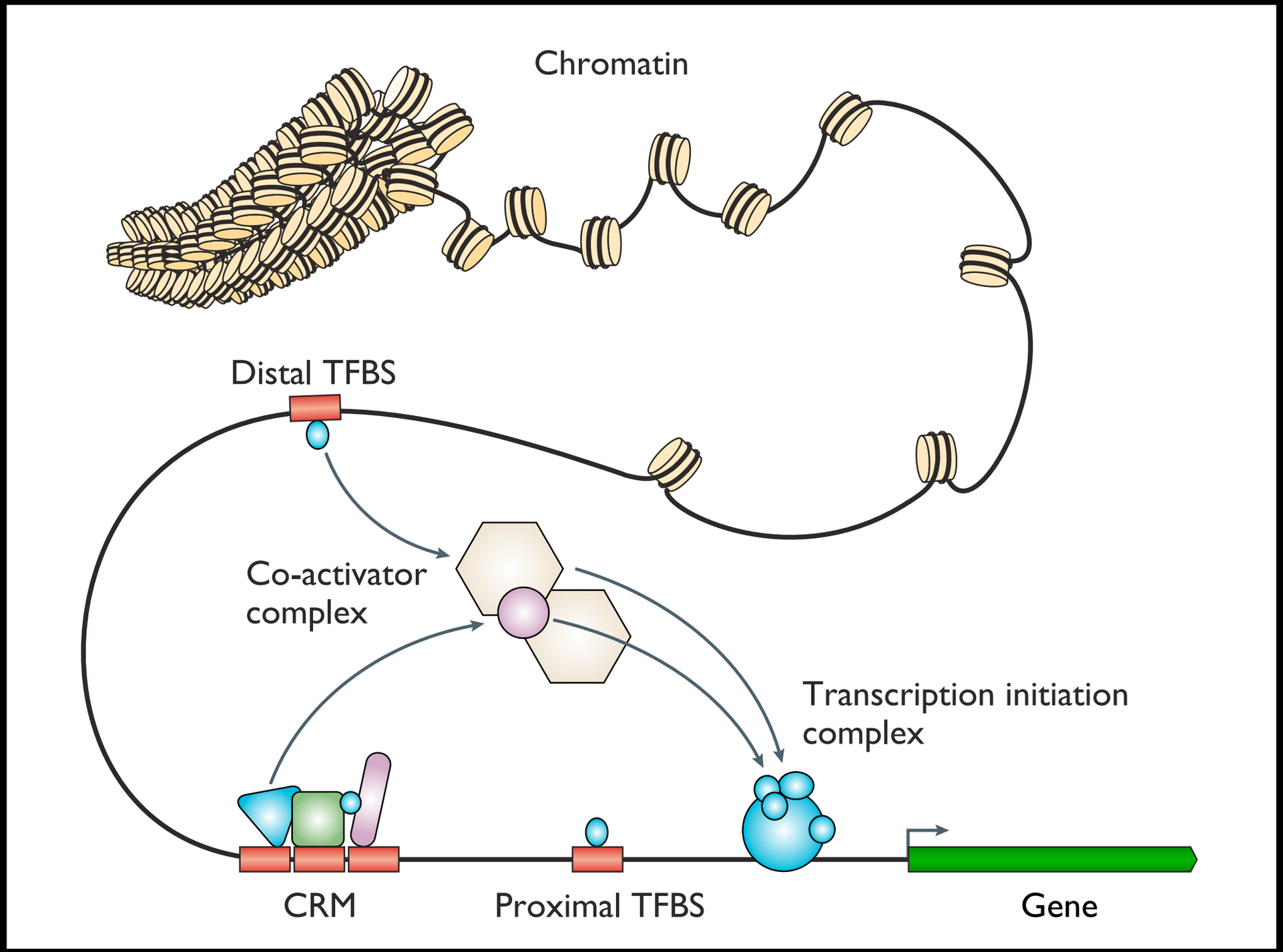
“Regulatory genomics”

Regulation of gene transcription



Wasserman and Sandelin. *Nature Review Genetics*. 2004.

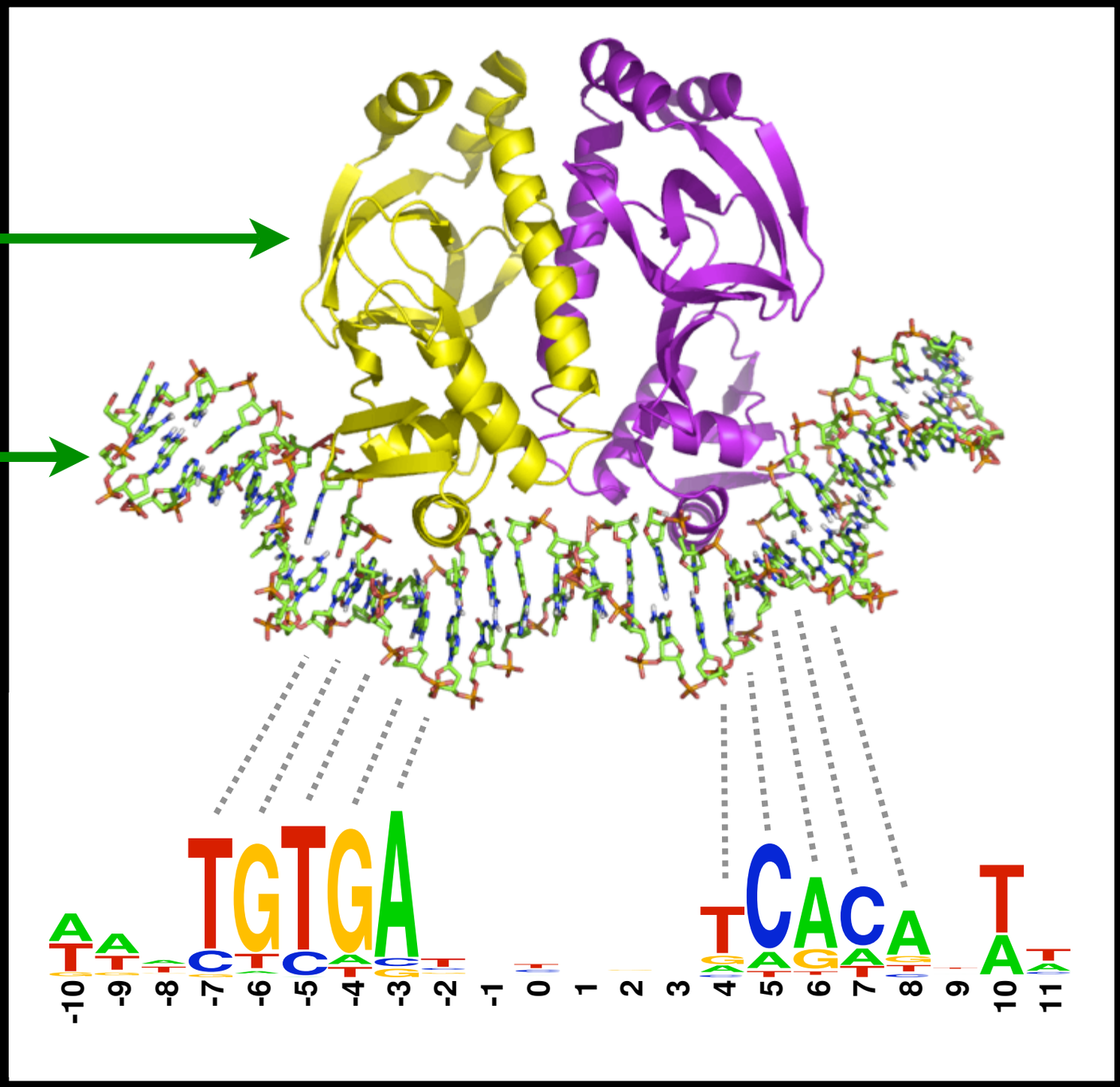
If only it were even *that* simple...

Sequence specific binding yields constraint

CAP protein (homodimer)

Bound DNA

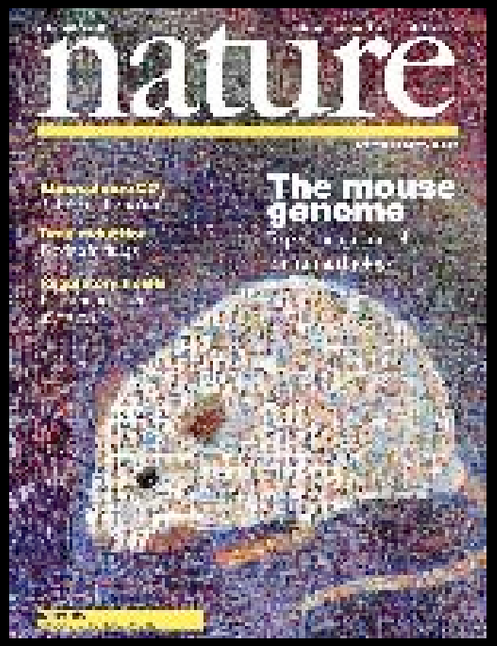
Motif from 59 bound sites



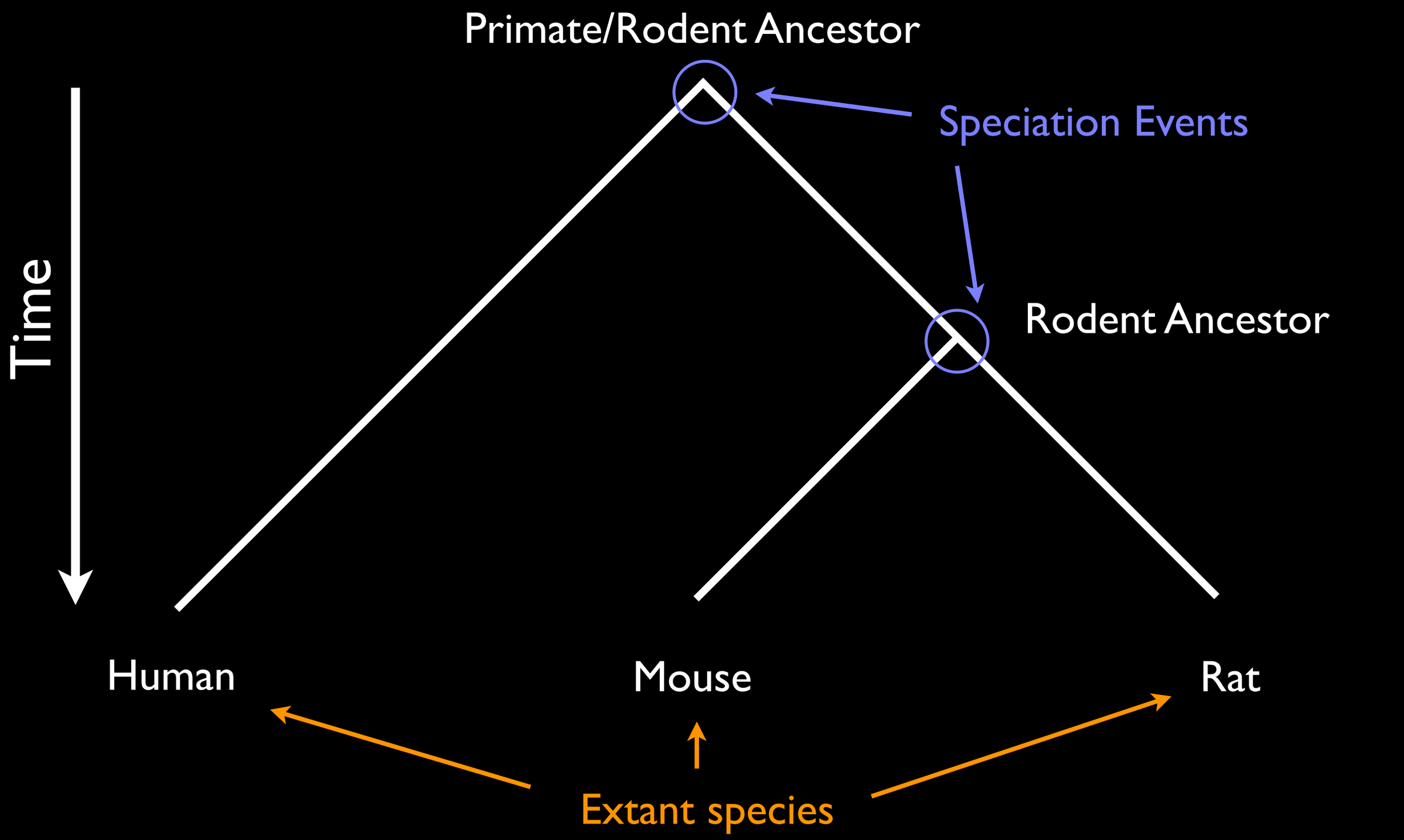
Structure: Schultz et al. *Science*. 1991, Logo software: Crooks et al. *Genome Research*. 2004

The genomic era...

Compârative



Evolution of functional elements



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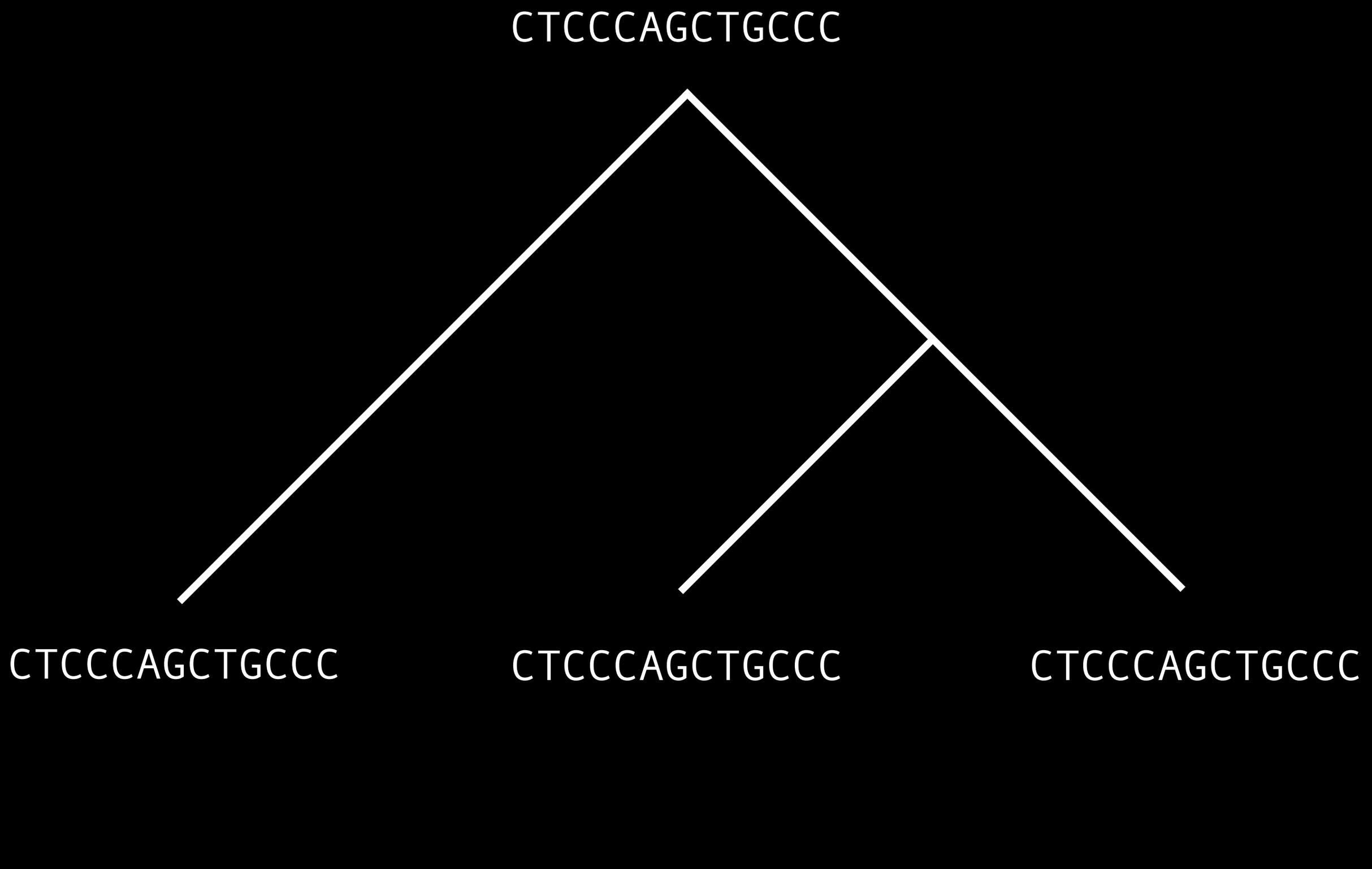
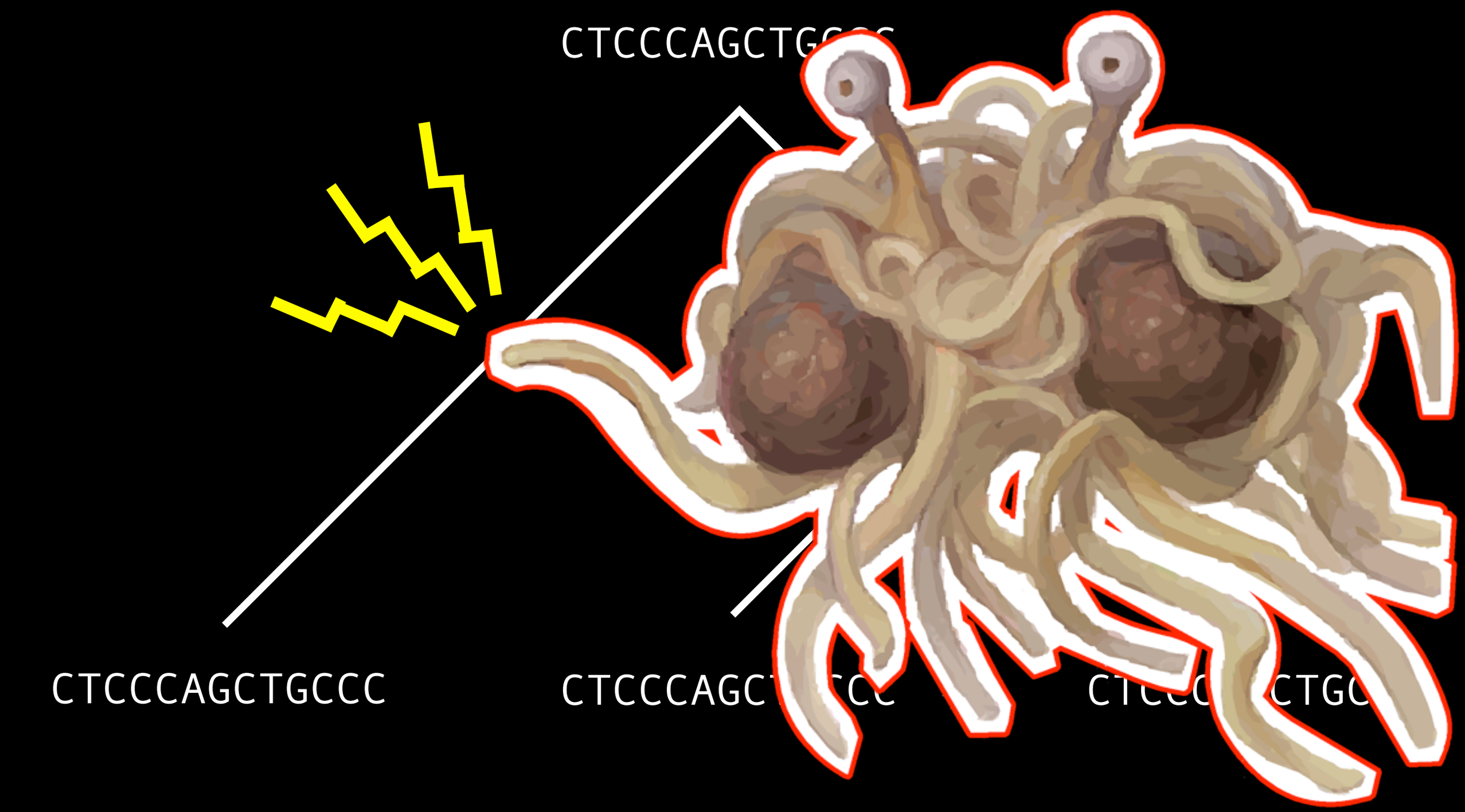


Evolution of functional elements



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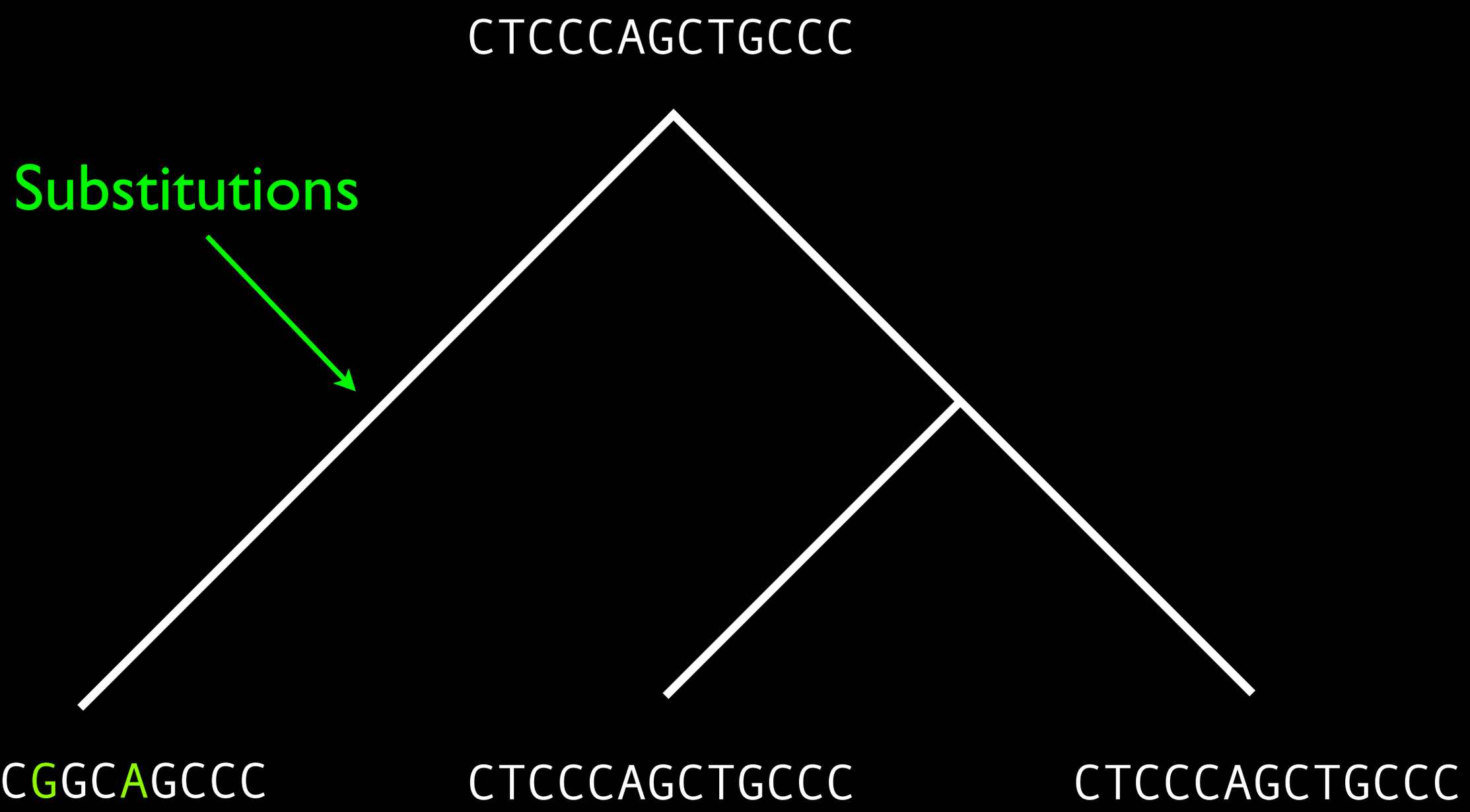

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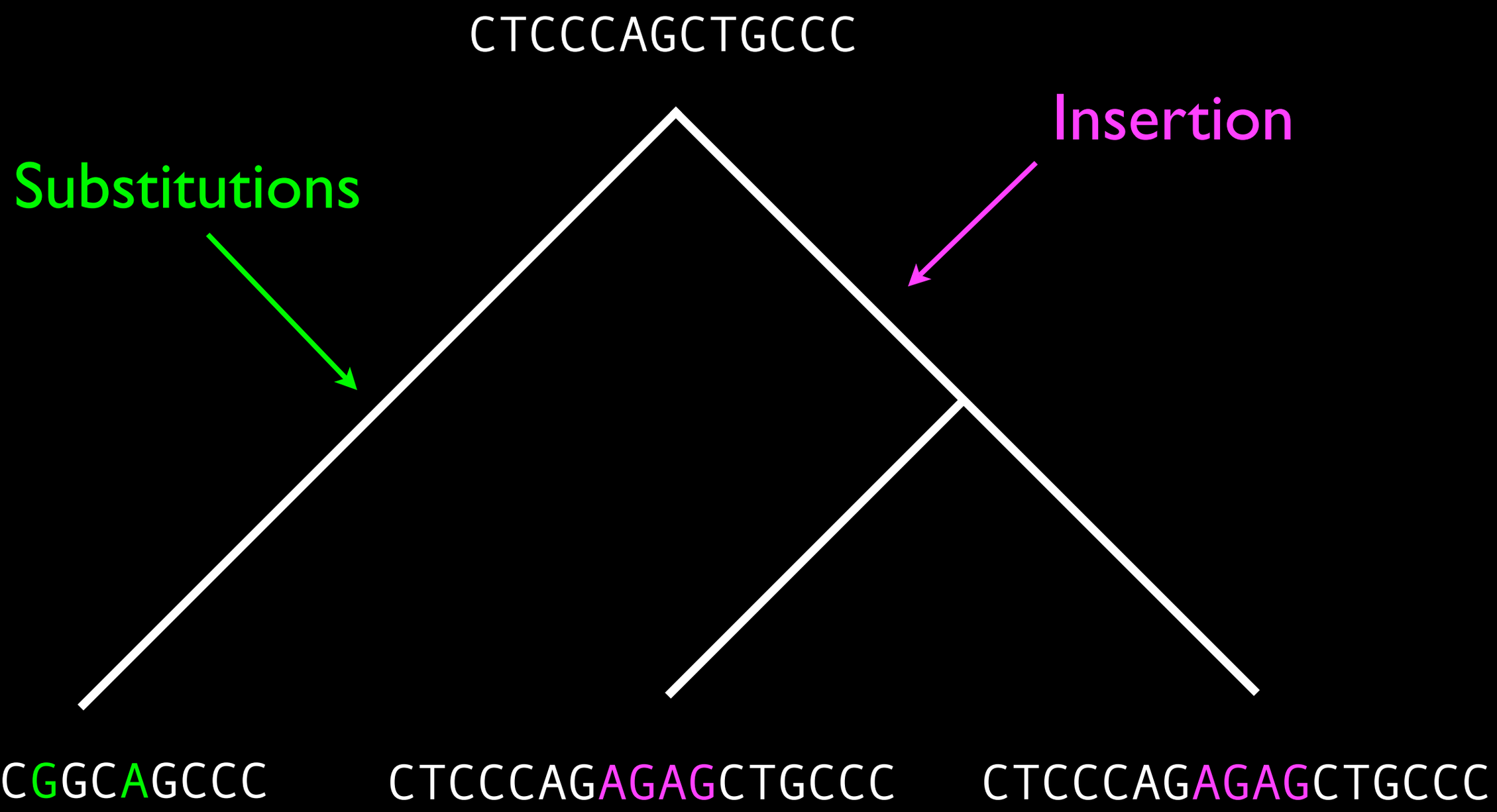

