Repeatable plant pathology bioinformatic analysis: Not everything is NGS data.

Peter Cock & Leighton Pritchard

Genomics for Non-Model Organisms

ISMB/ECCB - Workshop 6

Vienna, Austria

19 July 2011

The James Hutton Institute

JHI Plant Pathology

- We work on a range of organisms
  - Plant Viruses
  - Bacteria
  - Oomycetes
  - Fungi
  - Nematodes
  - Aphids (as virus vectors)
- Many genome sequences now available…

JHI Dundee site, formerly SCRI (Scottish Crop Research Institute)

Plant Pathogen Genomics

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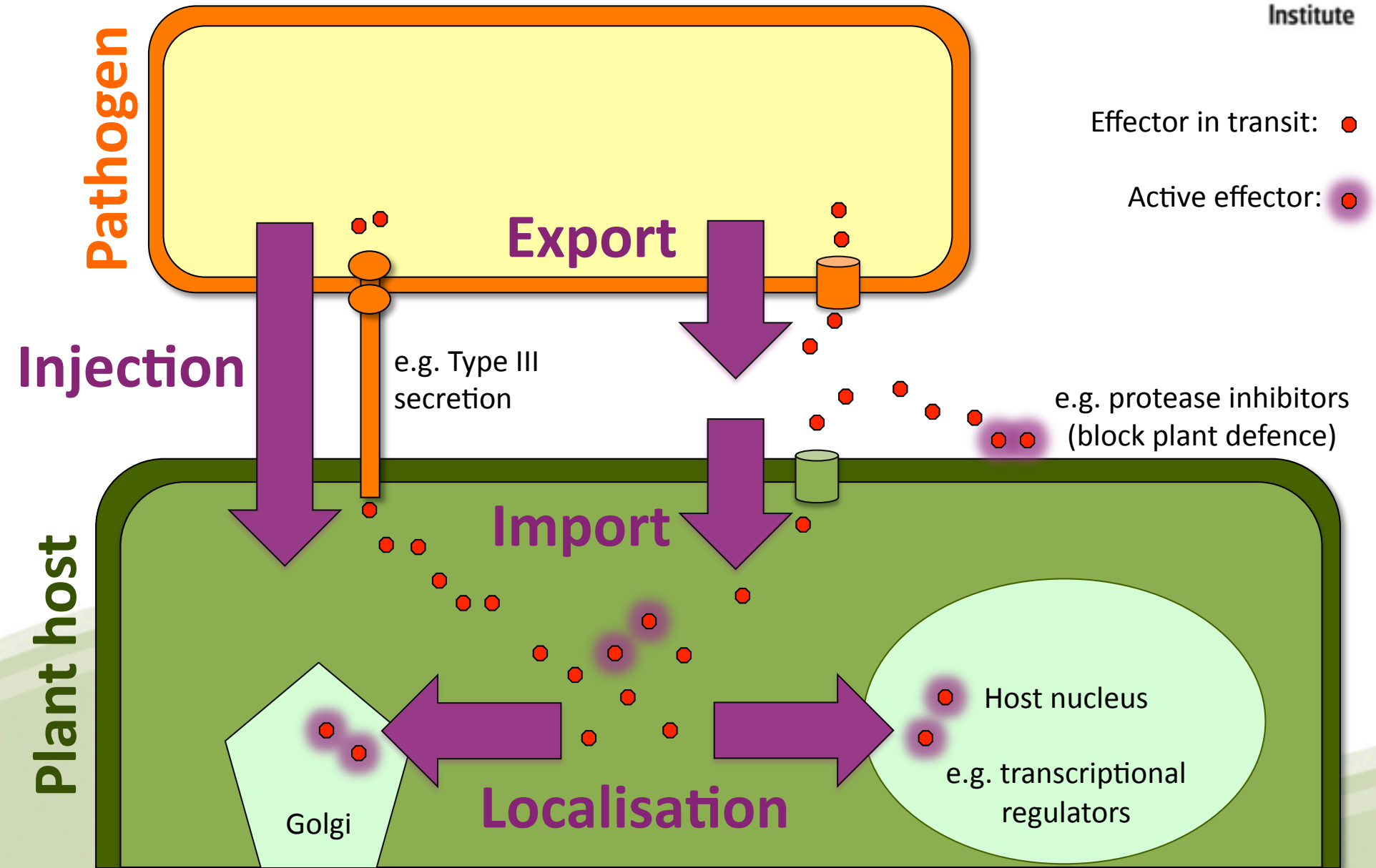
- Sequencing of plant pathogens becoming common
  - I will focus on the protein complement today (i.e. What happens *after* assembly of NGS data)
- Often looking at first genome for a genus
  - Automated gene annotation from other species limited
- In particular we want to find “effectors”
  - i.e. proteins used to manipulate host

Effector Protein Analysis



Example: Effector Protein Analysis

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- Want to identify effector genes, e.g.
  - Similarity to known effectors (e.g. with BLAST)
  - Signal peptides
  - Localization signals
  - Possible horizontal gene transfer (e.g. different GC%)
- Part of larger task of automated gene annotation, e.g.
  - HMMER or RPS-BLAST domain searches
  - GO annotation with Blast2GO

Example: Nematode Effector Proteins

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- To identify candidate effector genes:
  - Want a signal peptide (for export)
  - Don't want a transmembrane domain (not secreted)
- How? Initially used a Python script calling
  - SignalP 3.0
  - TMHMM 2.0
- Now we make this easy to use, thanks to Galaxy…

See Jones *et al.* (2009), Molecular Plant Pathology

What is Galaxy?

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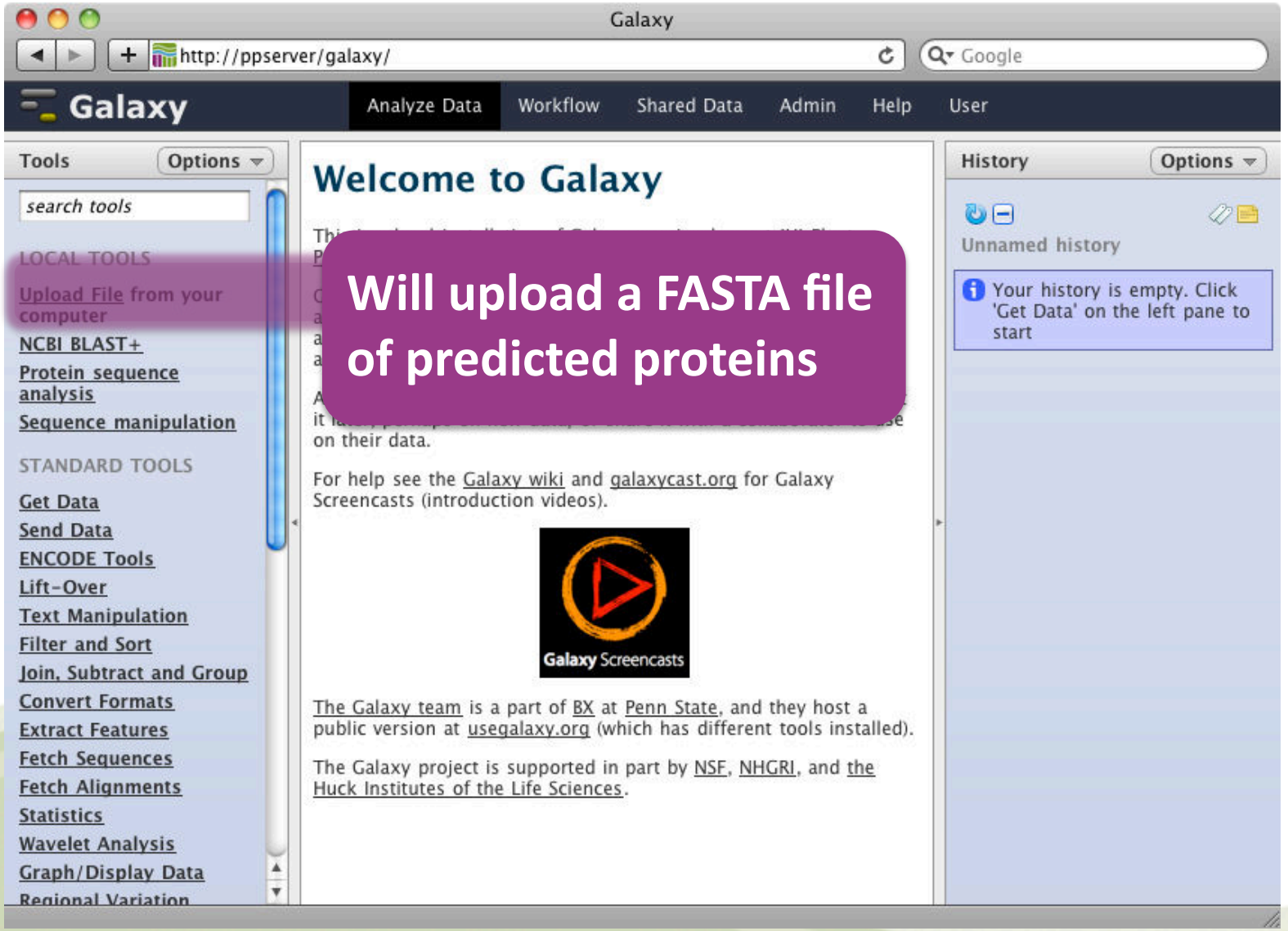
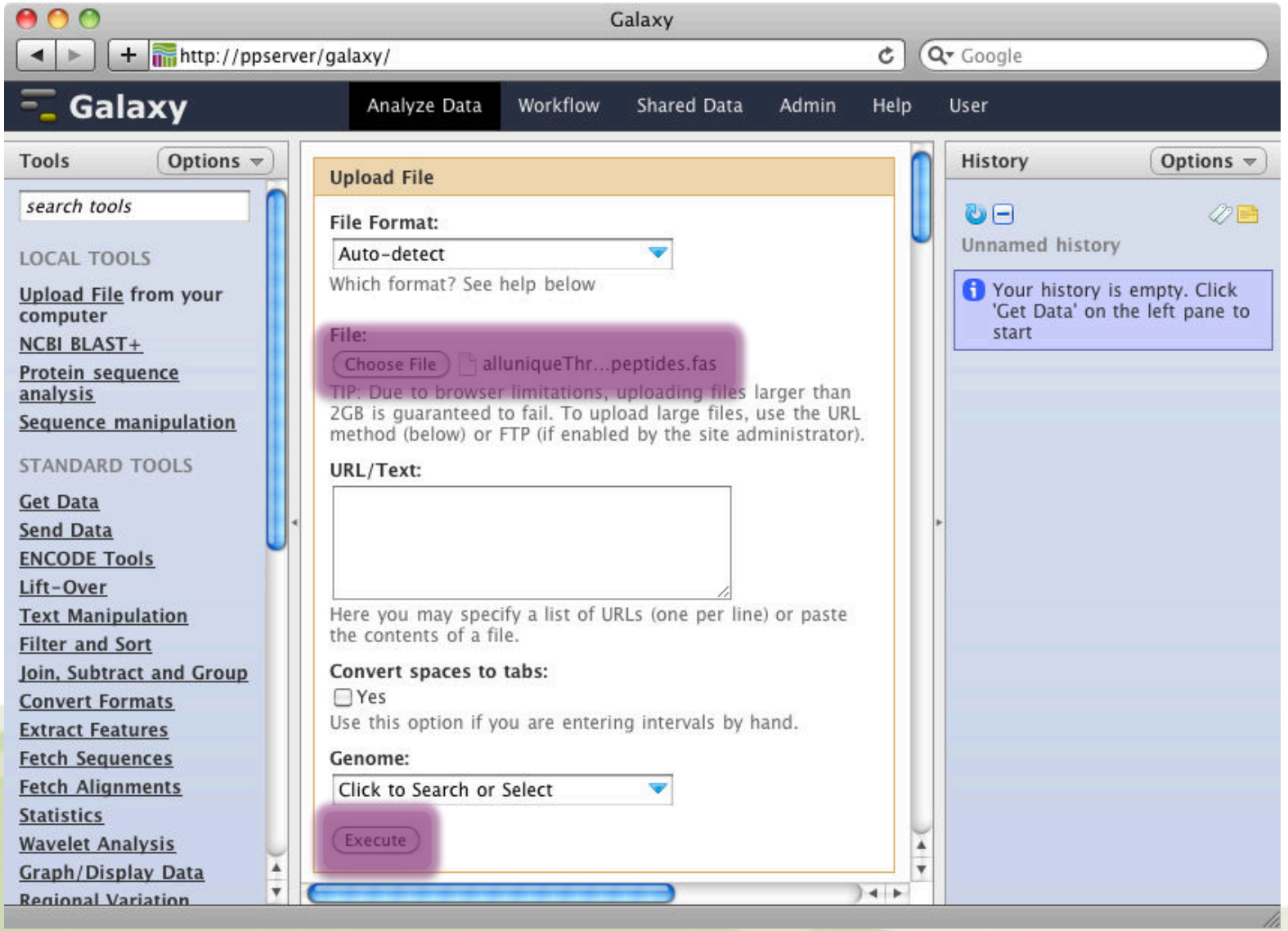
- Web system for running many analysis tools remotely:
  - Upload your data to Galaxy (or access shared data)
  - Run analysis on Galaxy server/cluster
  - Download results (or share them)
- Designed to link multiple analysis steps as workflows:
  - Repeatable
  - Shareable

