



# Oqtans: Online Quantitative Transcriptome Analysis with Galaxy

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## What is Galaxy

Galaxy is an open source, web-based platform for accessible, reproducible, and transparent computational biomedical research.

### 1 Accessibility

Galaxy enables users without programming experience to easily specify parameters and run tools and workflows.

### 2 Reproducibility

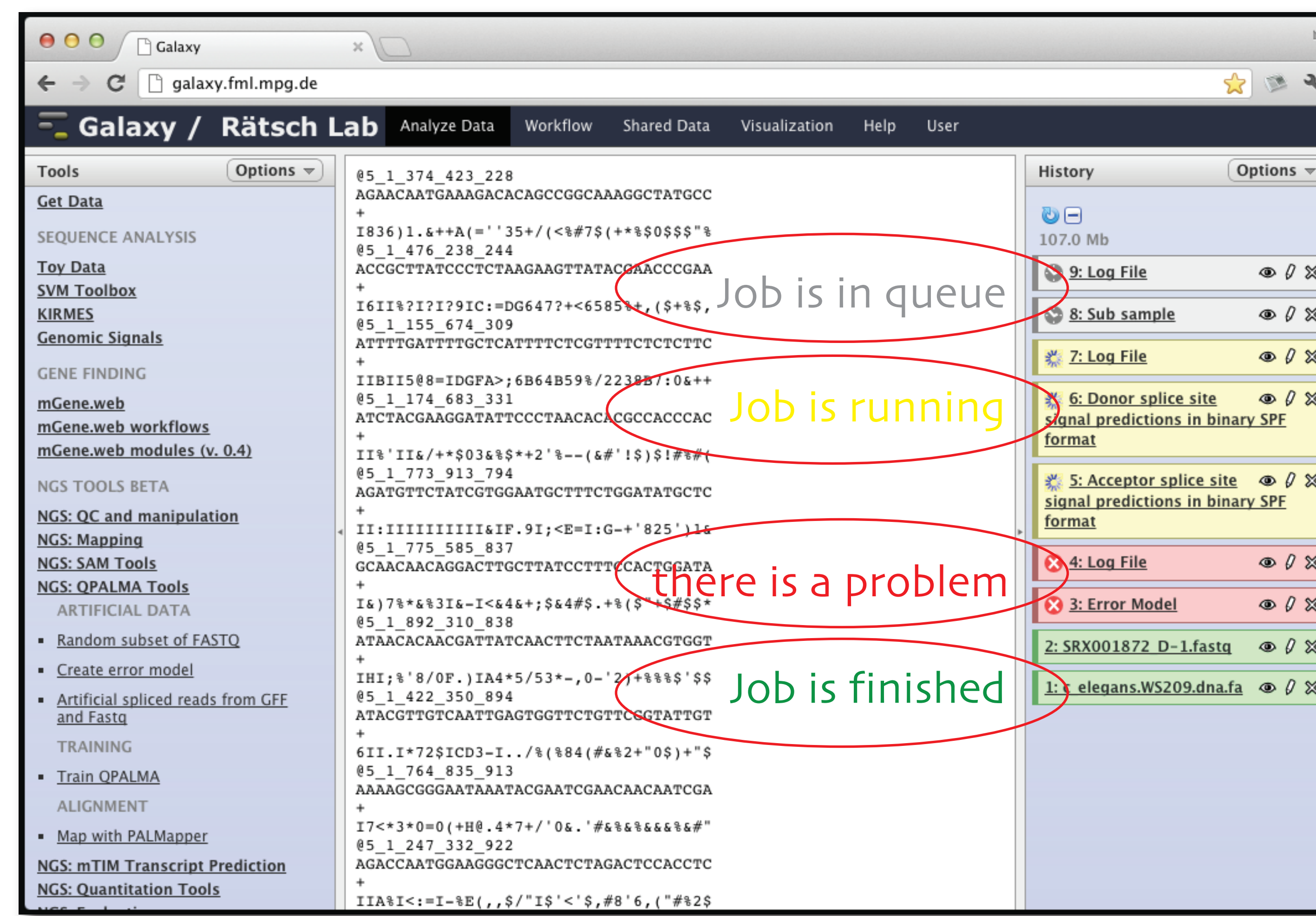
Galaxy captures all information necessary so that any user can repeat and understand a complete computational analysis.