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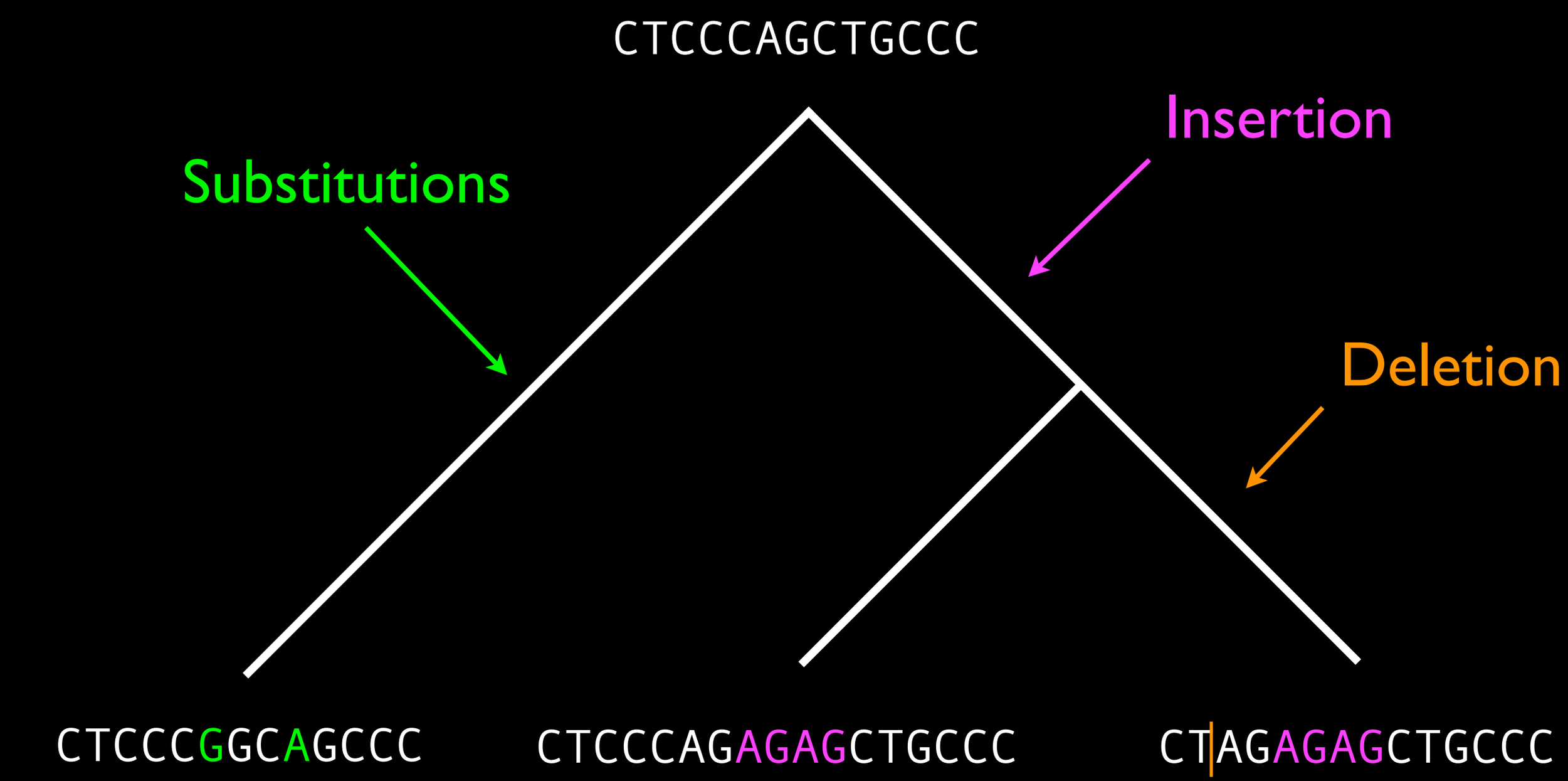
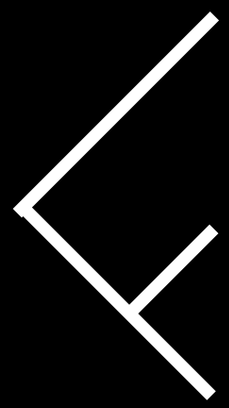


Sequence alignment



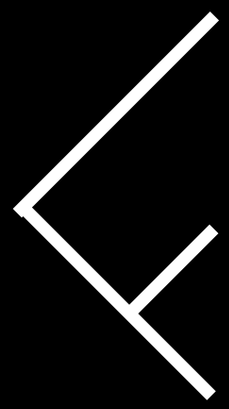
CTCCCGGCAGCCC

CTCCCAGAGAGCTGCCC

CTAGAGAGCTGCCC

Review: Batzoglou *Briefings in Bioinformatics* 2005

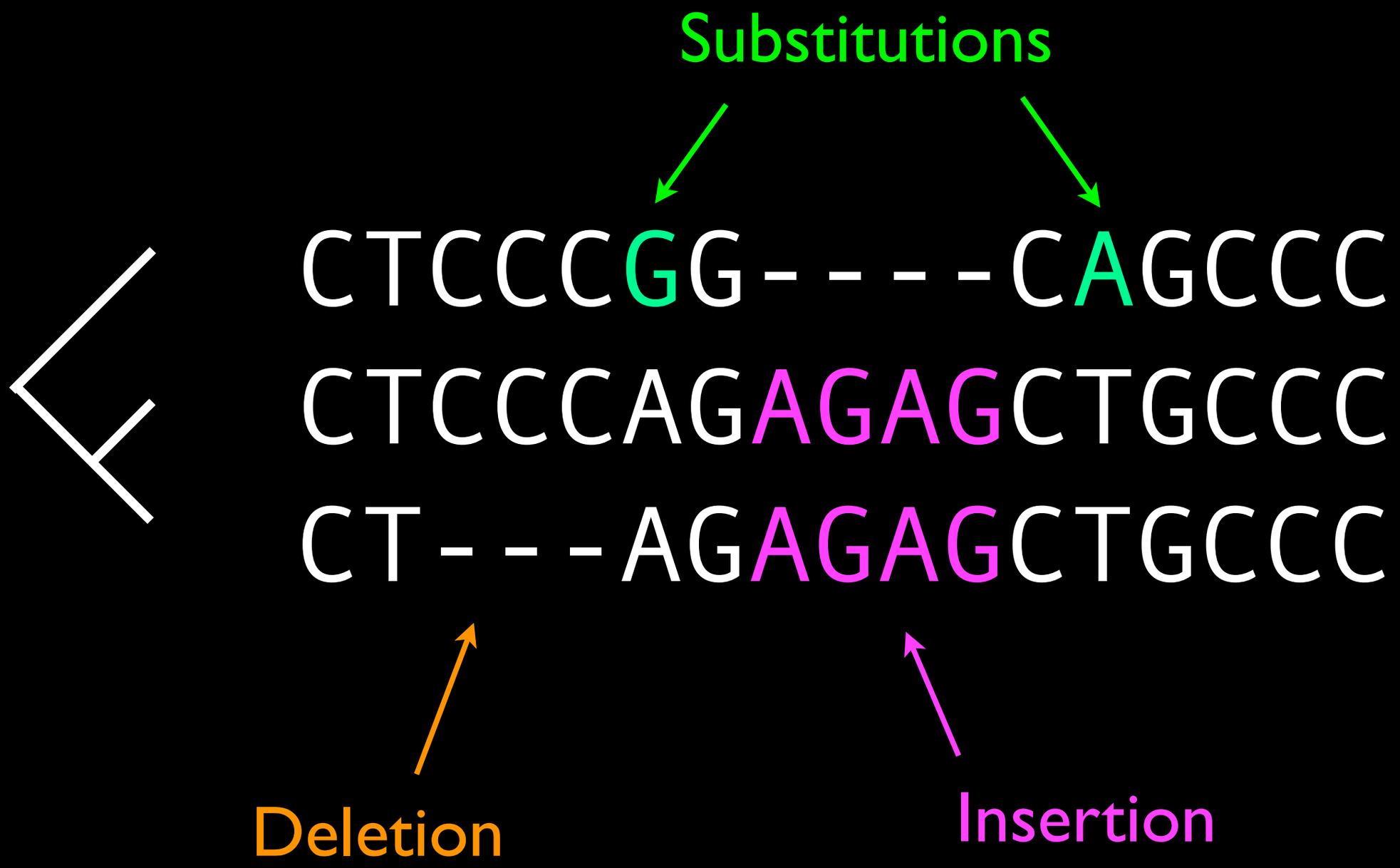
Sequence alignment



```
CTCCCGG----CAGCCC
CTCCCAGAGAGCTGCCC
CT---AGAGAGCTGCCC
```

Review: Batzoglou *Briefings in Bioinformatics* 2005

Sequence alignment



Review: Batzoglou *Briefings in Bioinformatics* 2005

Evolutionary constraint

- After speciation different changes occur in each lineage
- Events occur randomly, but selection determines if events are tolerated
- Constraint due to function may prevent certain changes, resulting in a different pattern of change in functional regions

ESPERR

(Evolutionary and Sequence Pattern Extraction through Reduced Representation)

ESPERR: Learning strong and weak signals in genomic sequence alignments to identify functional elements

James Taylor,[1] Svitlana Tyekucheva, David C. King, Ross C. Hardison, Webb Miller, and Francesca Chiaromonte[1]

Center for Comparative Genomics and Bioinformatics, The Pennsylvania State University, University Park, Pennsylvania 16802, USA

Genomic sequence signals—such as base composition, presence of particular motifs, or evolutionary constraint—have been used effectively to identify functional elements. However, approaches based only on specific signals known to correlate with function can be quite limiting. When training data are available, application of computational learning algorithms to multispecies alignments has the potential to capture broader and more informative sequence and evolutionary patterns that better characterize a class of elements. However, effective exploitation of patterns in multispecies alignments is impeded by the vast number of possible alignment columns and by a limited understanding of which particular strings of columns may characterize a given class. We have developed a computational method, called ESPERR (evolutionary and sequence pattern extraction through reduced representations), which uses training examples to learn encodings of multispecies alignments into reduced forms tailored for the prediction of chosen classes of functional elements. ESPERR produces a greatly improved Regulatory Potential score, which can discriminate regulatory regions from neutral sites with excellent accuracy (~94%). This score captures strong signals (GC content and conservation), as well as subtler signals (with small contributions from many different alignment patterns) that characterize the regulatory elements in our training set. ESPERR is also effective for predicting other classes of functional elements, as we show for DNaseI hypersensitive sites and highly conserved regions with developmental enhancer activity. Our software, training data, and genome-wide predictions are available from our Web site (http://www.bx.psu.edu/projects/esperr).

[Supplemental material is available online at www.genome.org.]

Identification of functional elements within genome sequences often relies on specific characteristic signals, typically based on known biological examples. For instance, prediction of protein-coding exons and genes relies on knowledge of the genetic code and splicing signals. These predictions can be improved by incorporating evolutionary information from orthologous regions of other species through sequence alignments. In particular, in most ubiquitous promoters, and (3) evolutionary patterns, particularly a high level of interspecies conservation, which should characterize functional regions under purifying selection.

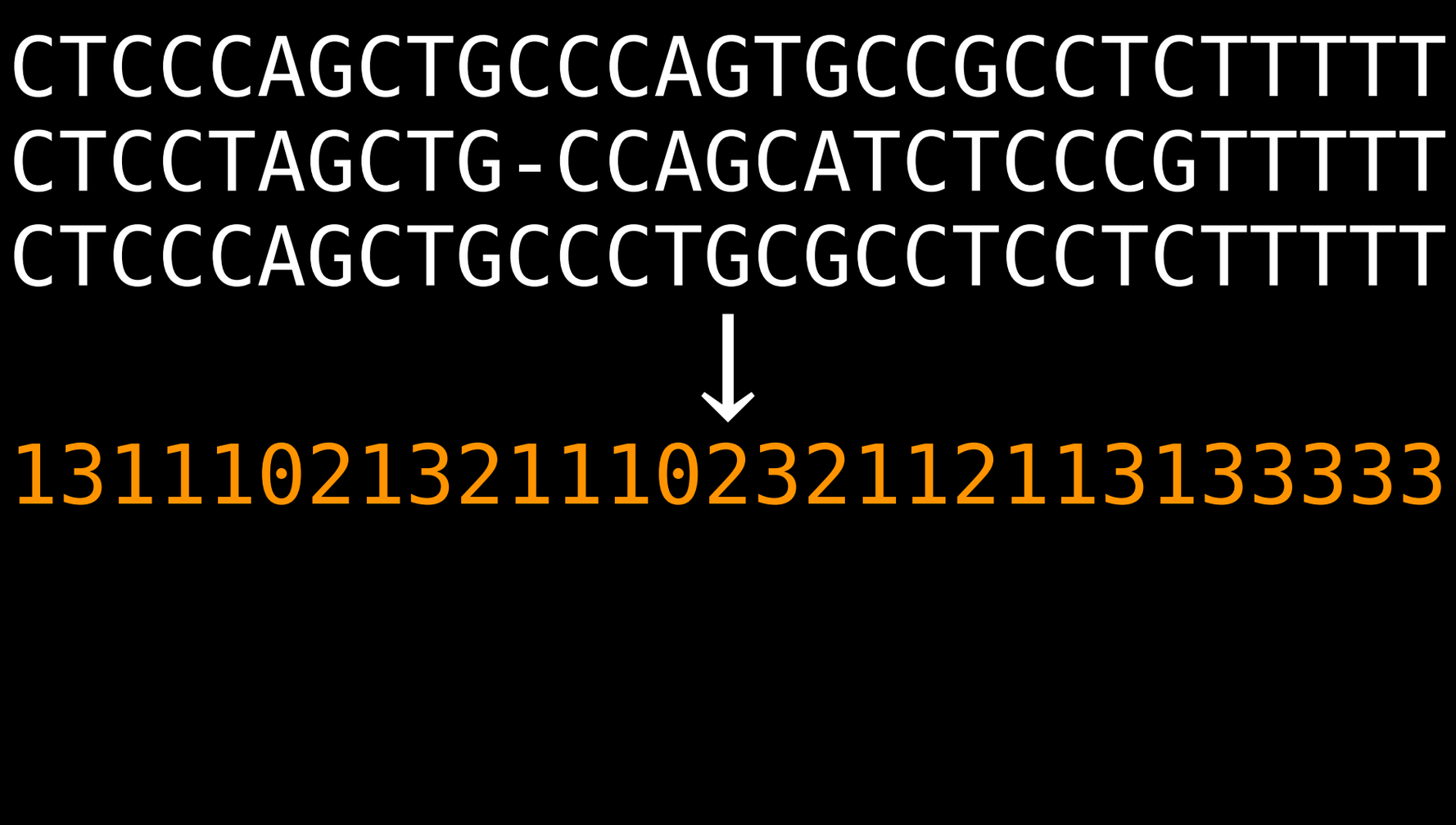
While each of these signals is associated with some *cis*-regulatory modules, all of them have limitations (Tompa et al. 2005). Motif-based approaches can have high specificity, particu-

A different approach

- Don’t assume a database of known binding motifs
- Don’t assume strict conservation of the important sequence signals
- Instead, use alignments of **validated examples** to learn sequence and evolutionary patterns that characterize a class of elements

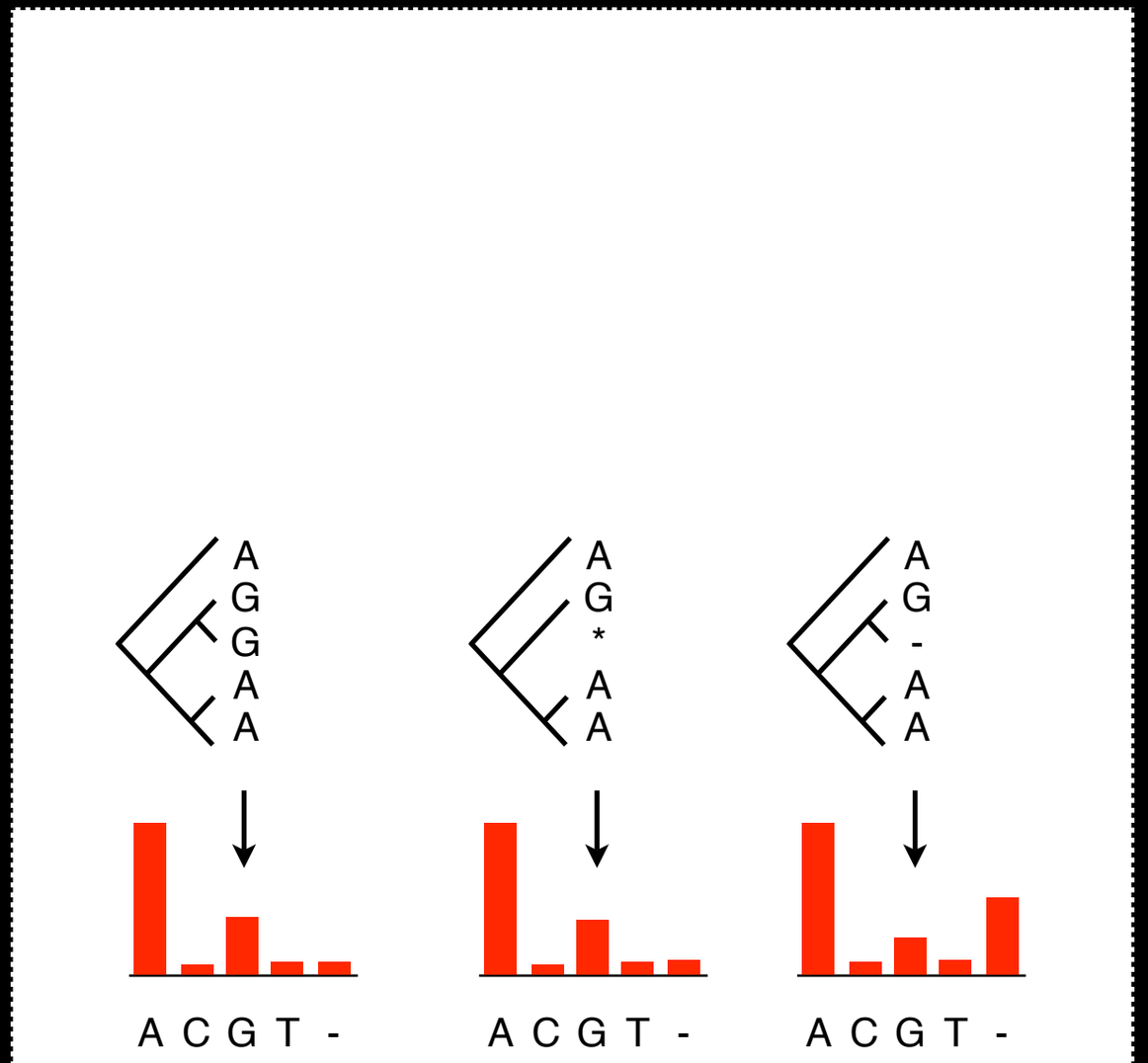
Objective

Find a mapping from alignment columns into a smaller alphabet that maintains the “right” information for some classification problem



Ancestral probability distribution

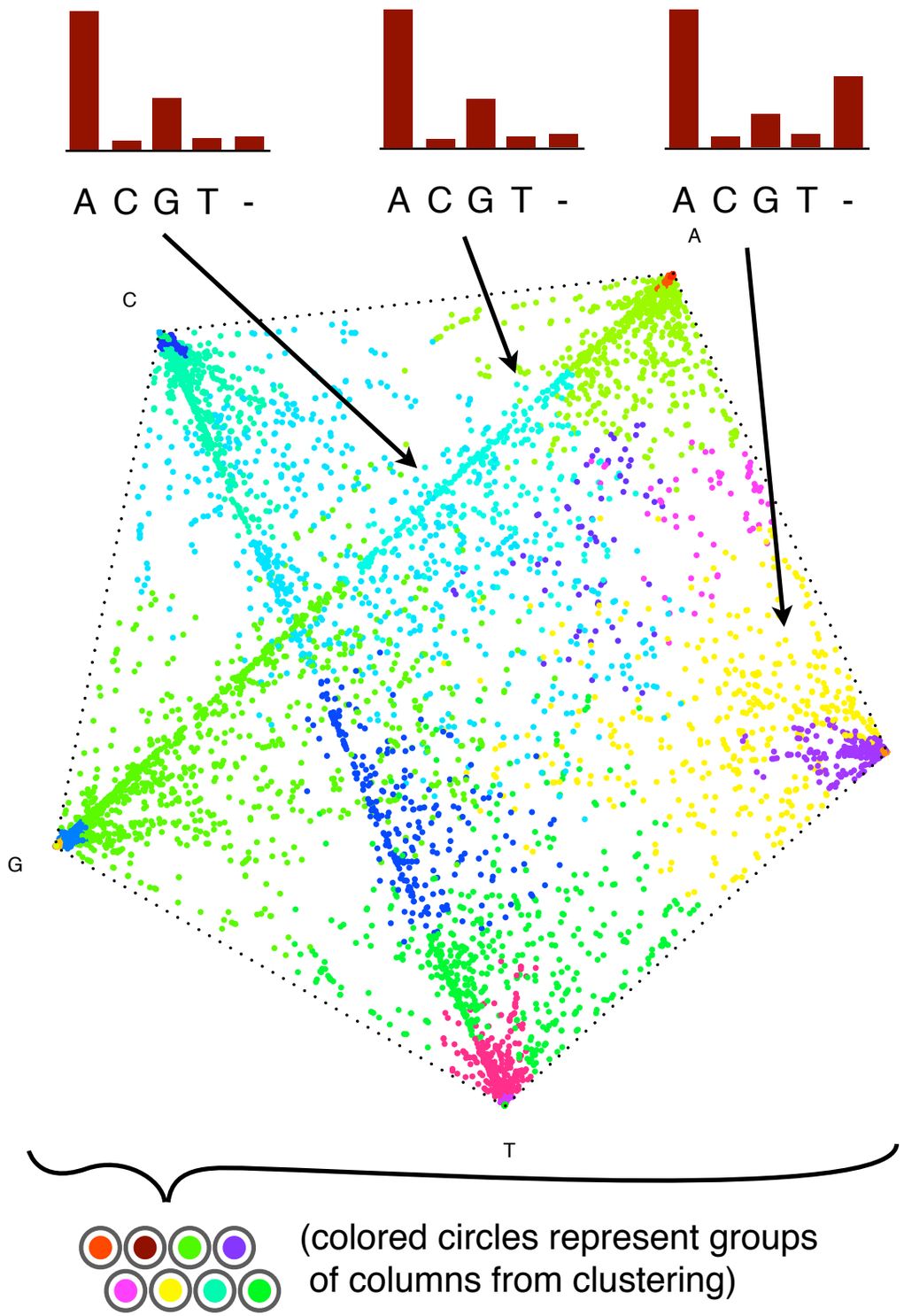
Map each possible column of a multiple alignment to a probability distribution of the nucleotide in that position in the common ancestor.



