Ablynx

Running Galaxy workflows using the Clc Main Workbench

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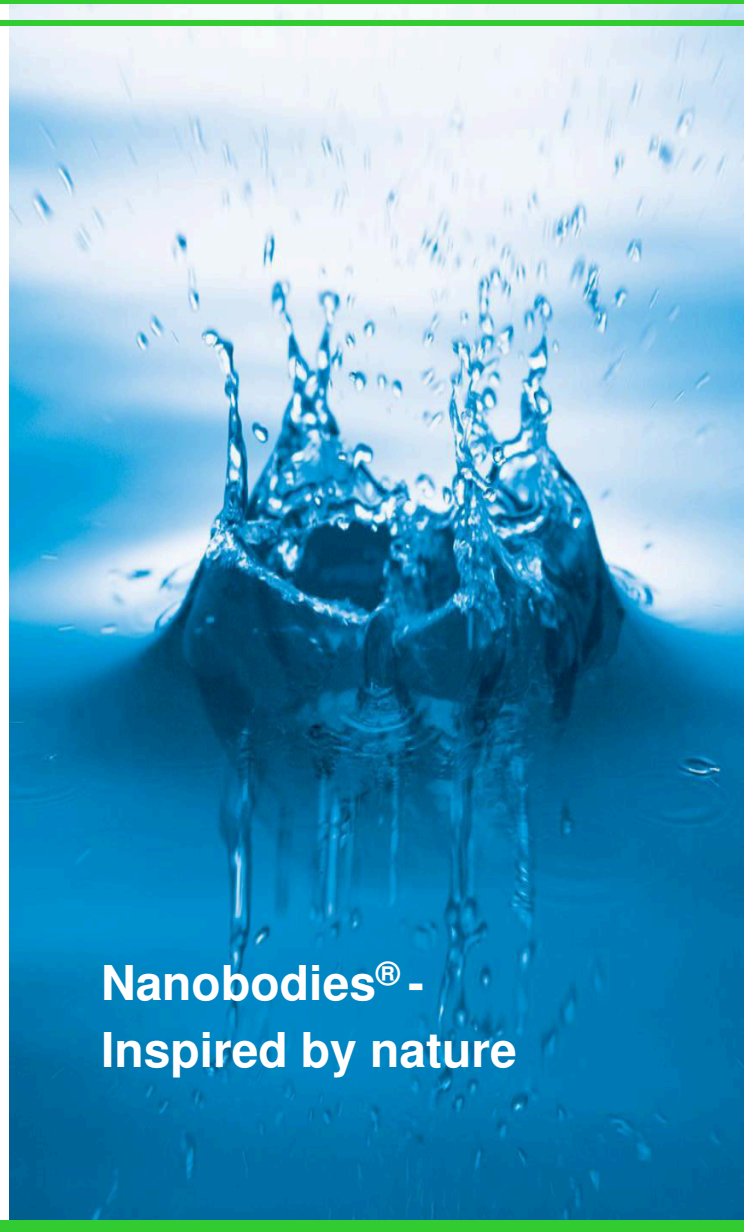
Galaxy Community Conference 2013

July 2nd



Ablynx – company overview

- Drug discovery and development company based in Ghent, Belgium
- A pioneer in next generation biologics - Nanobodies®
- Worldwide exclusive rights to commercialise Nanobody products in human healthcare
- ~25 programmes in the R&D pipeline
- Two products achieved clinical proof-of-concepts in RA
- 6 Nanobody products in the clinic - 3 Phase II & 3 Phase I
- Exclusive rights to >500 patent applications and granted patents
- Partnerships with Boehringer Ingelheim, Merck Serono, Novartis and Merck & Co
- Cash at 31 March 2013 of €82.2M
- >250 employees

What ?

- Transparently run Galaxy workflows in the Main Workbench of Clc bio

Why ?

