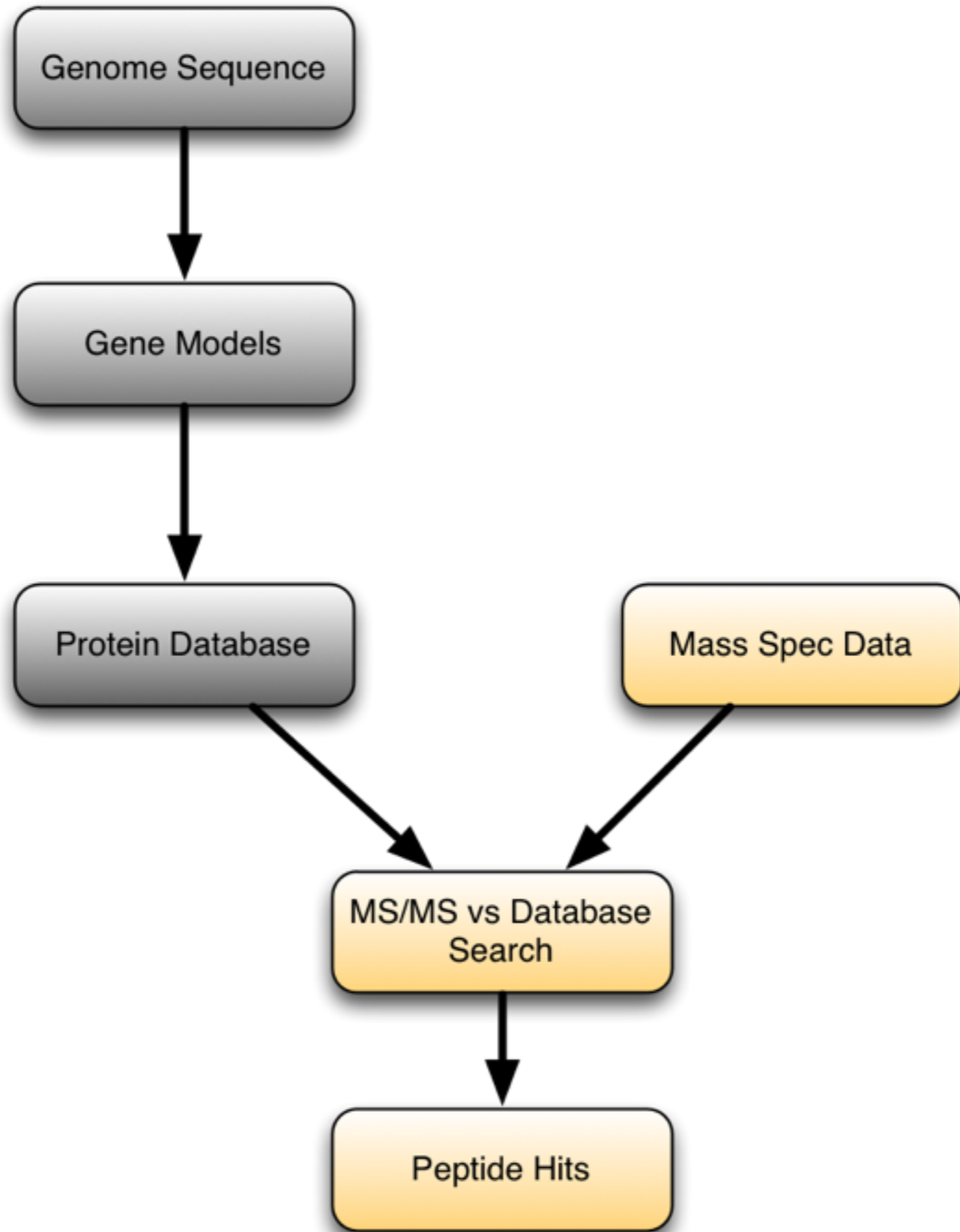