Clustering spatially and distributionally

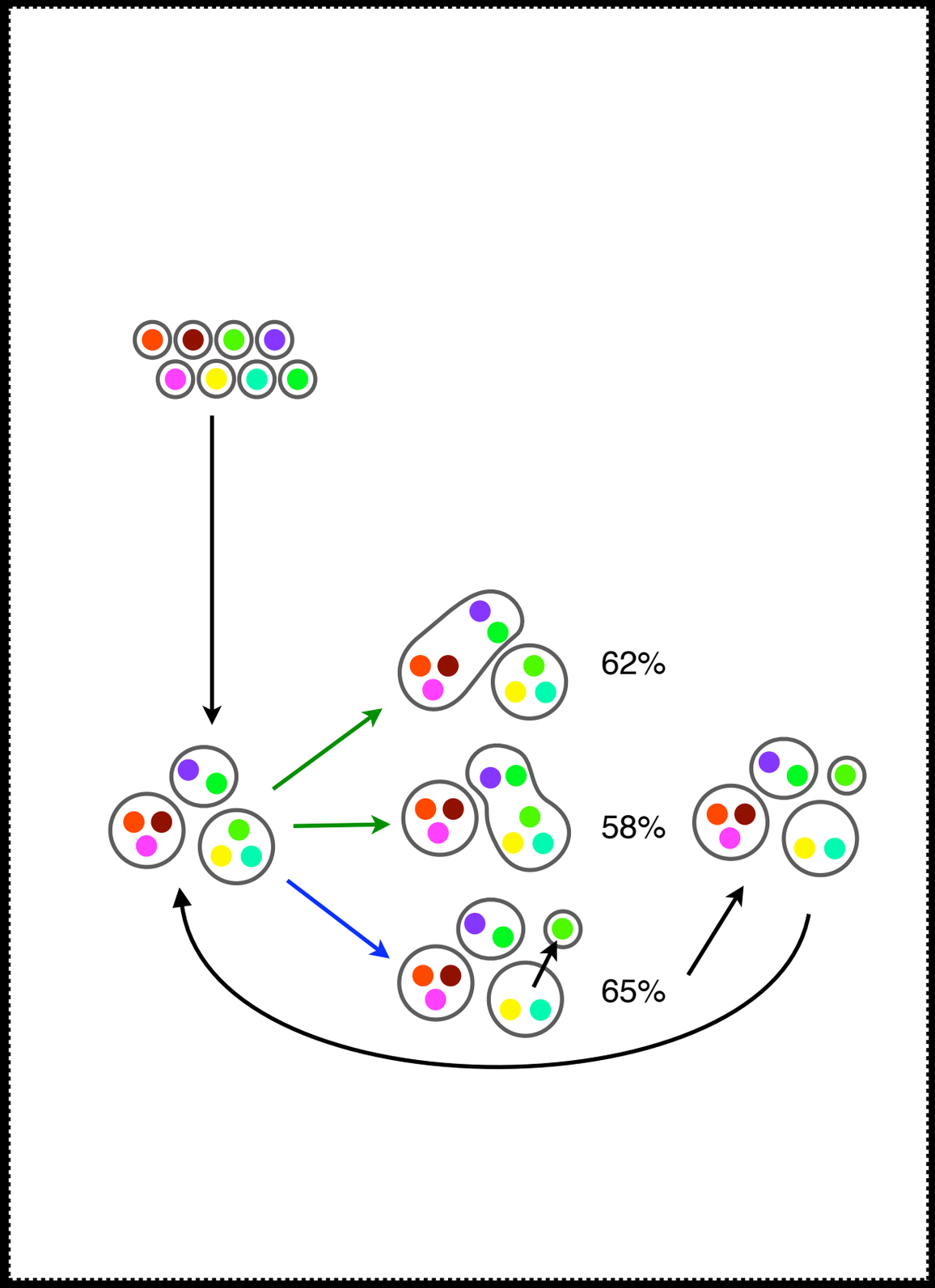
Consider the observed column frequencies as a discrete distribution over the probability simplex, and find a distribution on a smaller number of points that preserves:

- spatial structure: merge only neighboring points
- distributional structure: select mergers that maximize mutual information

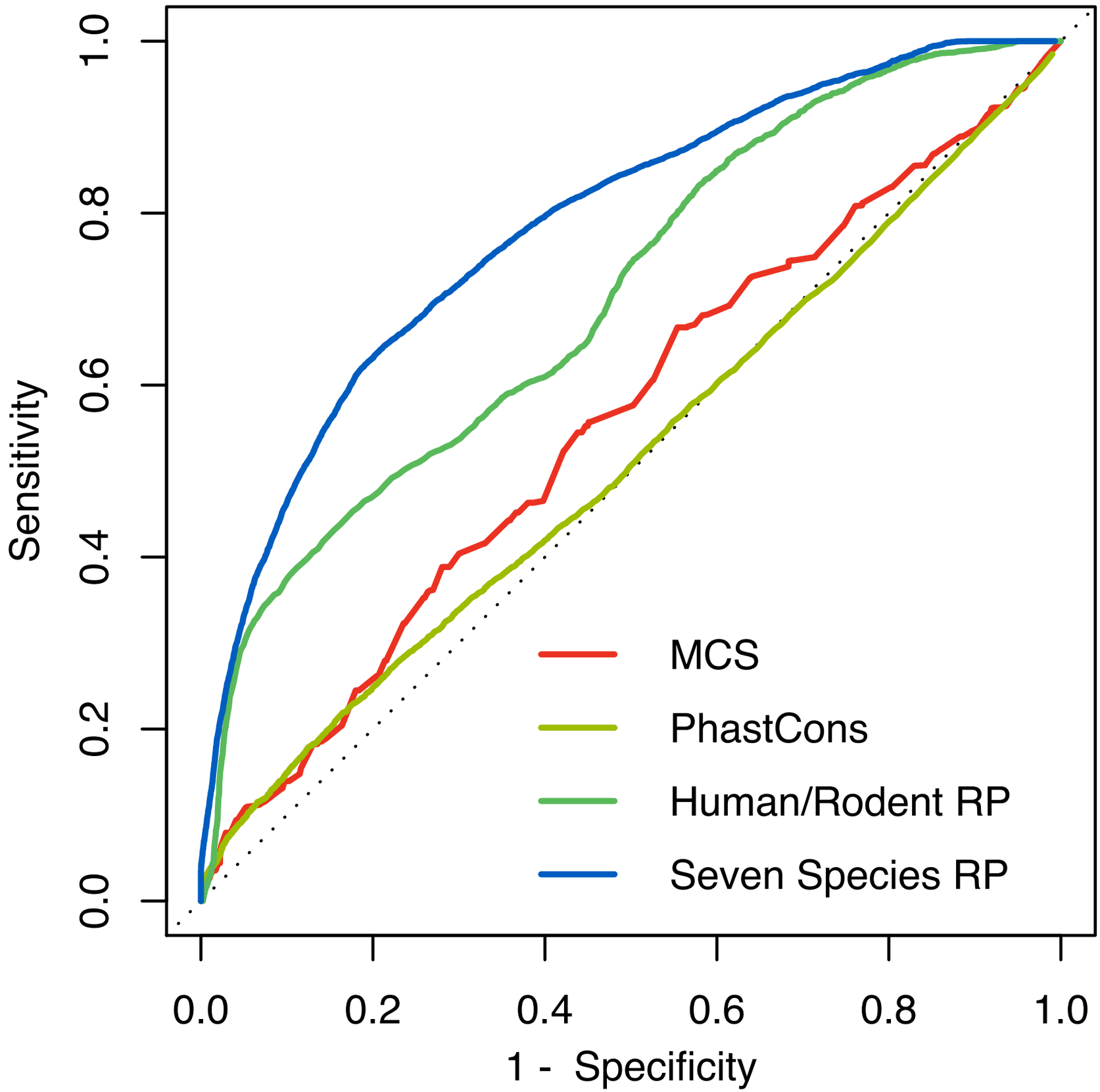


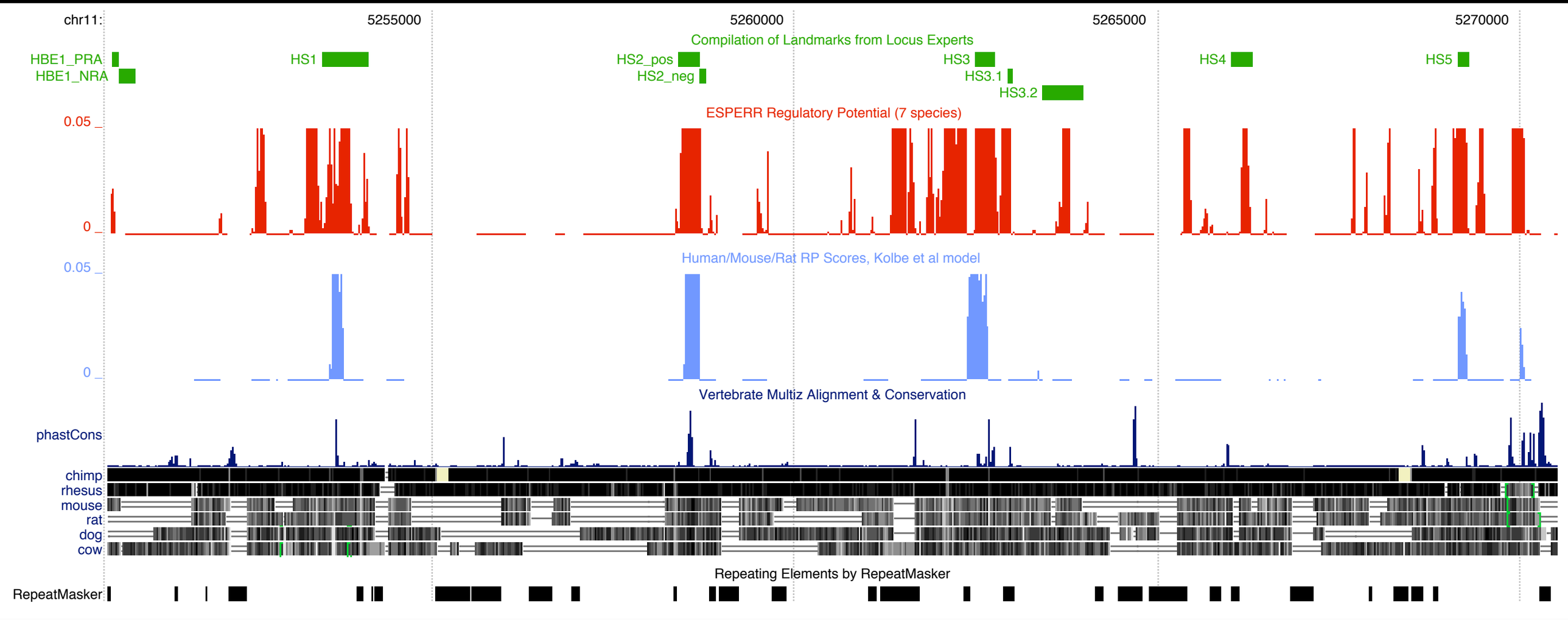
Searching for encodings

- Random / heuristic search through space of possible encodings



Some validation


Sensitivity
0.0
0.2
0.4
0.6
0.8
1.0
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0
MCS
PhastCons
Human/Rodent RP
Seven Species RP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5260000
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5270000
Compilation of Landmarks from Locus Experts
HBE1_PRA
HBE1_NRA
HS1
HS2_pos
HS2_neg
HS3
HS3.1
HS3.2
HS4
HS5
ESPERR Regulatory Potential (7 species)
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Human/Mouse/Rat RP Scores, Kolbe et al model
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mouse
rat
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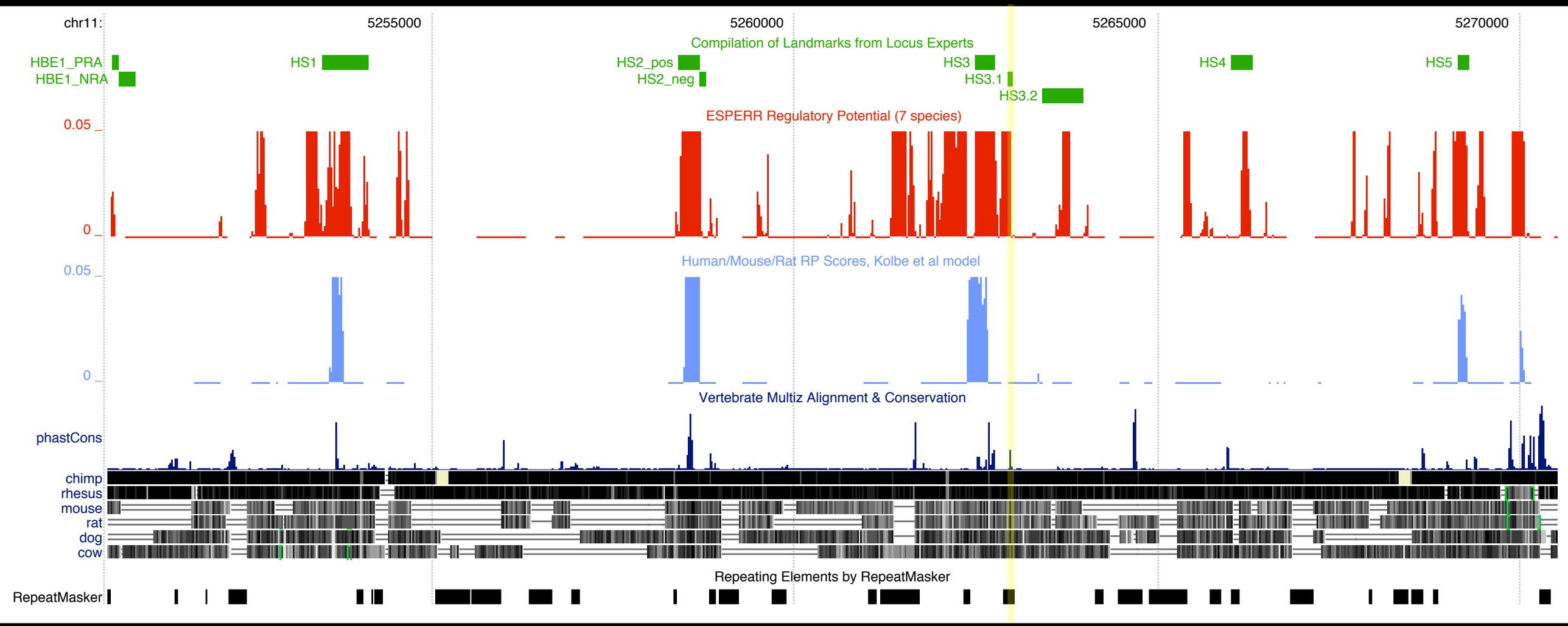
cow
Repeating Elements by RepeatMasker
RepeatMasker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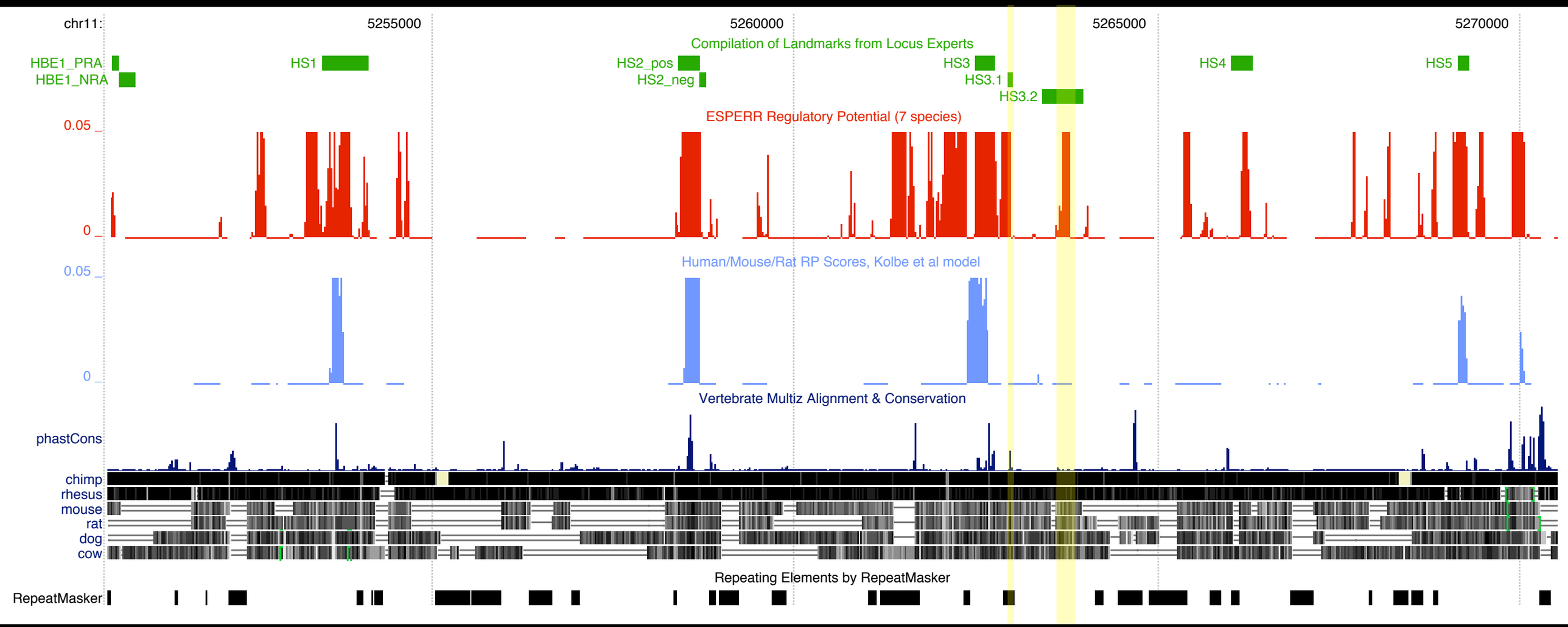
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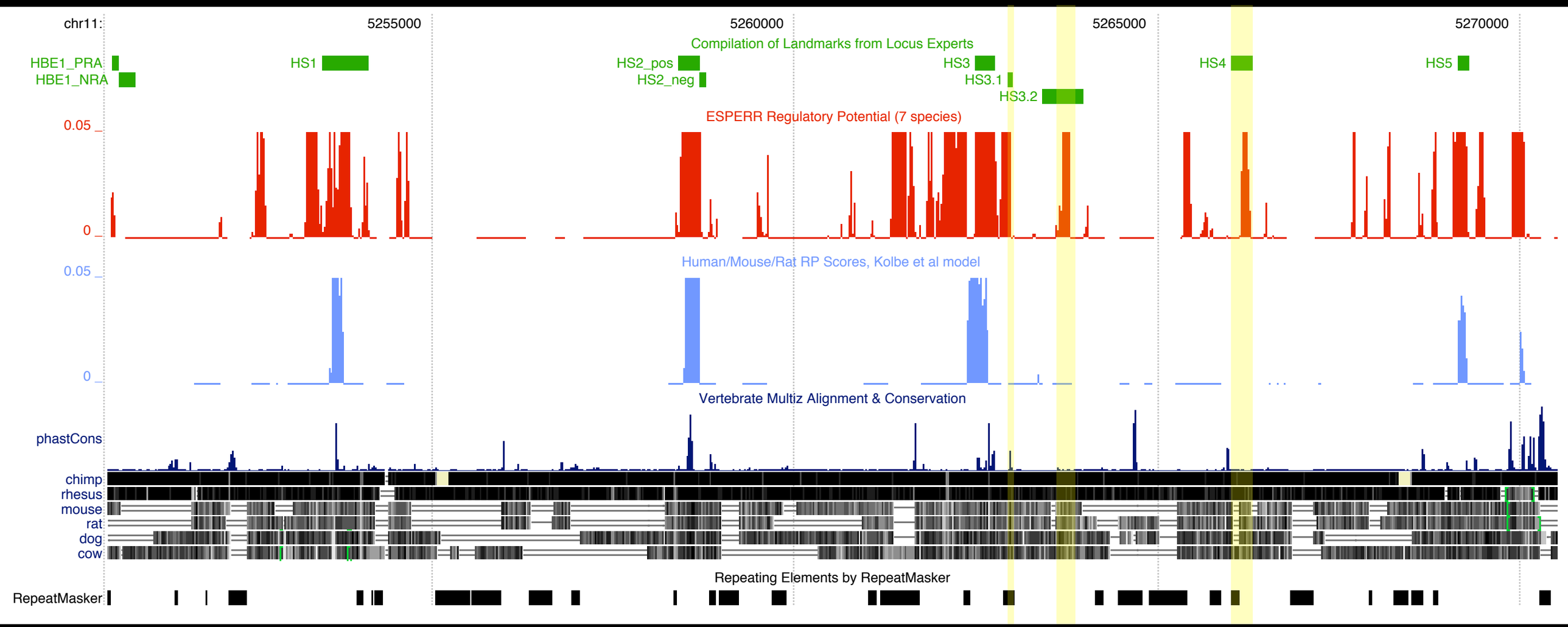
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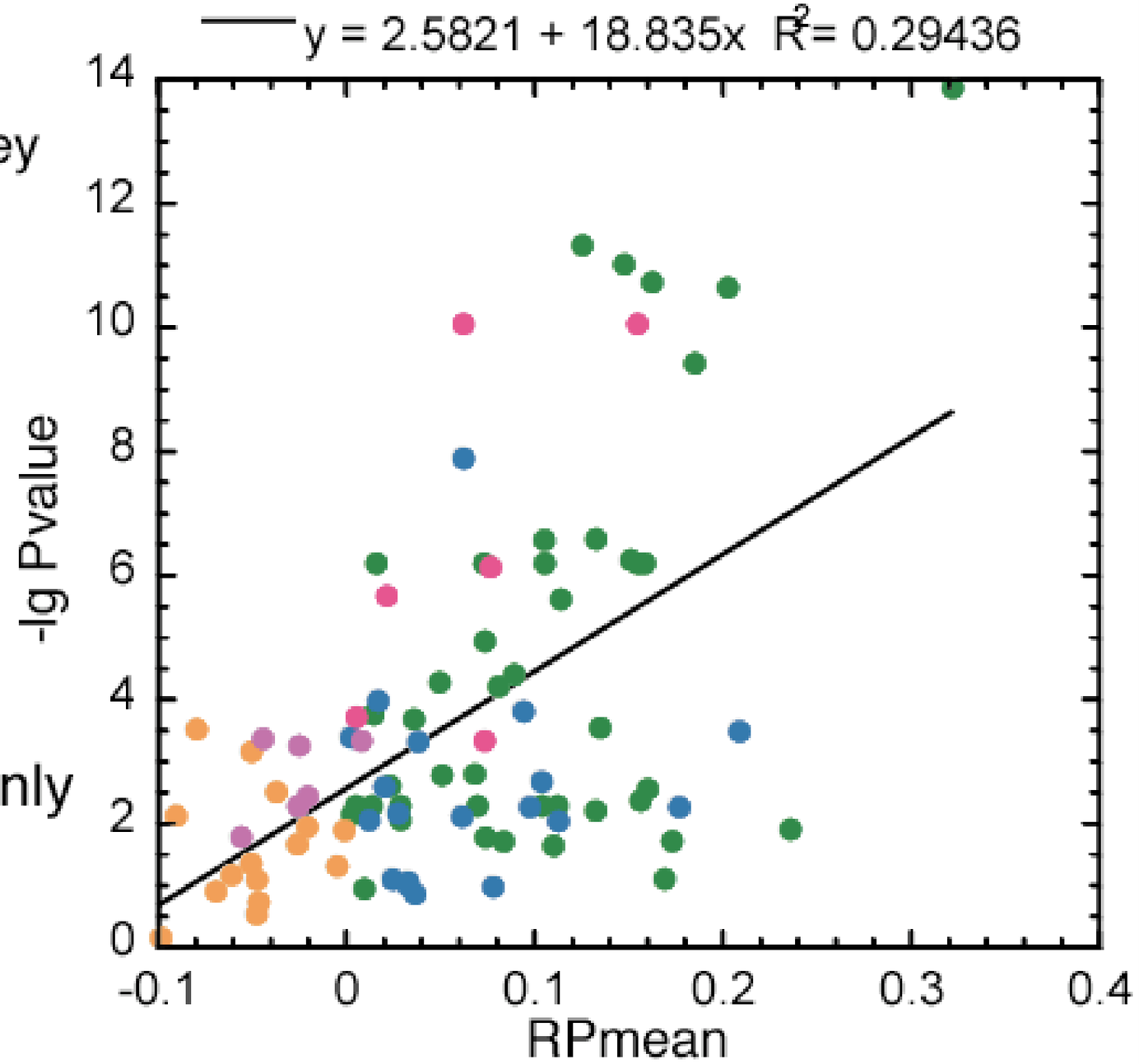
Enhancer activity correlates with RP score

Pvalue: derived from Mann-Whitney test for tested transient or stable (min for 7 days) assays.

- preCRMcc
- preCRMcnc
- preNeutral
- NegRPw/ccGATA1
- PosiRPw/GATA1mouseonly



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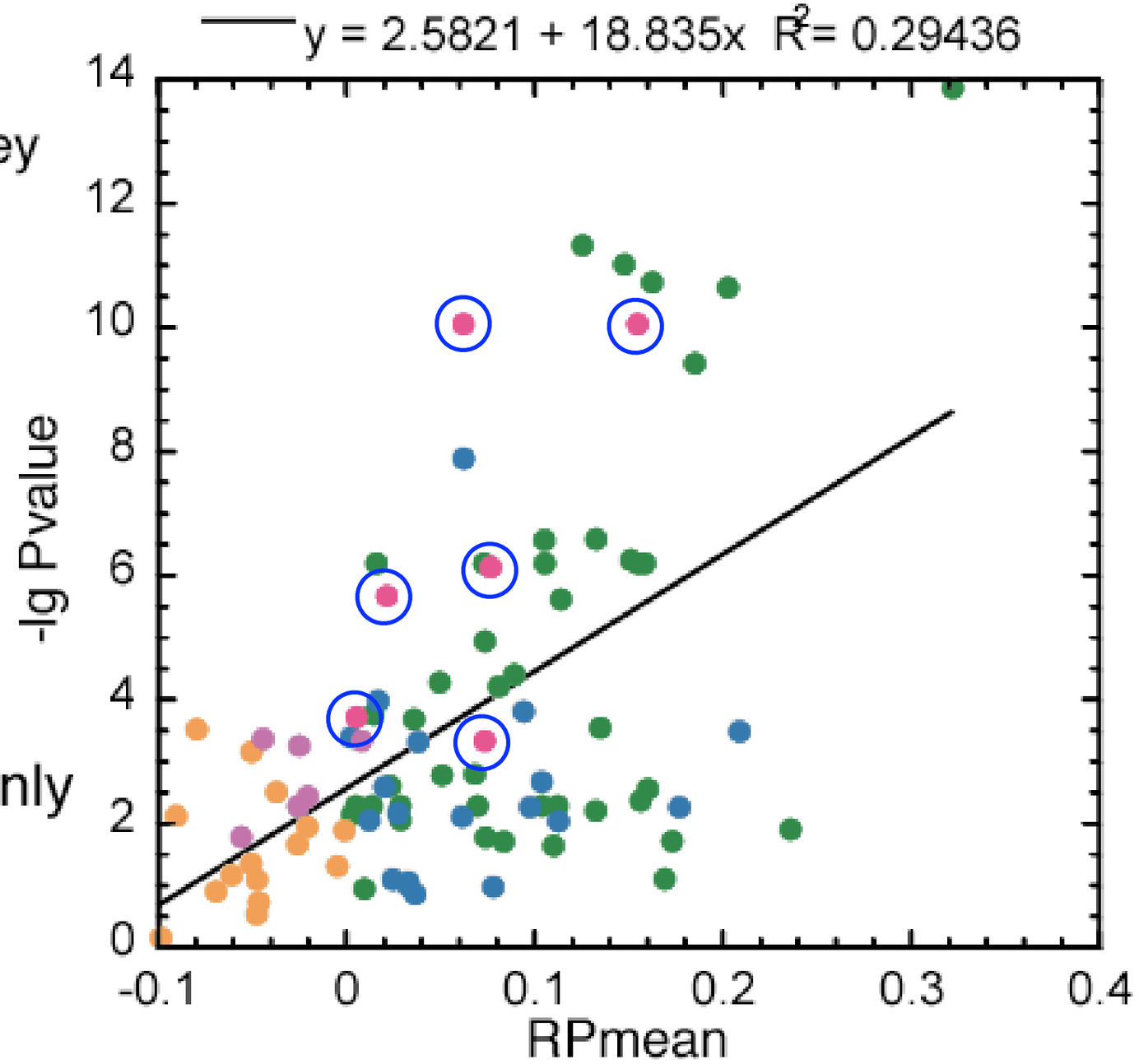
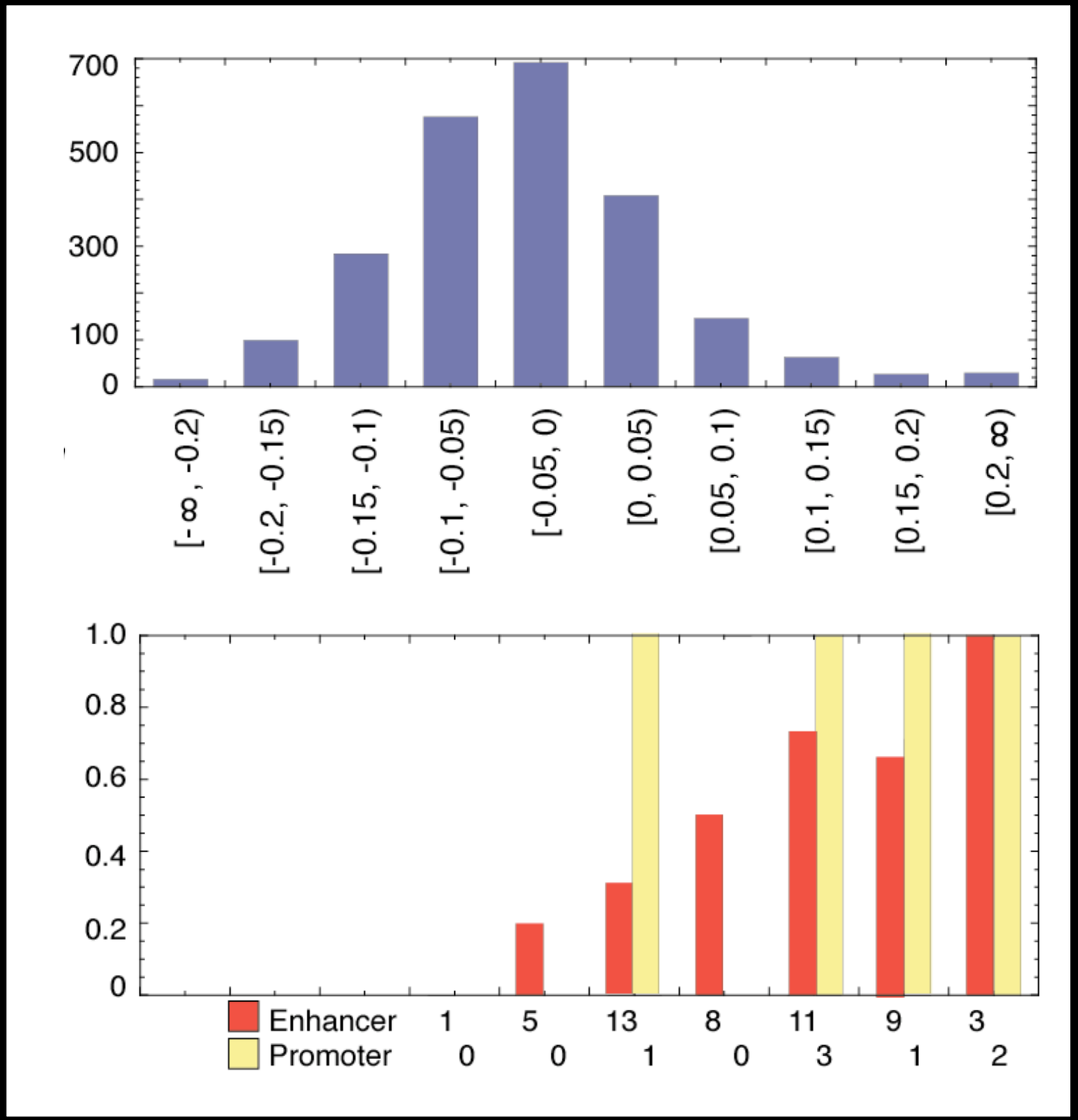


Higher RP scores yield better validation rates



RP distribution across loci of interest

Validation rate of test loci falling in the RP score bin

Galaxy

(http://g2.bx.psu.edu)

Biological data explosion

- Genome sequences and alignments
- Large scale genotyping and resequencing
- Gene expression and other high throughput functional assays
- “Meta genomics”

Genomic data management successes

- Data warehouses and query interfaces
  - NCBI
  - UCSC Table Browser
  - Biomart
- Data visualization
  - UCSC Genome browser
  - Ensembl
  - GBrowse

Many computational methods

- An enormous number of methods / application note papers are being published
  - Usually with some kind of working implementation!
- But what about interfaces? Are these methods accessible to data producers?

