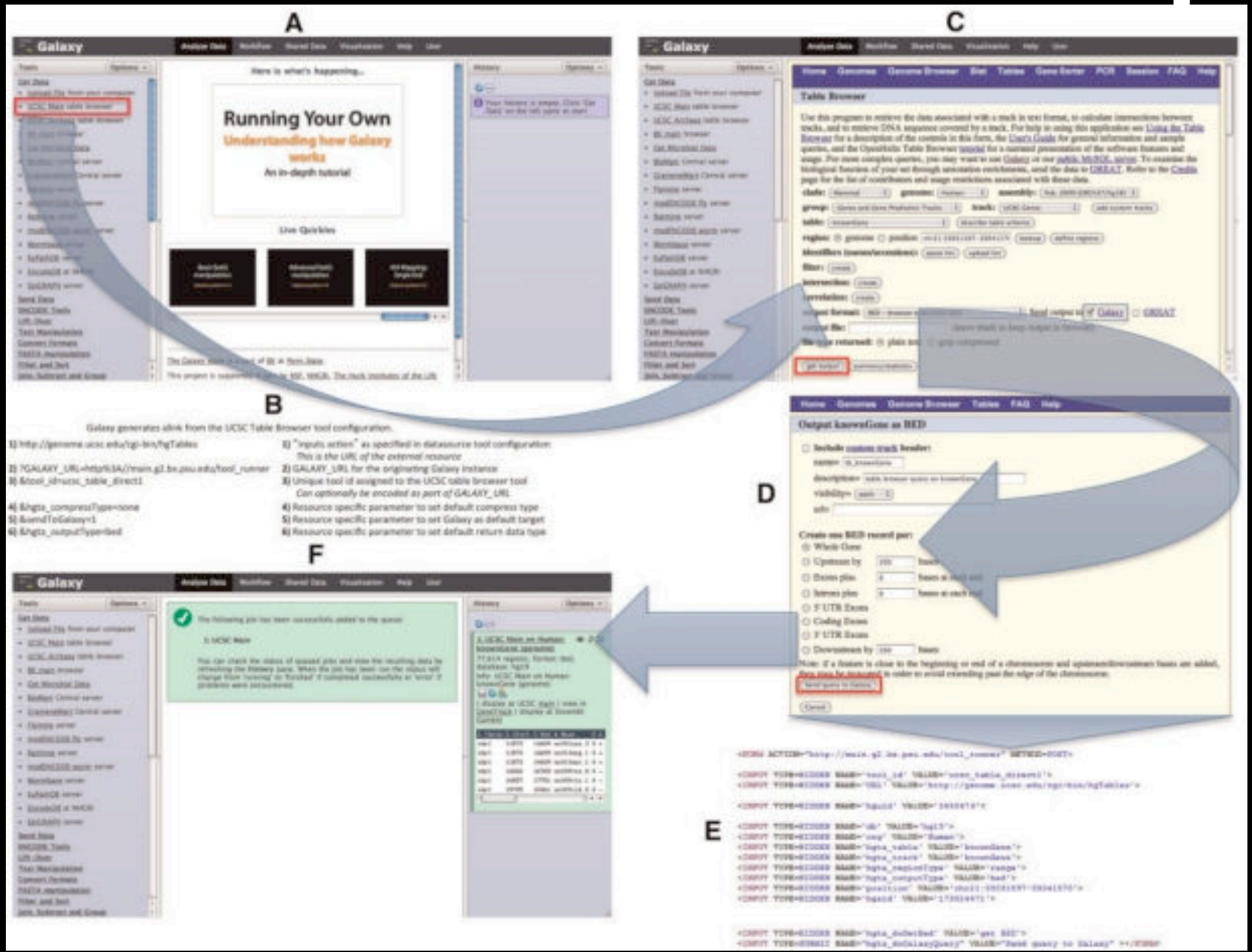
https://bitbucket.org/galaxy/galaxy-central/wiki/DataSources

Blankenberg D, Coraor N, Von Kuster G, Taylor J, Nekrutenko A and The Galaxy Team. Integrating diverse databases into an unified analysis framework: a Galaxy approach. Database (Oxford). 2011 Apr 29.