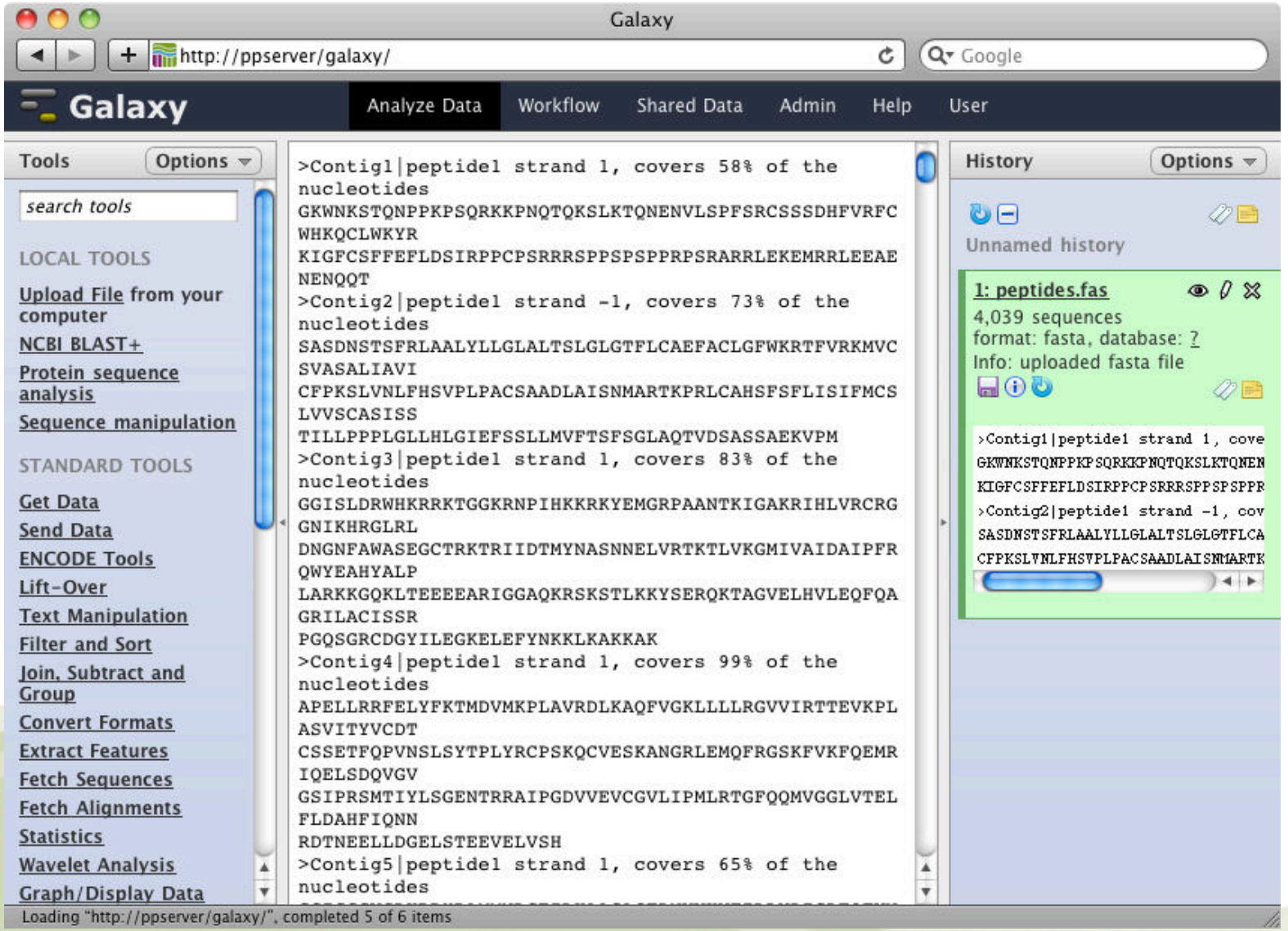
Our local Galaxy Server



Step 1 – Upload FASTA file



Step 1 – Upload FASTA file



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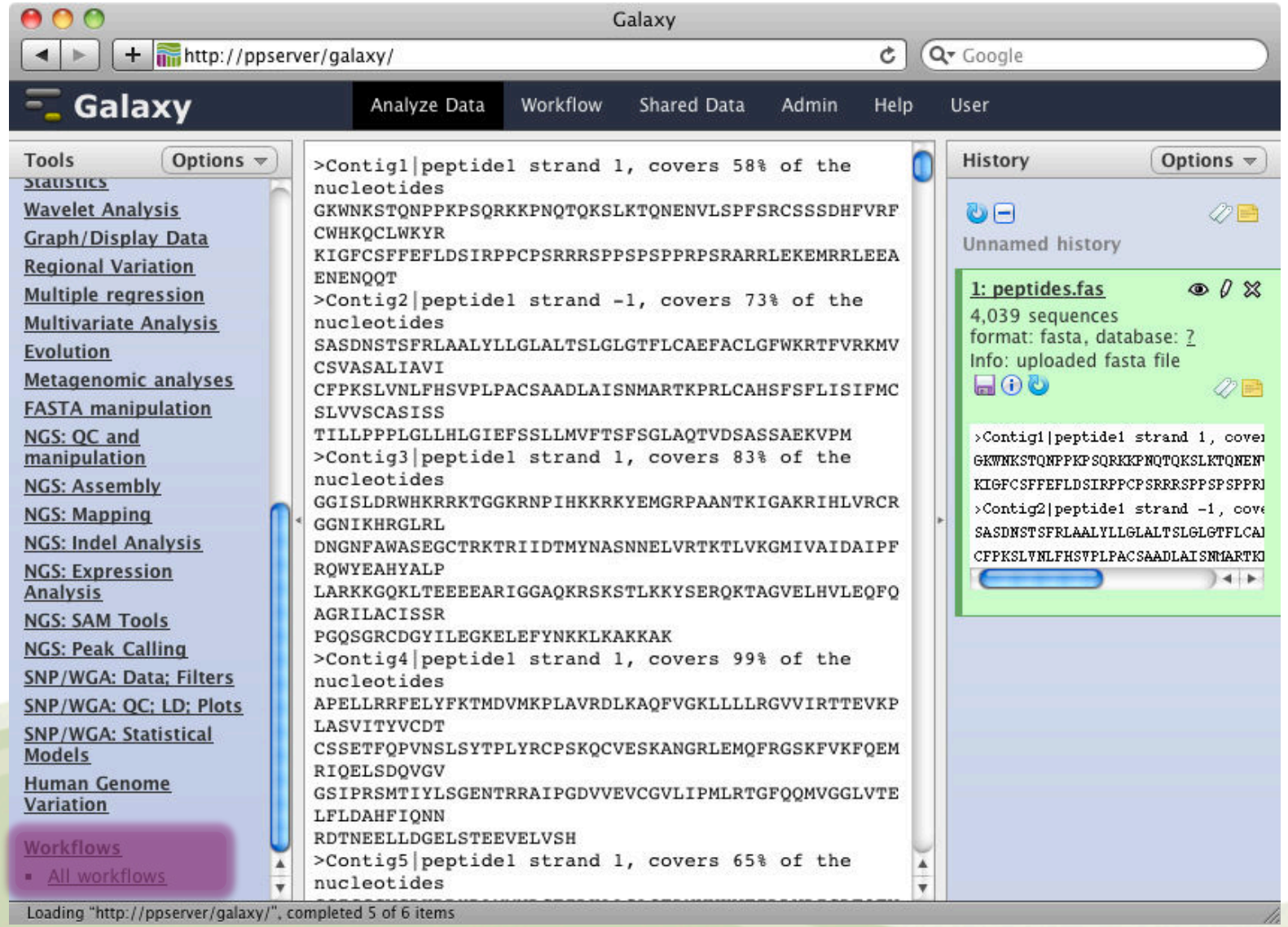

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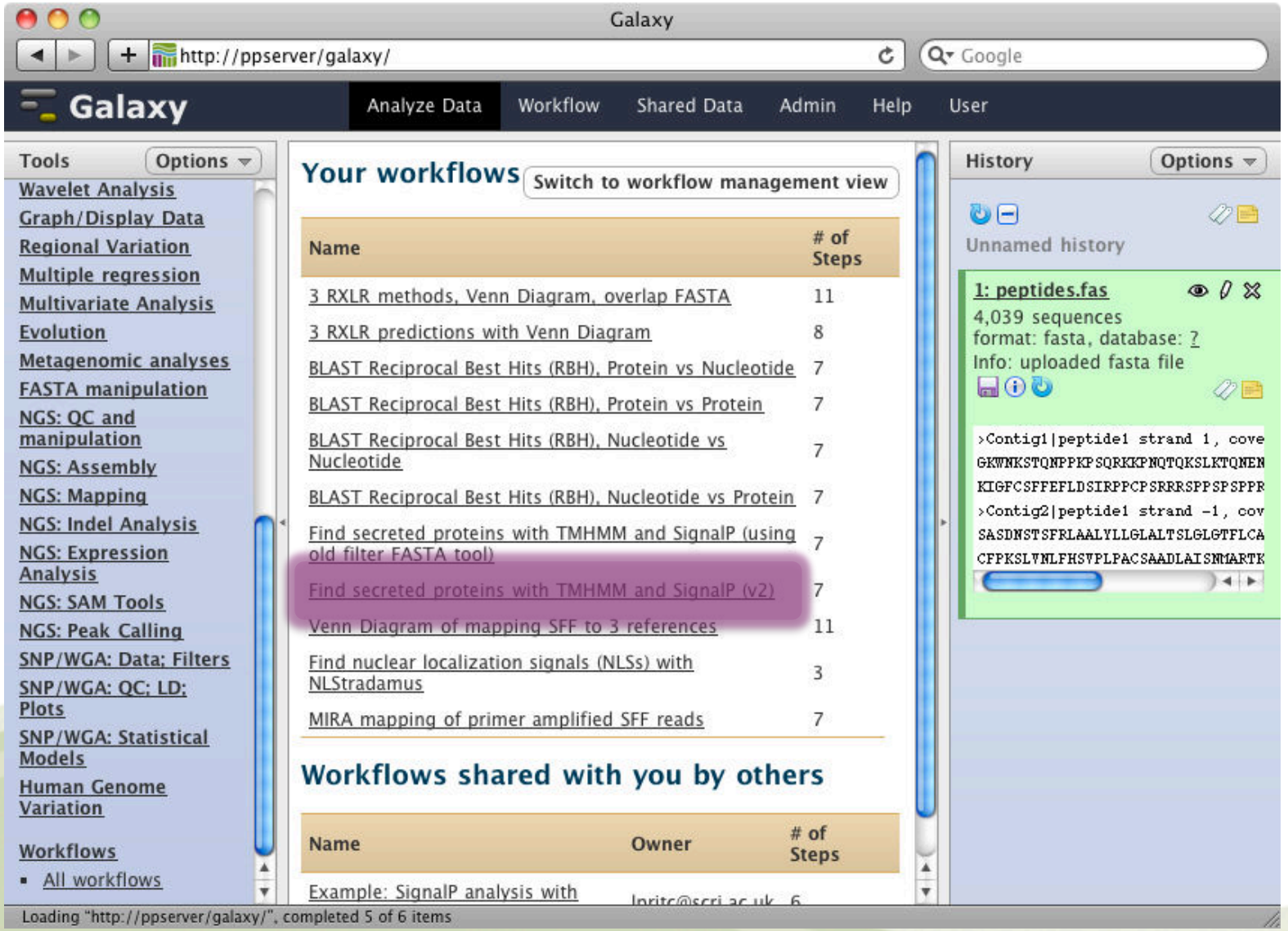
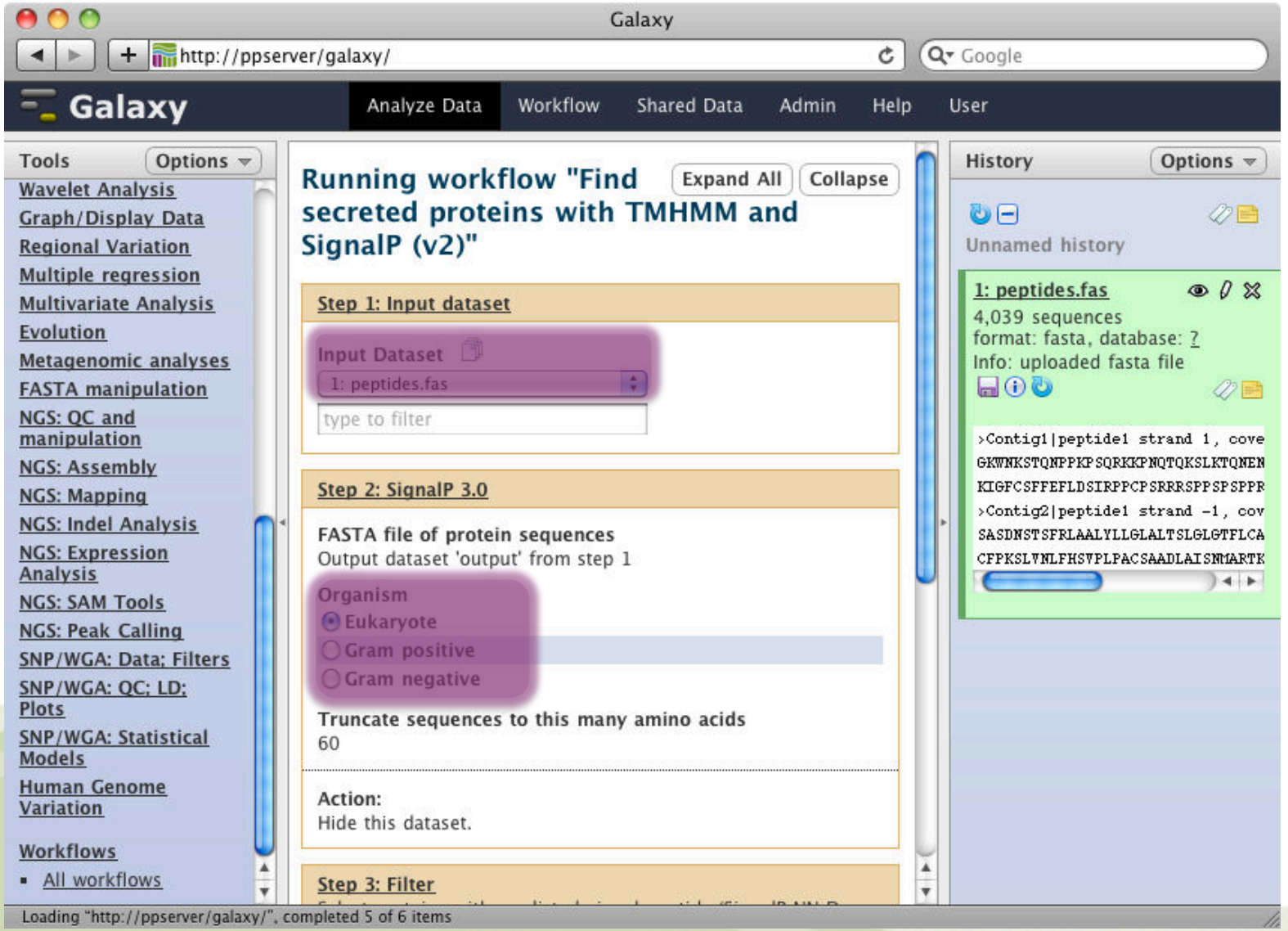