Developing interfaces: Scenario 1

- Developer simply provides scripts or programs with a (usually non-standard) command line interface
- Experimentalist hires a grad student who hacks it together with Excel / some perl script / manual labor
- ...or just re-implements the method from scratch with all new bugs

Developing interfaces: Scenario 2

- Developer builds an interface to their tool that is usable without computational expertise
    - Requires more maintenance, more work to move to new platforms
    - Most of the effort in building interfaces is highly repetitive, substantial waste of developers time
    - Even with a good interface, the tool is not integrated with other tools and datasources, still wasting effort moving data around manually, converting, et cetera.

Integration

- The primary problem is how do we integrate tools and datasources
  - Give tools a usable and *common* interface
  - Facilitate building complex analysis that use multiple data sources and tools
  - Make it easy to work with large datasets and long running analysis

Galaxy

What is **Galaxy**?

- An open-source framework for integrating various computational tools and databases into a cohesive workspace
- A web-based service we (Penn State) provide, integrating many popular tools and resources for comparative genomics
- A completely self-contained Python application for building your own **Galaxy** style sites

Galaxy's web user interface

Tools

Get Data
Get ENCODE Data
ENCODE Tools
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
EMBOSS
HYPHY

Galaxy at ISMB/ECCB2007 in Vienna (July 21-25)

- July 19 10:00am | *The Galaxy Framework for Computational Biology Tool Integration*
- July 25 10:15am Room L | *GALAXY: a simple web application for the analysis of enormous datasets*
- July 25 11:10am Room L | *Effortless integration of tools into simple, scalable, multiuser, pythonic framework*

Two Galaxy sessions at the 57th Annual Meeting of the American Society for Human Genetics (October 23-27)!
The first session will be designed for biomedical researchers and will concentrate on analyses of genomic and disease association data. The second session will be organized as a hands-on software development workshop for bioinformaticians and computational biologists. For more information click here.

Unsequenced Genomes of the World | July 2007

Giraffe (Giraffa camelopardalis) | Eastern Cape, SAR

Why use Galaxy? It is not a database or a browser. It is an analysis medium that enables multiple tools to be applied to existing data in a simple unified way. Click here to learn more. Don't like to read manuals? Then watch a movie (QuickTime required). Here are some reasons why users love it:

History (options)

refresh | collapse all

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Operate on Genomic Intervals

- Intersect the intervals of two queries
- Subtract the intervals of two queries
- Merge the overlapping intervals of a query
- Concatenate two queries into one query
- Base Coverage of all intervals
- Coverage of a set of intervals on second set of intervals
- Complement intervals of a query
- Cluster the intervals of a query
- Join the intervals of two queries side-by-side
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Upload File

File: Browse...

URL/Text:

Here you may specify a list of URLs (one per line) or paste the contents of a file.

Convert spaces to tabs: Yes

Use this option if you are entering intervals by hand.

File Format: Auto-detect

BED or Interval? See help below

Genome: unspecified (?)

Execute

Auto-detect

The system will attempt to detect AXT, FASTA, Gff, HTML, LAV, Maf, Wiggle, BED and Interval (BED with headers) formats. Other formats will be set to generic text files. If your file is not detected properly as one of the known formats, it most likely means that it has some format problems (e.g., different number of columns on different rows). You can still coerce the system to set your data to the format you think it should be (please send us a note if you see a case when a valid format is not detected).

BED

- Tab delimited format (tabular)
- Does not require header line
- Contains 3 required fields:
  - chrom - The name of the chromosome (e.g. chr3, chrY, chr2_random) or contig (e.g. ctgY1).
  - chromStart - The starting position of the feature in the chromosome or contig. The first base in a chromosome is numbered 0.
  - chromEnd - The ending position of the feature in the chromosome or contig. The chromEnd base is not included in the display of the feature. For example, the first 100 bases of a chromosome are defined as chromStart=0, chromEnd=100,

History (options)

refresh | collapse all

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

Tools
Get Data
- Upload File from your computer
- UCSC Main table browser
- UCSC Archaea table browser
- Get Microbial Data
- BioMart Central server

Get ENCODE Data
ENCODE Tools
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
EMBOSS
HYPHY

Upload File

File: Browse...

URL/Text:

```
chr1  147971133  148471133
ENr231
chr2  51570355  52070355
ENr112
chr2  118010803  118510803
ENr121
```

Here you may specify a list of URLs (one per line) or paste the contents of a file.

Convert spaces to tabs: Yes

Use this option if you are entering intervals by hand.

File Format: Auto-detect

BED or Interval? See help below

Genome: Human May 2004 (hg17)

Execute

History (options)
refresh | collapse all
Your history is empty. Click 'Get Data' on the left pane to start

Auto-detect

The system will attempt to detect AXT, FASTA, Gff, HTML, LAV, Maf, Wiggle, BED and Interval (BED with headers) formats. Other formats will be set to generic text files. If your file is not detected properly as one of the known formats, it most likely means that it has some format problems (e.g., different number of columns on different rows). You can still coerce the system to set your data to the format you think it should be (please send us a note if you see a case when a valid format is not detected).

BED

- Tab delimited format (tabular)
- Does not require header line
- Contains 3 required fields:
  - chrom - The name of the chromosome (e.g. chr3, chrY, chr2_random) or contig (e.g. ctgY1).
  - chromStart - The starting position of the feature in the chromosome or contig. The first base in a chromosome is numbered 0.
  - chromEnd - The ending position of the feature in the chromosome or contig. The chromEnd base is not included in the display of the feature. For example, the first 100 bases of a chromosome are defined as chromStart=0, chromEnd=100,

The following job has been succesfully added to the queue:

3: Pasted Entry

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 succesfully or 'error' if problems were encountered.

Tools

Get Data
- Upload File from your computer
- UCSC Main table browser
- UCSC Archaea table browser
- Get Microbial Data
- BioMart Central server

Get ENCODE Data
ENCODE Tools
Text Manipulation
Filter and Sort
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Convert Formats
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Fetch Sequences
Fetch Alignments
Get Genomic Scores
Operate on Genomic Intervals
Statistics
Graph/Display Data
EMBOSS
HYPHY

The following job has been succesfully added to the queue:

3: Pasted Entry

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 succesfully or 'error' if problems were encountered.

History (options)

refresh | collapse all

3: Pasted Entry

Galaxy

Info: report bugs | wiki | screencasts Account: create | login

Tools

Get Data
- Upload File from your computer
- UCSC Main table browser
- UCSC Archaea table browser
- Get Microbial Data
- BioMart Central server

Get ENCODE Data
ENCODE Tools
Text Manipulation
Filter and Sort
Join, Subtract and Group
Convert Formats
Extract Features
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Get Genomic Scores
Operate on Genomic Intervals
Statistics
Graph/Display Data
EMBOSS
HYPHY

The following job has been succesfully added to the queue:

3: Pasted Entry

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 succesfully or 'error' if problems were encountered.

History (options)

refresh | collapse all

3: Pasted Entry

44 regions, format: bed, database: hg17
Info: pasted entry
save | display at UCSC main test

1	2	3	4
chr1	147971133	148471133	ENr231
chr2	51570355	52070355	ENr112
chr2	118010803	118510803	ENr121
chr2	220102850	220602850	ENr331
chr2	234273824	234773888	ENr131
chr4	118604258	119104258	ENr113

Tools

Get Data
- Upload File from your computer
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- UCSC Archaea table browser
- Get Microbial Data
- BioMart Central server

Get ENCODE Data
ENCODE Tools
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
EMBOSS
HYPHY

The following job has been succesfully added to the queue:

3: Pasted Entry

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 succesfully or 'error' if problems were encountered.

History (options)

refresh | collapse all

3: Pasted Entry

Galaxy

Info: report bugs | wiki | screencasts Account: create | login

Tools

Get Data
- Upload File from your computer
- UCSC Main table browser
- UCSC Archaea table browser
- Get Microbial Data
- BioMart Central server

Get ENCODE Data
ENCODE Tools
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
EMBOSS
HYPHY

The following job has been succesfully added to the queue:

4: UCSC Main

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 succesfully or 'error' if problems were encountered.

History (options)

refreshing in 9 sec | collapse all

4: UCSC Main

3: Pasted Entry

Tools

Get Data
Get ENCODE Data
ENCODE Tools
Text Manipulation
Filter and Sort
Join, Subtract and Group
Convert Formats
Extract Features
Fetch Sequences
Fetch Alignments
Get Genomic Scores
Operate on Genomic Intervals

- Intersect the intervals of two queries
- Subtract the intervals of two queries
- Merge the overlapping intervals of a query
- Concatenate two queries into one query
- Base Coverage of all intervals
- Coverage of a set of intervals on second set of intervals
- Complement intervals of a query
- Cluster the intervals of a query
- Join the intervals of two queries side-by-side
- Get flanks returns flanking region/s for every gene

Statistics
Graph/Display Data
EMBOSS
HYPHY

The following job has been succesfully added to the queue:

5: Intersect on data 3 and data 4

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 succesfully or 'error' if problems were encountered.

History (options)

refreshing in 8 sec | collapse all

5: Intersect on data 3 and data 4
4: UCSC Main on Human: knownGene (genome)
3: Pasted Entry

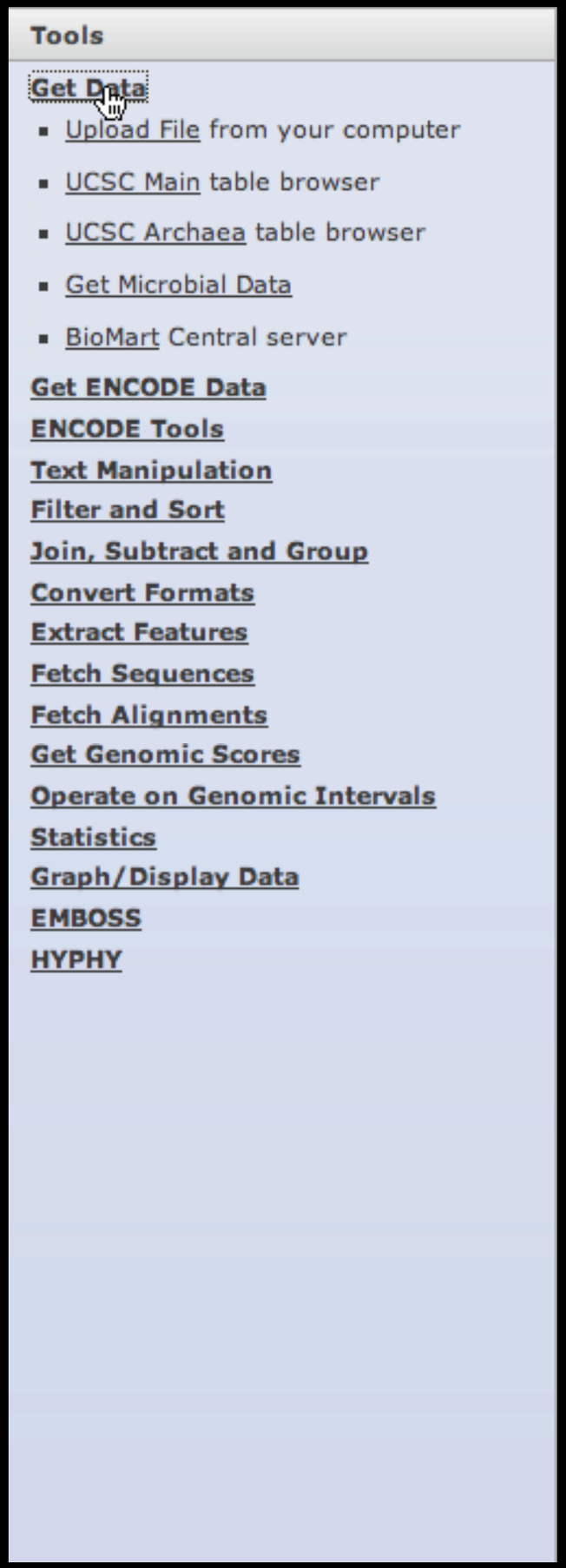
Integrating tools into **Galaxy**

Tools

Get Data

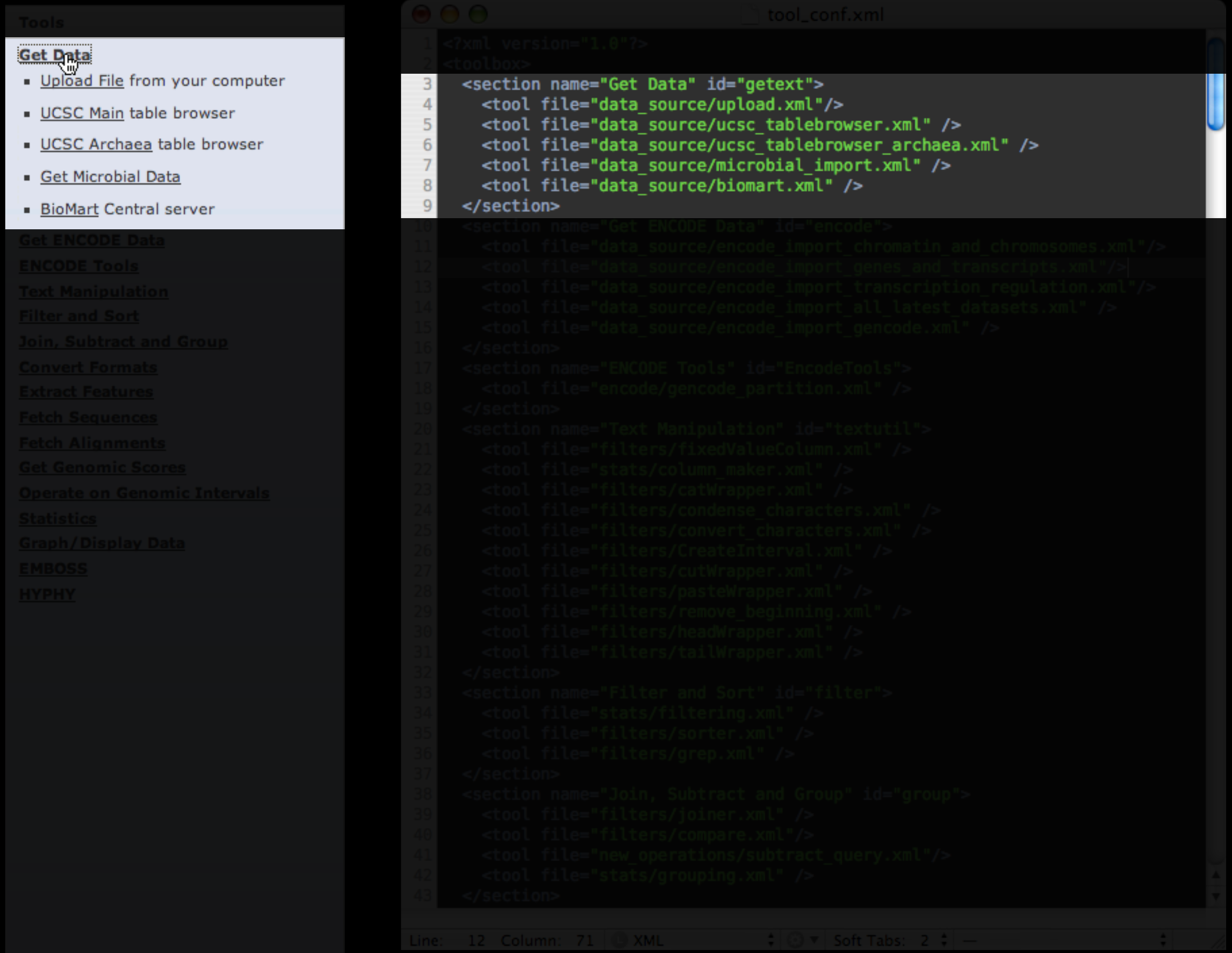
- Upload File from your computer
- UCSC Main table browser
- UCSC Archaea table browser
- Get Microbial Data
- BioMart Central server

Get ENCODE Data
ENCODE Tools
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
EMBOSS
HYPHY



tool_conf.xml

```
<?xml version="1.0"?>
<toolbox>
  <section name="Get Data" id="getext">
    <tool file="data_source/upload.xml"/>
    <tool file="data_source/ucsc_tablebrowser.xml" />
    <tool file="data_source/ucsc_tablebrowser_archaea.xml" />
    <tool file="data_source/microbial_import.xml" />
    <tool file="data_source/biomart.xml" />
  </section>
  <section name="Get ENCODE Data" id="encode">
    <tool file="data_source/encode_import_chromatin_and_chromosomes.xml"/>
    <tool file="data_source/encode_import_genes_and_transcripts.xml"/>
    <tool file="data_source/encode_import_transcription_regulation.xml"/>
    <tool file="data_source/encode_import_all_latest_datasets.xml" />
    <tool file="data_source/encode_import_gencode.xml" />
  </section>
  <section name="ENCODE Tools" id="EncodeTools">
    <tool file="encode/gencode_partition.xml" />
  </section>
  <section name="Text Manipulation" id="textutil">
    <tool file="filters/fixedValueColumn.xml" />
    <tool file="stats/column_maker.xml" />
    <tool file="filters/catWrapper.xml" />
    <tool file="filters/condense_characters.xml" />
    <tool file="filters/convert_characters.xml" />
    <tool file="filters/CreateInterval.xml" />
    <tool file="filters/cutWrapper.xml" />
    <tool file="filters/pasteWrapper.xml" />
    <tool file="filters/remove_beginning.xml" />
    <tool file="filters/headWrapper.xml" />
    <tool file="filters/tailWrapper.xml" />
  </section>
  <section name="Filter and Sort" id="filter">
    <tool file="stats/filtering.xml" />
    <tool file="filters/sorter.xml" />
    <tool file="filters/grep.xml" />
  </section>
  <section name="Join, Subtract and Group" id="group">
    <tool file="filters/joiner.xml" />
    <tool file="filters/compare.xml"/>
    <tool file="new_operations/subtract_query.xml"/>
    <tool file="stats/grouping.xml" />
  </section>
```


Tools
Get Data
Upload File from your computer
UCSC Main table browser
UCSC Archaea table browser
Get Microbial Data
BioMart Central server
Get ENCODE Data
ENCODE Tools
Text Manipulation
Filter and Sort
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Statistics
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EMBOSS
HYPHY
tool_conf.xml
<?xml version="1.0"?>
<toolbox>
<section name="Get Data" id="getext">
<tool file="data_source/upload.xml"/>
<tool file="data_source/ucsc_tablebrowser.xml" />
<tool file="data_source/ucsc_tablebrowser_archaea.xml" />
<tool file="data_source/microbial_import.xml" />
<tool file="data_source/biomart.xml" />
</section>
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<tool file="data_source/encode_import_genes_and_transcripts.xml"/>
<tool file="data_source/encode_import_transcription_regulation.xml"/>
<tool file="data_source/encode_import_all_latest_datasets.xml" />
<tool file="data_source/encode_import_gencode.xml" />
</section>
<section name="ENCODE Tools" id="EncodeTools">
<tool file="encode/gencode_partition.xml" />
</section>
<section name="Text Manipulation" id="textutil">
<tool file="filters/fixedValueColumn.xml" />
<tool file="stats/column_maker.xml" />
<tool file="filters/catWrapper.xml" />
<tool file="filters/condense_characters.xml" />
<tool file="filters/convert_characters.xml" />
<tool file="filters/CreateInterval.xml" />
<tool file="filters/cutWrapper.xml" />
<tool file="filters/pasteWrapper.xml" />
<tool file="filters/remove_beginning.xml" />
<tool file="filters/headWrapper.xml" />
<tool file="filters/tailWrapper.xml" />
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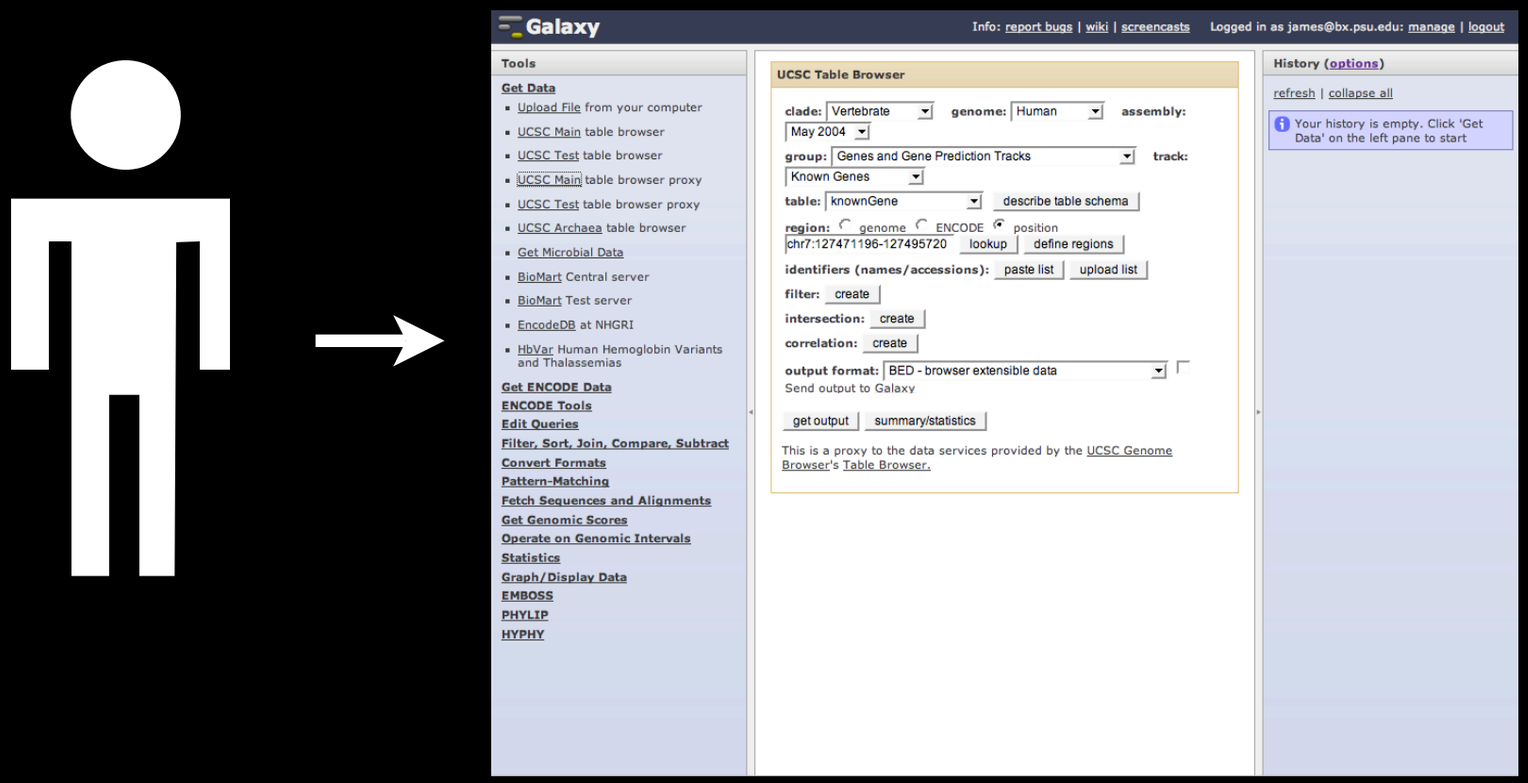
<section name="Filter and Sort" id="filter">
<tool file="stats/filtering.xml" />
<tool file="filters/sorter.xml" />
<tool file="filters/grep.xml" />
</section>
<section name="Join, Subtract and Group" id="group">
<tool file="filters/joiner.xml" />
<tool file="filters/compare.xml"/>
<tool file="new_operations/subtract_query.xml"/>
<tool file="stats/grouping.xml" />
</section>
Line: 12 Column: 71 XML Soft Tabs: 2