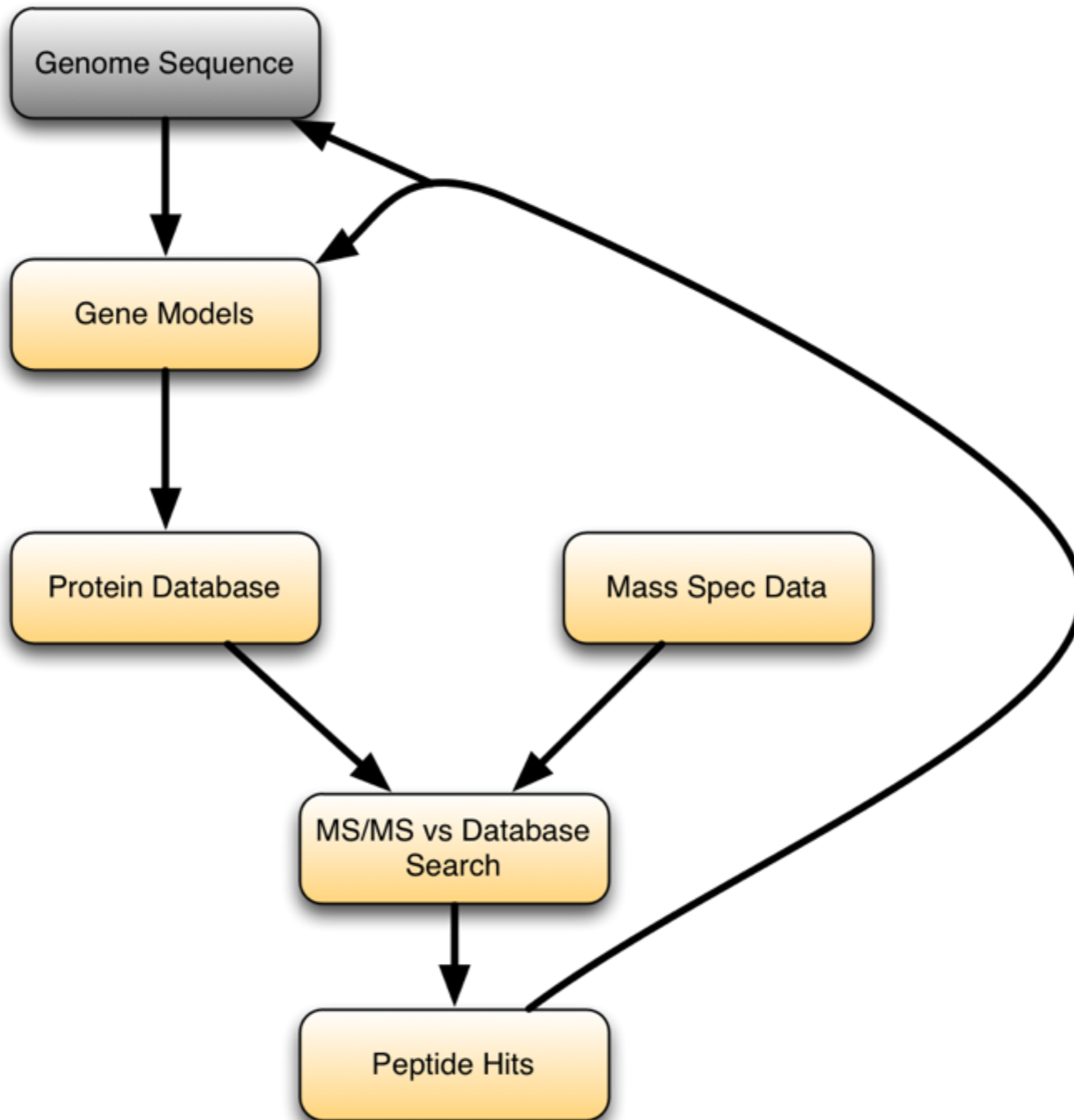