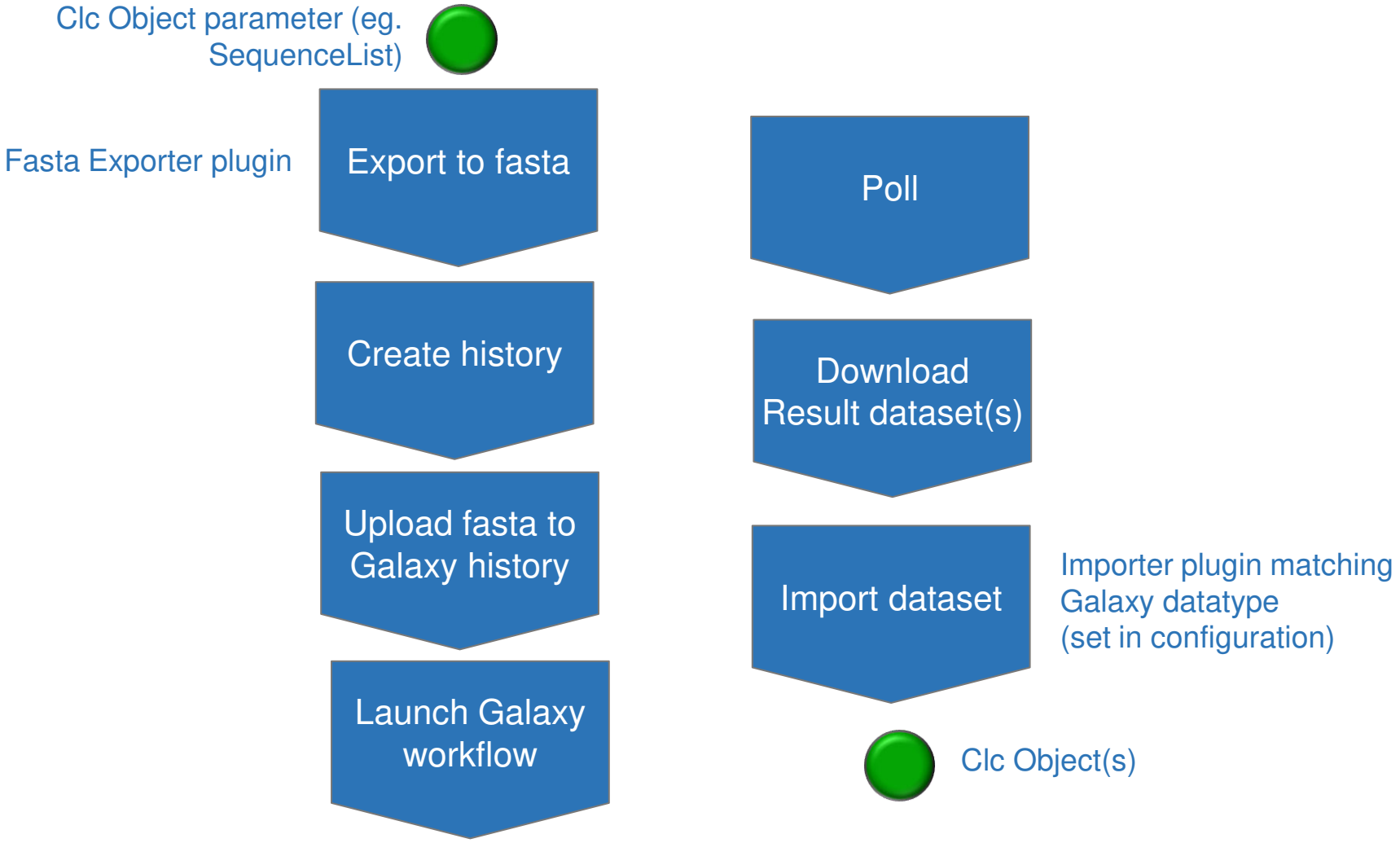
- Users don’t like change
  - Yet Another Tool to learn
- User friendly
  - Stay in comfort zone
  - No copy/paste or (manual) export of data needed

How ?