# Synchronous Datasource Tools

- When the user has finished at the external site, the external site directs the user back to Galaxy
- Parameters and a retrieval URL are provided
- In the background, Galaxy creates a new dataset and then uses provided URL and parameters to retrieve the new dataset content

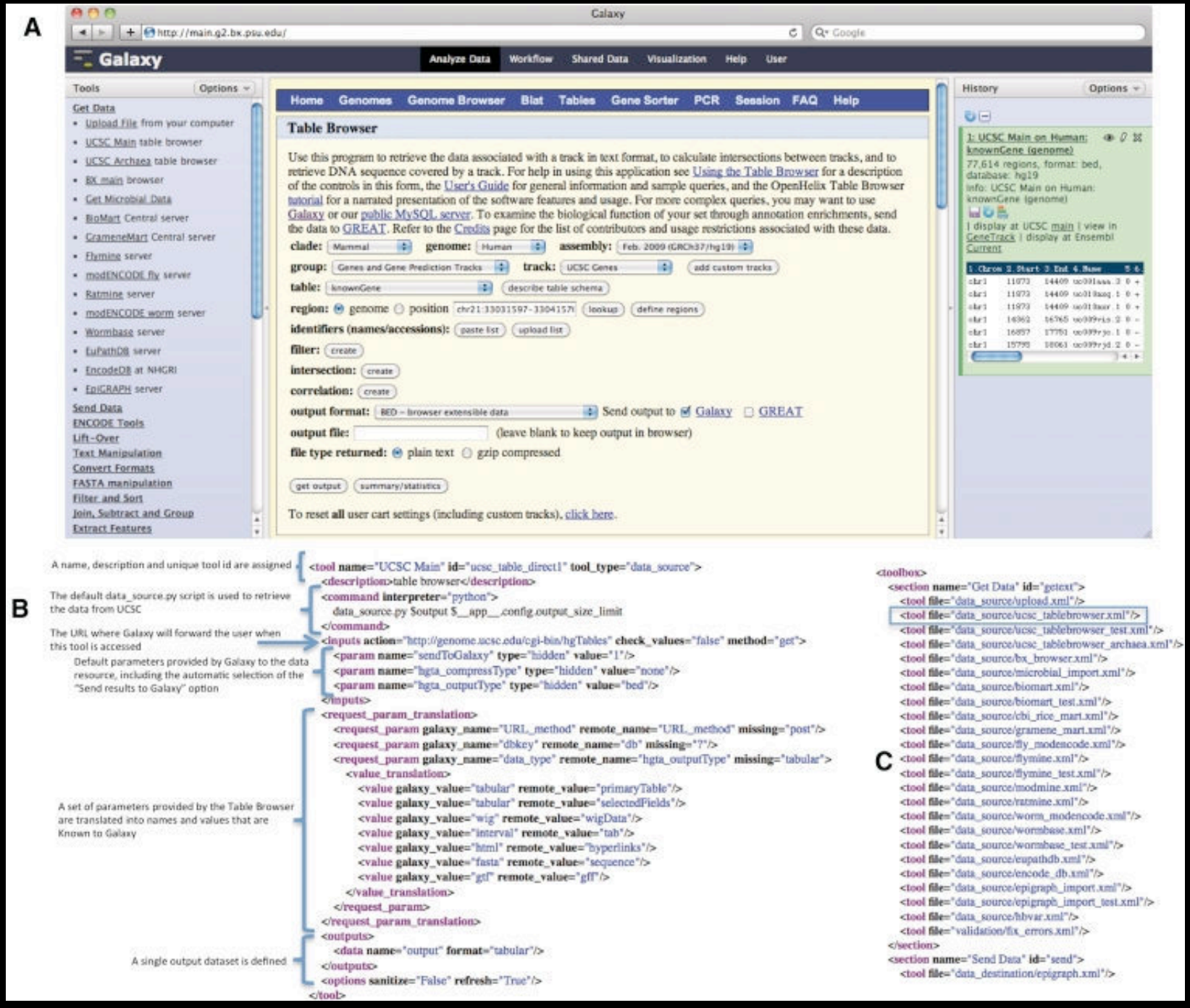
# UCSC Table Browser Example



# Asynchronous Datasource Tools

- When the user has finished at the external site, the external site directs the user back to Galaxy
- Parameters and an URL is provided
- In the background, Galaxy creates a new dataset and then creates a new GALAXY_URL (uniquely identifying this new dataset) and sends this and provided parameters to the data source
- External data source then runs processes to generate dataset contents and sends a URL back to GALAXY_URL

