

Visualising Proteomics Data in Galaxy

Ira Cooke



Protviz

Galaxy

10.211.55.24/root

Galaxy

Analyze Data Workflow Shared Data Admin Help User

Using 2.7 Gb

Tools

- Get Data
- Send Data
- ENCODE Tools
- Lift-Over
- Text Manipulation
- Filter and Sort
- Join, Subtract and Group
- Convert Formats
- Extract Features
- Fetch Sequences
- Fetch Alignments
- Get Genomic Scores
- Operate on Genomic Intervals
- Statistics
- Wavelet Analysis
- Graph/Display Data
- Regional Variation
- Multiple regression
- Multivariate Analysis
- Evolution
- Motif Tools
- Multiple Alignments
- Metagenomic analyses
- FASTA manipulation
- NCBI BLAST+
- NGS: QC and manipulation
- NGS: Picard (beta)

Displaying all 31 results

Protein	Peptides	Coverage	Probability																																																																																																													
41_HUMAN	HSNLMLEDLDKSQEEIKK 2 more	5.7%	1.0																																																																																																													
B3AT_HUMAN	GTVLLDLOETSLAGVANQLLDR 1 more	4.5%	1.0																																																																																																													
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History

Test 45.8 Mb

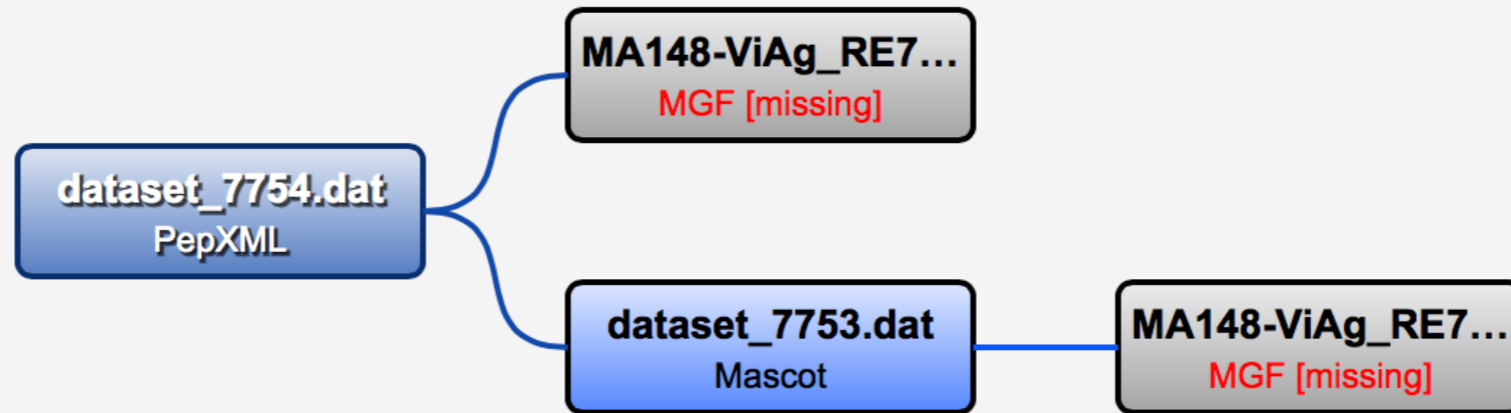
37: [protein_prophet.interprophet.peptide_prophet.omssa_vs_sphuman.MT669-9-TiloS3_BAF.d_pk.mzML.mgf.pepXML.pep.xml.protXML](#)
prot XML Search Results
format: protxml, database: ?
[view protXML in Proteomics Visualize](#)

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ase/job_work
<protein_summary_header ...
/database/files/000...
initial_min_peptide ... total
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35: [peptide_prophet.omssa_vs_sphuman.MT669-TiloS3_BAF.d_pk.mzML.mgf.pepXML](#)

[Hide Navigation](#)



Filter:

None of the 0 queries matched your filter

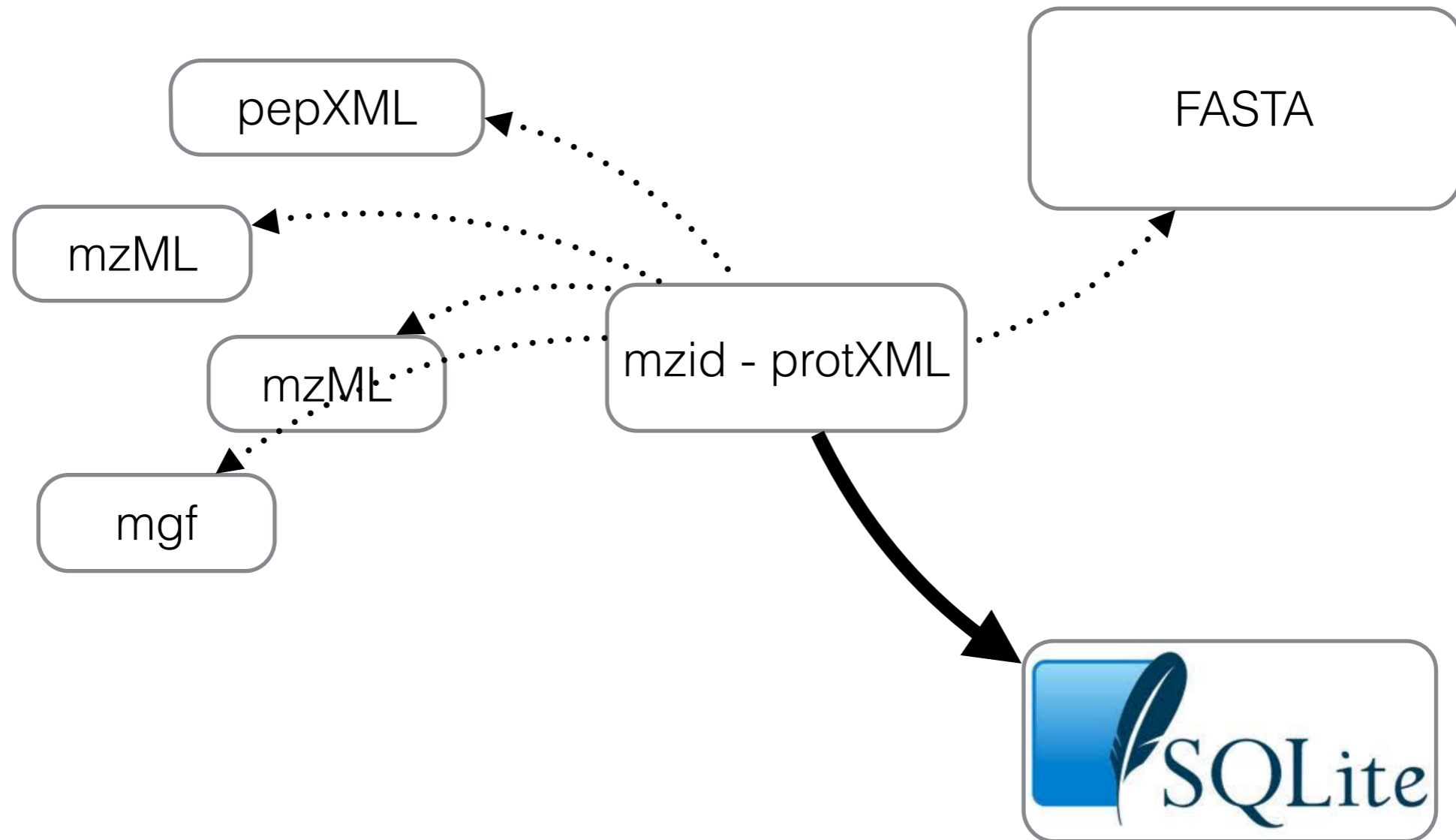
<u>Regional variation</u>
<u>Multiple regression</u>
...

```
<?xml version="1.0" encoding="UTF-8"?>  
<protein_summary xmlns="http://regis-w
```

Problems

- Data is spread over many (possibly hundreds) of files with dozens of formats
- Long load times for visualisation
- Results files are not self-contained
- Difficult to install and maintain

Gather Data Up-Front



Galaxy Visualisation Plugin

- Toolshed Installable?! SQLite Data provider and custom datatype. All Visualisation code in a plugin template.
- Full access to data via SQLite data provider.

Tools ↑

search tools ×

Get Data

- [Upload File](#) from your computer
- [UCSC Main](#) table browser
- [UCSC Test](#) table browser
- [UCSC Archaea](#) table browser
- [EBI SRA](#) [ENA SRA](#)
- [Get Microbial Data](#)
- [BioMart Central](#) server
- [BioMart Test](#) server
- [CBI Rice Mart](#) rice mart
- [GrameneMart](#) Central server
- [modENCODE fly](#) server
- [modENCODE worm](#) server
- [WormBase](#) server
- [Wormbase](#) test server
- [EuPathDB](#) server
- [HbVar](#) Human Hemoglobin

Name	Description	Probability	Num Peptides
lcl comp57626_c0_seq1m.151088	RecName: Thymidylate synthase; 278197 COG0207 Identity: 25.49 EValue:9.4	0.999	3
<p>3 G C P S F A Q T E P K D A L M Q T I M D L I Q E Q M T S N K N D G K E M D E A L I K L I K E V T E F F</p> <p>psms</p>			
lcl comp55716_c2_seq1m.99931	RecName: Activating transcription factor 7- interacting protein 1; 9031 NOG82478 Identity: 50.79 EValue:2.0e-30	0.9908	2
lcl comp289902_c0_seq1m.166463	RecName: WD repeat-containing protein 65; 10090 COG2319 Identity: 46.73 EValue:4.0e- 66	0.9862	2
lcl comp50482_c0_seq2m.63494	RecName: UPF0658 Golgi apparatus membrane protein C23H3.04; 284812 NOG68074 Identity: 26.17 EValue:0.08	0.9824	2

History ↺ ⚙

Unnamed history
60.4 MB 🔍 ✓ 🗑 💬

30: squid.psqlite 👁 ✎ ✕
2.2 MB
format: **psqlite**, database: ?
uploaded psqlite file
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PSqliteViewer
Trackster

28: mt272.psqlite 👁 ✎ ✕
2.8 MB
format: **psqlite**, database: ?
uploaded psqlite file
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Proteomics SQLite File

27: mt272.psqlite 👁 ✎ ✕
2.8 MB