Step 2 – Run workflow



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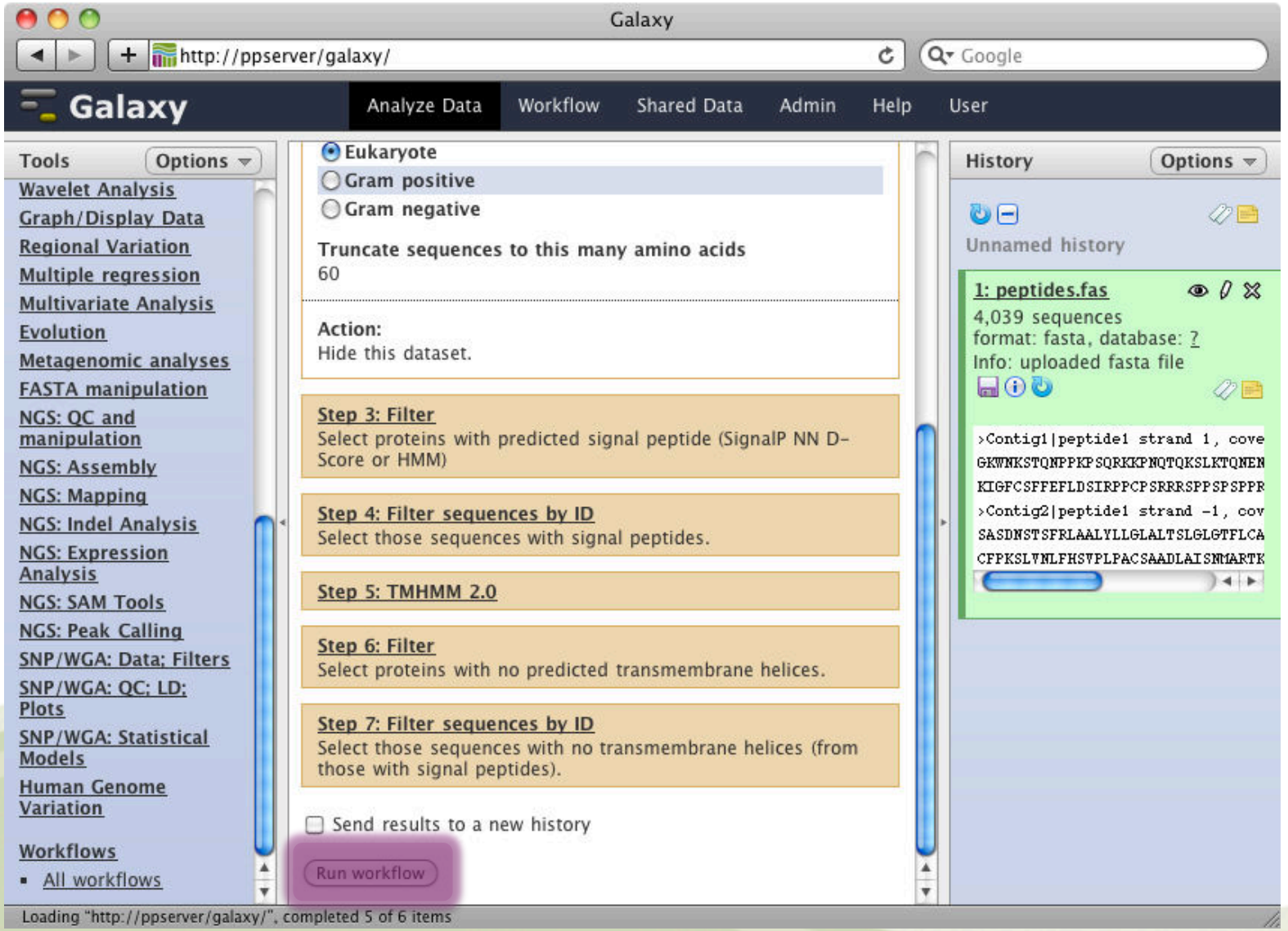
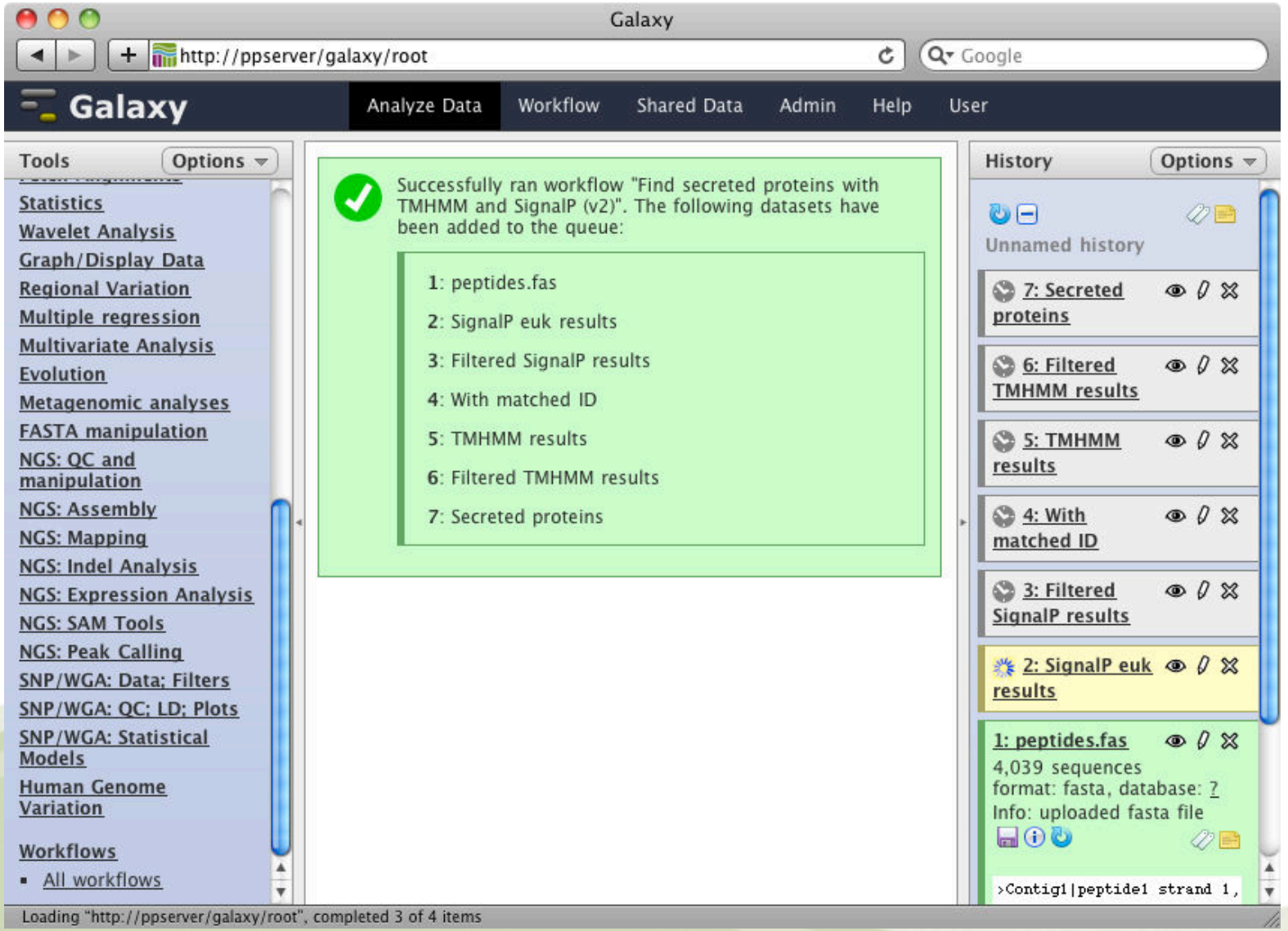


Step 2 – Run workflow



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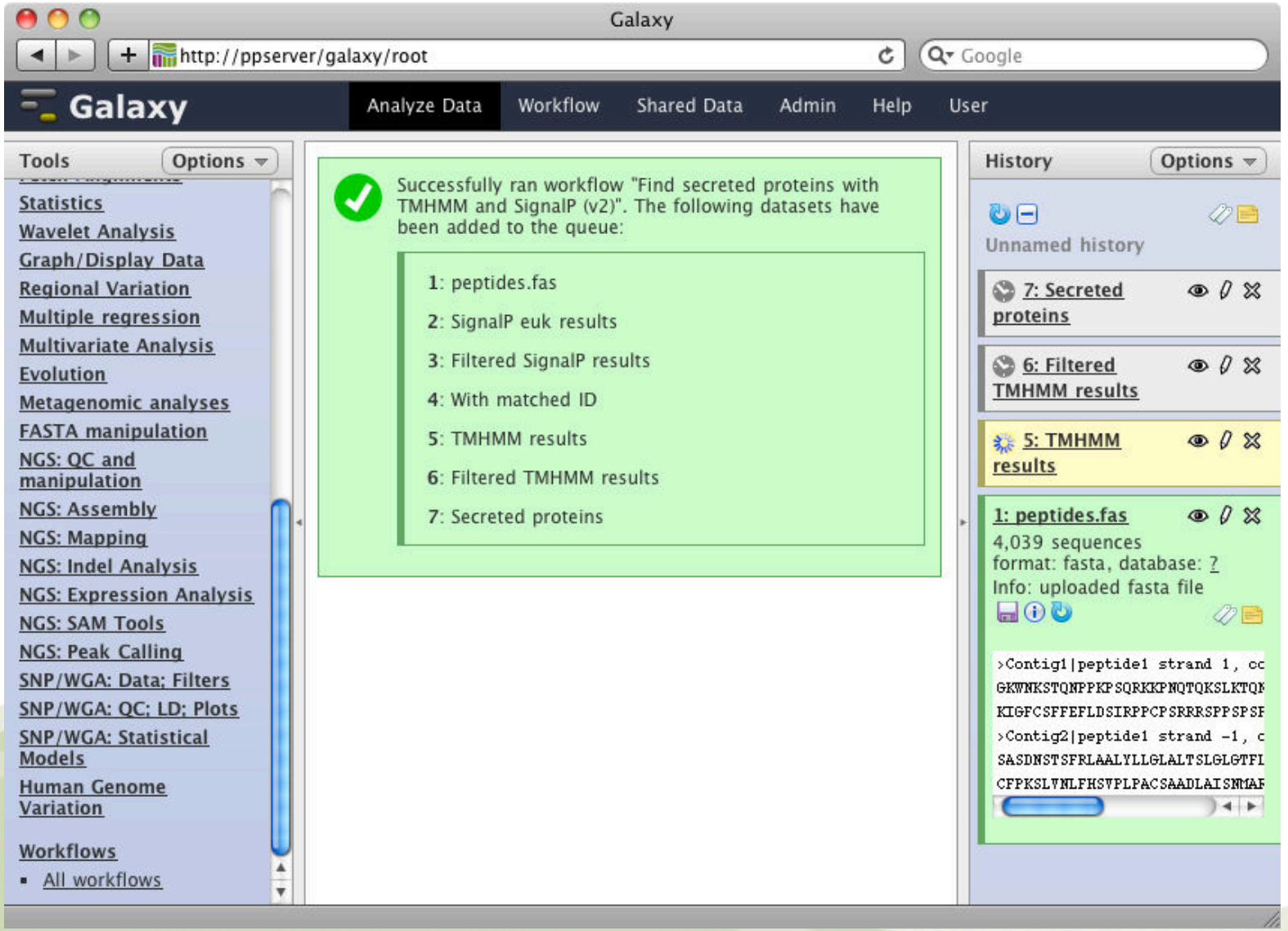
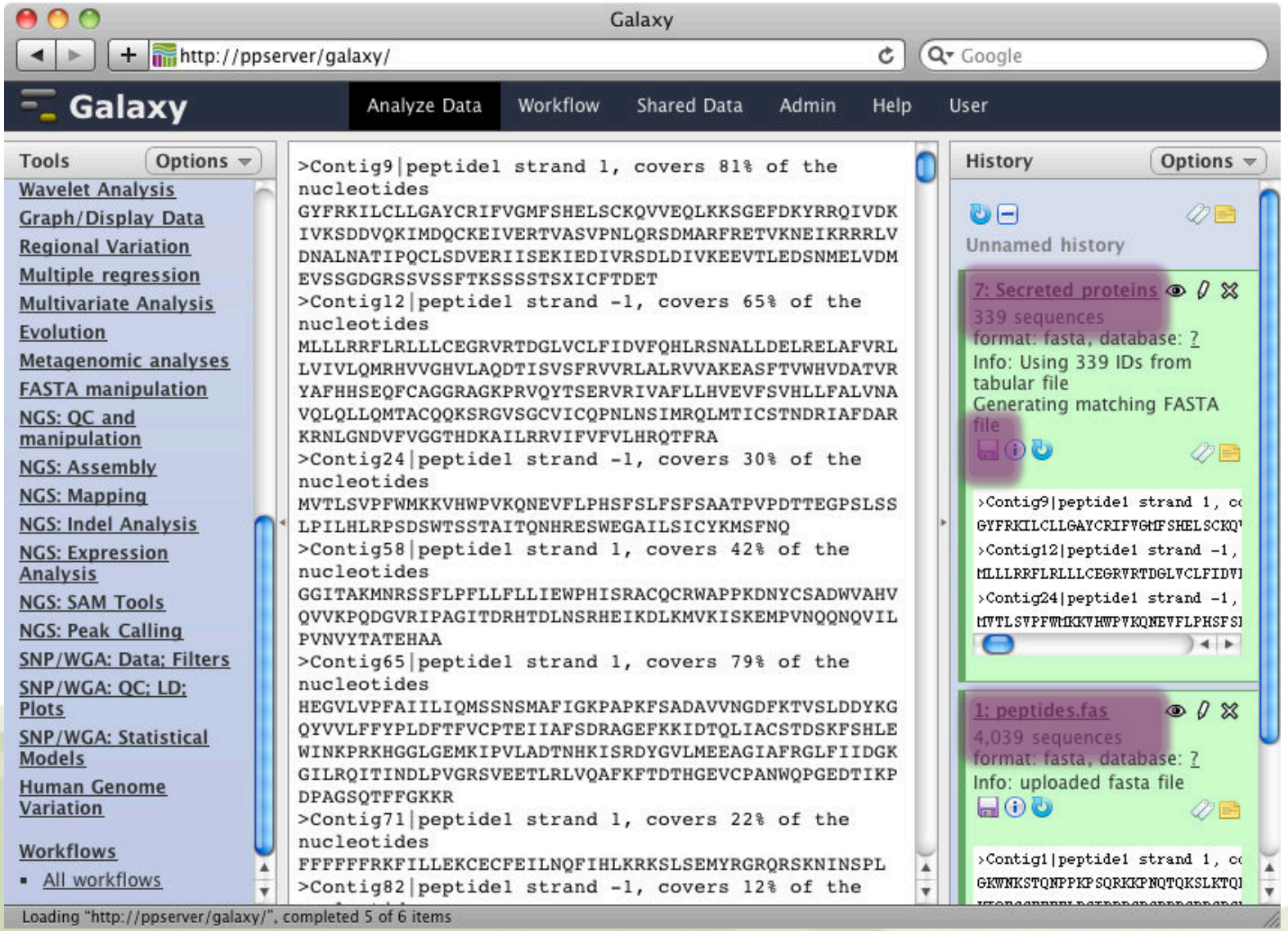