# UCSC Table Browser Example



# Setting Attributes of Newly obtained Datasets

| Parameter name | Usage |
|---|---|
| Name | The external resource can provide a descriptive name for the retrieved data set. If not provided, a default name based upon the name provided in the XML tool configuration is used. |
| Info | A free-form text string that a resource can use to provide additional information about the data set. |
| data_type | The type of data returned to Galaxy. Examples include bed, sam, gff and maf. |
| Dbkey | If the data belongs to a single reference genome, this string is used to store this information. Examples include hg18, mm9 and canFam2. |
| URL | The user's history will be populated with a new data set containing the results returned by submitting all provided parameters to this URL. |

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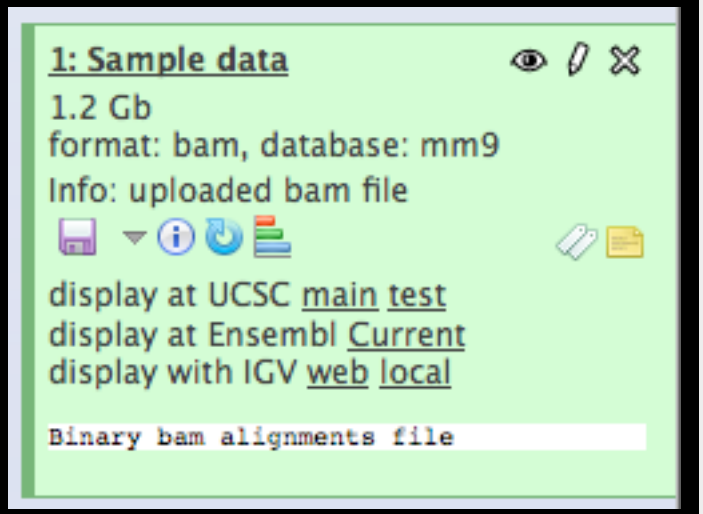
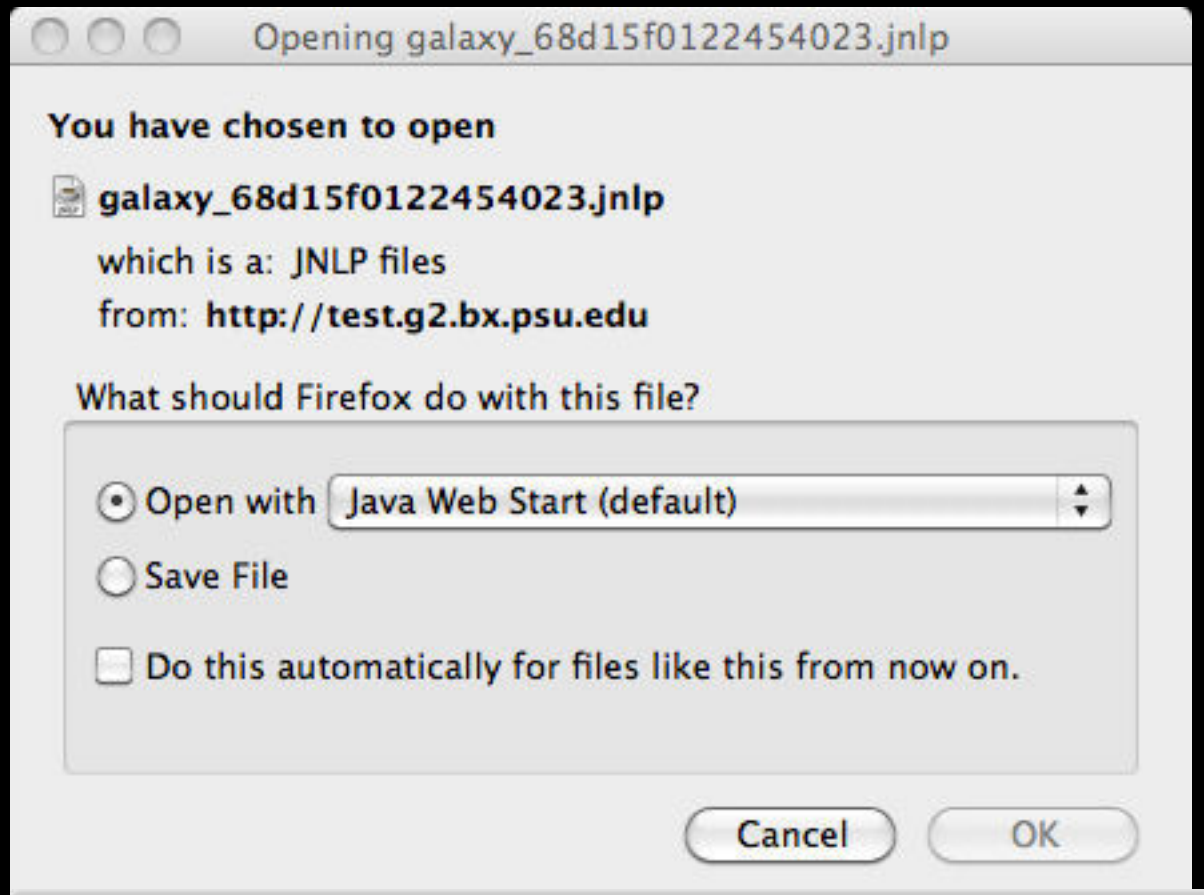
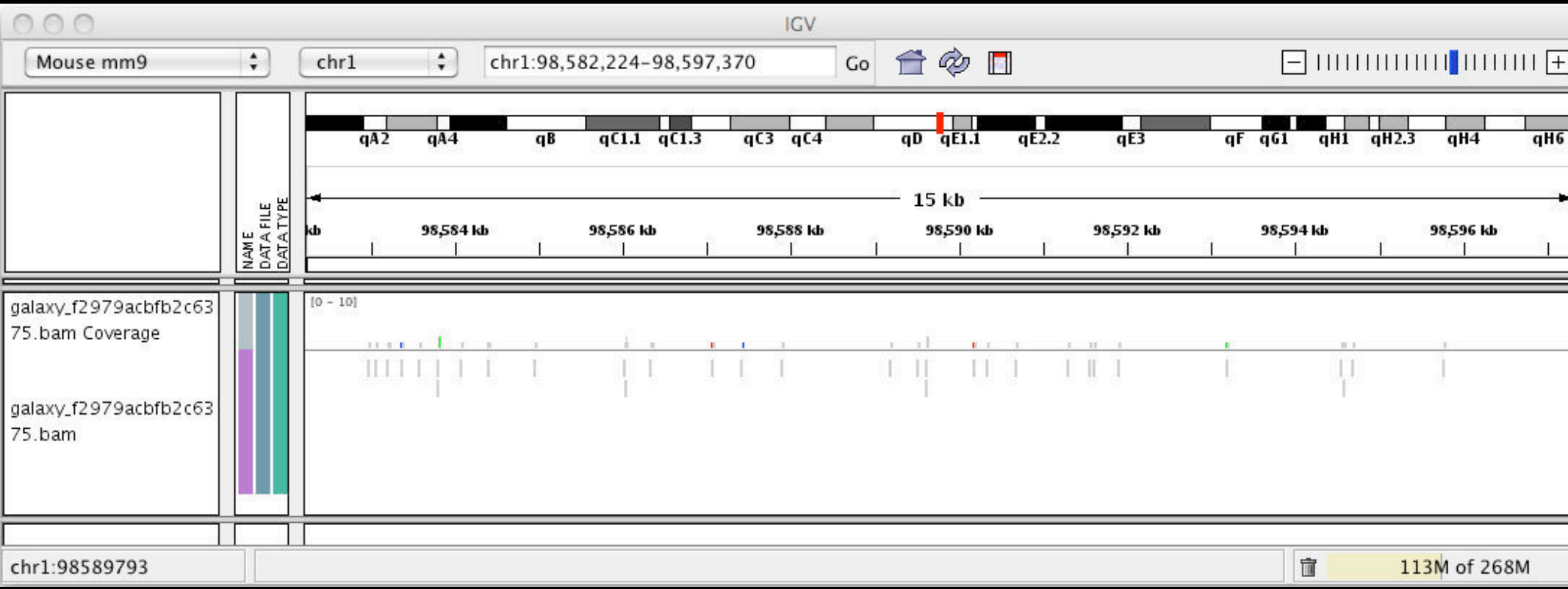