# Using Galaxy for Proteogenomics

Ira Cooke



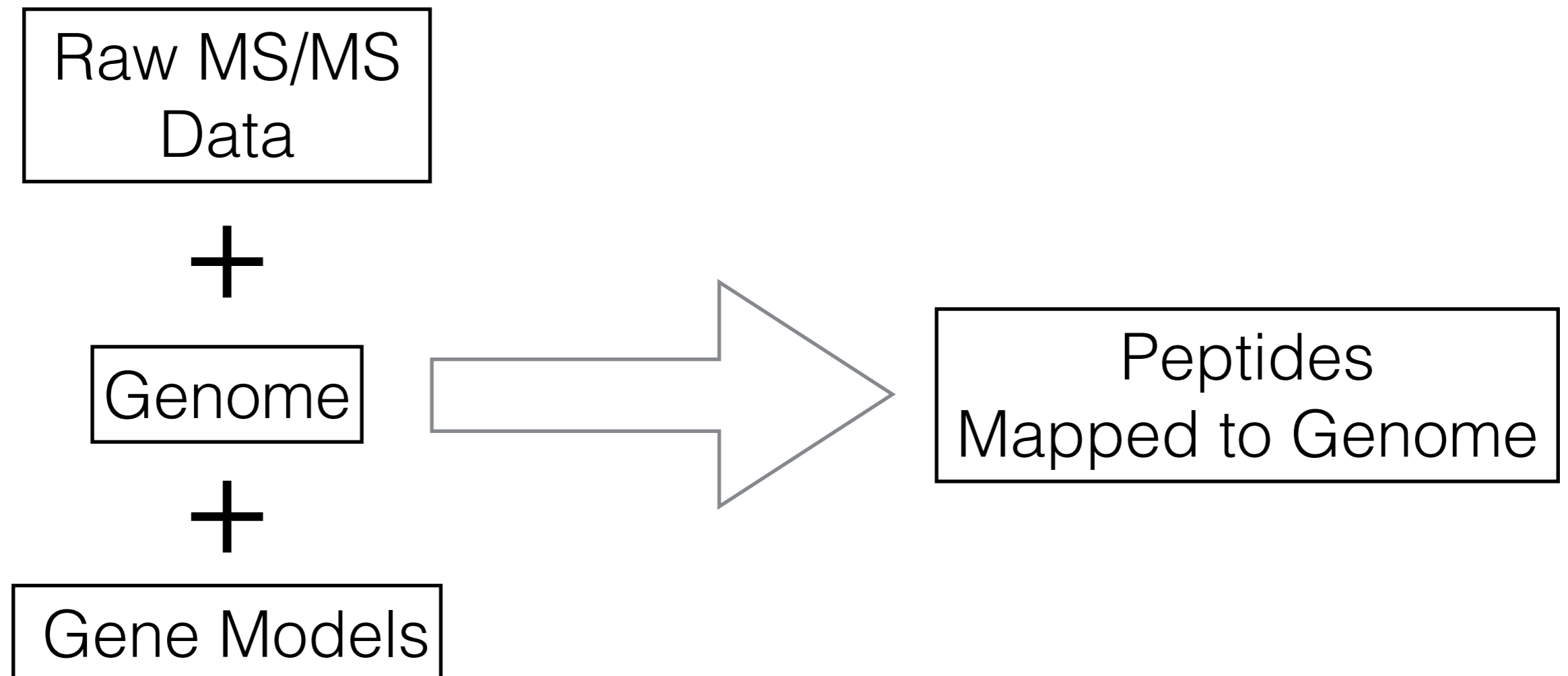


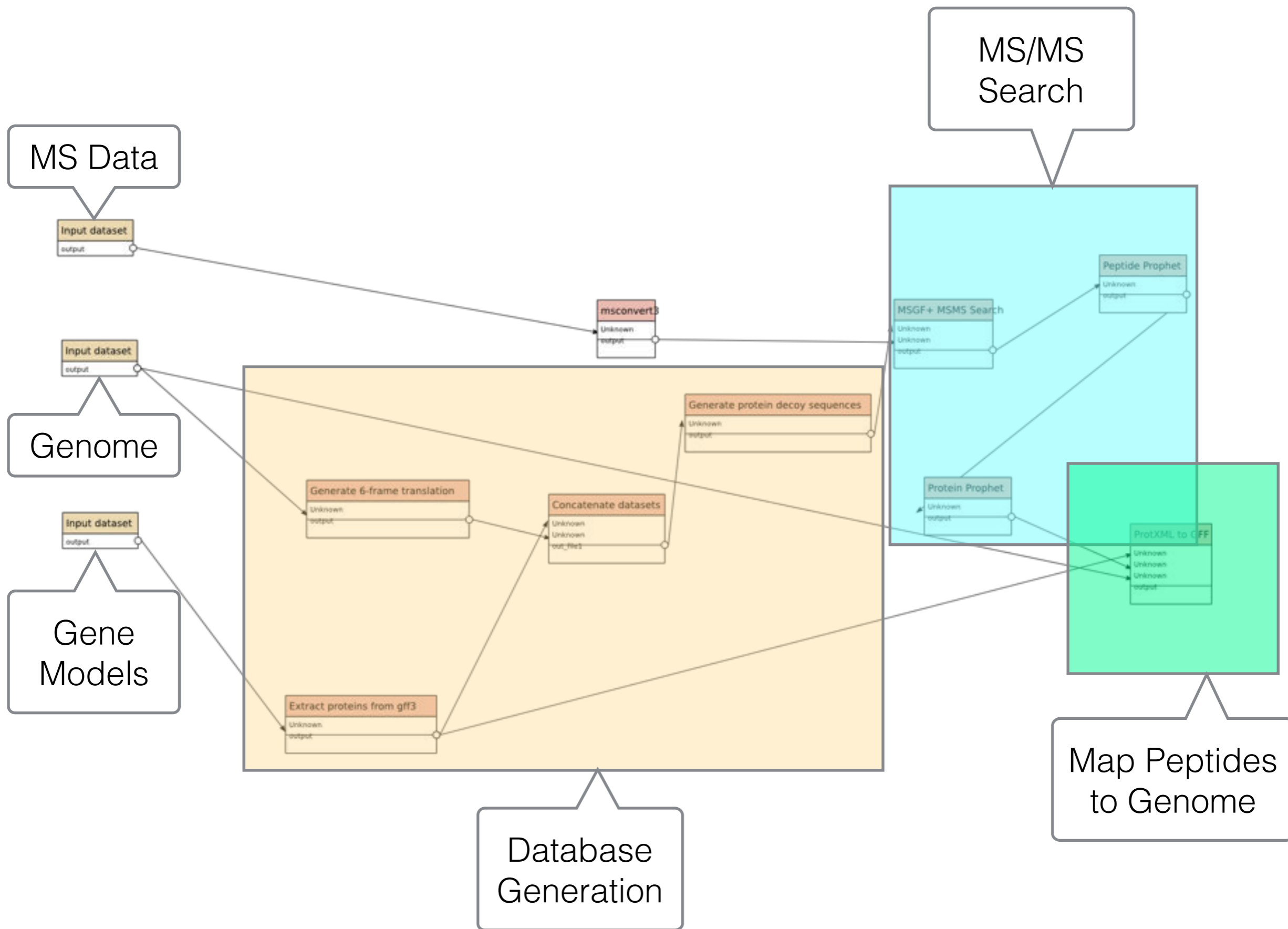


# What can Proteogenomics tell us?

- Locations of “Novel” Genes
- Confirm gene models