Step 3 – Get results



Example: Effector Protein Analysis

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- To identify candidate effector genes:
  - Want a signal peptide (for export)
  - Don't want a transmembrane domain (not secreted)
- Now use Galaxy workflow calling:
  - SignalP 3.0
  - TMHMM 2.0
- I can share this workflow:
  - Easily available to anyone using our Server
  - If tools installed, could share with other Galaxy Servers
- Easy for our Biologists to apply workflow to their own data

See Jones *et al.* (2009), Molecular Plant Pathology & Kikuchi et al. (2011), PLoS Pathogens

Workflow Editor – Effector finding

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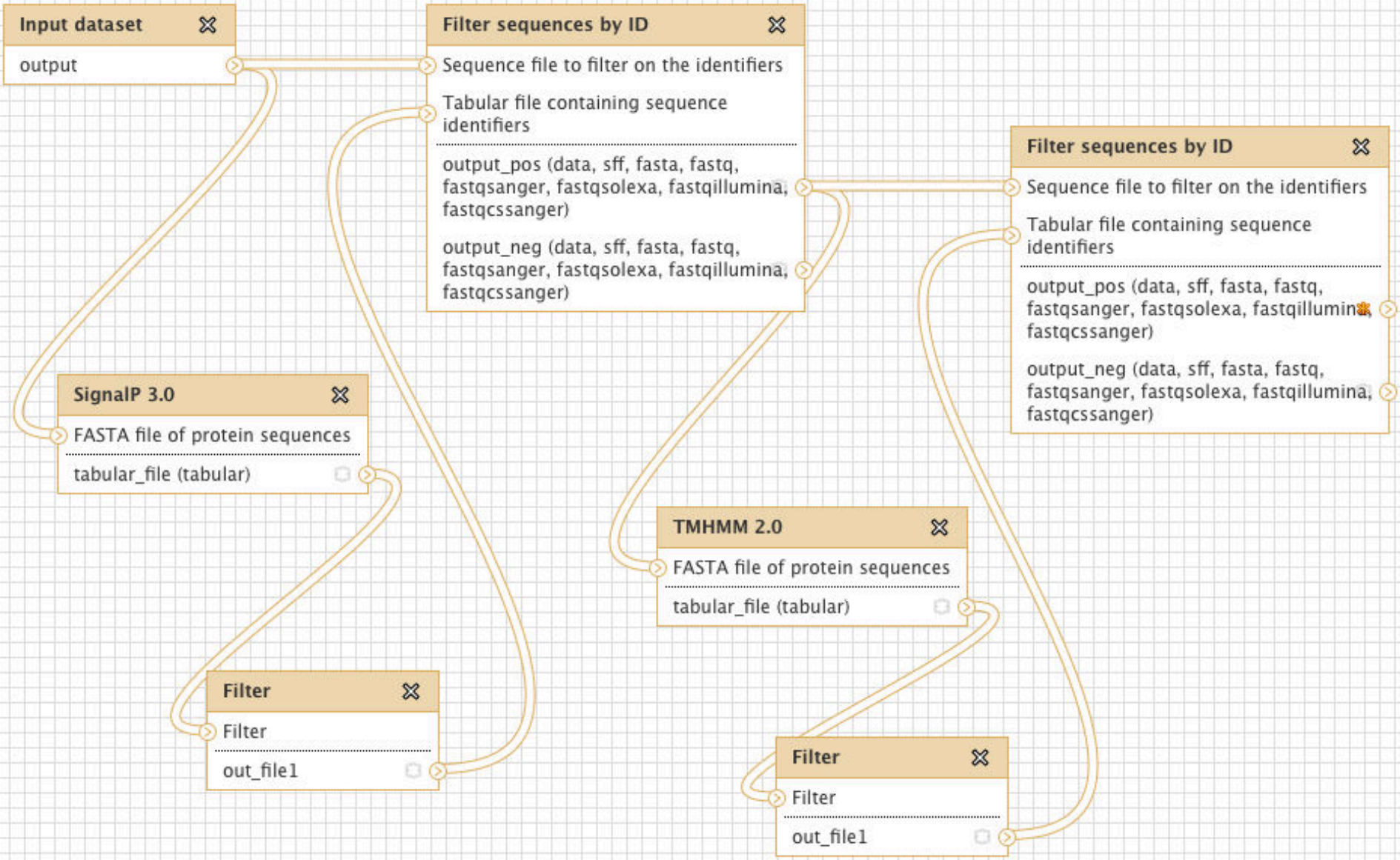

Why Galaxy?

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- Hi Peter, could you run a big BLAST job for me?
  - Everyone using standalone BLAST is not practical
  - Want a local BLAST web interface with multiple-query support
- Group *XXX* have just published the *YYY* genome – could you look for *ZZZ* proteins please?
  - With a suitable interface, lots of analyses are simple enough for non-bioinformaticians to run and interpret
- You remember that analysis we did last year? I want to do it again on this new genome
  - Running old scripts on new data is tedious
  - Workflows should be reproducible

Why Galaxy? Plus Points

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- Don’t have to worry about local software installation
  - Mostly Windows here at JHI, most tools need Linux
- Uniform web based GUI for wrapped tools
  - Web interfaces are all different
  - Command line tools are scary
- Coupling tools together as sharable repeatable workflows
- Can share data files (better than email/shared drives)
- Open Source (extendable, free)
- Almost any tool can be added

Why Galaxy? Downsides

- Investment in training users
  - But interface is consistent across tools
- Bugs in Galaxy
  - Most issues arise when wrapping tools
- Missing tools
  - Have to invest time wrapping things we need

Protein Analysis Tools in our Galaxy

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All take a FASTA protein file as input, return a tabular file.

- Sequence similarity
  - NCBI BLAST+
  - Blast2GO
- Transmembrane domains
  - TMHMM
- Signal Peptides/Motifs
  - SignalP
  - EffectiveT3
  - RXLR
- Nuclear Localisation
  - PredictNLS
  - NLStradamus
- Nucleolus Localisation
  - NoD
- Sub-cellular Localisation
  - PSORTB (*)
  - WoLF PSORT

(*) Konrad Paszkiewicz's wrapper from Galaxy Tool Shed, other wrappers written by us.

Observations from Wrapping Tools

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- Tabular output for Galaxy
  - Most tools' output needed reformatting
- Some tools are not threaded
  - Galaxy team working on "embarrassing parallel" case
- Interaction with tool authors can be productive and informative, and improve their tools
- To tool authors
  - Offer tabular output (if appropriate)
  - Better error handling (e.g. zero length sequences)

Workflow example - RXLR motifs

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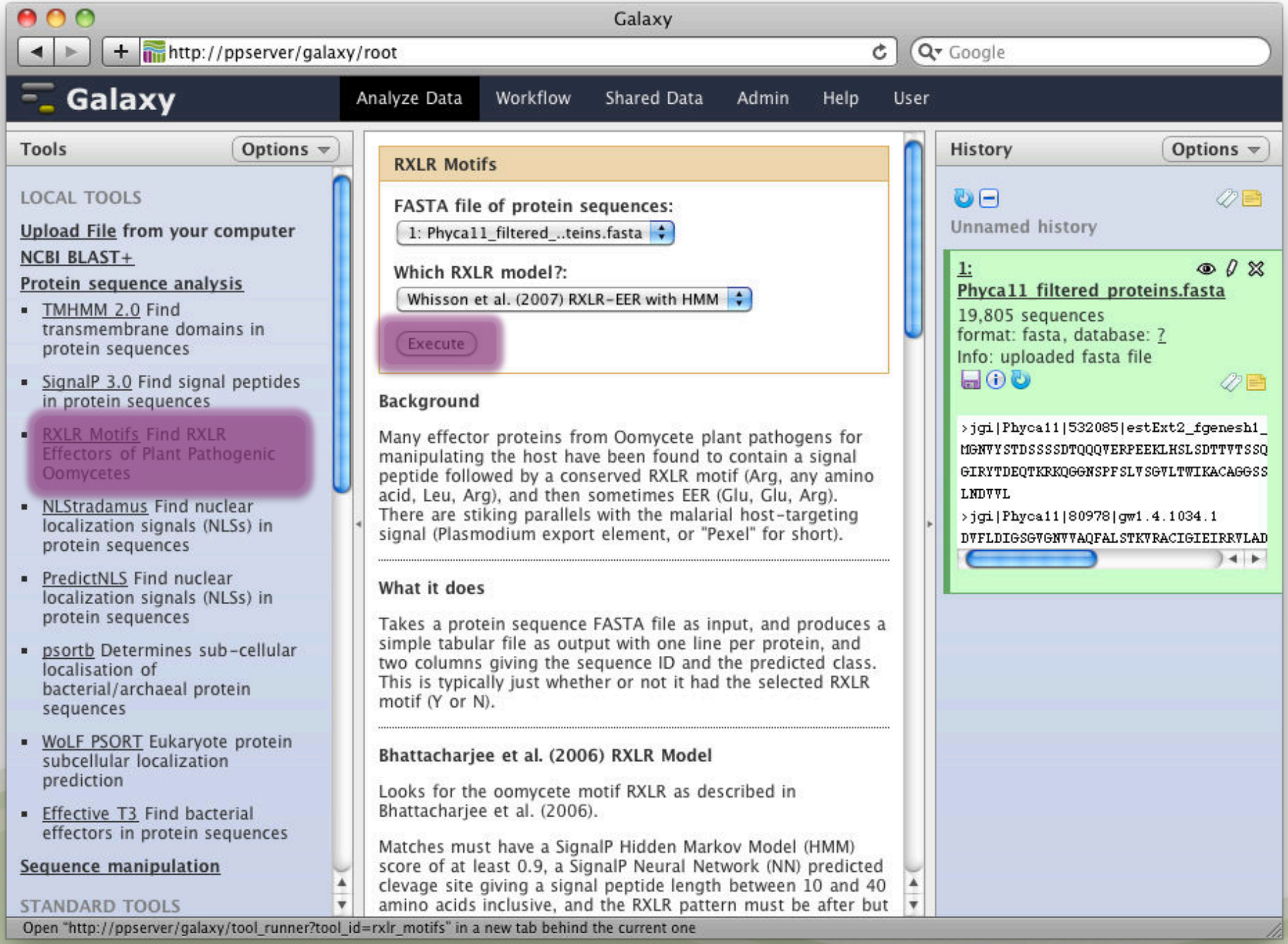
- Important translocation motif in oomycetes
- We have implemented three methods in Galaxy:
  - Bhattacharjee et al. (2006)
  - Win et al. (2007)
  - Whisson et al. (2007)
- Venn Diagram comparing the three methods