# Integrative Genomics Viewer (IGV)



# Adding your Own

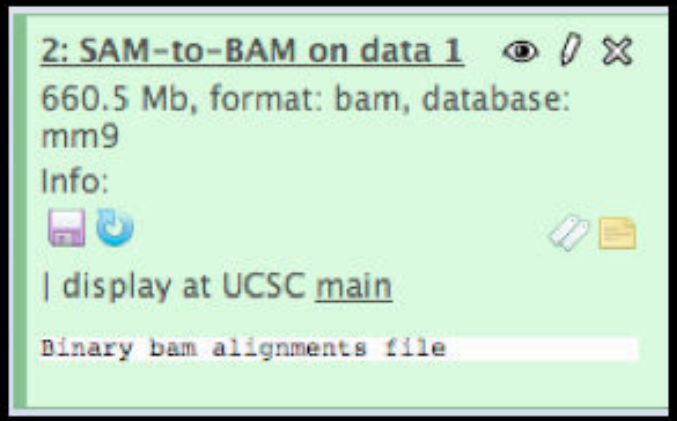
- Define An XML configuration which describes how and where to present the data to the External Web Application
  - Static
  - Dynamic - display options can be loaded from a file
- Inform Galaxy about the new display by adding to the appropriate datatype in datatypes_conf.xml

https://bitbucket.org/galaxy/galaxy-central/wiki/ExternalDisplayApplications/Tutorial