- Extend functionality of Main Workbench with plugin
  - SDK (http://www.clcbio.com/customized-solutions/software-developer-kit/)
- blend4j (John Chilton)
  - Github (https://github.com/biologghe/blend4j)

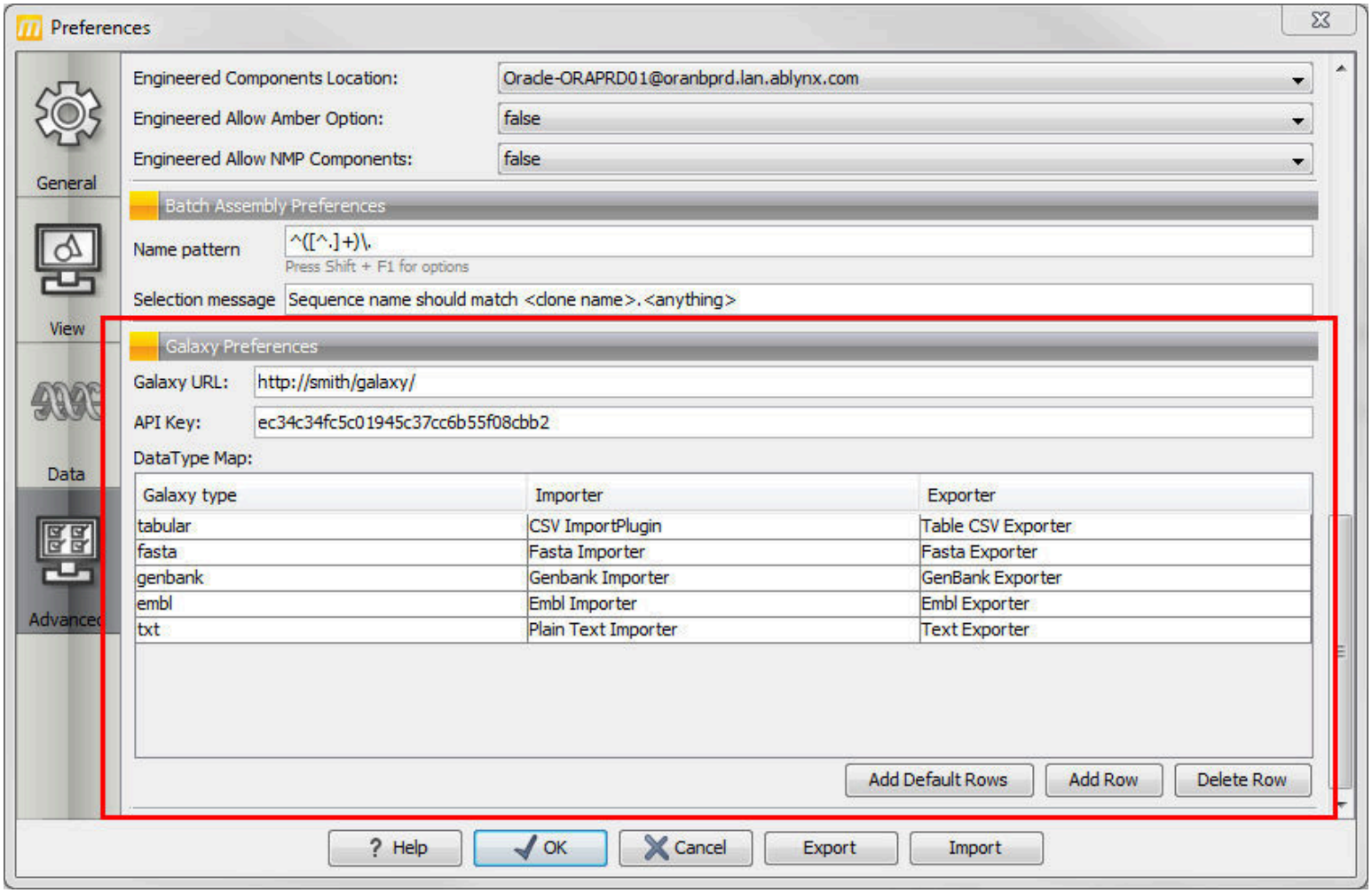
How ?