Galaxy
http://ppserver/galaxy/root
Google
Galaxy
Analyze Data
Workflow
Shared Data
Admin
Help
User
Tools
Options
LOCAL TOOLS
Upload File from your computer
NCBI BLAST+
Protein sequence analysis
TMHMM 2.0 Find transmembrane domains in protein sequences
SignalP 3.0 Find signal peptides in protein sequences
RXLR Motifs Find RXLR Effectors of Plant Pathogenic Oomycetes
NLStradamus Find nuclear localization signals (NLSs) in protein sequences
PredictNLS Find nuclear localization signals (NLSs) in protein sequences
psortb Determines sub-cellular localisation of bacterial/archaeal protein sequences
WoLF PSORT Eukaryote protein subcellular localization prediction
Effective T3 Find bacterial effectors in protein sequences
Sequence manipulation
STANDARD TOOLS
RXLR Motifs
FASTA file of protein sequences:
1: Phyca11_filtered_..teins.fasta
Which RXLR model?:
Whisson et al. (2007) RXLR-EER with HMM
Execute
Background
Many effector proteins from Oomycete plant pathogens for manipulating the host have been found to contain a signal peptide followed by a conserved RXLR motif (Arg, any amino acid, Leu, Arg), and then sometimes EER (Glu, Glu, Arg). There are stiking parallels with the malarial host-targeting signal (Plasmodium export element, or "Pexel" for short).
What it does
Takes a protein sequence FASTA file as input, and produces a simple tabular file as output with one line per protein, and two columns giving the sequence ID and the predicted class. This is typically just whether or not it had the selected RXLR motif (Y or N).
Bhattacharjee et al. (2006) RXLR Model
Looks for the oomycete motif RXLR as described in Bhattacharjee et al. (2006).
Matches must have a SignalP Hidden Markov Model (HMM) score of at least 0.9, a SignalP Neural Network (NN) predicted clevage site giving a signal peptide length between 10 and 40 amino acids inclusive, and the RXLR pattern must be after but
History
Options
Unnamed history
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Phyca11_filtered_proteins.fasta
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format: fasta, database: ?
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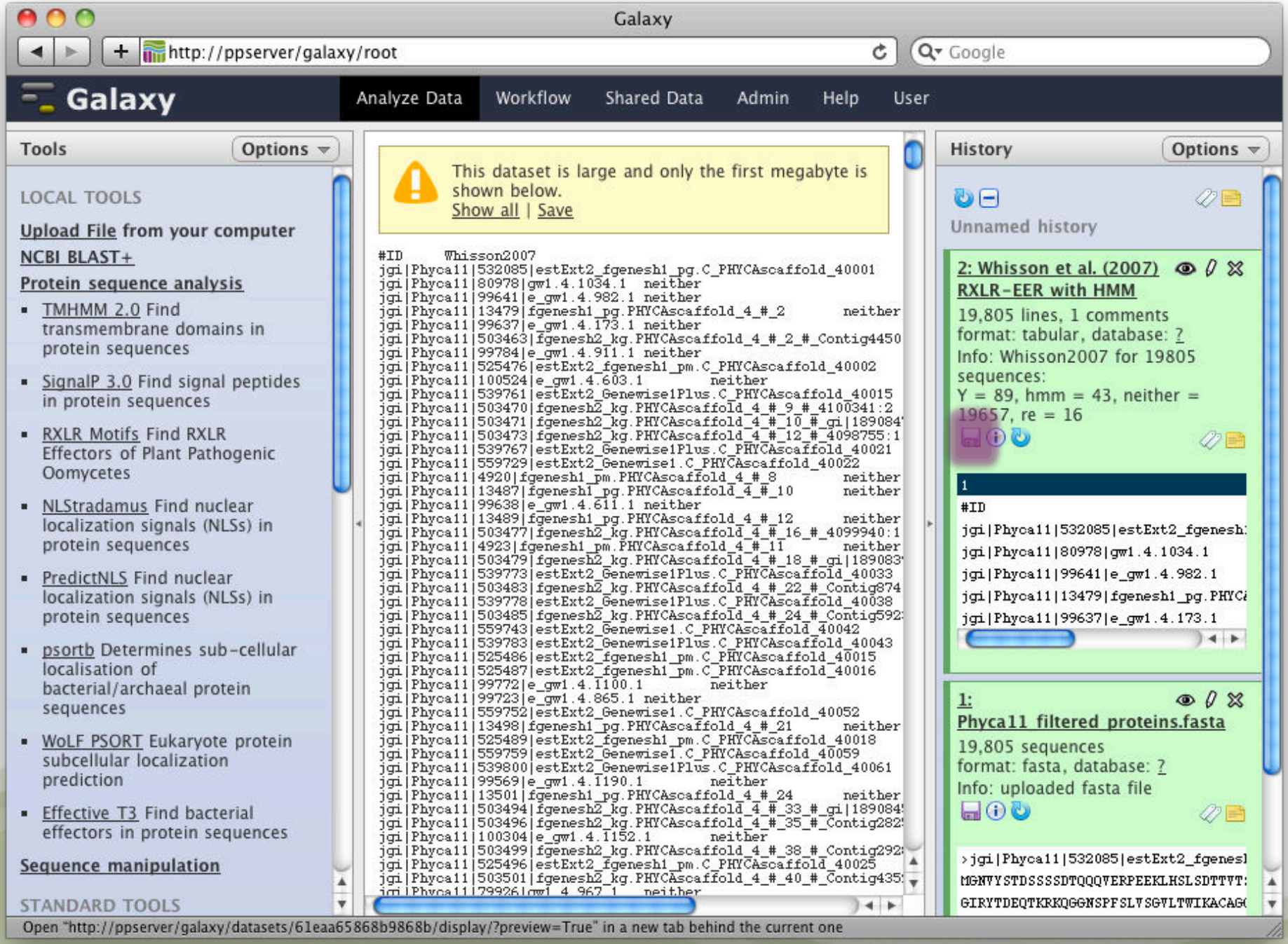
Galaxy
http://ppserver/galaxy/root
Google
Galaxy
Analyze Data
Workflow
Shared Data
Admin
Help
User
Tools
Options
LOCAL TOOLS
Upload File from your computer
NCBI BLAST+
Protein sequence analysis
TMHMM 2.0 Find transmembrane domains in protein sequences
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RXLR Motifs Find RXLR Effectors of Plant Pathogenic Oomycetes
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WoLF PSORT Eukaryote protein subcellular localization prediction
Effective T3 Find bacterial effectors in protein sequences
Sequence manipulation
STANDARD TOOLS
This dataset is large and only the first megabyte is shown below.
Show all | Save
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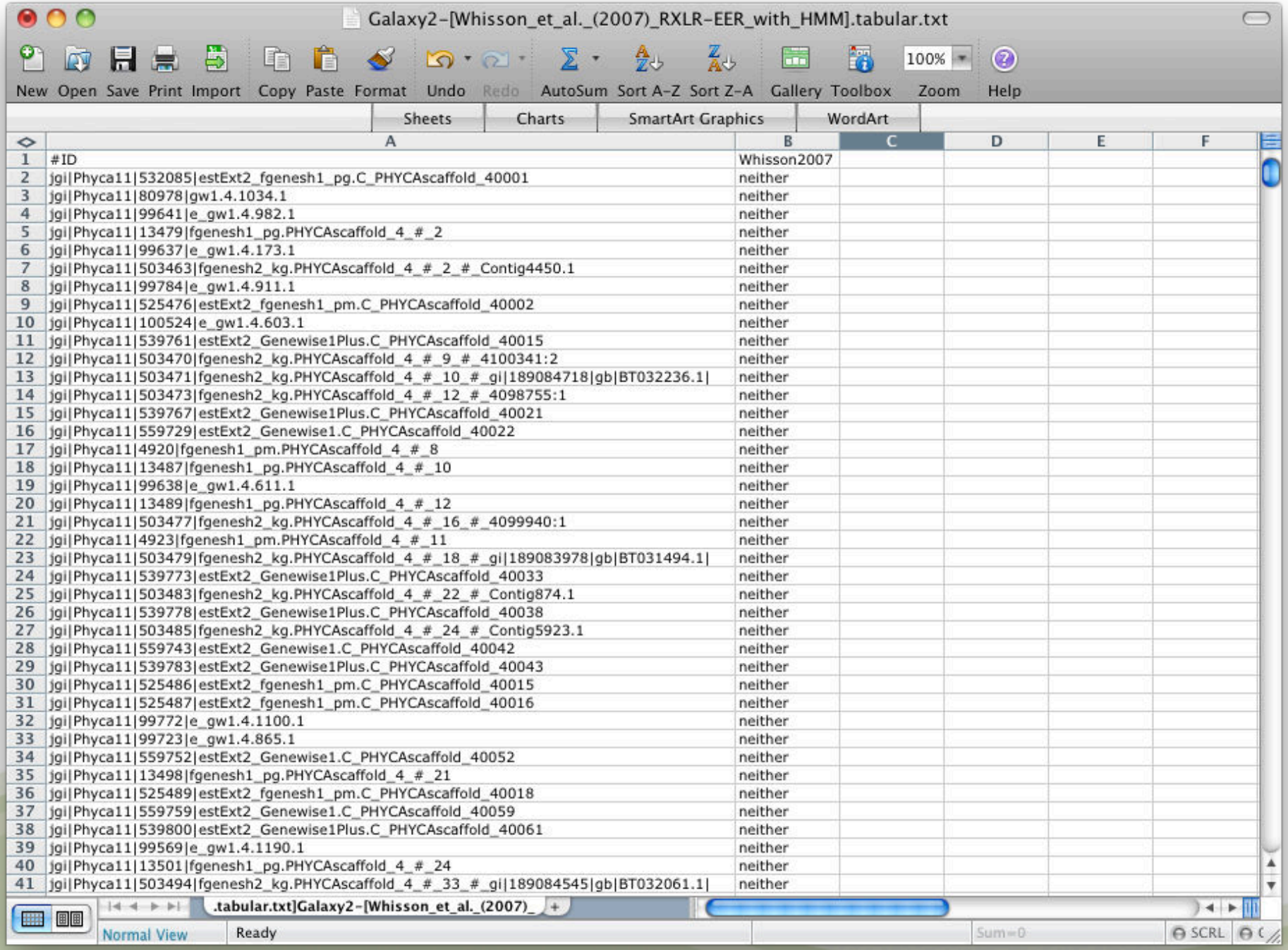
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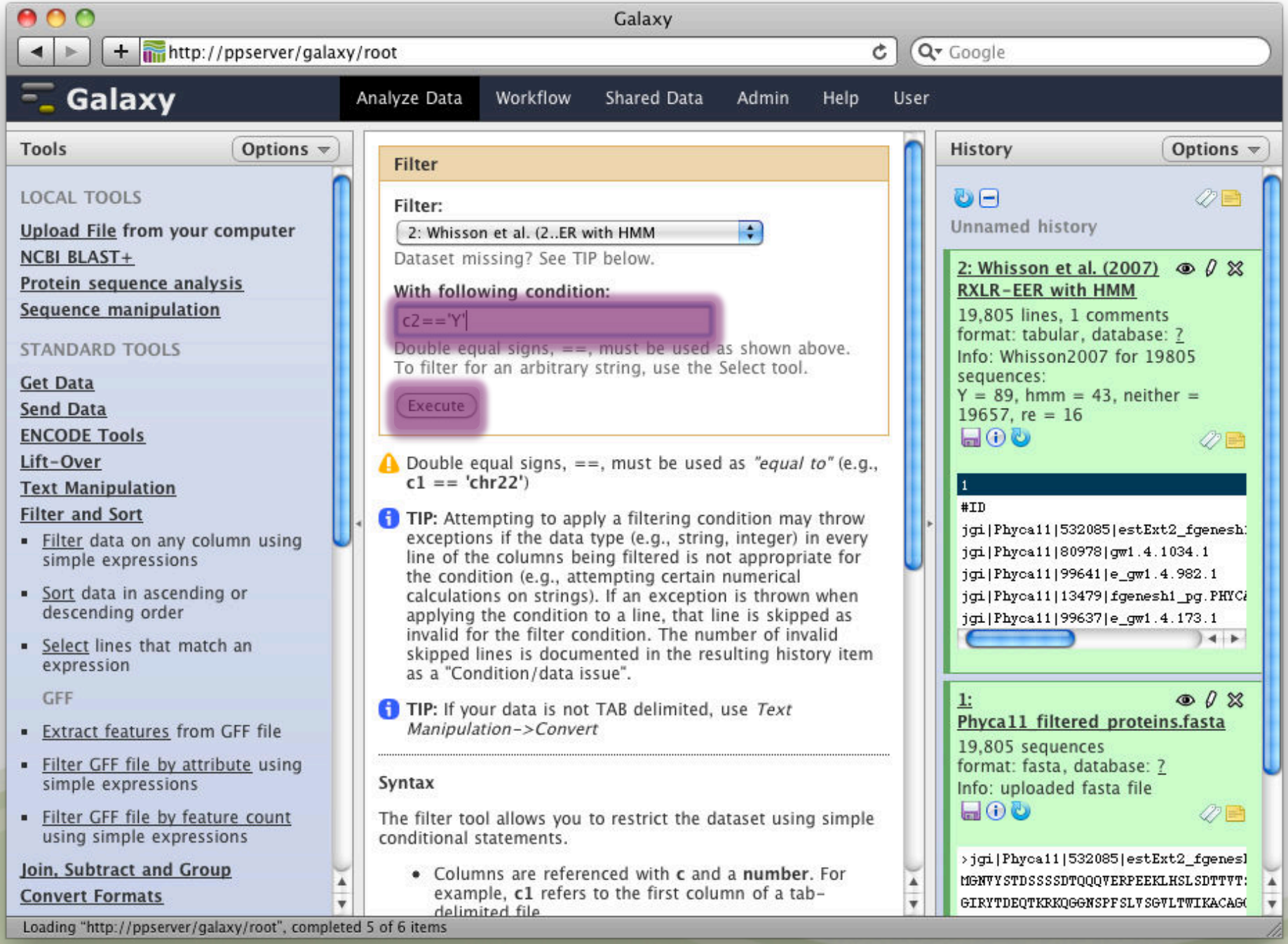
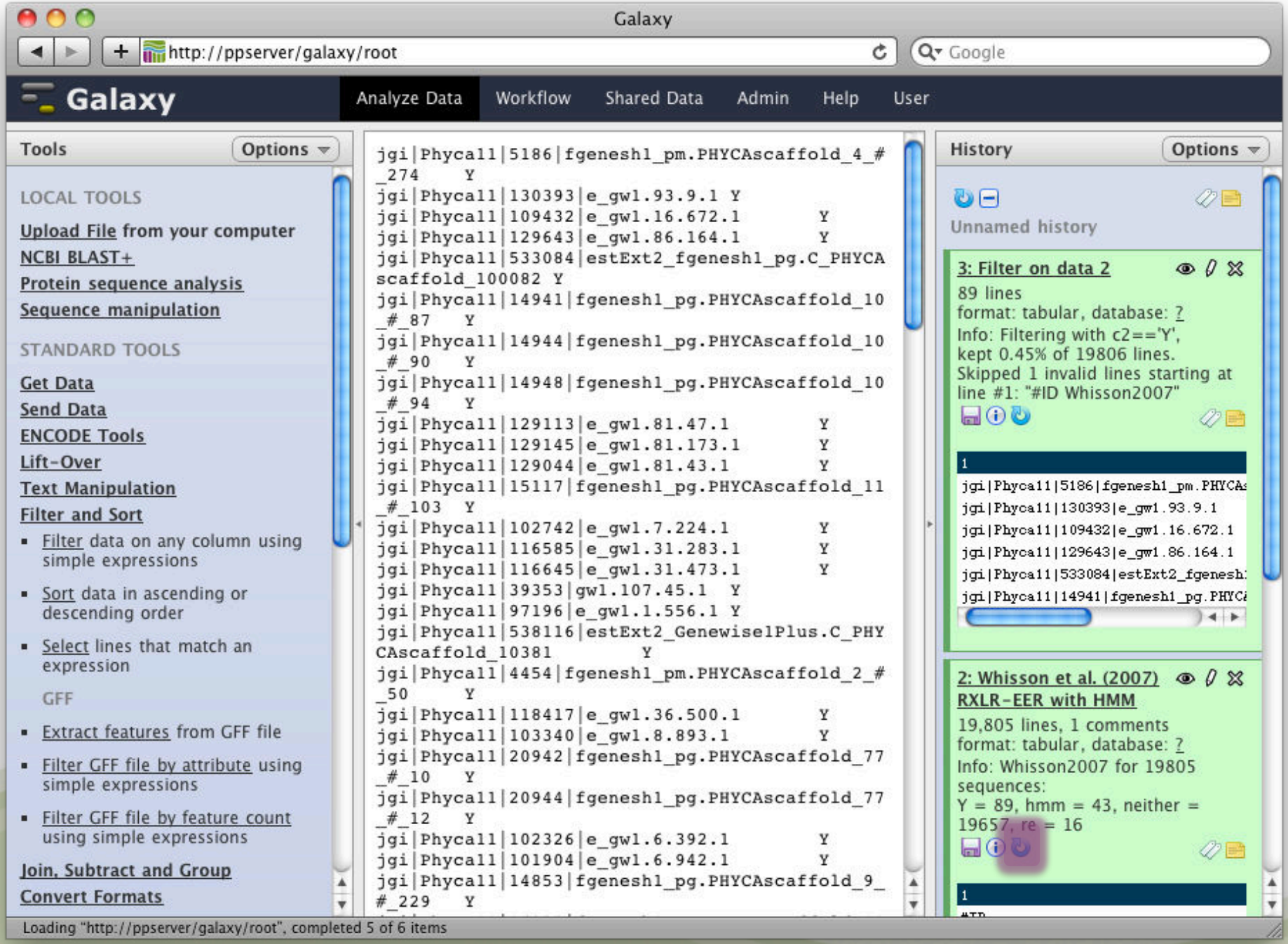
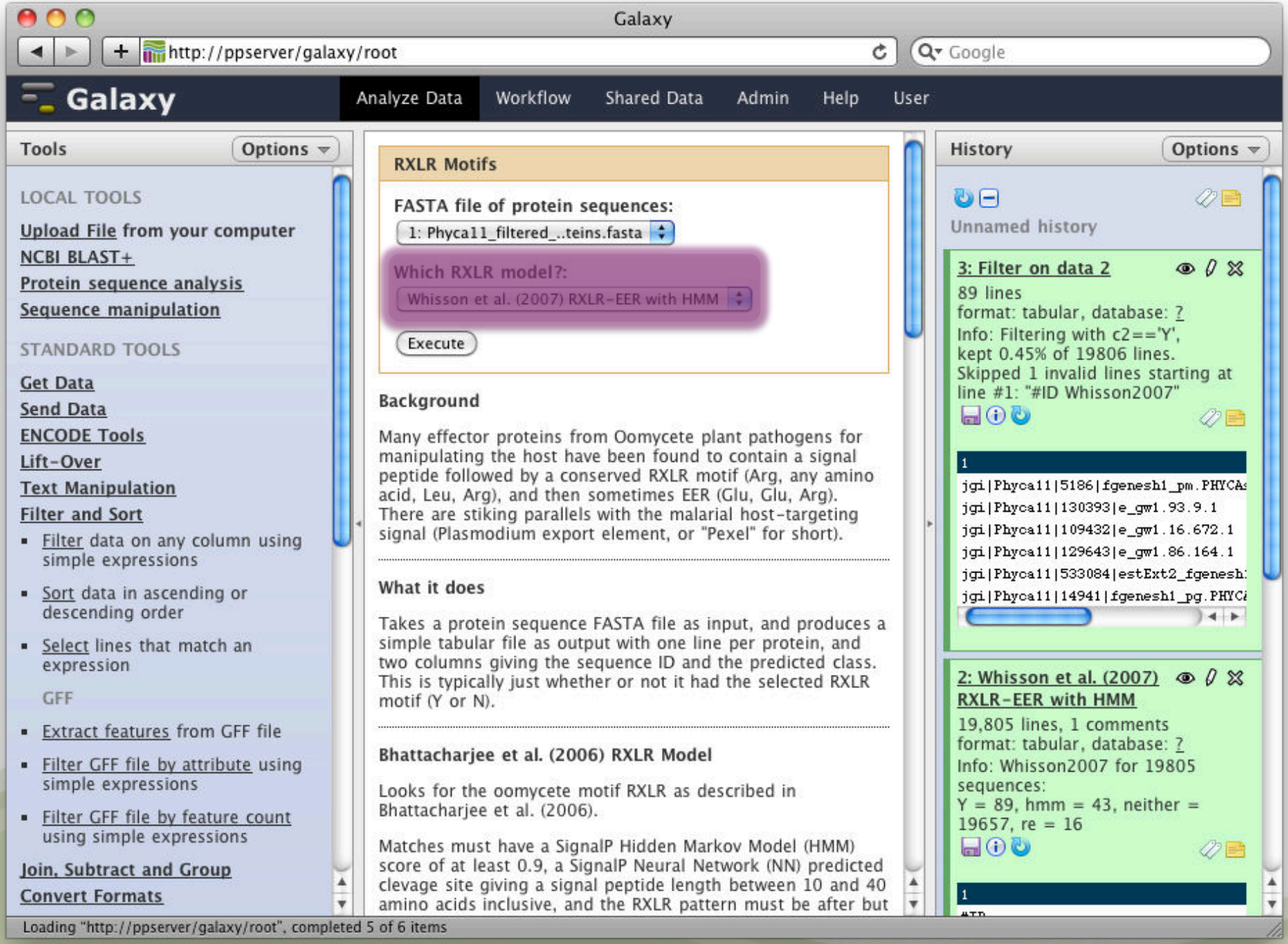
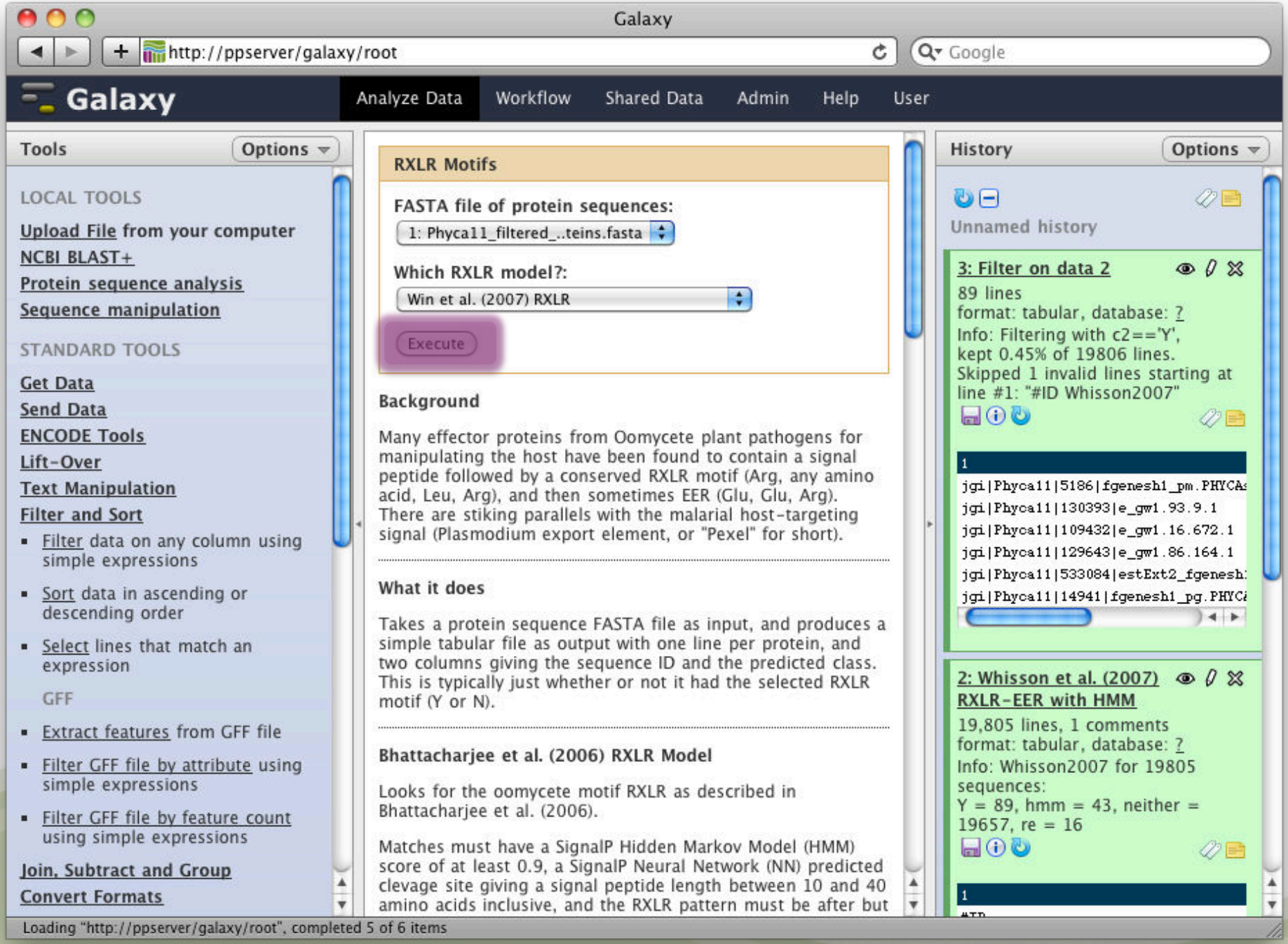