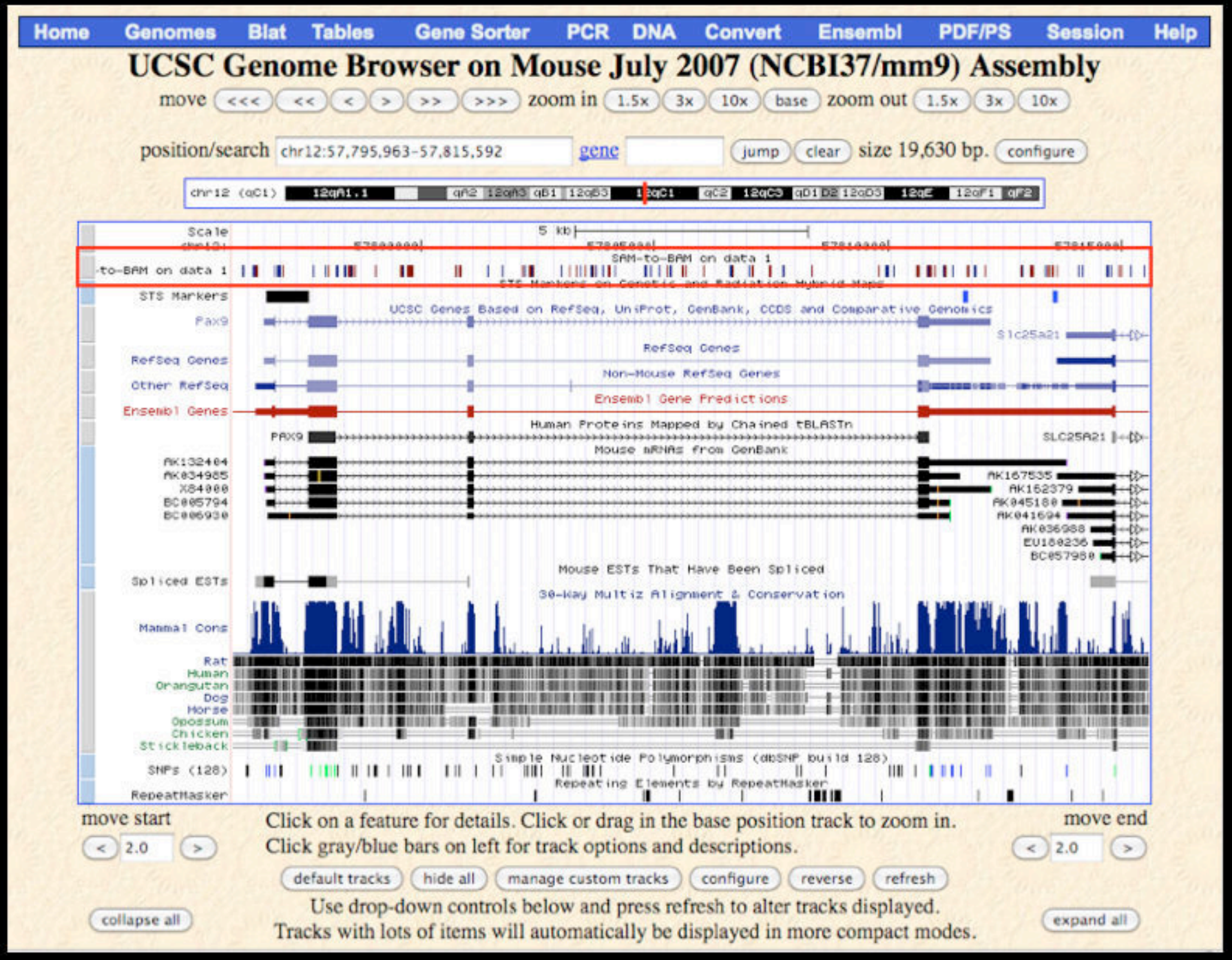
# Static External Display Application

```
<display id="ucsc_bam" version="1.0.0" name="display at UCSC">
    <link id="main" name="main">
        <url>http://genome.ucsc.edu/cgi-bin/hgTracks?db=${qp($bam_file.dbkey)}&amp;hgt.customText=${qp($track.url)}</url>
        <param type="data" name="bam_file" url="galaxy.bam" strip_https="True" />
        <param type="data" name="bai_file" url="galaxy.bam.bai" metadata="bam_index" strip_https="True" />
        <param type="template" name="track" viewable="True" strip_https="True">
            track type=bam name="${bam_file.name}" bigDataUrl=${bam_file.url} db=${bam_file.dbkey}
        </param>
    </link>
</display>
```

```
<datatype extension="bam" type="galaxy.datatypes.binary:Bam"
    mimetype="application/octet-stream" display_in_upload="true">
    <display file="ucsc/bam.xml" />
</datatype>
```