- Correct gene models
- Post-translational processing

# Core Task of Proteogenomics



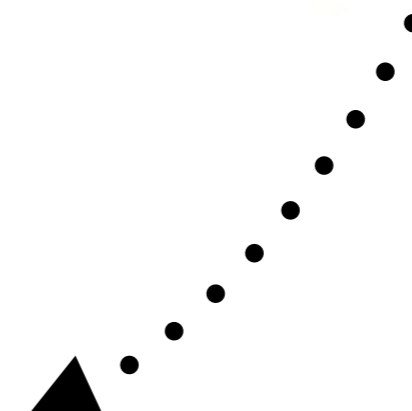
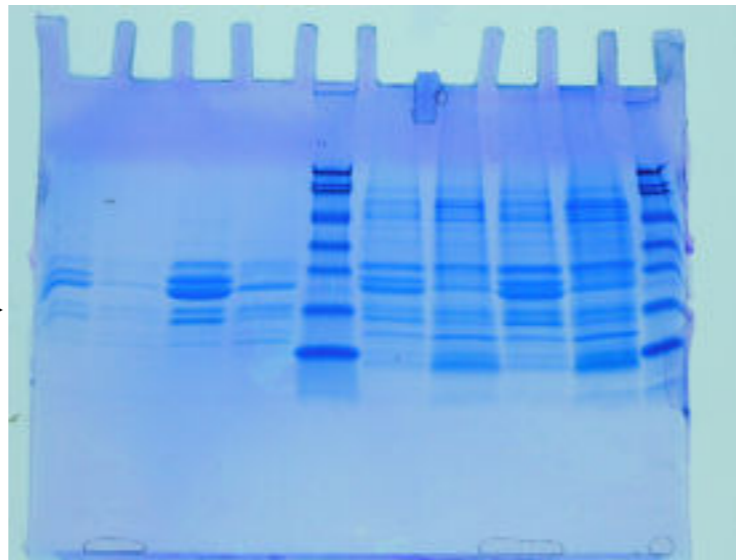
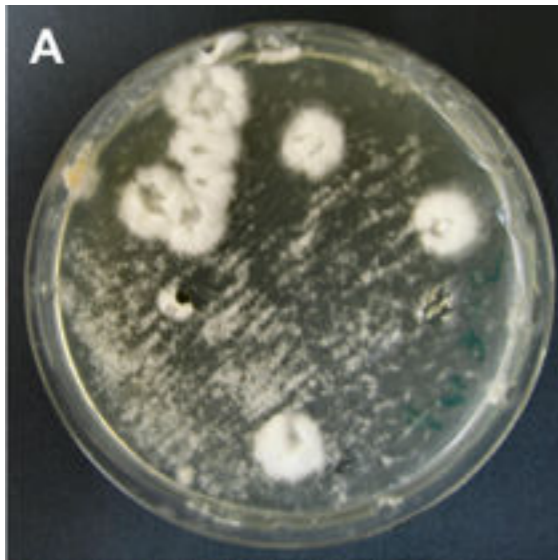