Galaxy
http://ppserver/galaxy/root
Google
Galaxy
Analyze Data
Workflow
Shared Data
Admin
Help
User
Tools
Options
LOCAL TOOLS
Upload File from your computer
NCBI BLAST+
Protein sequence analysis
Sequence manipulation
STANDARD TOOLS
Get Data
Send Data
ENCODE Tools
Lift-Over
Text Manipulation
Filter and Sort
Filter data on any column using simple expressions
Sort data in ascending or descending order
Select lines that match an expression
GFF
Extract features from GFF file
Filter GFF file by attribute using simple expressions
Filter GFF file by feature count using simple expressions
Join, Subtract and Group
Convert Formats
Filter
Filter:
2: Whisson et al. (2..ER with HMM
Dataset missing? See TIP below.
With following condition:
c2=='Y'
Double equal signs, ==, must be used as shown above.
To filter for an arbitrary string, use the Select tool.
Execute
Double equal signs, ==, must be used as "equal to" (e.g., c1 == 'chr22')
TIP: Attempting to apply a filtering condition may throw exceptions if the data type (e.g., string, integer) in every line of the columns being filtered is not appropriate for the condition (e.g., attempting certain numerical calculations on strings). If an exception is thrown when applying the condition to a line, that line is skipped as invalid for the filter condition. The number of invalid skipped lines is documented in the resulting history item as a "Condition/data issue".
TIP: If your data is not TAB delimited, use Text Manipulation->Convert
Syntax
The filter tool allows you to restrict the dataset using simple conditional statements.
Columns are referenced with c and a number. For example, c1 refers to the first column of a tab-delimited file
History
Options
Unnamed history
2: Whisson et al. (2007) RXLR-EER with HMM
19,805 lines, 1 comments
format: tabular, database: ?
Info: Whisson2007 for 19805 sequences:
Y = 89, hmm = 43, neither = 19657, re = 16
1
#ID
jgi|Phyca11|532085|estExt2_fgenesh1
jgi|Phyca11|80978|gw1.4.1034.1
jgi|Phyca11|99641|e_gw1.4.982.1
jgi|Phyca11|13479|fgenesh1_pg.PHYCA
jgi|Phyca11|99637|e_gw1.4.173.1
1: Phyca11_filtered_proteins.fasta
19,805 sequences
format: fasta, database: ?
Info: uploaded fasta file
>jgi|Phyca11|532085|estExt2_fgenesl
MGNVYSTDSSSSDTQQQVERPEEKLHSLSDTTVT
GIRYTDEQTKRKQGGNSPFSLVSGVLTWIKACAG
Loading "http://ppserver/galaxy/root", completed 5 of 6 items


Galaxy
http://ppserver/galaxy/root
Google
Galaxy
Analyze Data
Workflow
Shared Data
Admin
Help
User
Tools
Options
LOCAL TOOLS
Upload File from your computer
NCBI BLAST+
Protein sequence analysis
Sequence manipulation
STANDARD TOOLS
Get Data
Send Data
ENCODE Tools
Lift-Over
Text Manipulation
Filter and Sort
Filter data on any column using simple expressions
Sort data in ascending or descending order
Select lines that match an expression
GFF
Extract features from GFF file
Filter GFF file by attribute using simple expressions
Filter GFF file by feature count using simple expressions
Join, Subtract and Group
Convert Formats
jgi|Phycal1|5186|fgeneshl_pm.PHYCAscaffold_4_#_274 Y
jgi|Phycal1|130393|e_gw1.93.9.1 Y
jgi|Phycal1|109432|e_gw1.16.672.1 Y
jgi|Phycal1|129643|e_gw1.86.164.1 Y
jgi|Phycal1|533084|estExt2_fgeneshl_pg.C_PHYCAscaffold_100082 Y
jgi|Phycal1|14941|fgeneshl_pg.PHYCAscaffold_10_#_87 Y
jgi|Phycal1|14944|fgeneshl_pg.PHYCAscaffold_10_#_90 Y
jgi|Phycal1|14948|fgeneshl_pg.PHYCAscaffold_10_#_94 Y
jgi|Phycal1|129113|e_gw1.81.47.1 Y
jgi|Phycal1|129145|e_gw1.81.173.1 Y
jgi|Phycal1|129044|e_gw1.81.43.1 Y
jgi|Phycal1|15117|fgeneshl_pg.PHYCAscaffold_11_#_103 Y
jgi|Phycal1|102742|e_gw1.7.224.1 Y
jgi|Phycal1|116585|e_gw1.31.283.1 Y
jgi|Phycal1|116645|e_gw1.31.473.1 Y
jgi|Phycal1|39353|gw1.107.45.1 Y
jgi|Phycal1|97196|e_gw1.1.556.1 Y
jgi|Phycal1|538116|estExt2_GenewiselPlus.C_PHYCAscaffold_10381 Y
jgi|Phycal1|4454|fgeneshl_pm.PHYCAscaffold_2_#_50 Y
jgi|Phycal1|118417|e_gw1.36.500.1 Y
jgi|Phycal1|103340|e_gw1.8.893.1 Y
jgi|Phycal1|20942|fgeneshl_pg.PHYCAscaffold_77_#_10 Y
jgi|Phycal1|20944|fgeneshl_pg.PHYCAscaffold_77_#_12 Y
jgi|Phycal1|102326|e_gw1.6.392.1 Y
jgi|Phycal1|101904|e_gw1.6.942.1 Y
jgi|Phycal1|14853|fgeneshl_pg.PHYCAscaffold_9_#_229 Y
History
Options
Unnamed history
3: Filter on data 2
89 lines
format: tabular, database: ?
Info: Filtering with c2=='Y', kept 0.45% of 19806 lines.
Skipped 1 invalid lines starting at line #1: "#ID Whisson2007"
1
jgi|Phyca11|5186|fgeneshl_pm.PHYCAs
jgi|Phyca11|130393|e_gw1.93.9.1
jgi|Phyca11|109432|e_gw1.16.672.1
jgi|Phyca11|129643|e_gw1.86.164.1
jgi|Phyca11|533084|estExt2_fgenesh
jgi|Phyca11|14941|fgeneshl_pg.PHYCA
2: Whisson et al. (2007) RXLR-EER with HMM
19,805 lines, 1 comments
format: tabular, database: ?
Info: Whisson2007 for 19805 sequences:
Y = 89, hmm = 43, neither = 19657, re = 16
1
Loading "http://ppserver/galaxy/root", completed 5 of 6 items