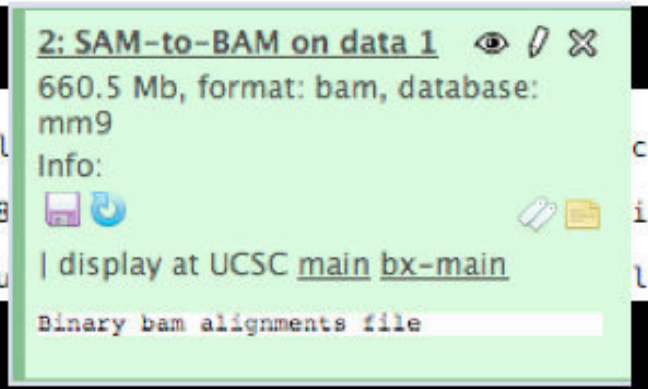
# BAM at UCSC


Home Genomes Blat Tables Gene Sorter PCR DNA Convert Ensembl PDF/PS Session Help
UCSC Genome Browser on Mouse July 2007 (NCBI37/mm9) Assembly
move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x
position/search chr12:57,795,963-57,815,592 gene jump clear size 19,630 bp. configure
Scale
5 kb
SAM-to-BAM on data 1
STS Markers
UCSC Genes Based on RefSeq, UniProt, GenBank, CCDS and Comparative Genomics
Pax9
Slc25a21
RefSeq Genes
Non-Mouse RefSeq Genes
Other RefSeq
Ensembl Gene Predictions
Ensembl Genes
Human Proteins Mapped by Chained tBLASTn
PAX9
SLC25A21
Mouse mRNAs from GenBank
AK132404
AK034985
X84000
BC005794
BC006930
AK167535
AK152379
AK045180
AK041694
AK036988
EU160236
BC057950
Mouse ESTs That Have Been Spliced
Spliced ESTs
30-Way Multiz Alignment & Conservation
Mammal Cons
Rat
Human
Orangutan
Dog
Horse
Opossum
Chicken
Stickleback
Simple Nucleotide Polymorphisms (dbSNP build 128)
SNPs (128)
Repeating Elements by RepeatMasker
RepeatMasker
move start
move end
Click on a feature for details. Click or drag in the base position track to zoom in.
Click gray/blue bars on left for track options and descriptions.
default tracks hide all manage custom tracks configure reverse refresh
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.
collapse all
expand all

# Dynamic External Display Application

```
<display id="ucsc_bam" version="1.0.0" name="display at UCSC">
    <!-- Load links from file: one line to one link -->
    <dynamic_links from_file="tool-data/shared/ucsc/ucsc_build_sites.txt" skip_startswith="#" id="0" name="0">

        <!-- Define parameters by column from file, allow splitting on builds -->
        <dynamic_param name="site_id" value="0"/>
        <dynamic_param name="ucsc_link" value="1"/>
        <dynamic_param name="builds" value="2" split="True" separator="," />

        <!-- Filter out some of the links based upon matching site_id to a Galaxy application configuration parameter and b
        <filter>${site_id in $APP.config.ucsc_display_sites}</filter>
        <filter>${dataset.dbkey in $builds}</filter>

        <!-- We define url and params as normal, but values defined in dynamic_param are available by specified name -->
        <url>${ucsc_link}db=${qp($bam_file.dbkey)}&amp;hgt.customText=${qp($track.url)}</url>
        <param type="data" name="bam_file" url="galaxy_${DATASET_HASH}.bam" strip_https="True" />
        <param type="data" name="bai_file" url="galaxy_${DATASET_HASH}.bam.bai" metadata="bam_index" strip_https="True" />
        <param type="template" name="track" viewable="True" strip_https="True">
            track type=bam name="${bam_file.name}" bigDataUrl=${bam_file.url} db=${bam_file.dbkey}
        </param>

    </dynamic_links>
</display>
```

```
#Harvested from http://genome.ucsc.edu/cgi-bin/das/dsn
main    http://genome.ucsc.edu/cgi-bin/hgTracks?    anoCar1,ce6,ce4,ce2,rn3,l
#Harvested from http://archaea.ucsc.edu/cgi-bin/das/dsn
archaea http://archaea.ucsc.edu/cgi-bin/hgTracks?   therSibi1,symbTher_IAM148
#Harvested from http://main.genome-browser.bx.psu.edu/cgi-bin/das/dsn
bx-main http://main.genome-browser.bx.psu.edu/cgi-bin/hgTracks? oviAri1,eriEu
```



# But I don't want to send my data to an external site

- Galaxy Trackster and Visual Analytics
  - Jeremy Goecks
  - 1:35 today

# Using Galaxy

- Use public Galaxy server: UseGalaxy.org
- Download Galaxy source: GetGalaxy.org
- Galaxy Wiki: GalaxyProject.org
- Screencasts: GalaxyCast.org
- Public Mailing Lists
  - galaxy-bugs@bx.psu.edu
  - galaxy-user@bx.psu.edu
  - galaxy-dev@bx.psu.edu

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