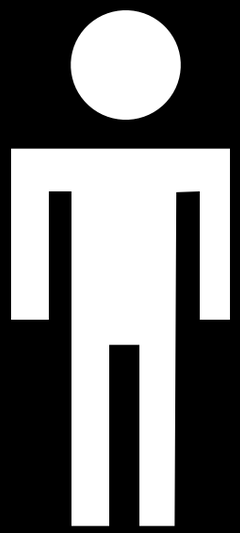
How **Galaxy** integrates existing web-based tools

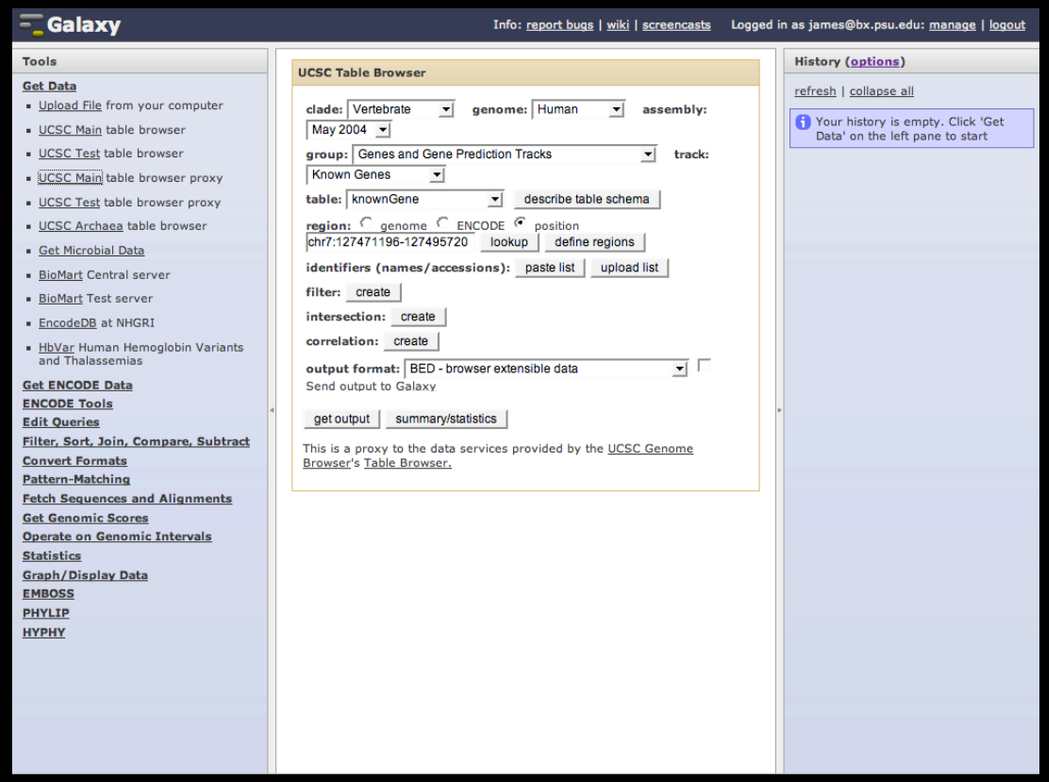
Proxy based tools

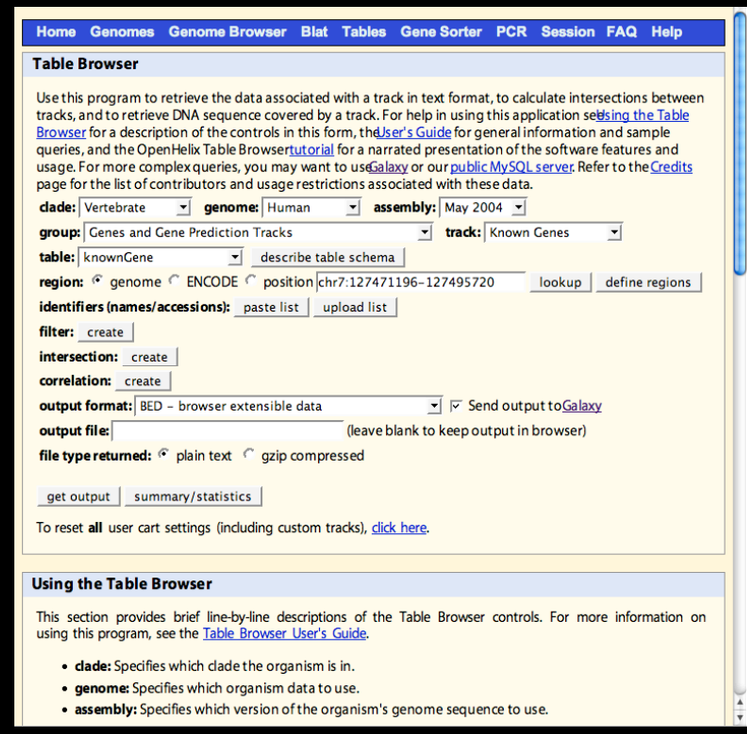


User makes request to Galaxy

Proxy based tools

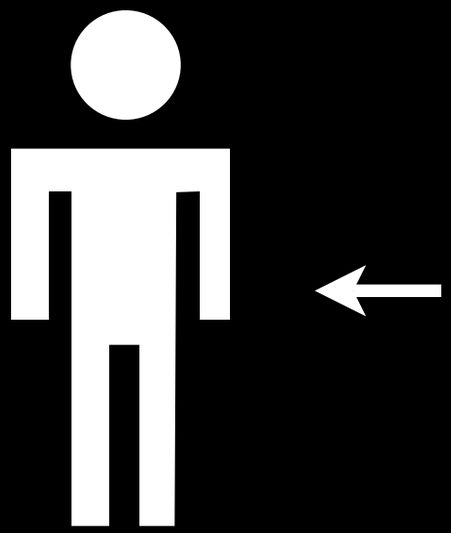


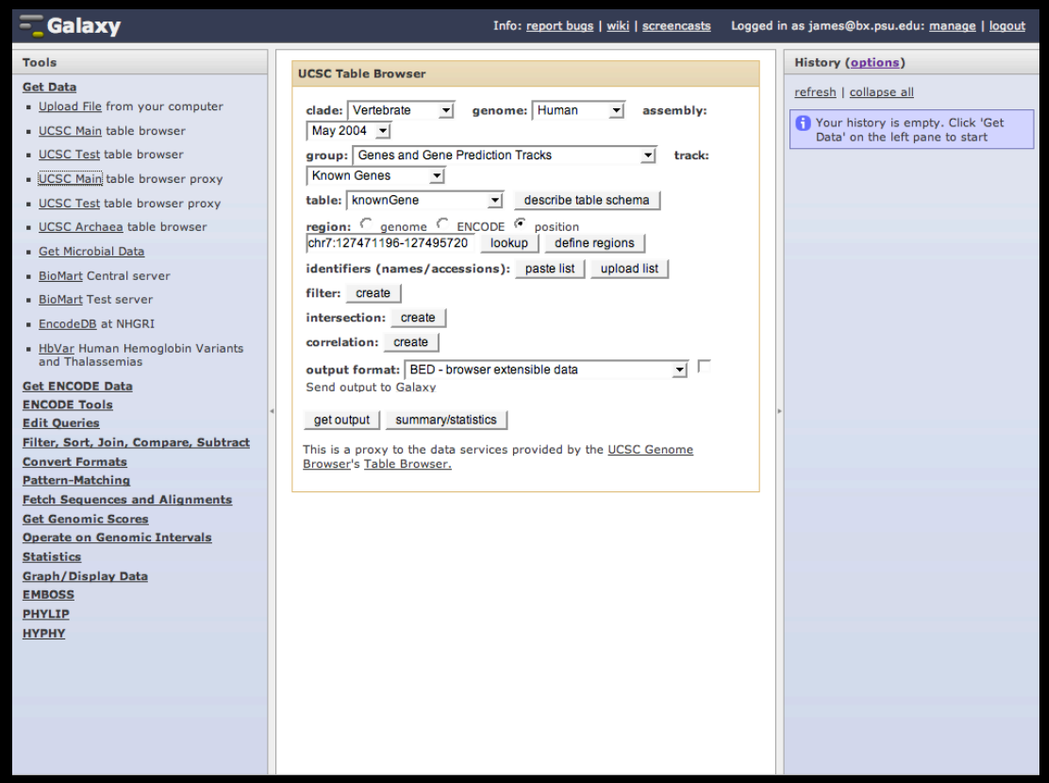


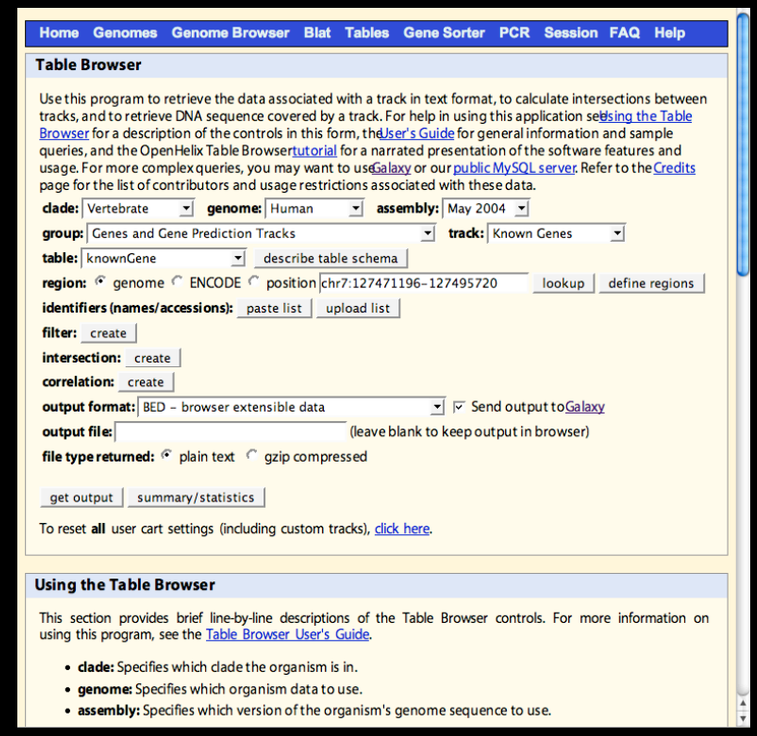


Galaxy delegates request to external site

Proxy based tools



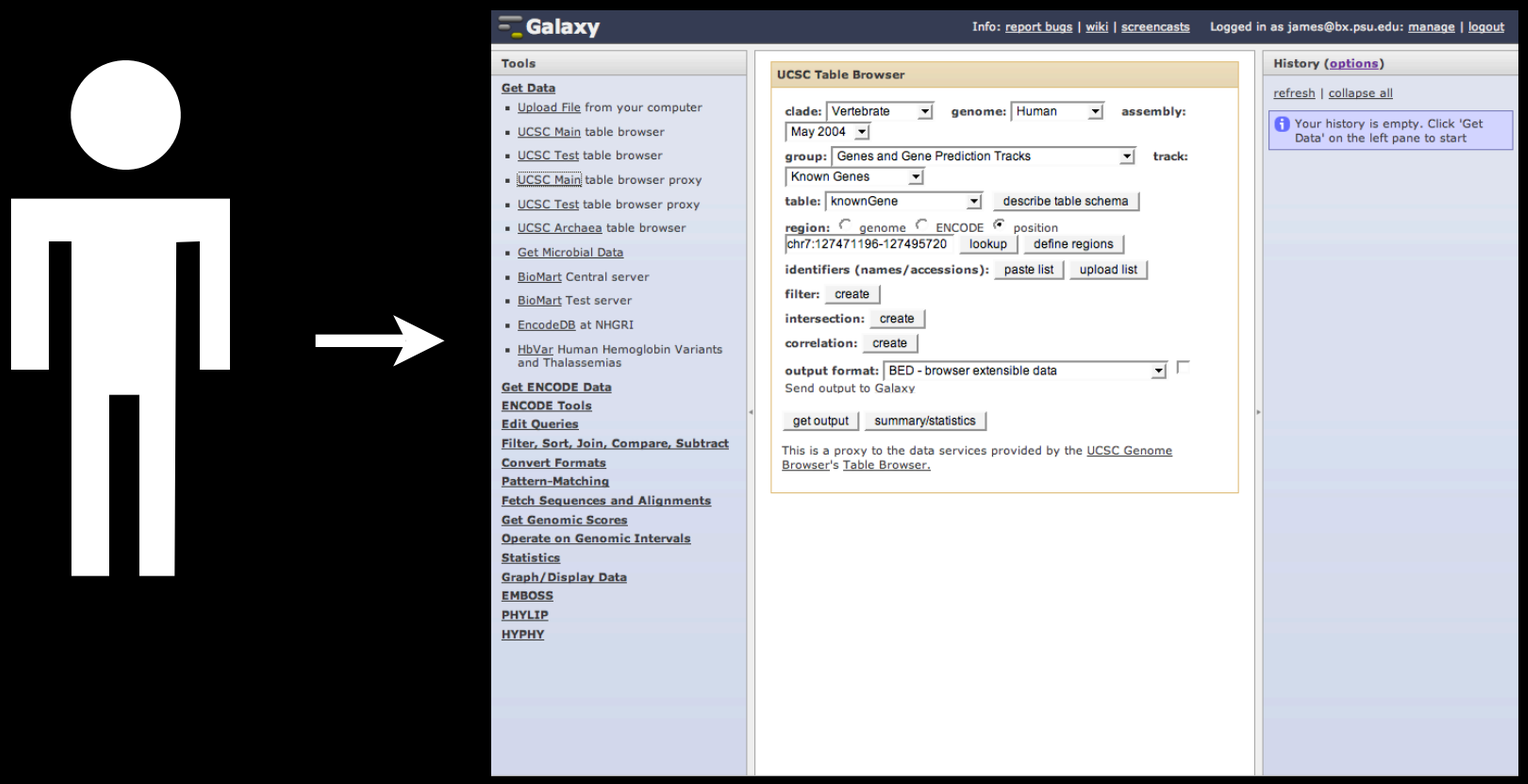




External site generates response

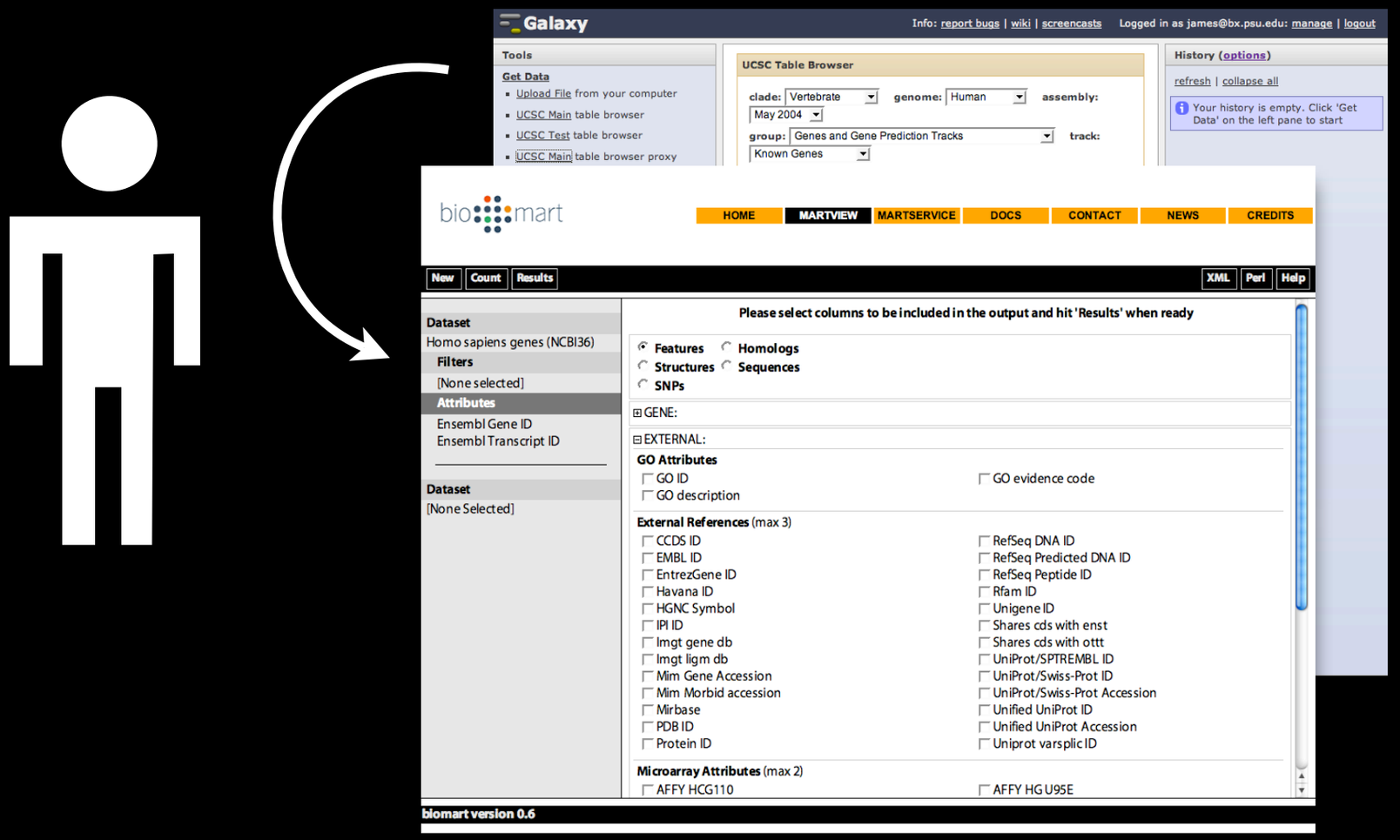
- If data, Galaxy determines type, processes, and adds to ‘history’
- Otherwise, return response to user

External tools



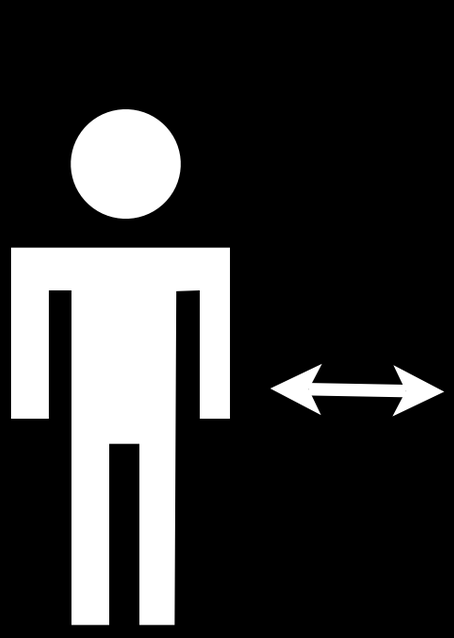
User makes request to Galaxy

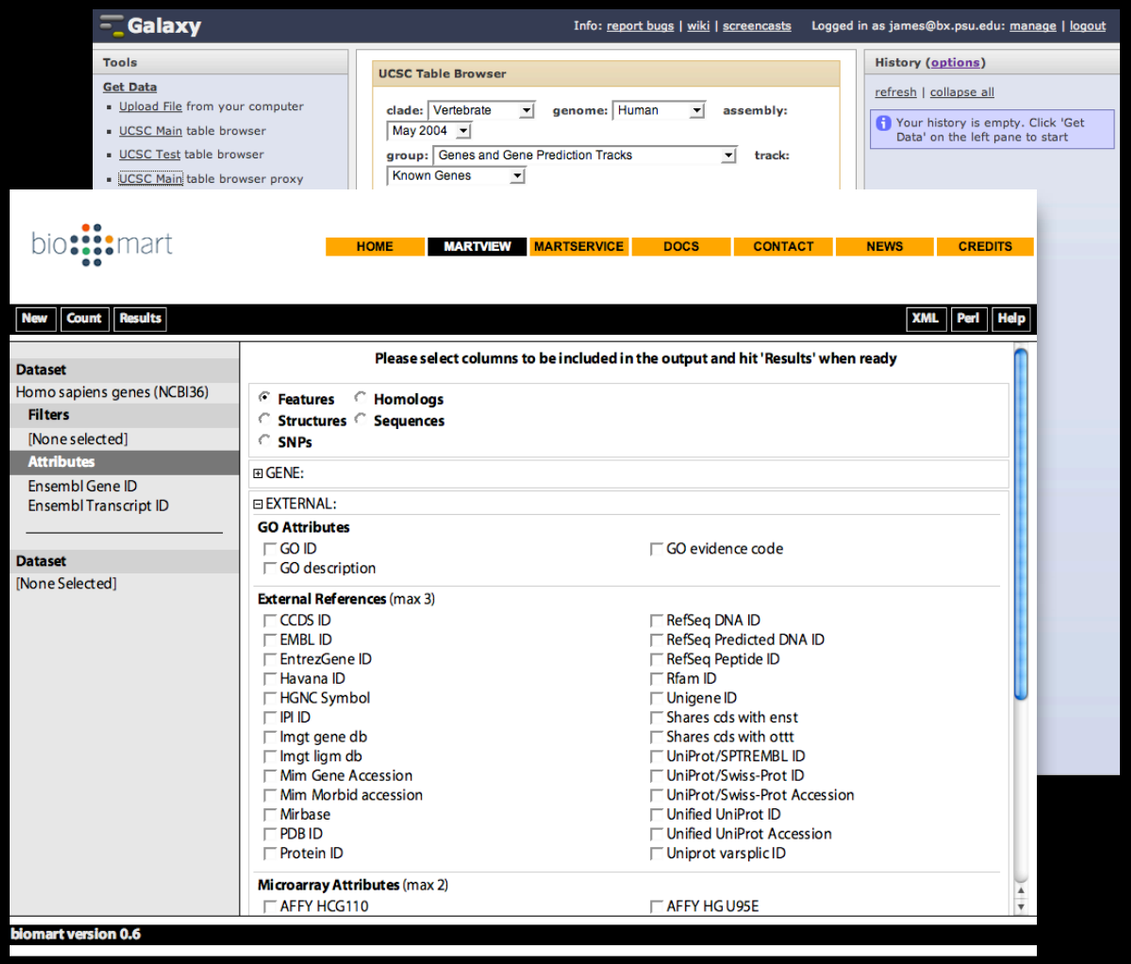
External tools



Galaxy sends user directly to external site with extra URL data

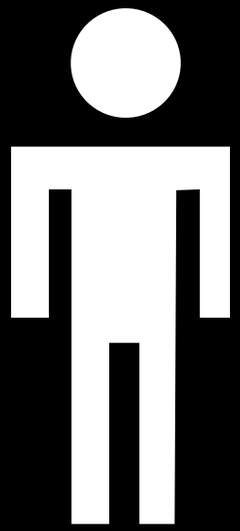
External tools

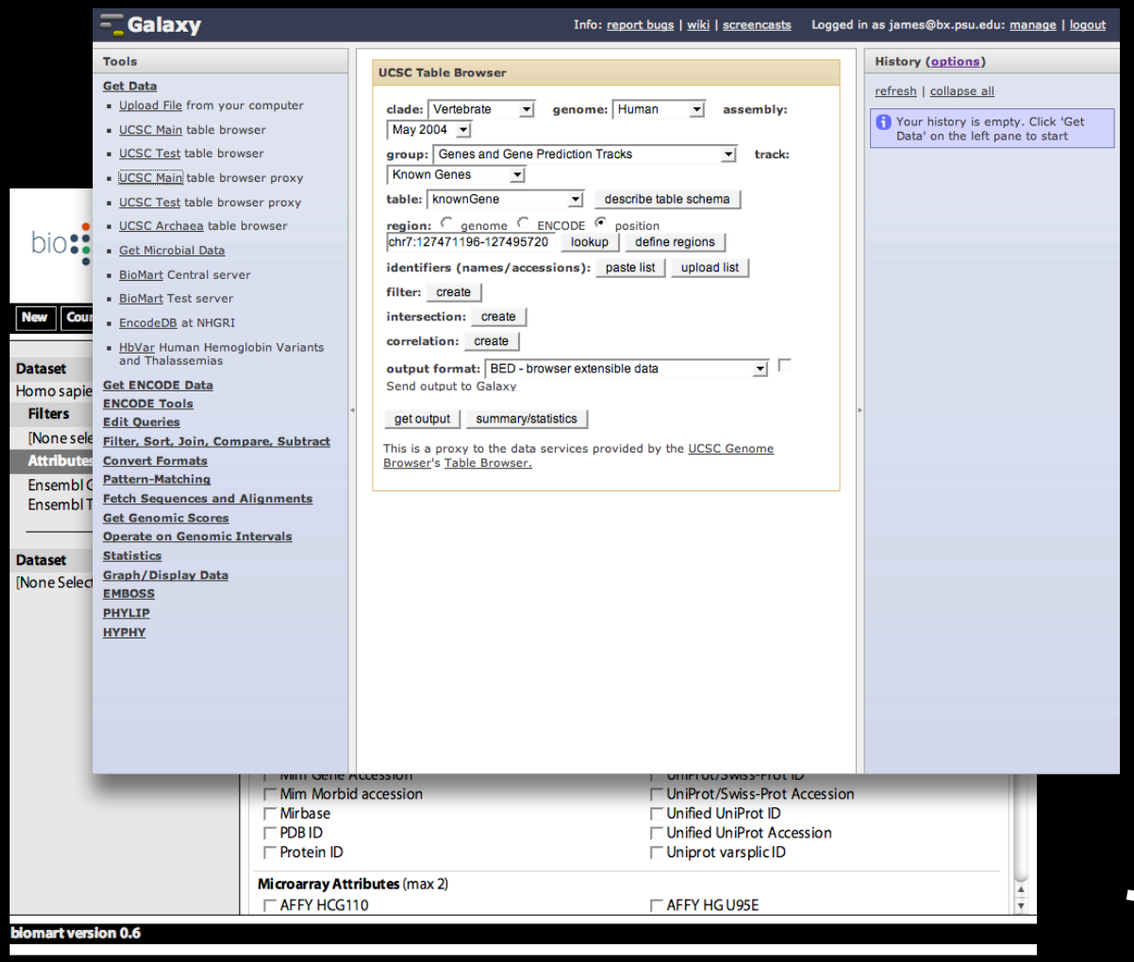




User interacts directly with external site

External tools





When data is generated the user is sent back to Galaxy. Data can be fetched immediately, or wait for notification from the external site

Tools

Get Data
- Upload File from your computer
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- UCSC Archaea table browser
- Get Microbial Data
- BioMart Central server

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ENCODE Tools
Text Manipulation
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Extract Features
Fetch Sequences
Fetch Alignments
Get Genomic Scores
Operate on Genomic Intervals
Statistics
Graph/Display Data
EMBOSS
HYPHY

Table Browser

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, and 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 want to use Galaxy or our public MySQL server. Refer to the Credits page for the list of contributors and usage restrictions associated with these data.

clade: Vertebrate **genome:** Human **assembly:** May 2004

group: Genes and Gene Prediction Tracks **track:** Known Genes

table: knownGene describe table schema

region: genome ENCODE position chr7:127471196-127495720 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

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.