- Steps executed by plugin

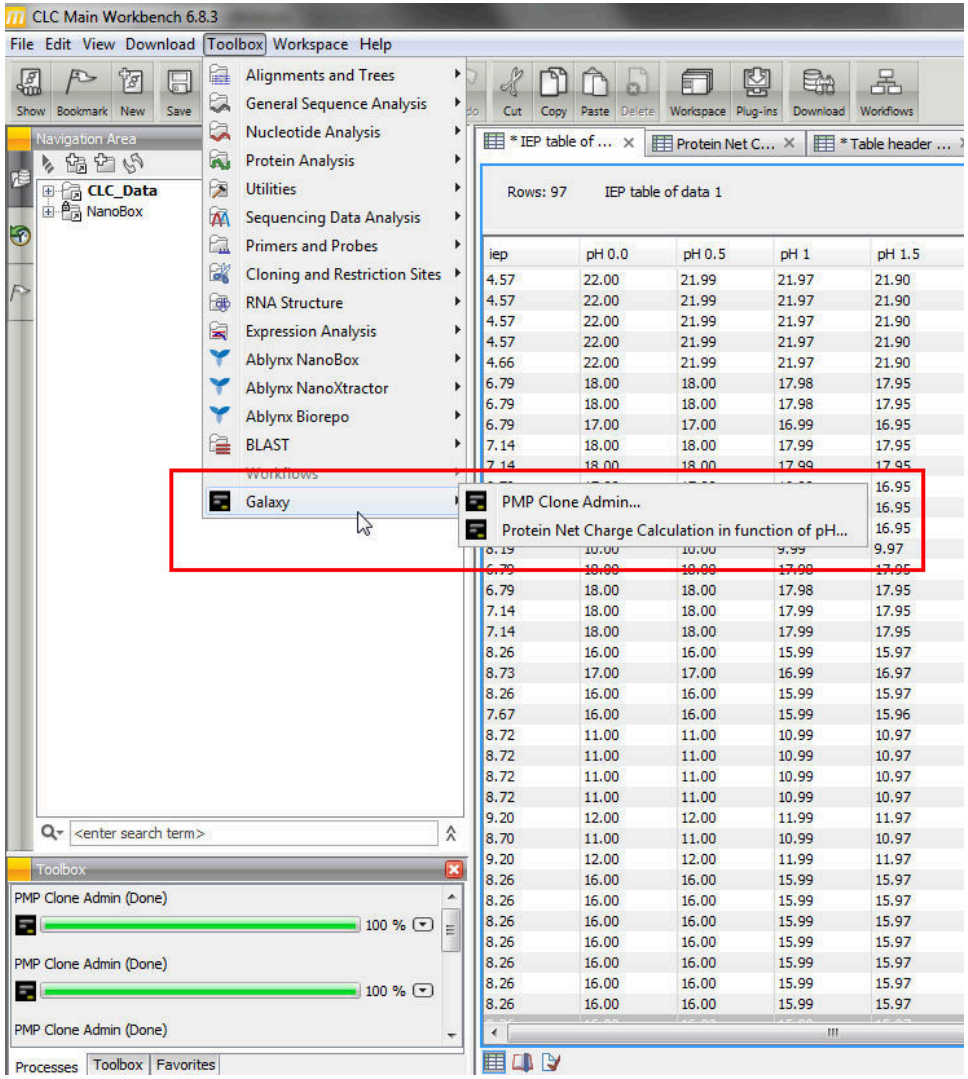


Configuration of Galaxy plugin