# Example: Pear Scab

- Important crop pest
- Small genome ( 50 Mb )
- “Effector” proteins crucial to fungal invasion are small



# Experiments

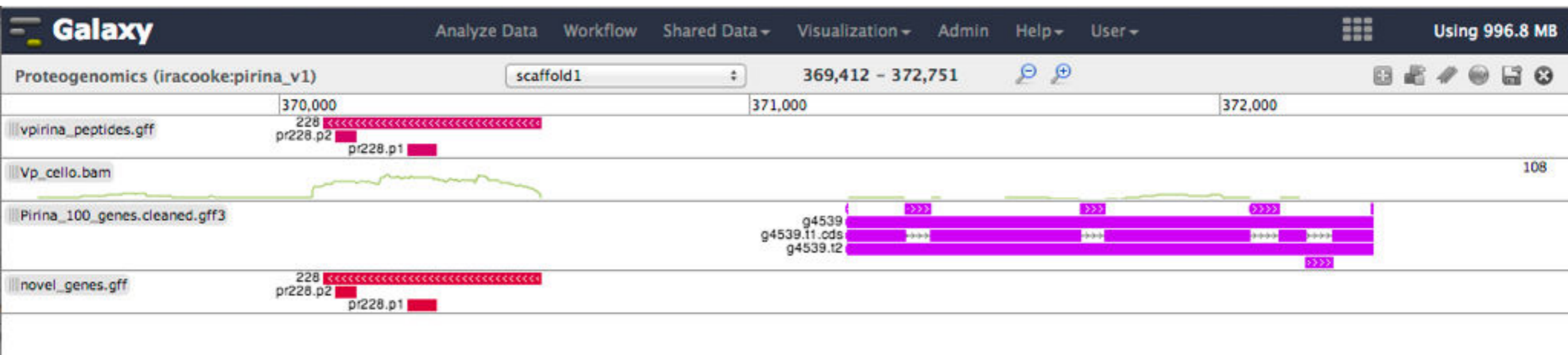




# Results

- Confirmed ~1000 Predicted Genes (17 Effectors)
- “Discovered” 32 New Genes (13 Effectors)
- Confirmed 30 Post-translational Cleavages (22 Signal Peps, 2 Propeps, 6 Mitochondrial Targeting)
- 6 Gene Extensions, 490 Confirmed splice sites

# Novel Genes in Trackster





# Where to get the tools

- **Proteogenomics Workflow**

Under Proteomics on the *Test* Toolshed  
[proteogenomics\\_msms\\_to\\_gff\\_workflow](#)

- **MS/MS Visualisations**

[https://bitbucket.org/Andrew\\_Brock/proteomics-visualise](https://bitbucket.org/Andrew_Brock/proteomics-visualise)

- **Vagrant VM**

[https://bitbucket.org/iracooke/protk\\_vagrant\\_ubuntumin](https://bitbucket.org/iracooke/protk_vagrant_ubuntumin)

- **Proteomics Tools**

<https://github.com/iracooke/protk>

# Acknowledgements

## ★ Venturia Biology & Mass Spec

Kim Plummer, Suresh Mathivanan, Pierre Faou, Daniel Jones, Vignesh Jayachandran

## ★ Galaxy Community

Bjoern Groening, John Chilton

## ★ Funding

VLSCI, LaTrobe e-Research, LaTrobe University