Using the Table Browser

This section provides brief line-by-line descriptions of the Table Browser controls. For more information on using this program, see the Table Browser User's Guide.

Tools

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- UCSC Archaea table browser
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- BioMart Central server

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Filter and Sort
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Statistics
Graph/Display Data
EMBOSS
HYPHY

Output knownGene as BED

☐ **Include custom track header:**

name= tb_knownGene

description= table browser query on knownGene

visibility= pack

url=

Create one BED record per:

- ○ Whole Gene
- ○ Upstream by 200 bases
- ○ Exons plus 0 bases at each end
- ○ Introns plus 0 bases at each end
- ○ 5' UTR Exons
- ◉ Coding Exons
- ○ 3' UTR Exons
- ○ Downstream by 200 bases

Note: if a feature is close to the beginning or end of a chromosome and upstream/downstream bases are added, they may be truncated in order to avoid extending past the edge of the chromosome.

Send query to Galaxy

Cancel

Tools

Get Data
- Upload File from your computer
- UCSC Main table browser
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- Get Microbial Data
- BioMart Central server

Get ENCODE Data
ENCODE Tools
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
EMBOSS
HYPHY

The following job has been succesfully added to the queue:

6: UCSC Main

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 succesfully or 'error' if problems were encountered.

History (options)

refreshing in 8 sec | collapse all

6: UCSC Main on Human: knownGene (genome)

5: Intersect on data 3 and data 4

4: UCSC Main on Human: knownGene (genome)

3: Pasted Entry

Galaxy

Info: report bugs | wiki | screencasts Account: create | login

Tools

Get Data
- Upload File from your computer
- UCSC Main table browser
- UCSC Archaea table browser
- Get Microbial Data
- BioMart Central server

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ENCODE Tools
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Extract Features
Fetch Sequences
Fetch Alignments
Get Genomic Scores
Operate on Genomic Intervals
Statistics
Graph/Display Data
EMBOSS
HYPHY

biomart

HOME | MARTVIEW | MARTSERVICE | DOCS | CON

New | Count | Results | XML | Perl | Help

Dataset

[None selected]

- CHOOSE DATABASE -

biomart version 0.6

Galaxy

Info: report bugs | wiki | screencasts Account: create | login

Tools

Get Data
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- BioMart Central server

Get ENCODE Data
ENCODE Tools
Text Manipulation
Filter and Sort
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Convert Formats
Extract Features
Fetch Sequences
Fetch Alignments
Get Genomic Scores
Operate on Genomic Intervals
Statistics
Graph/Display Data
EMBOSS
HYPHY

biomart

HOME | MARTVIEW | MARTSERVICE | DOCS | CON

New | Count | Results | XML | Perl | Help

Dataset
Homo sapiens genes (NCBI36)

Filters
[None selected]

Attributes
Ensembl Gene ID
Ensembl Transcript ID
Transcript Start (bp)
Transcript End (bp)
Chromosome Name

Dataset
[None Selected]

Export all results to: Galaxy | TSV | Unique results only | Go

Email notification to:

View 10 rows as TSV | Unique results only

Ensembl Gene ID	Ensembl Transcript ID	Transcript	Sta
ENSG00000184895	ENST00000383070	2714896	2715740 Y
ENSG00000184895	ENST00000327563	2715030	2715644 Y
ENSG00000129824	ENST00000322114	2769527	2794997 Y
ENSG00000129824	ENST00000250784	2769623	2794995 Y
ENSG00000067646	ENST00000383052	2863322	2910547 Y
ENSG00000067646	ENST00000155093	2863546	2909891 Y
ENSG00000176679	ENST00000383049	3507096	3508082 Y
ENSG00000176679	ENST00000321217	3507126	3508080 Y
ENSG00000099715	ENST00000333703	4928267	5033485 Y
ENSG00000099715	ENST00000362095	4928267	5033485 Y

biomart version 0.6

Tools

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Convert Formats
Extract Features
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Operate on Genomic Intervals
Statistics
Graph/Display Data
EMBOSS
HYPHY

The following job has been succesfully added to the queue:

7: BioMart

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 succesfully or 'error' if problems were encountered.

History (options)

refreshing in 8 sec | collapse all

7: BioMart

6: UCSC Main on Human: knownGene (genome)

5: Intersect on data 3 and data 4

4: UCSC Main on Human: knownGene (genome)

3: Pasted Entry

Tools

Get Data
- Upload File from your computer
- UCSC Main table browser
- UCSC Archaea table browser
- Get Microbial Data
- BioMart Central server

Get ENCODE Data
ENCODE Tools
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
EMBOSS
HYPHY

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History (options)

refresh | collapse all

7: Homo sapiens genes (NCBI36)

52,160 lines, format: tabular, database: ?
Info: Homo sapiens genes (NCBI36)
save

1	2
Ensembl Gene ID	Ensembl Transcri
ENSG00000184895	ENST00000383070
ENSG00000184895	ENST00000327563
ENSG00000129824	ENST00000322114
ENSG00000129824	ENST00000250784
ENSG00000067646	ENST00000383052

6: UCSC Main on Human: knownGene (genome)

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How **Galaxy** integrates existing command line tools

Tools

Get Data
Get ENCODE Data
ENCODE Tools
Text Manipulation
Filter and Sort
Join, Subtract and Group
Convert Formats
Extract Features
Fetch Sequences
Fetch Alignments
Get Genomic Scores
Operate on Genomic Intervals

- Intersect the intervals of two queries
- Subtract the intervals of two queries
- Merge the overlapping intervals of a query
- Concatenate two queries into one query
- Base Coverage of all intervals
- Coverage of a set of intervals on second set of intervals
- Complement intervals of a query
- Cluster the intervals of a query
- Join the intervals of two queries side-by-side
- Get flanks returns flanking region/s for every gene

Statistics
Graph/Display Data
EMBOSS
HYPHY

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

Screencasts!

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

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 overlap.
- **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.
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- **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.

Example

History (options)

refresh | collapse all

- **7: Homo sapiens genes (NCBI36)**
- **6: UCSC Main on Human: knownGene (genome)**
- **5: Intersect on data 3 and data 4**
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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">
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  <inputs>
    <param format="interval" name="input1" type="data">
      <label>Cluster intervals of</label>
    </param>
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    </param>
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.. 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

-----

**Syntax**

- **Maximum distance** is greatest distance in base pairs allowed betw
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```
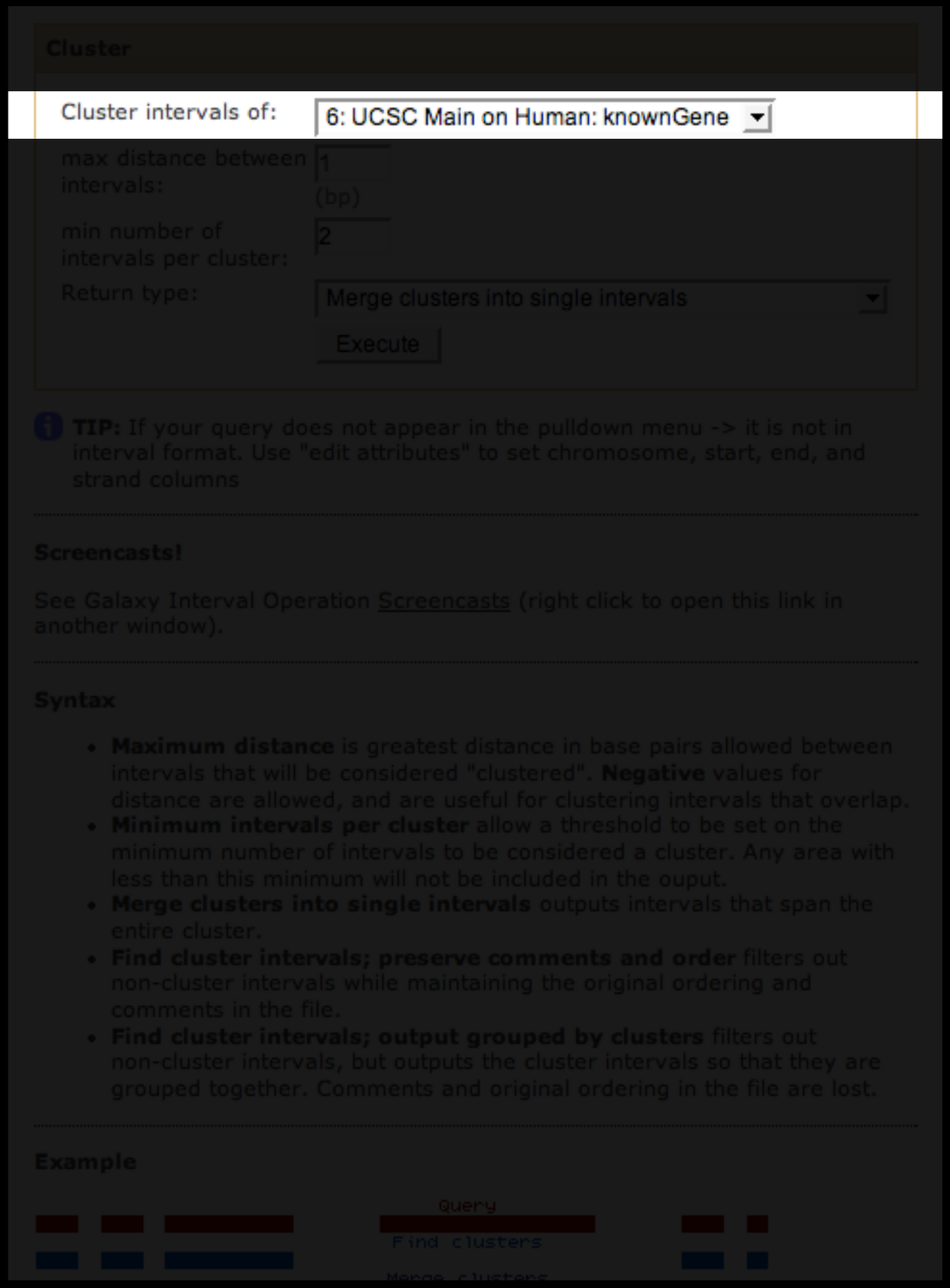
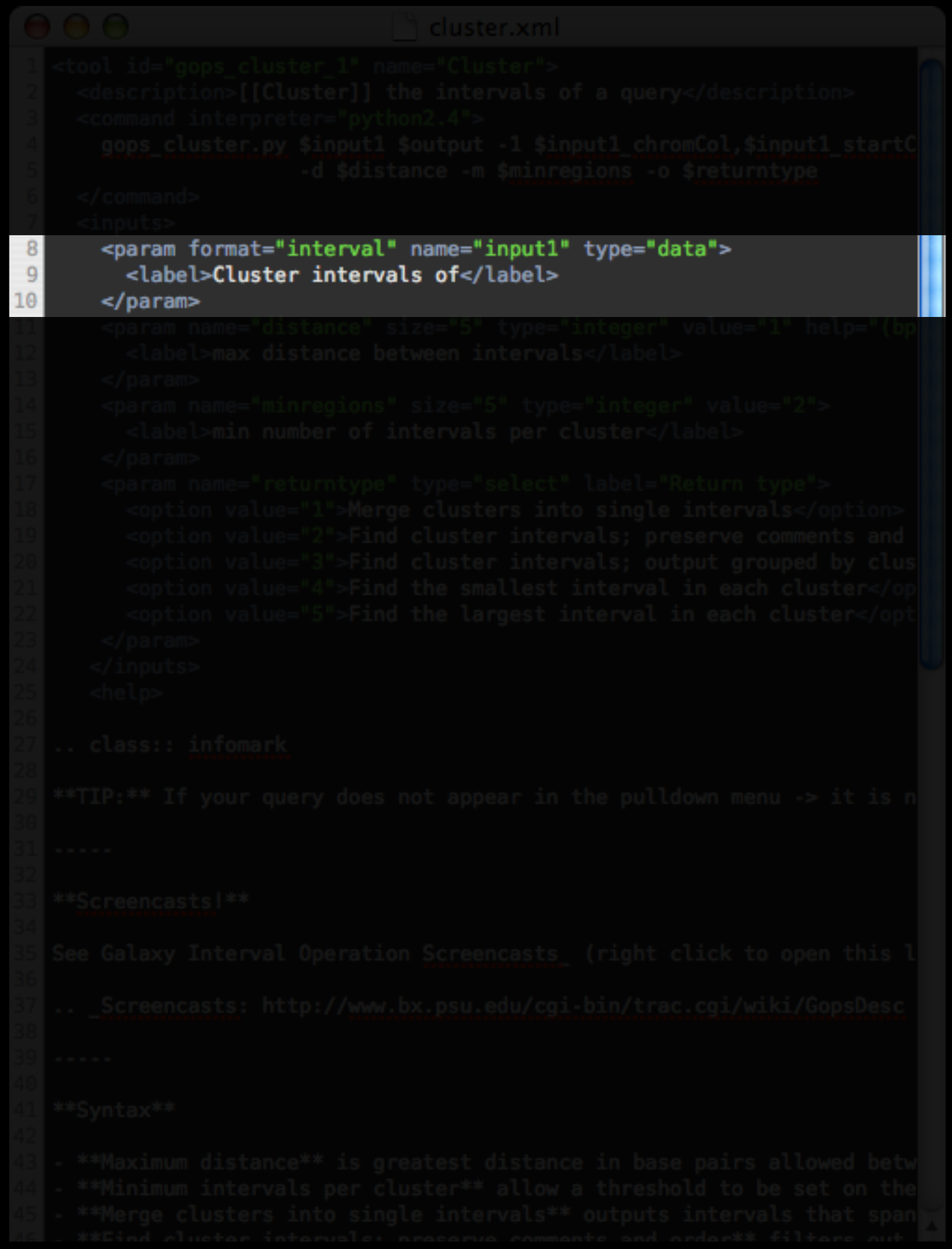

Line: 87 Column: 8 XML Soft Tabs: 2





HTML inputs generated from abstract parameter description

Cluster

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

max distance between intervals: 1 (bp)

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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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.. class:: infomark

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**Screencasts!**

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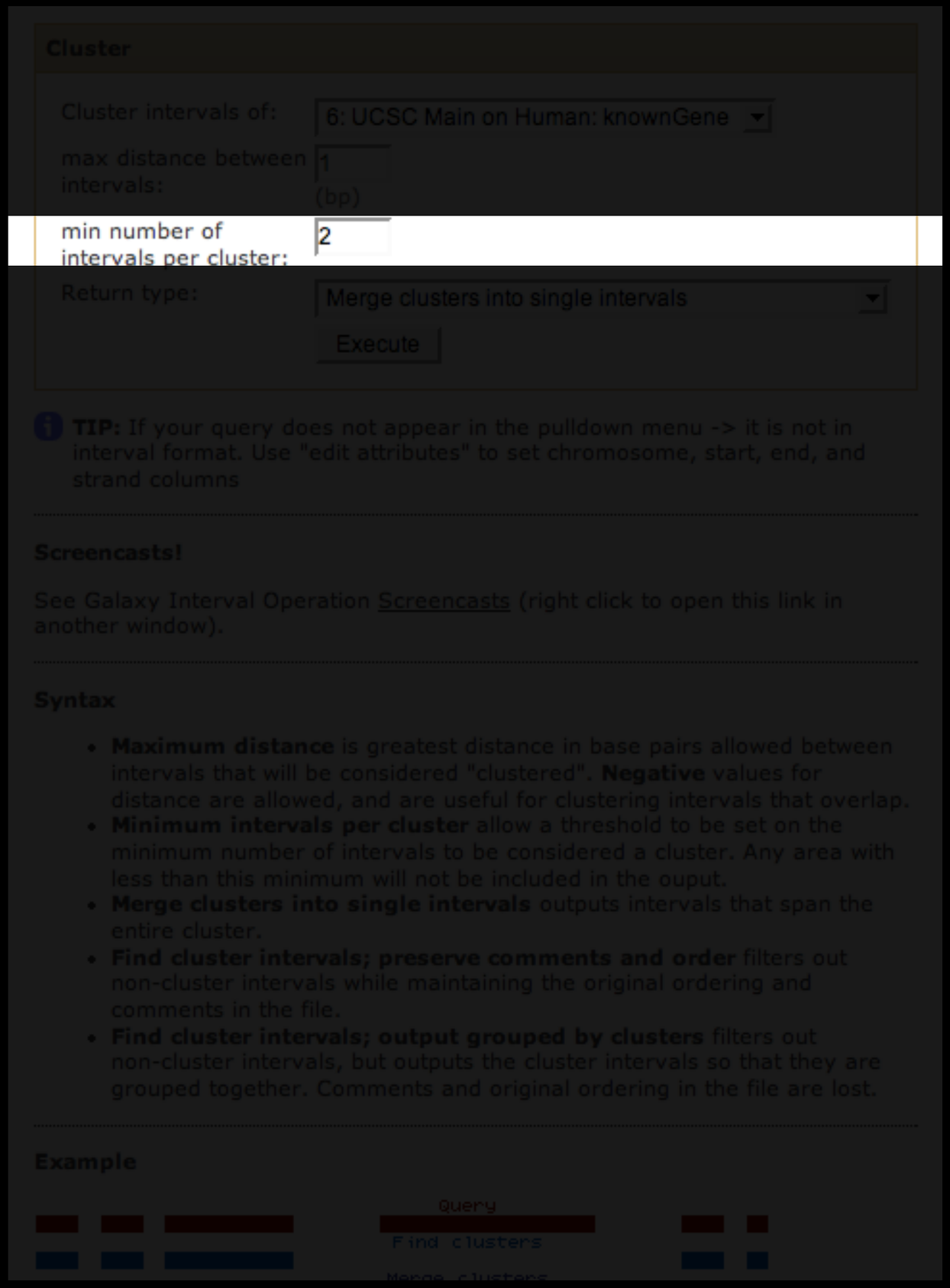

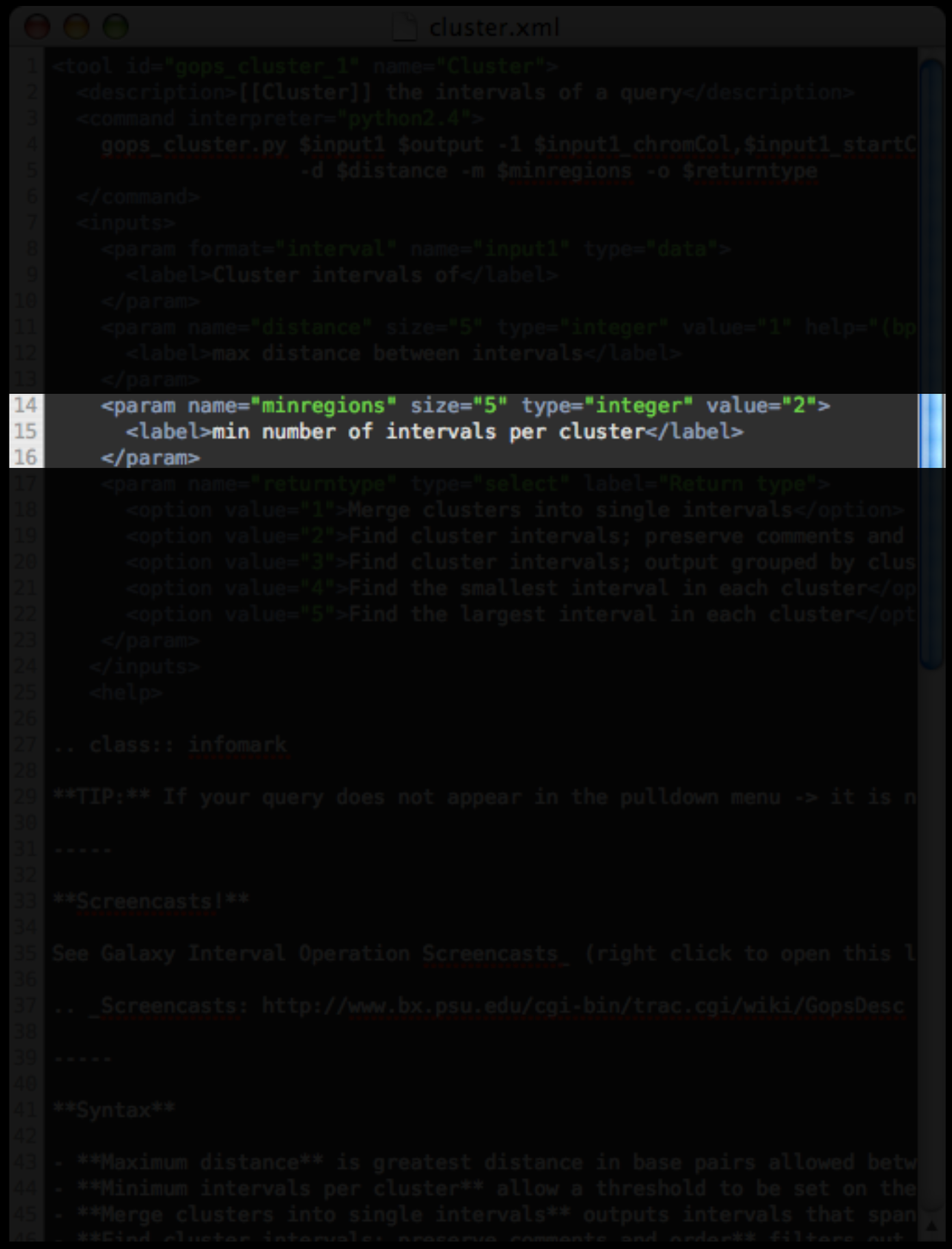

HTML inputs generated from abstract parameter description

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

Screencasts!

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.. class:: infomark

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**Screencasts!**

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

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HTML inputs generated from abstract parameter description

Tool help generated from a simple text format

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

max distance between intervals: 1 (bp)

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Line: 87 Column: 8 XML Soft Tabs: 2

One or more errors were found in the input you provided. The specific errors are marked below.

Cluster

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

max distance between intervals: seven

An integer is required

min number of intervals per cluster: 2

Return type: Merge clusters into single intervals

Execute

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Automatic input validation based on type, or more...

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Line: 61 Column: 45 XML Soft Tabs: 2

cluster.xml

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Line: 61 Column: 45 XML Soft Tabs: 2

} Template for generating command line from parameter values

cluster.xml

```
41 **Syntax**
42
43 - **Maximum distance** is greatest distance in base pairs allowed between intervals tha
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48
49 -----
50
51 **Example**
52
53 .. image:: ../static/operation_icons/gops_cluster.gif
54
55 </help>
56
57   <outputs>
58     <data format="input" name="output" metadata_source="input1" />
59   </outputs>
60   <code file="operation_filter.py">
61     <hook exec_after_process="exec_after_cluster" />
62   </code>
63   <tests>
64     <test>
65       <param name="input1" value="1.bed" />
66       <param name="distance" value="1" />
67       <param name="minregions" value="2" />
68       <param name="returntype" value="1" />
69       <output name="output" file="gops-cluster-1.dat" />
70     </test>
71     <test>
72       <param name="input1" value="1.bed" />
73       <param name="distance" value="1" />
74       <param name="minregions" value="2" />
75       <param name="returntype" value="2" />
76       <output name="output" file="gops-cluster-2.dat" />
77     </test>
78     <test>
79       <param name="input1" value="1.bed" />
80       <param name="distance" value="1" />
81       <param name="minregions" value="2" />
82       <param name="returntype" value="3" />
83       <output name="output" file="gops-cluster-3.dat" />
84     </test>
85   </tests>
86
87 </tool>
```

Line: 61 Column: 45 XML Soft Tabs: 2

} Output datasets generated by the tool

cluster.xml

```
**Syntax**

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**Example**

.. image:: ../static/operation_icons/gops_cluster.gif

</help>

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      <param name="returntype" value="1" />
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    </test>
    <test>
      <param name="input1" value="1.bed" />
      <param name="distance" value="1" />
      <param name="minregions" value="2" />
      <param name="returntype" value="2" />
      <output name="output" file="gops-cluster-2.dat" />
    </test>
    <test>
      <param name="input1" value="1.bed" />
      <param name="distance" value="1" />
      <param name="minregions" value="2" />
      <param name="returntype" value="3" />
      <output name="output" file="gops-cluster-3.dat" />
    </test>
  </tests>

</tool>
```

Line: 61 Column: 45 XML Soft Tabs: 2

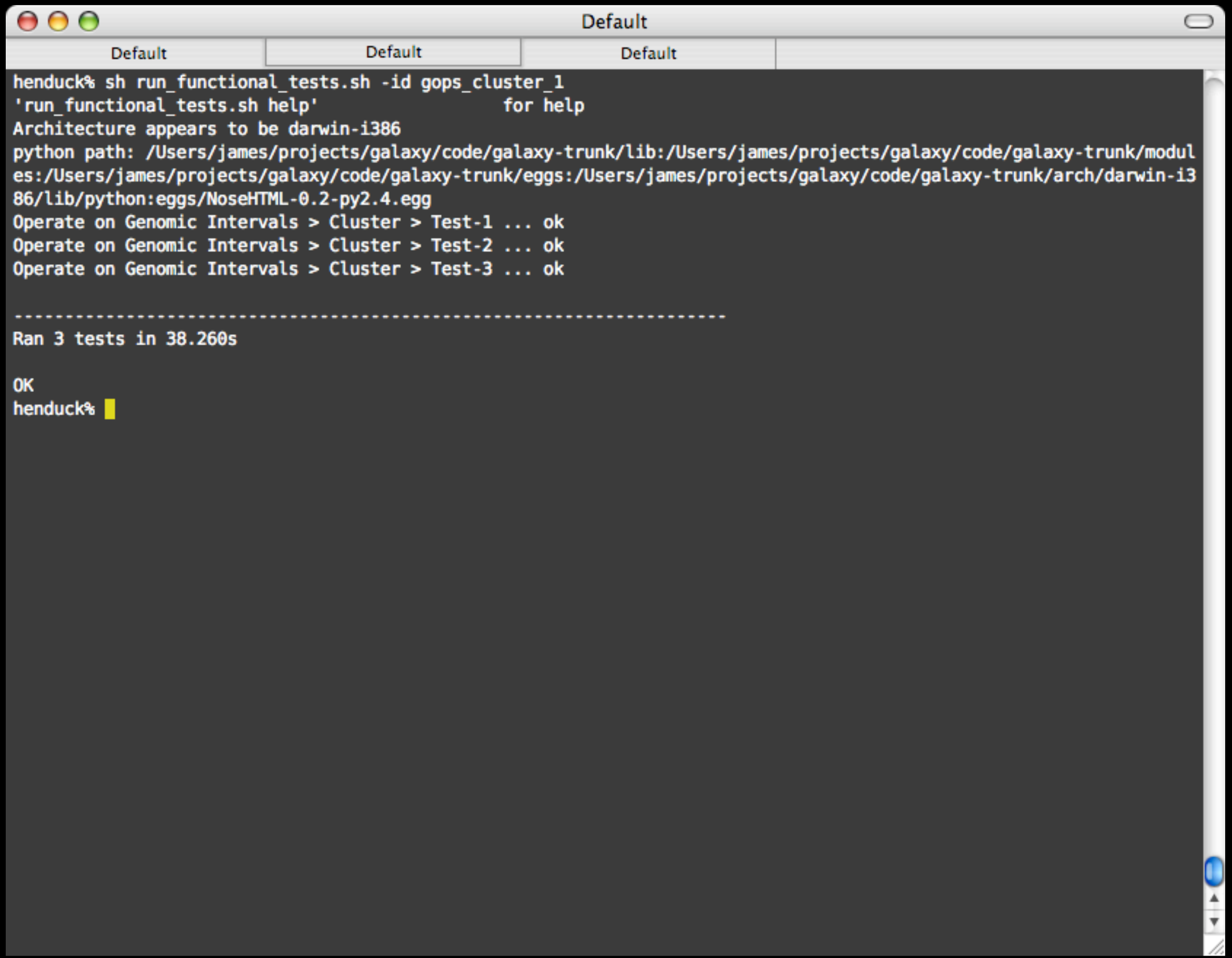
} Special actions to be run before / after execution

cluster.xml

```
**Syntax**

- **Maximum distance** is greatest distance in base pairs allowed between intervals tha
- **Minimum intervals per cluster** allow a threshold to be set on the minimum number o
- **Merge clusters into single intervals** outputs intervals that span the entire clust
- **Find cluster intervals; preserve comments and order** filters out non-cluster inter
- **Find cluster intervals; output grouped by clusters** filters out non-cluster interv

-----

**Example**

.. image:: ../static/operation_icons/gops_cluster.gif

</help>

  <outputs>
    <data format="input" name="output" metadata_source="input1" />
  </outputs>
  <code file="operation_filter.py">
    <hook exec_after_process="exec_after_cluster" />
  </code>
  <tests>
    <test>
      <param name="input1" value="1.bed" />
      <param name="distance" value="1" />
      <param name="minregions" value="2" />
      <param name="returntype" value="1" />
      <output name="output" file="gops-cluster-1.dat" />
    </test>
    <test>
      <param name="input1" value="1.bed" />
      <param name="distance" value="1" />
      <param name="minregions" value="2" />
      <param name="returntype" value="2" />
      <output name="output" file="gops-cluster-2.dat" />
    </test>
    <test>
      <param name="input1" value="1.bed" />
      <param name="distance" value="1" />
      <param name="minregions" value="2" />
      <param name="returntype" value="3" />
      <output name="output" file="gops-cluster-3.dat" />
    </test>
  </tests>

</tool>
```