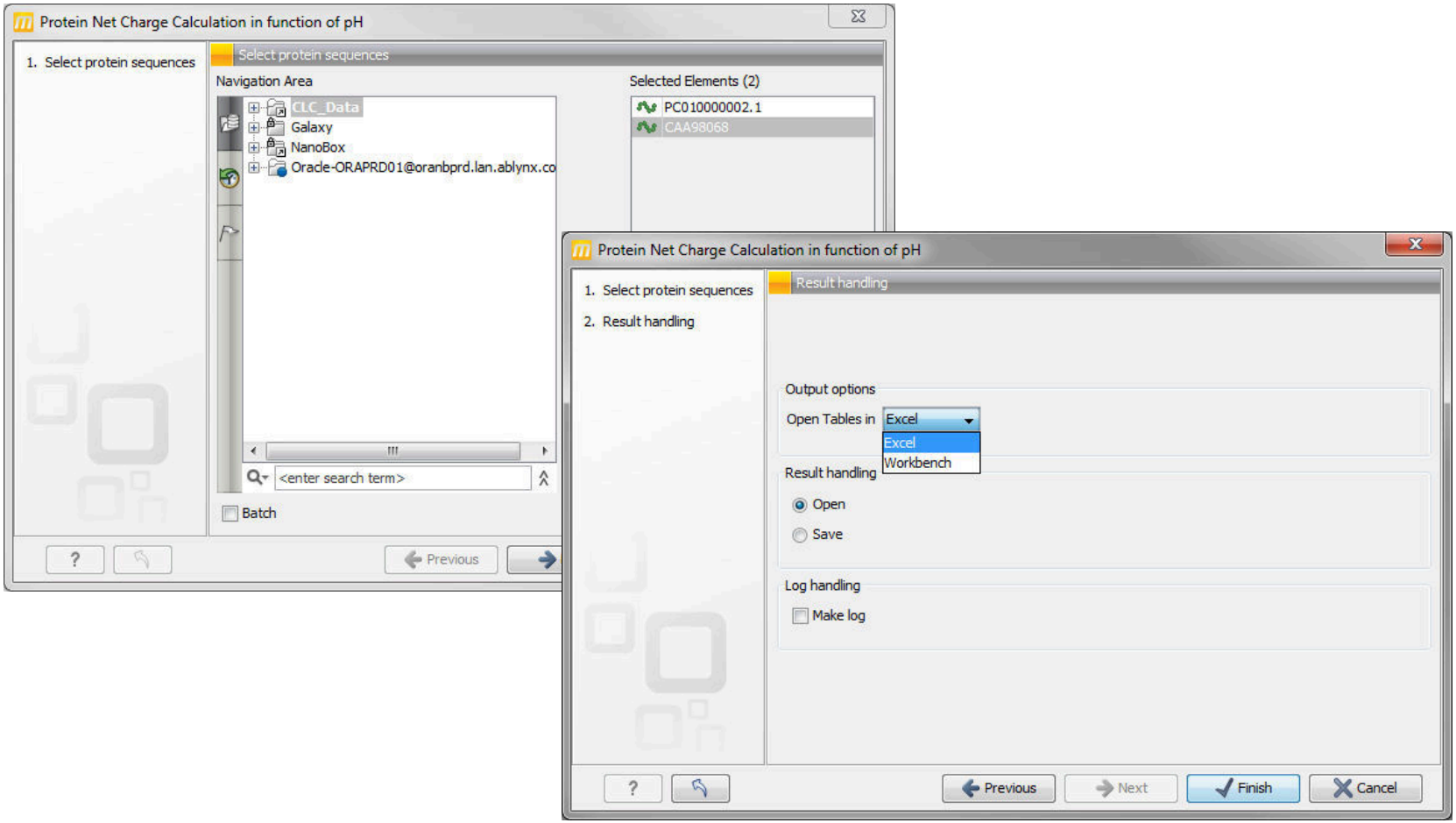
- Galaxy data type mapping using importer and exporter plugins