Galaxy
http://ppserver/galaxy/root
Google
Galaxy
Analyze Data
Workflow
Shared Data
Admin
Help
User
Tools
Options
LOCAL TOOLS
Upload File from your computer
NCBI BLAST+
Protein sequence analysis
Sequence manipulation
STANDARD TOOLS
Get Data
Send Data
ENCODE Tools
Lift-Over
Text Manipulation
Filter and Sort
Filter data on any column using simple expressions
Sort data in ascending or descending order
Select lines that match an expression
GFF
Extract features from GFF file
Filter GFF file by attribute using simple expressions
Filter GFF file by feature count using simple expressions
Join, Subtract and Group
Convert Formats
RXLR Motifs
FASTA file of protein sequences:
1: Phyca11_filtered_..teins.fasta
Which RXLR model?:
Whisson et al. (2007) RXLR-EER with HMM
Execute
Background
Many effector proteins from Oomycete plant pathogens for manipulating the host have been found to contain a signal peptide followed by a conserved RXLR motif (Arg, any amino acid, Leu, Arg), and then sometimes EER (Glu, Glu, Arg). There are stiking parallels with the malarial host-targeting signal (Plasmodium export element, or "Pexel" for short).
What it does
Takes a protein sequence FASTA file as input, and produces a simple tabular file as output with one line per protein, and two columns giving the sequence ID and the predicted class. This is typically just whether or not it had the selected RXLR motif (Y or N).
Bhattacharjee et al. (2006) RXLR Model
Looks for the oomycete motif RXLR as described in Bhattacharjee et al. (2006).
Matches must have a SignalP Hidden Markov Model (HMM) score of at least 0.9, a SignalP Neural Network (NN) predicted clevage site giving a signal peptide length between 10 and 40 amino acids inclusive, and the RXLR pattern must be after but
History
Options
Unnamed history
3: Filter on data 2
89 lines
format: tabular, database: ?
Info: Filtering with c2=='Y', kept 0.45% of 19806 lines.
Skipped 1 invalid lines starting at line #1: "#ID Whisson2007"
1
jgi|Phyca11|5186|fgenesh1_pm.PHYCA
jgi|Phyca11|130393|e_gw1.93.9.1
jgi|Phyca11|109432|e_gw1.16.672.1
jgi|Phyca11|129643|e_gw1.86.164.1
jgi|Phyca11|533084|estExt2_fgenesh
jgi|Phyca11|14941|fgenesh1_pg.PHYC
2: Whisson et al. (2007) RXLR-EER with HMM
19,805 lines, 1 comments
format: tabular, database: ?
Info: Whisson2007 for 19805 sequences:
Y = 89, hmm = 43, neither = 19657, re = 16
1
Loading "http://ppserver/galaxy/root", completed 5 of 6 items


Galaxy
http://ppserver/galaxy/root
Google
Galaxy
Analyze Data
Workflow
Shared Data
Admin
Help
User
Tools
Options
LOCAL TOOLS
Upload File from your computer
NCBI BLAST+
Protein sequence analysis
Sequence manipulation
STANDARD TOOLS
Get Data
Send Data
ENCODE Tools
Lift-Over
Text Manipulation
Filter and Sort
Filter data on any column using simple expressions
Sort data in ascending or descending order
Select lines that match an expression
GFF
Extract features from GFF file
Filter GFF file by attribute using simple expressions
Filter GFF file by feature count using simple expressions
Join, Subtract and Group
Convert Formats
RXLR Motifs
FASTA file of protein sequences:
1: Phyca11_filtered_..teins.fasta
Which RXLR model?:
Win et al. (2007) RXLR
Execute
Background
Many effector proteins from Oomycete plant pathogens for manipulating the host have been found to contain a signal peptide followed by a conserved RXLR motif (Arg, any amino acid, Leu, Arg), and then sometimes EER (Glu, Glu, Arg). There are stiking parallels with the malarial host-targeting signal (Plasmodium export element, or "Pexel" for short).
What it does
Takes a protein sequence FASTA file as input, and produces a simple tabular file as output with one line per protein, and two columns giving the sequence ID and the predicted class. This is typically just whether or not it had the selected RXLR motif (Y or N).
Bhattacharjee et al. (2006) RXLR Model
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History
Options
Unnamed history
3: Filter on data 2
89 lines
format: tabular, database: ?
Info: Filtering with c2=='Y', kept 0.45% of 19806 lines.
Skipped 1 invalid lines starting at line #1: "#ID Whisson2007"
1
jgi|Phyca11|5186|fgenesh1_pm.PHYCA
jgi|Phyca11|130393|e_gw1.93.9.1
jgi|Phyca11|109432|e_gw1.16.672.1
jgi|Phyca11|129643|e_gw1.86.164.1
jgi|Phyca11|533084|estExt2_fgenesh
jgi|Phyca11|14941|fgenesh1_pg.PHYC
2: Whisson et al. (2007) RXLR-EER with HMM
19,805 lines, 1 comments
format: tabular, database: ?
Info: Whisson2007 for 19805 sequences:
Y = 89, hmm = 43, neither = 19657, re = 16
1
Loading "http://ppserver/galaxy/root", completed 5 of 6 items

Next few steps omitted…

- Repeated RXLR search & filter using other two models
- Labelled some history entries

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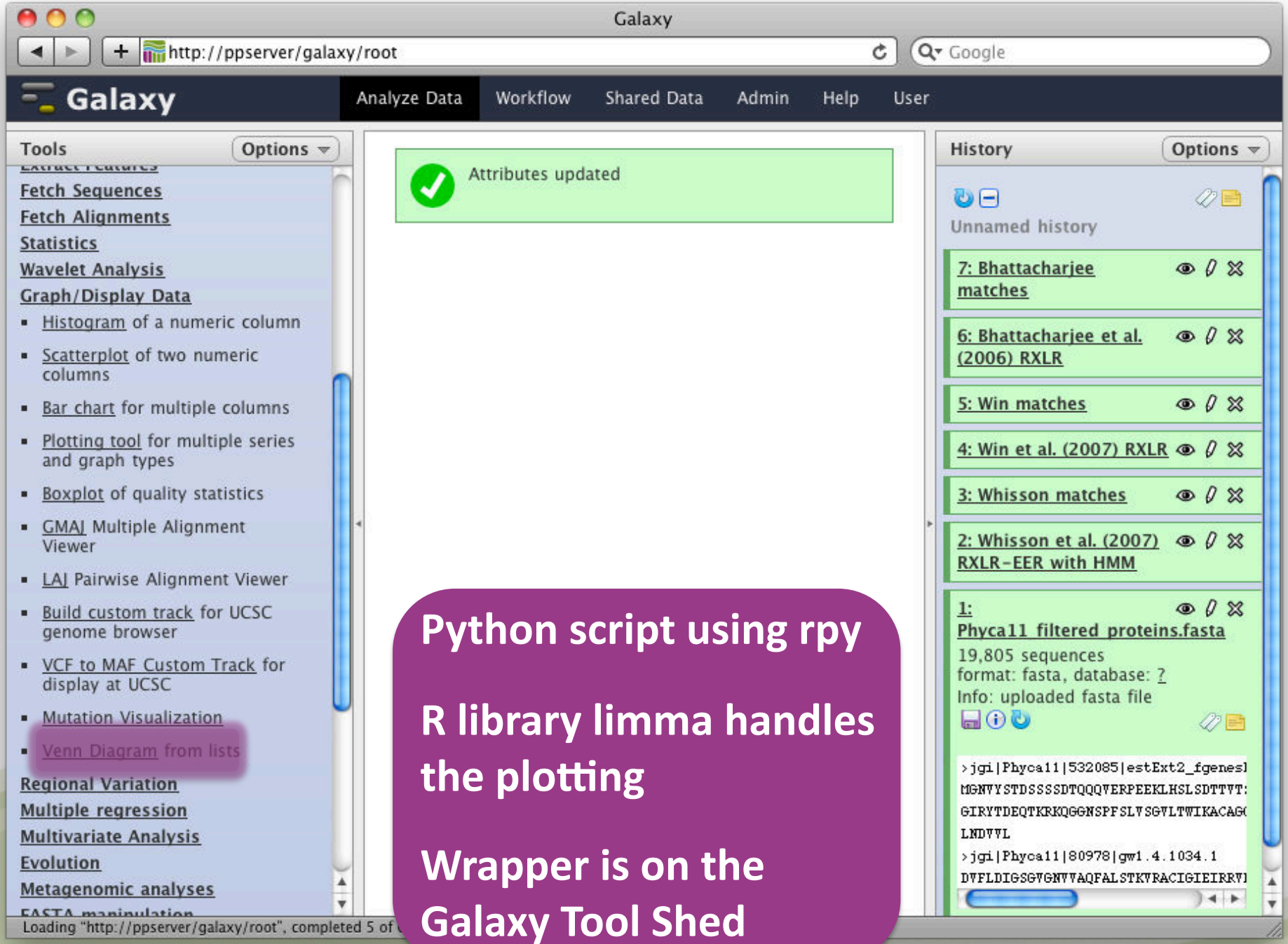
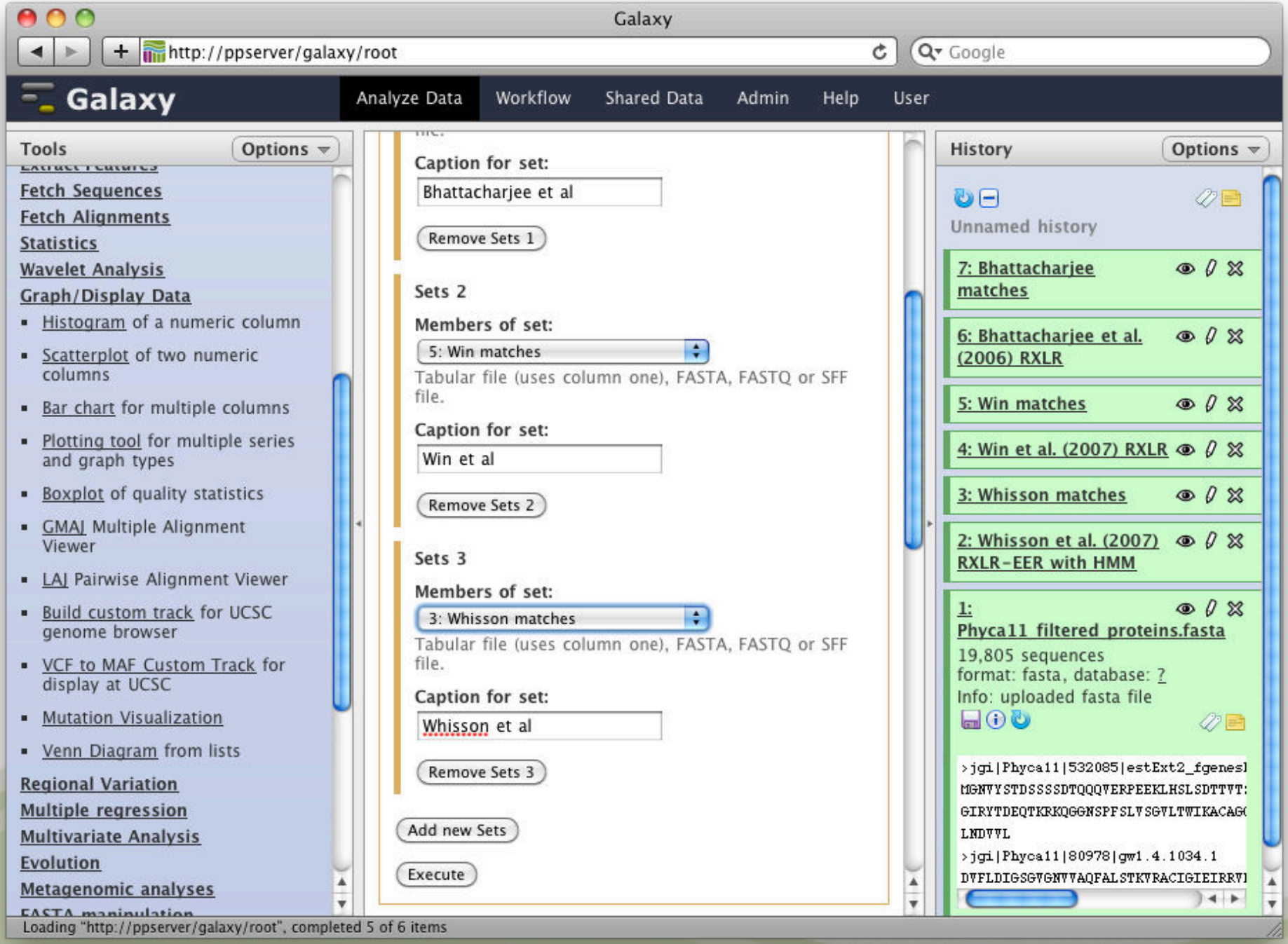