Line: 61 Column: 45 XML Soft Tabs: 2

Functional tests to be run with the “full stack” in place



Running functional tests for a specific tool on the command line

ID: functional.test_toolbox.GeneratedToolTestCase_gops_cluster_1.test_tool
Description: Operate on Genomic Intervals > Cluster > Test-1
Status: failure
Output: ...

```
galaxy.datatypes.registry WARNING 2007-07-16 18:55:30,380 unknown extension in data factory None
```

Exception: ...

```
Traceback (most recent call last):

  File "/Library/Frameworks/Python.framework/Versions/2.4//lib/python2.4/unittest.py", line 260, in run
    testMethod()

  File "/Users/james/projects/galaxy/code/galaxy-trunk/test/functional/test_toolbox.py", line 48, in test_tool
    self.do_it()

  File "/Users/james/projects/galaxy/code/galaxy-trunk/test/functional/test_toolbox.py", line 37, in do_it
    self.check_data( file )

  File "/Users/james/projects/galaxy/code/galaxy-trunk/test/base/twilltestcase.py", line 239, in check_data
    raise AssertionError( errmsg )

AssertionError: Data at history id 1 does not match expected, diff:
--- local_file
+++ history_data
@@ -1,4 +1,65 @@
-chr6    108640045       108640151
-chr6    108642394       108642519
-chr6    108650846       108650942
-chr6    108688656       108688818
+chr1    147962192       147962580       CCDS989.1_cds_0_0_chr1_147962193_r      0       -
+chr1    147984545       147984630       CCDS990.1_cds_0_0_chr1_147984546_f      0       +
+chr1    148078400       148078582       CCDS993.1_cds_0_0_chr1_148078401_r      0       -
+chr1    148185136       148185276       CCDS996.1_cds_0_0_chr1_148185137_f      0       +
```

Test results, on command line and as HTML report

Dealing with more complex interface needs

Tools

Get Data
Get ENCODE Data
ENCODE Tools
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 columns
- Scatterplot of two numeric columns
- XY Plot
- GMAJ Multiple Alignment Viewer
- Build custom track for UCSC genome browser

EMBOSS
HYPHY

Build custom track

Tracks

Track 1

Dataset: 6: UCSC Main on Human: knownGene
name: User Track
description: User Supplie
Color: Black
Visibility: Dense
Remove Track 1

Track 2

Dataset: 4: UCSC Main on Human: knownGene
name: User Track
description: User Supplie
Color: Magenta
Visibility: Full
Remove Track 2

Add new Track

Execute

Info

This tool displays the selected datasets with their custom track attributes (if any) in the UCSC genome browser.

This tool allows you to set the **Color** and **Visibility** attributes and you can edit the **Name** attribute of the dataset by clicking on **"edit attributes"** button (pencil icon) next to the dataset name in the history panel.

Please note that the primary dataset in step 1 of the tool sets the database build for the datasets in following steps. For example, if your first dataset belogs to hg18, you will only be able to select hg18 associated datasets on the next step.

History (options)

refresh | collapse all

7: Homo sapiens genes (NCBI36)
6: UCSC Main on Human: knownGene (genome)
5: Intersect on data 3 and data 4
4: UCSC Main on Human: knownGene (genome)
3: Pasted Entry

Build custom track

Tracks

Track 1

Dataset: 6: UCSC Main on Human: knownGene

name: User Track

description: User Supplie

Color: Black

Visibility: Dense

Remove Track 1

Track 2

Dataset: 4: UCSC Main on Human: knownGene

name: User Track

description: User Supplie

Color: Magenta

Visibility: Full

Remove Track 2

Add new Track

Execute

Info

This tool displays the selected datasets with their custom track attributes (if any) in the UCSC genome browser.

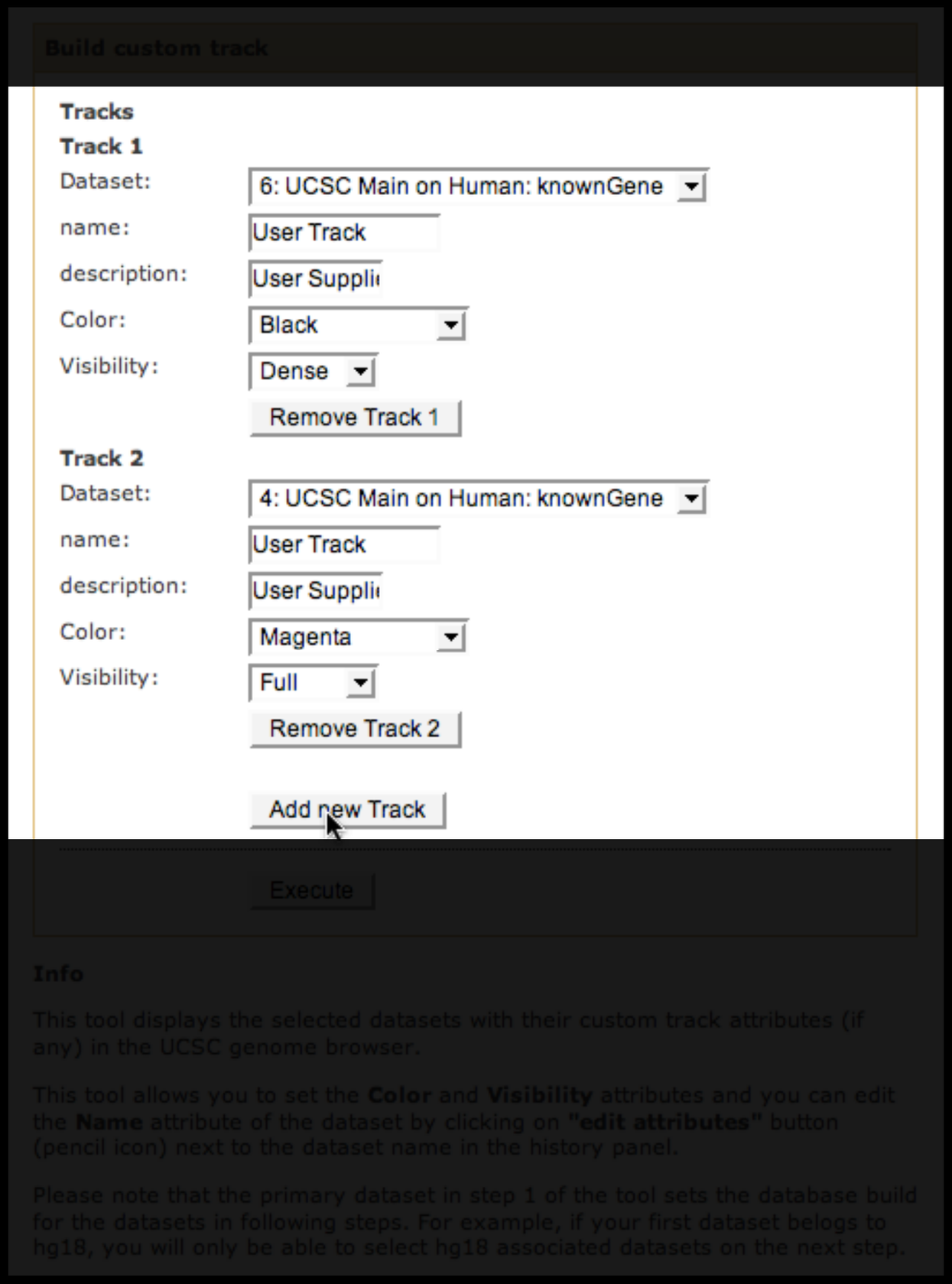
This tool allows you to set the **Color** and **Visibility** attributes and you can edit the **Name** attribute of the dataset by clicking on **"edit attributes"** button (pencil icon) next to the dataset name in the history panel.

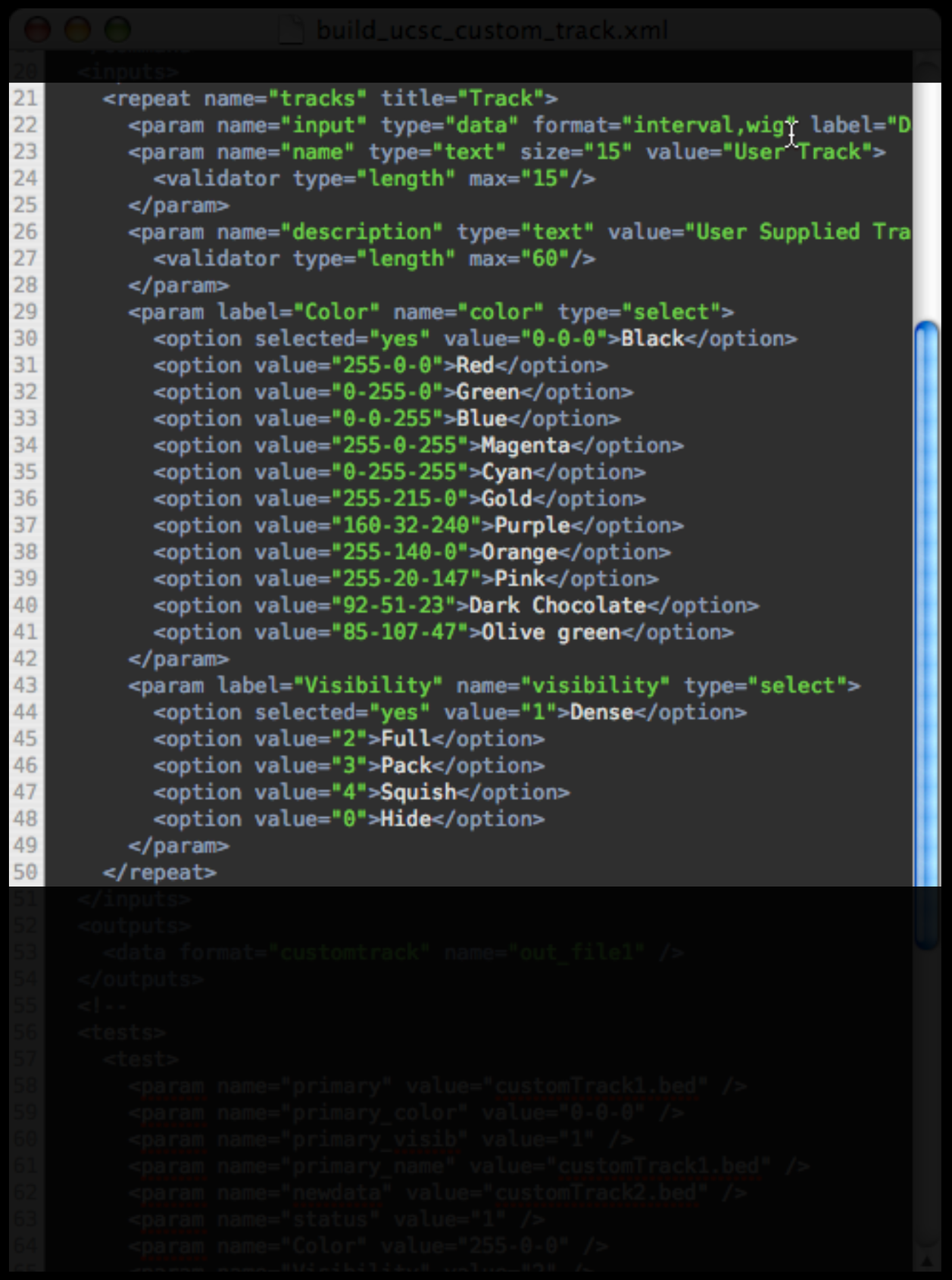
Please note that the primary dataset in step 1 of the tool sets the database build for the datasets in following steps. For example, if your first dataset belogs to hg18, you will only be able to select hg18 associated datasets on the next step.

build_ucsc_custom_track.xml

```
20  <inputs>
21    <repeat name="tracks" title="Track">
22      <param name="input" type="data" format="interval,wig" label="D
23      <param name="name" type="text" size="15" value="User Track">
24        <validator type="length" max="15"/>
25      </param>
26      <param name="description" type="text" value="User Supplied Tra
27        <validator type="length" max="60"/>
28      </param>
29      <param label="Color" name="color" type="select">
30        <option selected="yes" value="0-0-0">Black</option>
31        <option value="255-0-0">Red</option>
32        <option value="0-255-0">Green</option>
33        <option value="0-0-255">Blue</option>
34        <option value="255-0-255">Magenta</option>
35        <option value="0-255-255">Cyan</option>
36        <option value="255-215-0">Gold</option>
37        <option value="160-32-240">Purple</option>
38        <option value="255-140-0">Orange</option>
39        <option value="255-20-147">Pink</option>
40        <option value="92-51-23">Dark Chocolate</option>
41        <option value="85-107-47">Olive green</option>
42      </param>
43      <param label="Visibility" name="visibility" type="select">
44        <option selected="yes" value="1">Dense</option>
45        <option value="2">Full</option>
46        <option value="3">Pack</option>
47        <option value="4">Squish</option>
48        <option value="0">Hide</option>
49      </param>
50    </repeat>
51  </inputs>
52  <outputs>
53    <data format="customtrack" name="out_file1" />
54  </outputs>
55  <!--
56  <tests>
57    <test>
58      <param name="primary" value="customTrack1.bed" />
59      <param name="primary_color" value="0-0-0" />
60      <param name="primary_visib" value="1" />
61      <param name="primary_name" value="customTrack1.bed" />
62      <param name="newdata" value="customTrack2.bed" />
63      <param name="status" value="1" />
64      <param name="Color" value="255-0-0" />
65      <param name="Visibility" value="2" />
66      <param name="other names" value="customTrack2.bed" />
```

Line: 87 Column: 8 XML Soft Tabs: 2





Repeating sets of parameters

build_ucsc_custom_track.xml

```
<tool id="build_ucsc_custom_track_1" name="Build custom track">
  <description>for UCSC genome browser</description>
  <command interpreter="python2.4">
    build_ucsc_custom_track.py
      "$out_file1"
      #for $t in $tracks
        "${t.input.file_name}"
        "${t.input.ext}"
        #if $t.input.ext == "interval"
          ${t.input.metadata.chromCol},${t.input.metadata.startCol},${t.input.metadata.endCol},${t.input.metadata.strandCol}
        #else
          "NA"
        #end if
        "${t.name}"
        "${t.description}"
        "${t.color}"
        "${t.visibility}"
      #end for
  </command>
  <inputs>
    <repeat name="tracks" title="Track">
      <param name="input" type="data" format="interval,wig" label="Dataset" />
      <param name="name" type="text" size="15" value="User Track">
        <validator type="length" max="15"/>
      </param>
      <param name="description" type="text" value="User Supplied Track (from Galaxy)">
        <validator type="length" max="60"/>
      </param>
      <param label="Color" name="color" type="select">
        <option selected="yes" value="0-0-0">Black</option>
        <option value="255-0-0">Red</option>
        <option value="0-255-0">Green</option>
        <option value="0-0-255">Blue</option>
        <option value="255-0-255">Magenta</option>
        <option value="0-255-255">Cyan</option>
        <option value="255-215-0">Gold</option>
        <option value="160-32-240">Purple</option>
        <option value="255-140-0">Orange</option>
        <option value="255-20-147">Pink</option>
        <option value="92-51-23">Dark Chocolate</option>
        <option value="85-107-47">Olive green</option>
      </param>
```

Template language for building complex command lines

Tools

Get Data
Get ENCODE Data
ENCODE Tools
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 columns
- Scatterplot of two numeric columns
- XY Plot
- GMAJ Multiple Alignment Viewer
- Build custom track for UCSC genome browser

EMBOSS
HYPHY

XY Plot

Plot Title: Sample Plot
Label for x axis: Distance
Label for y axis: Count

Series

Series 1

Dataset: 5: Intersect on data 3 and data 4
Column for x axis: 1
Column for y axis: 2
Series Type: Line
Line Type: Solid
Line Color: Black
Line Width: 1.0

Remove Series 1

Series 2

Dataset: 7: Homo sapiens genes (NCBI36)
Column for x axis: 1
Column for y axis: 1
Series Type: Points
Point Type: Circle (hollow)
Point Color: Black
Point Scale: 1.0

Remove Series 2

Add new Series

Execute

History (options)

refresh | collapse all

7: Homo sapiens genes (NCBI36)
6: UCSC Main on Human: knownGene (genome)
5: Intersect on data 3 and data 4
4: UCSC Main on Human: knownGene (genome)
3: Pasted Entry

XY Plot

Plot Title: Sample Plot

Label for x axis: Distance

Label for y axis: Count

Series

Series 1

Dataset: 5: Intersect on data 3 and data 4

Column for x axis: 1

Column for y axis: 2

Series Type: Line

Line Type: Solid

Line Color: Black

Line Width: 1.0

Remove Series 1

Series 2

Dataset: 7: Homo sapiens genes (NCBI36)

Column for x axis: 1

Column for y axis: 1

Series Type: Points

Point Type: Circle (hollow)

Point Color: Black

Point Scale: 1.0

Remove Series 2

Add new Series

Execute

xy_plot.xml

```
<inputs>
  <param name="main" type="text"
         value="" size="30"
         label="Plot Title"/>
  <param name="xlab" type="text"
         value="" size="30"
         label="Label for x axis"/>
  <param name="ylab" type="text"
         value="" size="30"
         label="Label for y axis"/>
  <repeat name="series" title="Series">
    <param name="input"
           type="data" format="tabular"
           label="Dataset"/>
    <param name="xcol" type="integer"
           value="1" size="30"
           label="Column for x axis"/>
    <param name="ycol" type="integer"
           value="1" size="30"
           label="Column for y axis"/>
    <conditional name="series_type">
      <param name="type" type="select" label="Series Type">
        <option value="line" selected="true">Line</option>
        <option value="points">Points</option>
      </param>
      <when value="line">
        <param name="lty" type="select" label="Line Type">
          <option value="1">Solid</option>
          <option value="2">Dashed</option>
          <option value="3">Dotted</option>
        </param>
        <param name="col" type="select" label="Line Color">
          <option value="1">Black</option>
          <option value="2">Red</option>
          <option value="3">Green</option>
          <option value="4">Blue</option>
          <option value="5">Cyan</option>
          <option value="6">Magenta</option>
          <option value="7">Yellow</option>
          <option value="8">Gray</option>
        </param>
        <param name="lwd" type="float" label="Line Width" valu
      </when>
```

Line: 146 Column: 1 XML Soft Tabs: 2

XY Plot

Plot Title: Sample Plot

Label for x axis: Distance

Label for y axis: Count

Series

Series 1

Dataset: 5: Intersect on data 3 and data 4

Column for x axis: 1

Column for y axis: 2

Series Type: Line

Line Type: Solid

Line Color: Black

Line Width: 1.0

Remove Series 1

Series 2

Dataset: 7: Homo sapiens genes (NCBI36)

Column for x axis: 1

Column for y axis: 1

Series Type: Points

Point Type: Circle (hollow)

Point Color: Black

Point Scale: 1.0

Remove Series 2

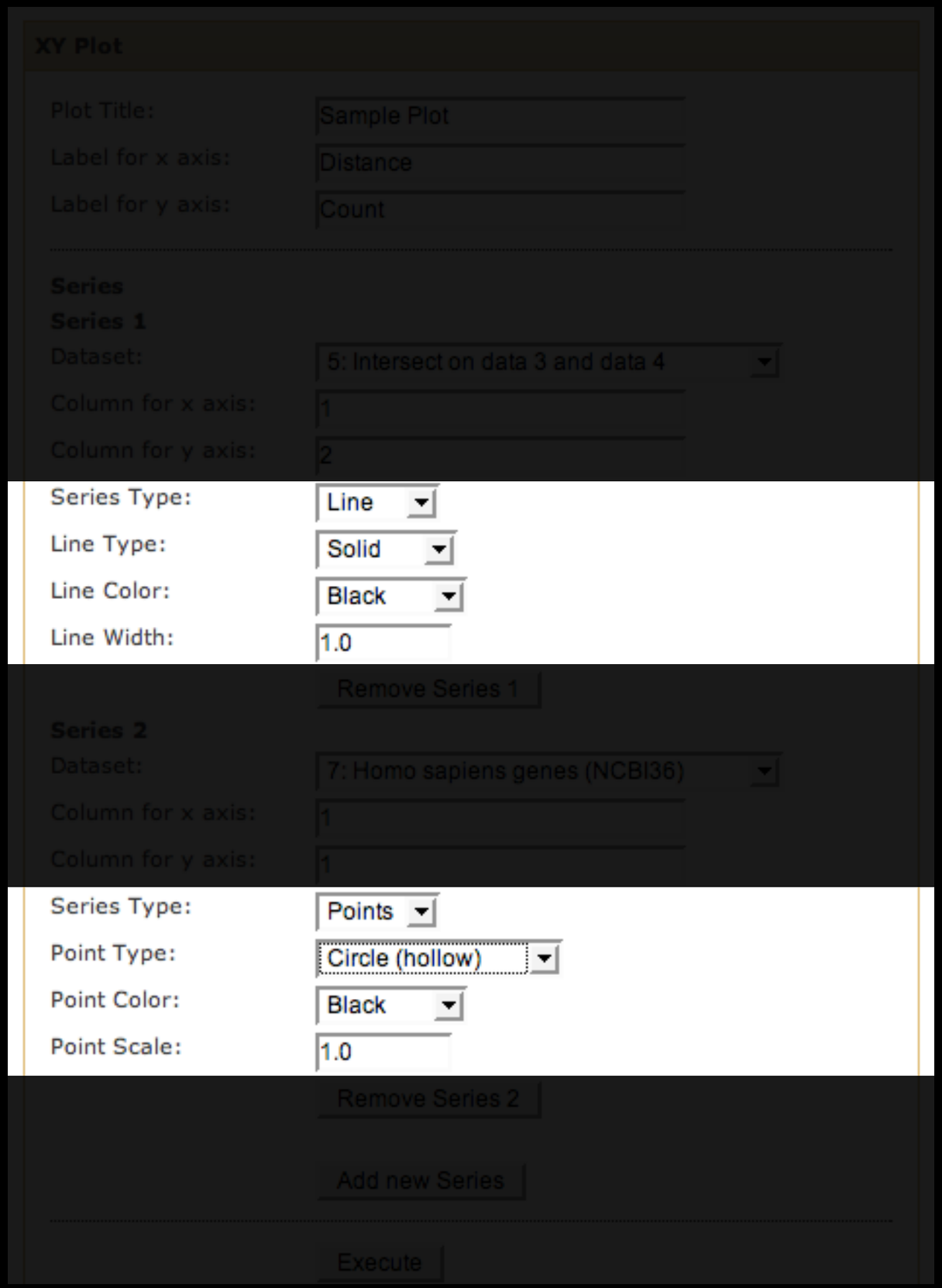
Add new Series

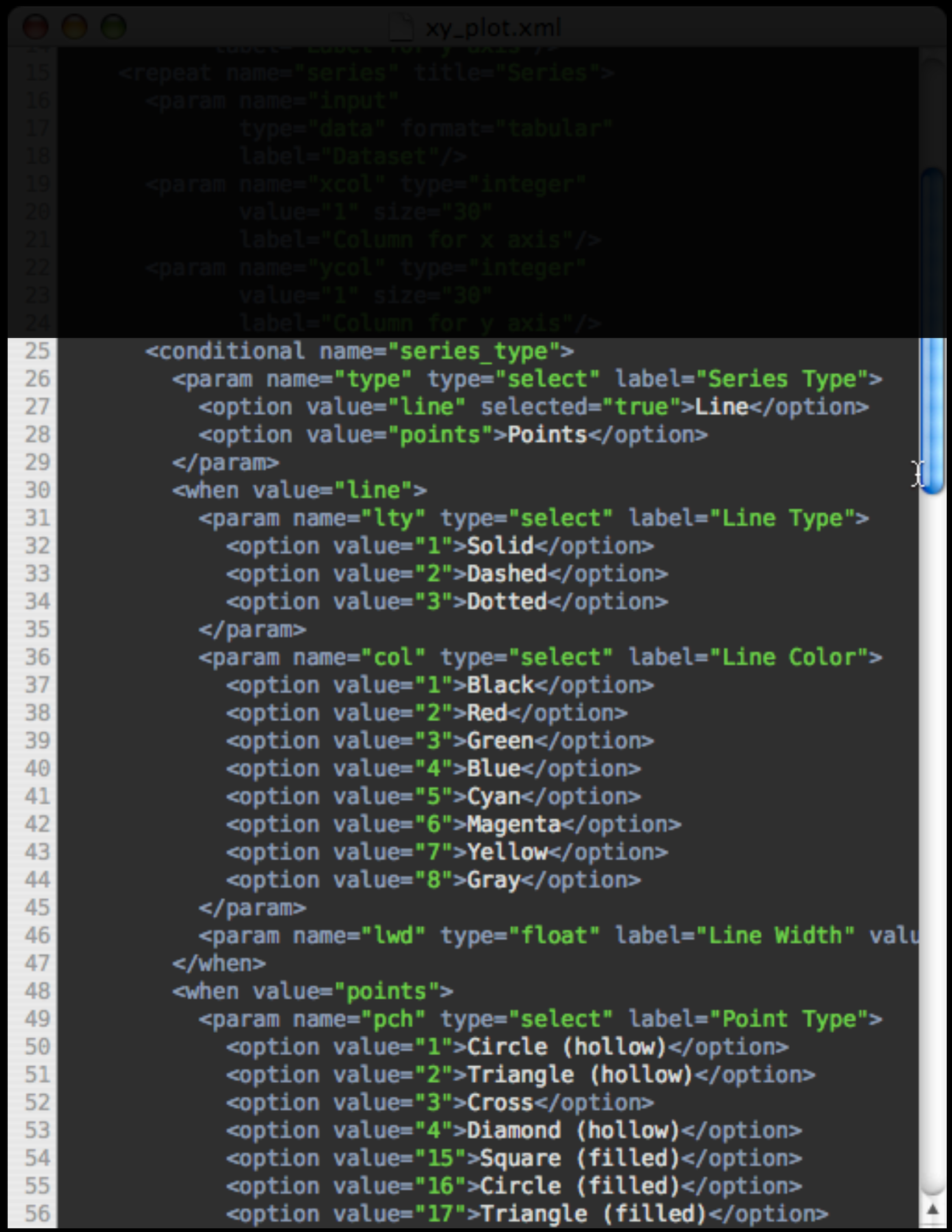
Execute

xy_plot.xml

```
15    <repeat name="series" title="Series">
16      <param name="input"
17             type="data" format="tabular"
18             label="Dataset"/>
19      <param name="xcol" type="integer"
20             value="1" size="30"
21             label="Column for x axis"/>
22      <param name="ycol" type="integer"
23             value="1" size="30"
24             label="Column for y axis"/>
25      <conditional name="series_type">
26        <param name="type" type="select" label="Series Type">
27          <option value="line" selected="true">Line</option>
28          <option value="points">Points</option>
29        </param>
30        <when value="line">
31          <param name="lty" type="select" label="Line Type">
32            <option value="1">Solid</option>
33            <option value="2">Dashed</option>
34            <option value="3">Dotted</option>
35          </param>
36          <param name="col" type="select" label="Line Color">
37            <option value="1">Black</option>
38            <option value="2">Red</option>
39            <option value="3">Green</option>
40            <option value="4">Blue</option>
41            <option value="5">Cyan</option>
42            <option value="6">Magenta</option>
43            <option value="7">Yellow</option>
44            <option value="8">Gray</option>
45          </param>
46          <param name="lwd" type="float" label="Line Width" valu
47        </when>
48        <when value="points">
49          <param name="pch" type="select" label="Point Type">
50            <option value="1">Circle (hollow)</option>
51            <option value="2">Triangle (hollow)</option>
52            <option value="3">Cross</option>
53            <option value="4">Diamond (hollow)</option>
54            <option value="15">Square (filled)</option>
55            <option value="16">Circle (filled)</option>
56            <option value="17">Triangle (filled)</option>
57          </param>
```