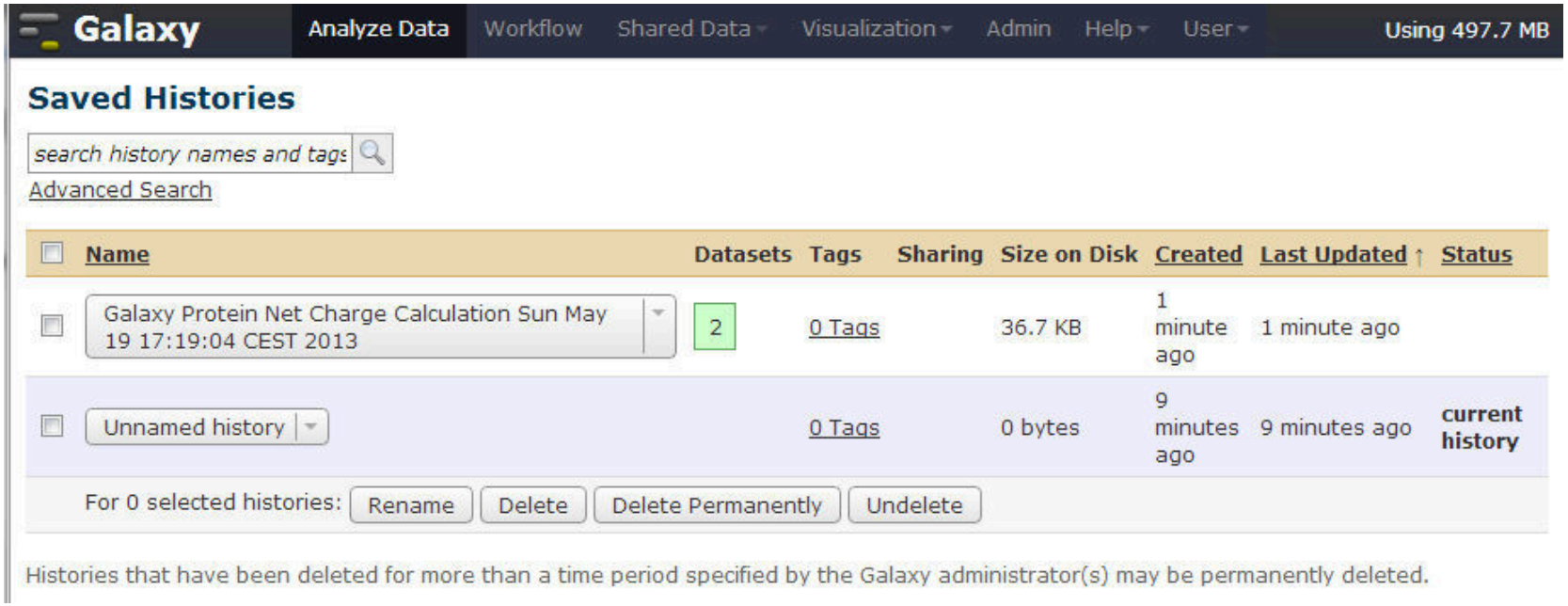
Galaxy workflows inToolbox



Set input parameters and launch

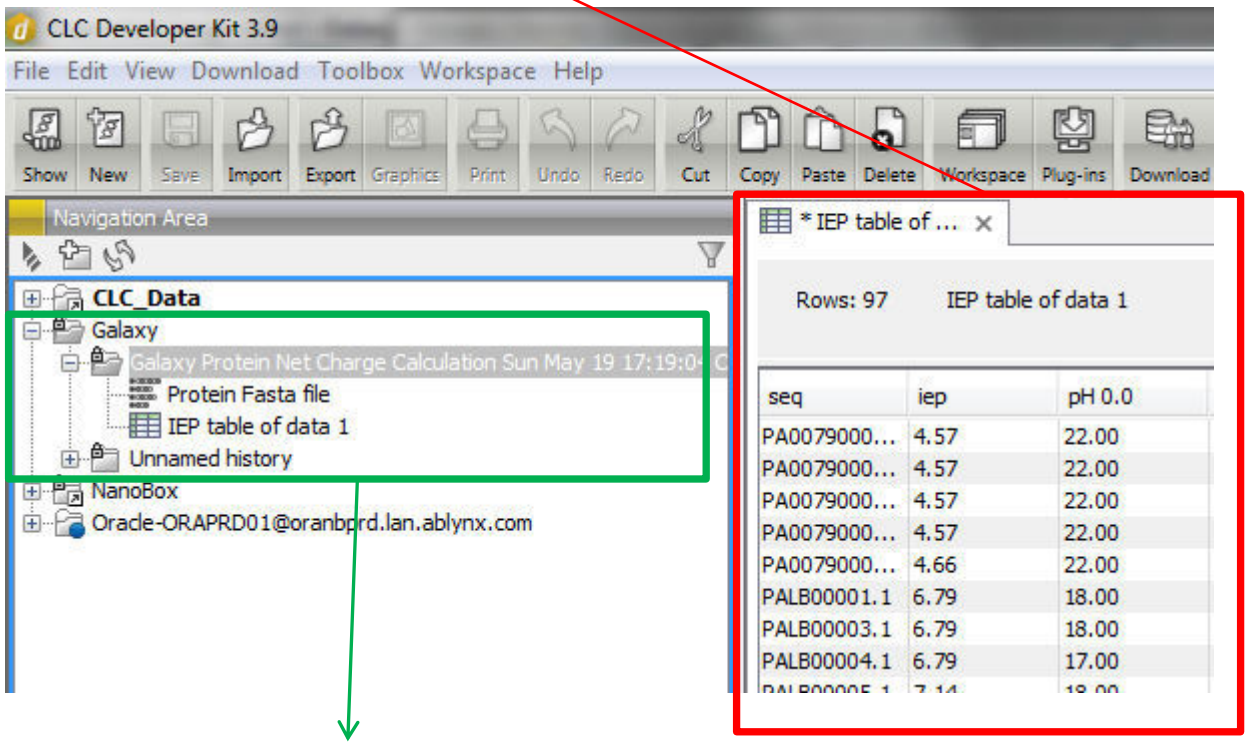


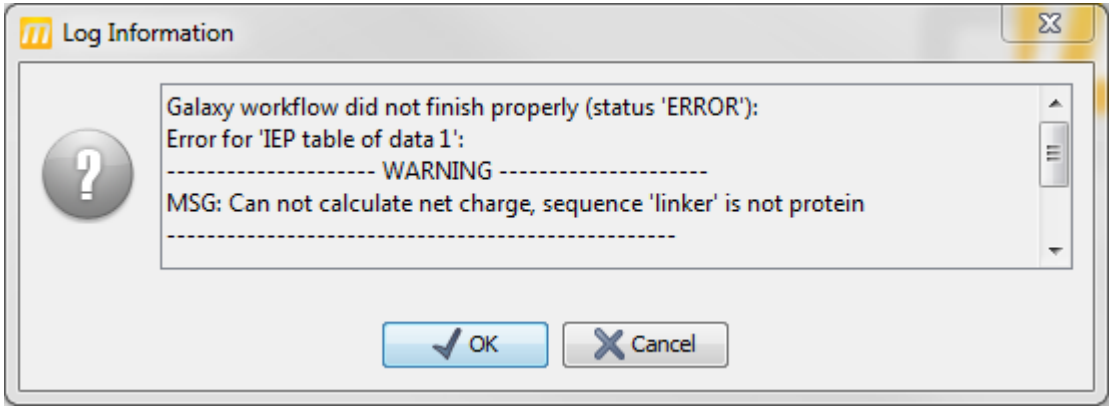
History is created



Result Dataset import and rendering

- As soon as workflow is finished, result is fetched, imported and rendered



- History visible in navigation area as well

Error handling