Galaxy
http://ppserver/galaxy/root
Google
Galaxy
Analyze Data
Workflow
Shared Data
Admin
Help
User
Tools
Options
Fetch Sequences
Fetch Alignments
Statistics
Wavelet Analysis
Graph/Display Data
Histogram of a numeric column
Scatterplot of two numeric columns
Bar chart for multiple columns
Plotting tool for multiple series and graph types
Boxplot of quality statistics
GMAJ Multiple Alignment Viewer
LAJ Pairwise Alignment Viewer
Build custom track for UCSC genome browser
VCF to MAF Custom Track for display at UCSC
Mutation Visualization
Venn Diagram from lists
Regional Variation
Multiple regression
Multivariate Analysis
Evolution
Metagenomic analyses
Attributes updated
History
Options
Unnamed history
7: Bhattacharjee matches
6: Bhattacharjee et al. (2006) RXLR
5: Win matches
4: Win et al. (2007) RXLR
3: Whisson matches
2: Whisson et al. (2007) RXLR-EER with HMM
1: Phyca11_filtered_proteins.fasta
19,805 sequences
format: fasta, database: ?
Info: uploaded fasta file
>jgi|Phyca11|532085|estExt2_fgenesl
MGNVYSTDSSSSDTQQQVERPEEKLHSLSDTTVT:
GIRYTDEQTKRKQGGNSPFSLVSGVLTWIKACAG
LNDVVL
>jgi|Phyca11|80978|gw1.4.1034.1
DVFLDIGSGVGNVVAQFALSTKVRACIGIEIRRV
Python script using rpy
R library limma handles the plotting
Wrapper is on the Galaxy Tool Shed
Loading "http://ppserver/galaxy/root", completed 5 of


Galaxy
http://ppserver/galaxy/root
Google
Galaxy
Analyze Data
Workflow
Shared Data
Admin
Help
User
Tools
Options
Fetch Sequences
Fetch Alignments
Statistics
Wavelet Analysis
Graph/Display Data
Histogram of a numeric column
Scatterplot of two numeric columns
Bar chart for multiple columns
Plotting tool for multiple series and graph types
Boxplot of quality statistics
GMAJ Multiple Alignment Viewer
LAJ Pairwise Alignment Viewer
Build custom track for UCSC genome browser
VCF to MAF Custom Track for display at UCSC
Mutation Visualization
Venn Diagram from lists
Regional Variation
Multiple regression
Multivariate Analysis
Evolution
Metagenomic analyses
Caption for set:
Bhattacharjee et al
Remove Sets 1
Sets 2
Members of set:
5: Win matches
Tabular file (uses column one), FASTA, FASTQ or SFF file.
Caption for set:
Win et al
Remove Sets 2
Sets 3
Members of set:
3: Whisson matches
Tabular file (uses column one), FASTA, FASTQ or SFF file.
Caption for set:
Whisson et al
Remove Sets 3
Add new Sets
Execute
History
Options
Unnamed history
7: Bhattacharjee matches
6: Bhattacharjee et al. (2006) RXLR
5: Win matches
4: Win et al. (2007) RXLR
3: Whisson matches
2: Whisson et al. (2007) RXLR-EER with HMM
1: Phyca11_filtered_proteins.fasta
19,805 sequences
format: fasta, database: ?
Info: uploaded fasta file
>jgi|Phyca11|532085|estExt2_fgenesl
MGNVYSTDSSSSDTQQQVERPEEKLHSLSDTTVT:
GIRYTDEQTKRKQGGNSPFSLVSGVLTWIKACAG
LNDVVL
>jgi|Phyca11|80978|gw1.4.1034.1
DVFLDIGSGVGNVVAQFALSTKVRACIGIEIRRV
Loading "http://ppserver/galaxy/root", completed 5 of 6 items

Galaxy

http://ppserver/galaxy/root

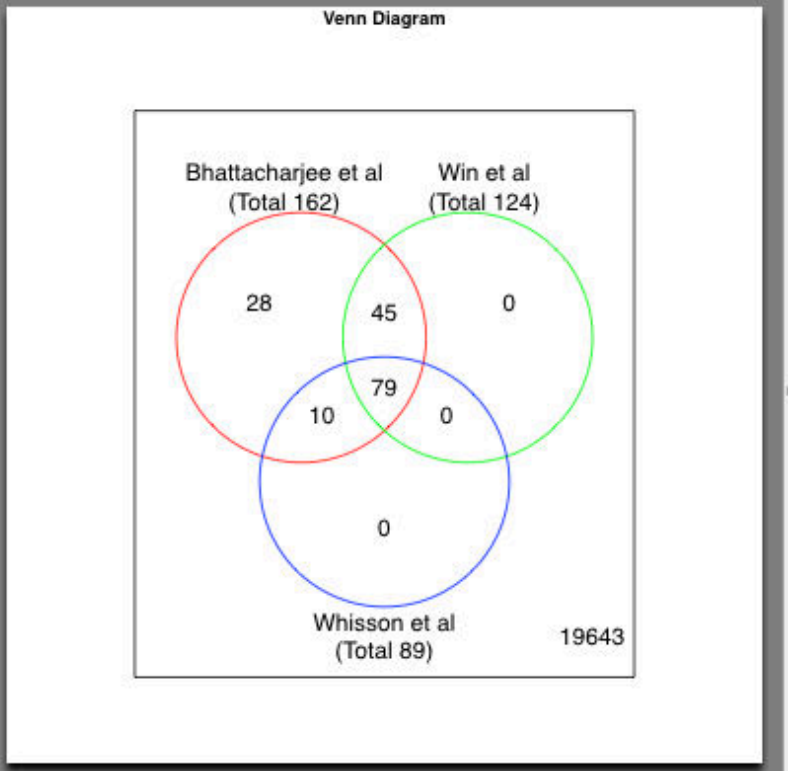
Google

Galaxy | Analyze Data | Workflow | Shared Data

Save this analysis as a workflow

Tools | Options

- Fetch Sequences
- Fetch Alignments
- Statistics
- Wavelet Analysis
- Graph/Display Data
  - Histogram of a numeric column
  - Scatterplot of two numeric columns
  - Bar chart for multiple columns
  - Plotting tool for multiple series and graph types
  - Boxplot of quality statistics
  - GMAJ Multiple Alignment Viewer
  - LAJ Pairwise Alignment Viewer
  - Build custom track for UCSC genome browser
  - VCF to MAF Custom Track for display at UCSC
  - Mutation Visualization
  - Venn Diagram from lists
- Regional Variation
- Multiple regression
- Multivariate Analysis
- Evolution
- Metagenomic analyses
- FASTA manipulation



Options

8: Venn Diagram on data 7, data 1, and others
19.5 Kb
format: pdf, database: ?
Info: Doing 3-way Venn Diagram
Total of 19805 IDs
162 in Bhattacharjee et al
124 in Win et al
89 in Whisson et al
Image in pdf format

7: Bhattacharjee matches

6: Bhattacharjee et al. (2006) RXLR

5: Win matches

4: Win et al. (2007) RXLR

3: Whisson matches

2: Whisson et al. (2007) RXLR-EER with HMM

1:

Loading "http://ppserver/galaxy/root", completed 5 of 6 items

Workflow editor view

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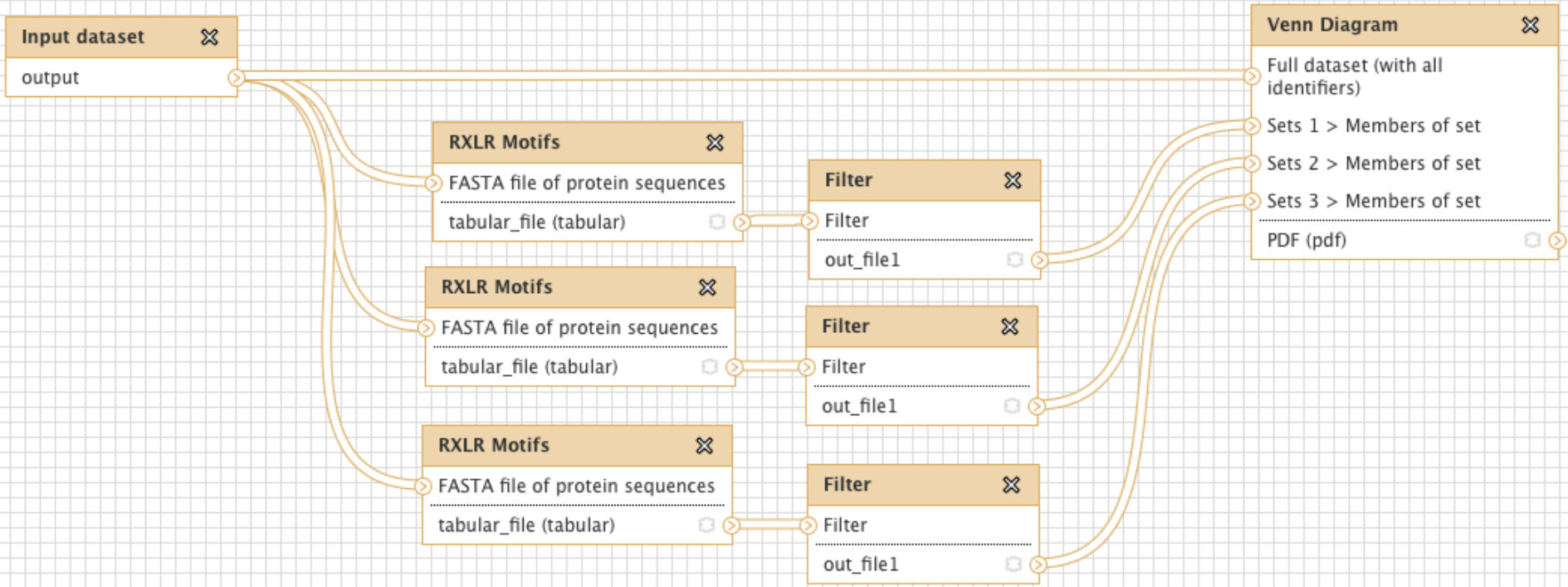
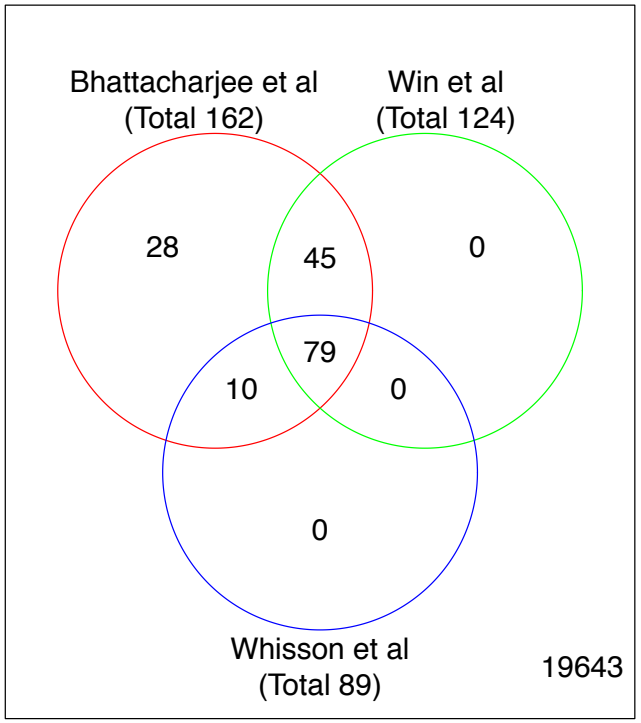
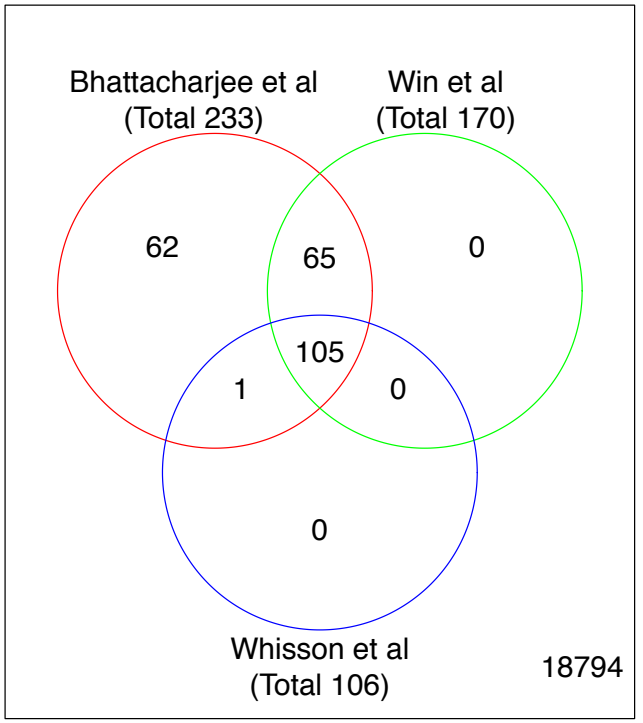


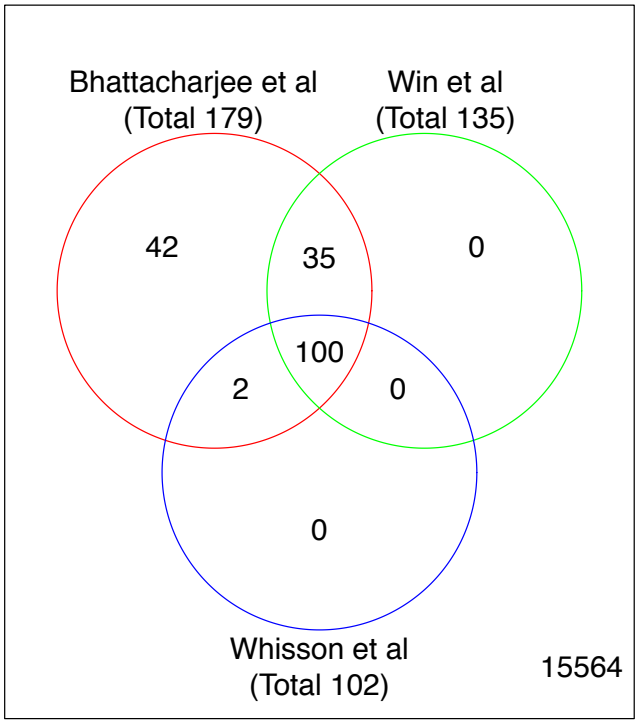
RXLRs in *Phytophthora* draft genomes



P. capsici
(19,805 proteins)



P. sojae
(19,027 proteins)



P. ramorum
(15,743 proteins)

Acknowledgements

- Helpful tool authors:
  - Alex Nguyen (NLStradamus)
  - Laszlo Kajan (PredictNLS)
  - Peter Troshin, Michelle Scott (NoD)
- JHI Testers:
  - John Jones, Remco Stam, Julietta Jupe
- The Galaxy Developers & mailing list community

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Conclusions

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- We like Galaxy
  - Consistent web interface for combining many tools
  - Open source and extensible
  - We can add tools of local interest
- Our Galaxy tool wrappers are on the Galaxy Tool Shed
  - http://usegalaxy.org/community
- Questions?