Line: 146 Column: 1 XML Soft Tabs: 2





Conditional groups, grouping constructs can be nested

xy_plot.xml

```
<tool id="XY_Plot_1" name="XY Plot">
  <description> of two numeric columns</description>
  <command interpreter="bash">r_wrapper.sh $script_file</command>

  <inputs>
    <param name="main" type="text"
           value="" size="30"
           label="Plot Title"/>
    <param name="xlab" type="text"
           value="" size="30"
           label="Label for x axis"/>
    <param name="ylab" type="text"
           value="" size="30"
           label="Label for y axis"/>
    <repeat name="series" title="Series">
      <param name="input"
             type="data" format="tabular"
             label="Dataset"/>
      <param name="xcol" type="integer"
             value="1" size="30"
             label="Column for x axis"/>
      <param name="ycol" type="integer"
             value="1" size="30"
             label="Column for y axis"/>
      <conditional name="series_type">
        <param name="type" type="select" label="Series Type">
          <option value="line" selected="true">Line</option>
          <option value="points">Points</option>
        </param>
        <when value="line">
          <param name="lty" type="select" label="Line Type">
            <option value="1">Solid</option>
            <option value="2">Dashed</option>
            <option value="3">Dotted</option>
          </param>
          <param name="col" type="select" label="Line Color">
            <option value="1">Black</option>
            <option value="2">Red</option>
            <option value="3">Green</option>
            <option value="4">Blue</option>
            <option value="5">Cyan</option>
            <option value="6">Magenta</option>
```

Command line tool expects a configuration file

xy_plot.xml

```
    </conditional>
  </repeat>
</inputs>

<configfiles>
  <configfile name="script_file">
    ## Setup R error handling to go to stderr
    options( show.error.messages=F,
             error = function () { cat( geterrmessage(), file=stderr() ); q( "no", 1, F ) } )
    ## Determine range of all series in the plot
    xrange = c( NULL, NULL )
    yrange = c( NULL, NULL )
    #for $i, $s in enumerate( $series )
      s${i} = read.table( "${s.input.file_name}" )
      x${i} = s${i}[,${s.xcol}]
      y${i} = s${i}[,${s.ycol}]
      xrange = range( x${i}, xrange )
      yrange = range( y${i}, yrange )
    #end for
    ## Open output PDF file
    pdf( "${out_file1}" )
    ## Dummy plot for axis / labels
    plot( NULL, type="n", xlim=xrange, ylim=yrange, main="${main}", xlab="${xlab}", ylab="${ylab}" )
    ## Plot each series
    #for $i, $s in enumerate( $series )
      #if $s.series_type['type'] == "line"
        lines( x${i}, y${i}, lty=${s.series_type.lty}, lwd=${s.series_type.lwd}, col=${s.series_type.col} )
      #elif $s.series_type.type == "points"
        points( x${i}, y${i}, pch=${s.series_type.pch}, cex=${s.series_type.cex}, col=${s.series_type.col} )
      #end if
    #end for
    ## Close the PDF file
    devname = dev.off()
  </configfile>
</configfiles>

<outputs>
  <data format="pdf" name="out_file1" />
</outputs>

<help>
.. class:: infomark
```

Configuration file is generated based on user input

Job execution in **Galaxy**

Flexible execution environment

- Dependencies between jobs handled by "JobManager" within **Galaxy**.
- Either in-process with the web application, or a separate process managing a queue to which multiple front-ends submit

Flexible execution environment

- Once jobs are ready, submitted to a “JobRunner”
  - Runners are pluggable
  - Can have multiple runners, and jobs to different runners depending on capabilities
- Current implementations:
  - Local runner executing a limited number of local processes
  - PBS runner dispatches to a cluster of worker nodes
  - Pluggable queueing policies

Core tools

Genomic interval analysis

- Set-like operations on intervals, base-level and interval level
  - Merge, intersect, subtract...
  - Interval clustering
- Relational-like operations
  - Join, group
- Data structures and high-level Python interfaces to all operations available as part of “bx-python”

Genomic alignment analysis

- Extracting features of interest from pairwise and multiple genome wide alignments
  - Dealing with gene / transcript structure
- Filtering alignments in many ways
- Tools for indexing alignments, fast random access, and all operations available in “bx-python”

Phylogenomic tools

- Built on top of HyPhy (http://hyphy.org)
  - Phylogenetic tree reconstruction
  - Selection detection
  - Hypothesis testing
  - Relative rate tests
  - Detecting recombination

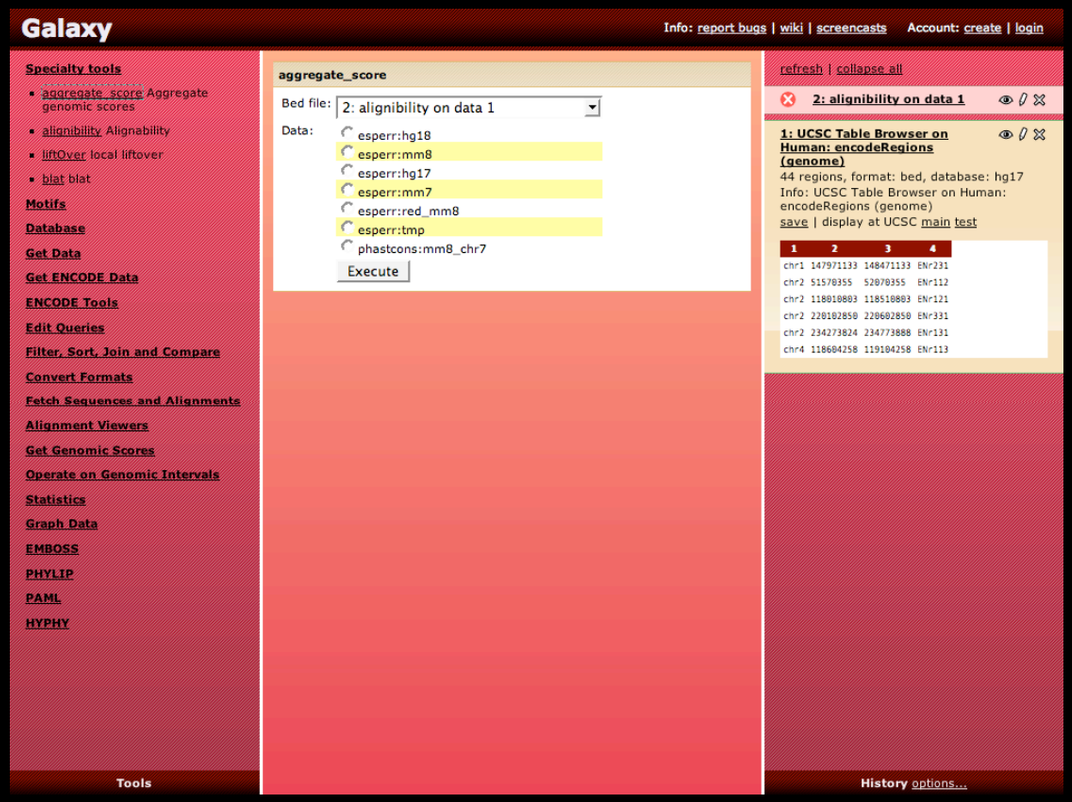
Statistical genetics

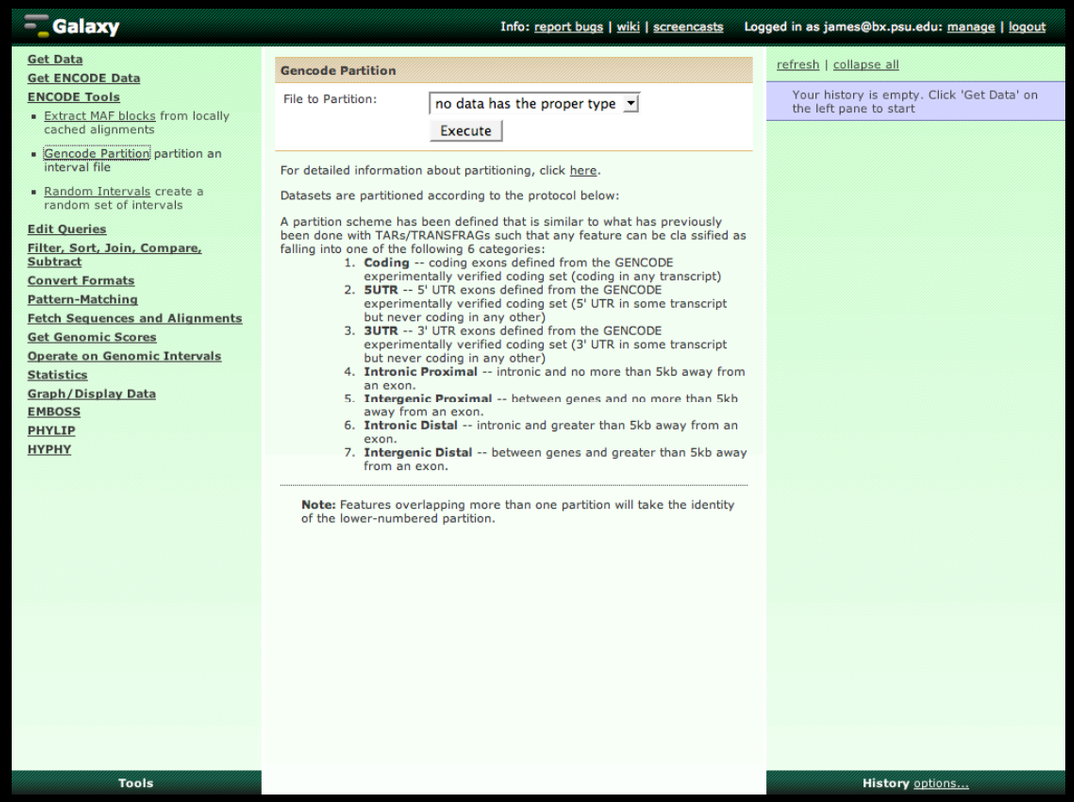
- Built with RGenetics (http://rgenetics.org)
  - Experiment design (including power and sample size calculations)
  - Quality control and filtering
  - Exploration of and adjustment for population substructure
  - Linkage disequlibrium visualization, data reduction based on LD (tag SNP identification)
  - Inference for pedigree and unrelated subject data

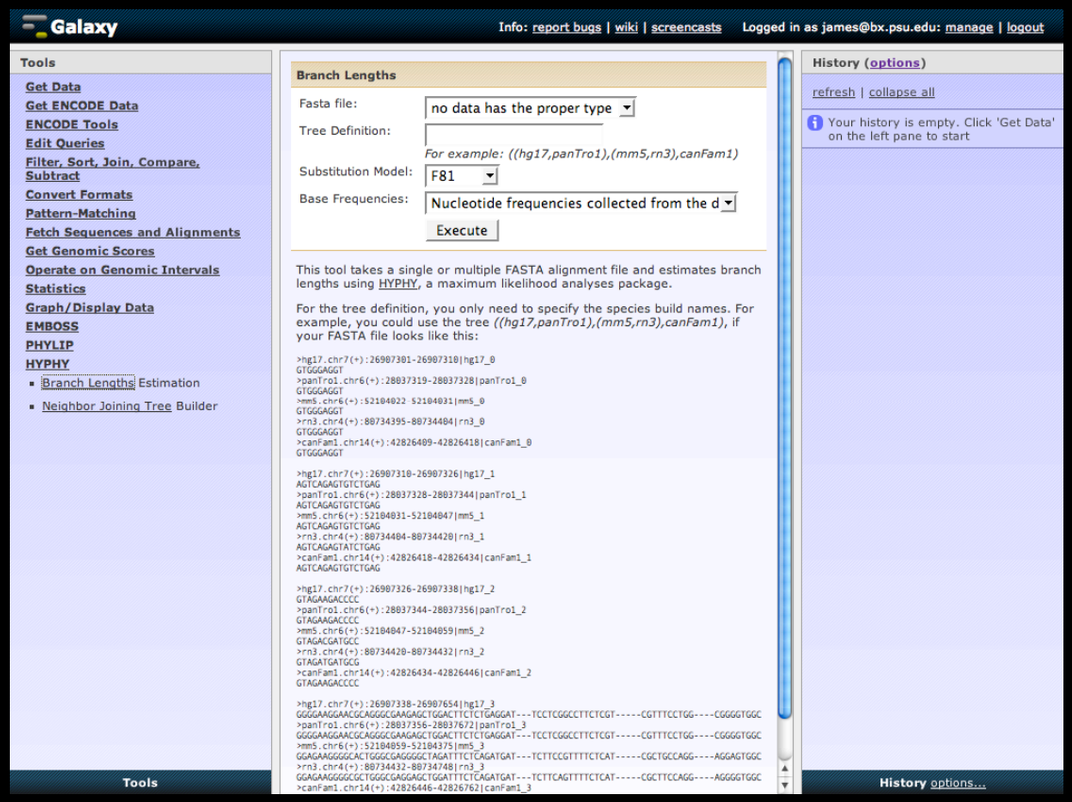
Metagenomics

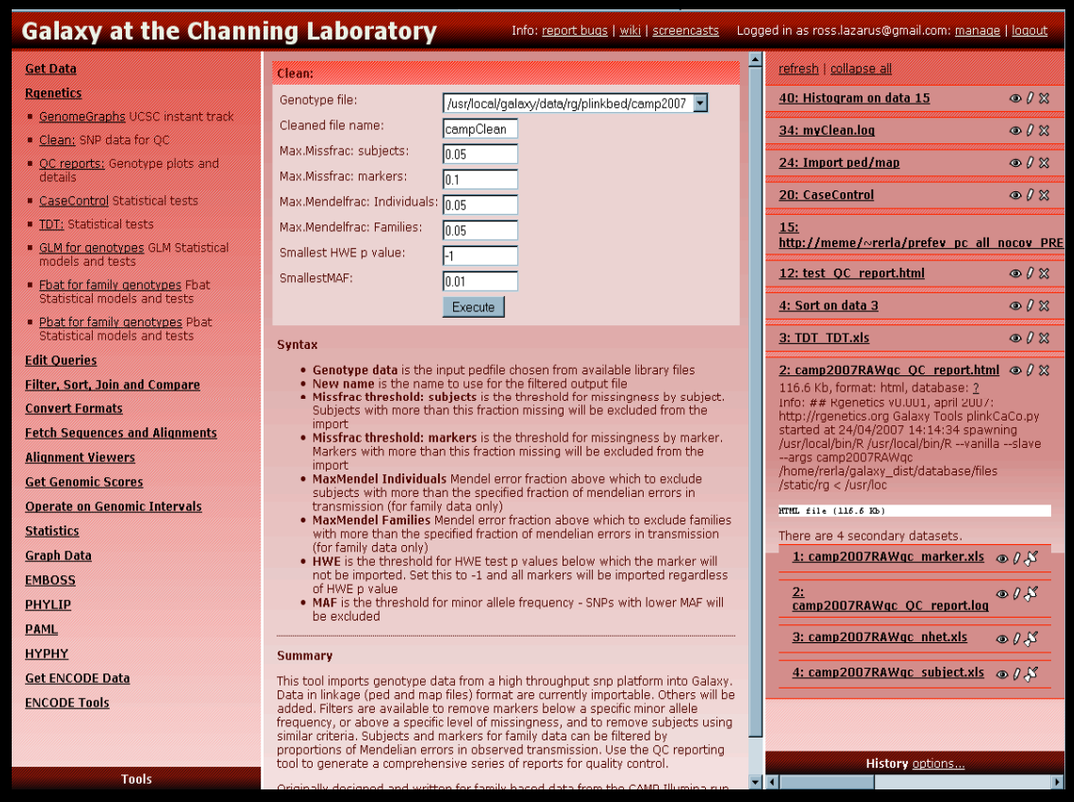
- Mapping “reads” onto protein databases
  - Need to figure out how to do this a lot faster!
- Visualizing
  - On the global phylogeny (MEGAN style)
- ...?

Deeper customization of **Galaxy**









Galaxy web interface is easily customized / branded

Datatypes

- Datatypes supported by a Galaxy instance can be configured at runtime
- Declarative definition of "metadata"
  - Easy way to define custom metadata
    - Automatically generated editing interfaces (similar to tool interfaces)
- Actions on datatypes (displaying at external sites, format conversion) all pluggable
- Nothing "genomics" specific hardcoded!

Reuse and reproducibility

Sharing histories

- A history in **Galaxy** is a complete record of a complex analysis
  - Histories in **Galaxy** can be easily be shared
    - A shared history is always a copy (the original analysis is always retained)
    - All of the details of any analysis can thus be inspected, rerun, ...

Workflows

- A series on analysis steps involving the invocation of multiple tools can be stored and reused
- Parameters within the workflow can be set in the workflow, or when the workflow is invoked (like any other tool)
- Support for repetitive invocation of tools and workflows, and aggregation of results
- Saving and sharing of workflows, reproducible!

Workflow construction

- Explicit workflow construction and editing
- Workflow construction by example
  - Users will continue to build analysis as they do now, and will be able to extraction portions of their histories as reusable workflows
  - Will work for most existing histories! (we've been saving the right data all along)

Some Technical Details

Under the hood

- Python 2.4, though some dependencies use CPython specific extensions (database access, tools)
- WSGI Web framework: PythonPaste, Routes, WebHelpers, Beaker, Cheetah, ...
- SQLAlchemy for database abstraction
- ♡ jQuery

Out of the box configuration

- Just checkout from subversion and run!
- All dependencies packaged as eggs
- Pure python HTTP server included (paste.httpserver)
- Embedded database (sqlite)
- Datasets stored on local filesystem
- Jobs run locally

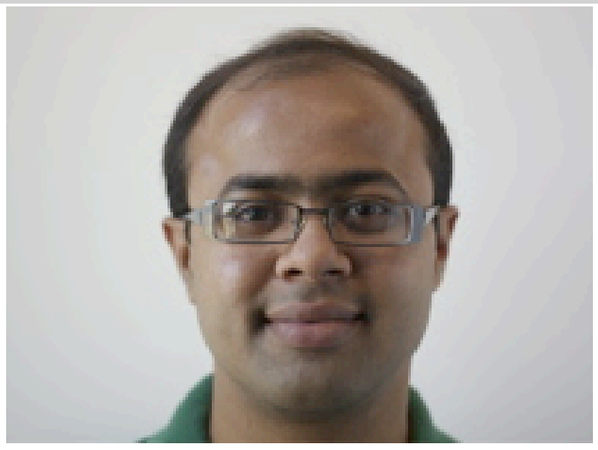
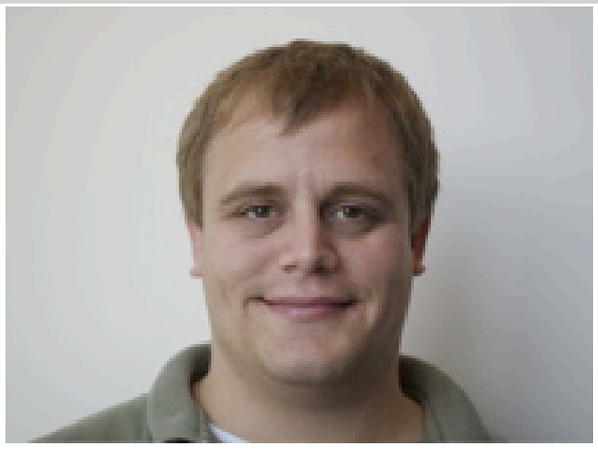
PSU production configuration

- Deployed behind Apache using mod_proxy
  - Python threads do not scale across CPUs, we use both forking and threading similar to Apache's worker MPM
- PostgreSQL
- Jobs dispatched to a PBS cluster using "pbs-python"

Acknowledgements

- **Galaxy** collaborators:
  - Ross Lazarus, Sergei Kosakovsky Pond
  - UCSC Genome Browser team
  - Biomart team
  - National Science Foundation

The core **Galaxy** development team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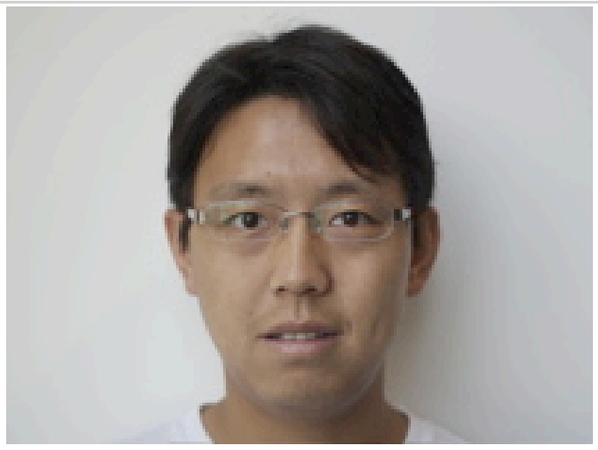	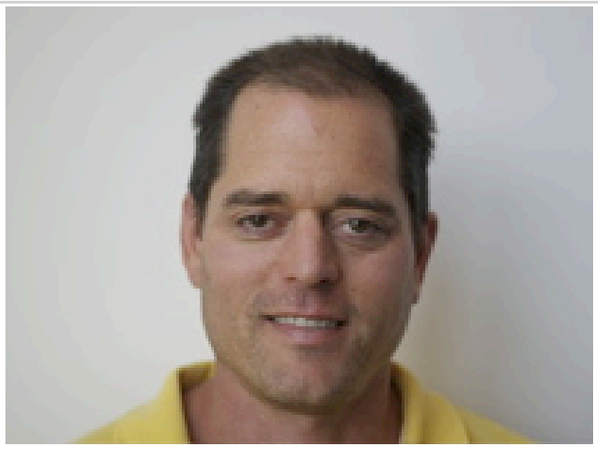	
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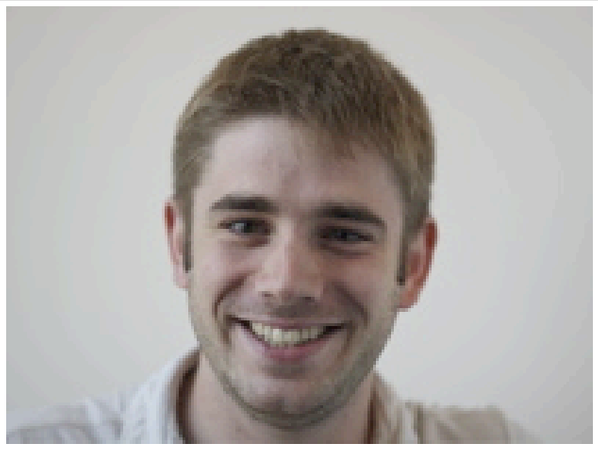		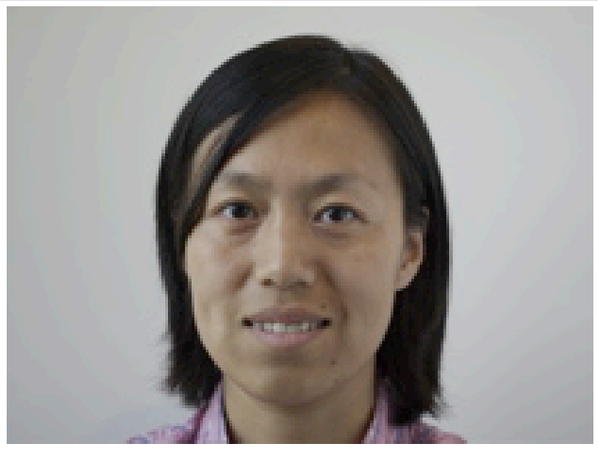
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