### 3 Transparency

Galaxy enables users to share and publish analyses via the web and create interactive, web-based documents that describe a complete analysis.

### 4 Customizable, Extensible...

## Galaxy Interface: Analyze Data



**Tool panel**  
Integrates many bioinformatics tools within one interface

**Display panel**  
Data display and tools dialog

**History panel**  
Dataset for each analysis are kept here

Workflows, Shared data libraries, Genome Track Browser...

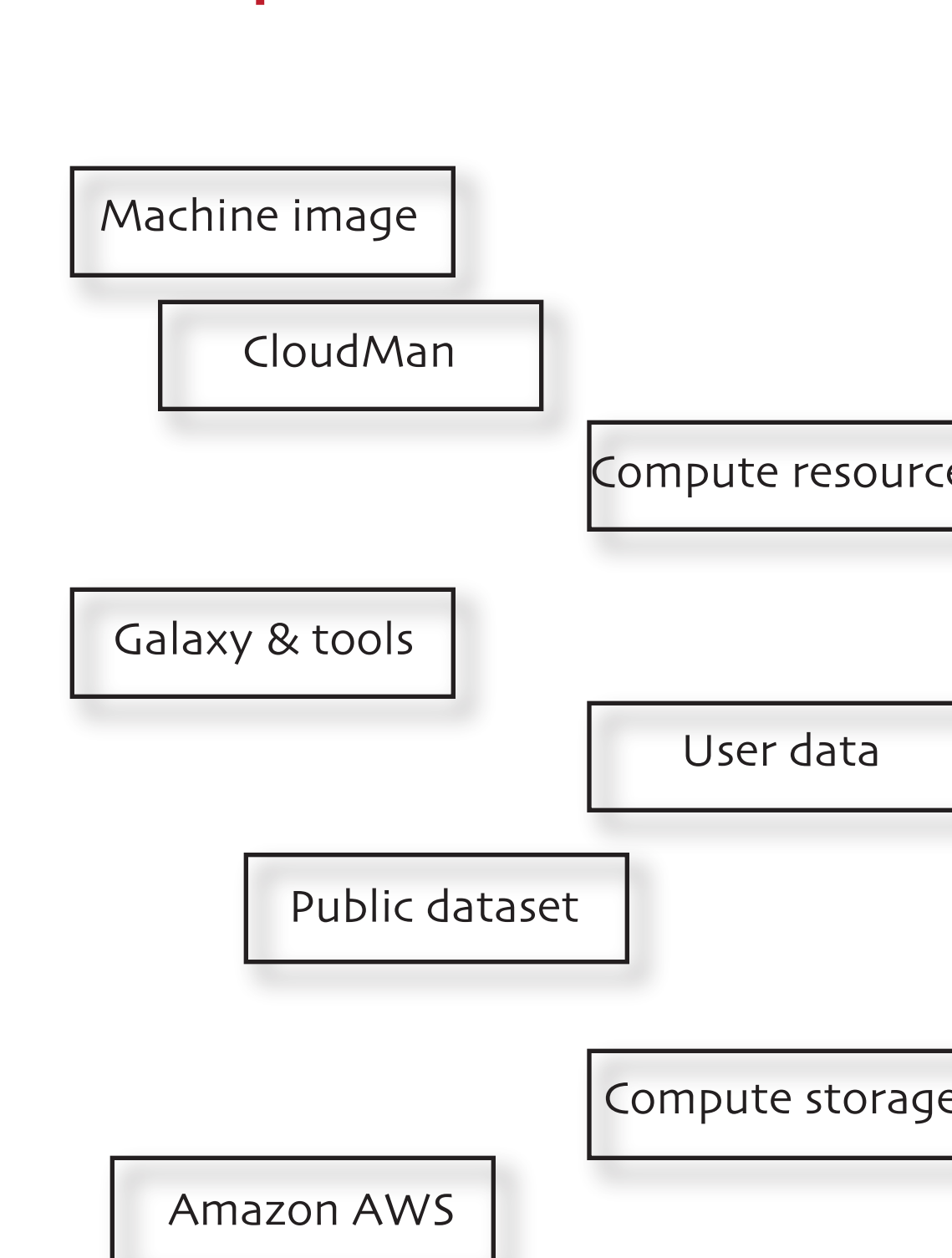
LOCAL instance, data is private!

## Galaxy CloudMan

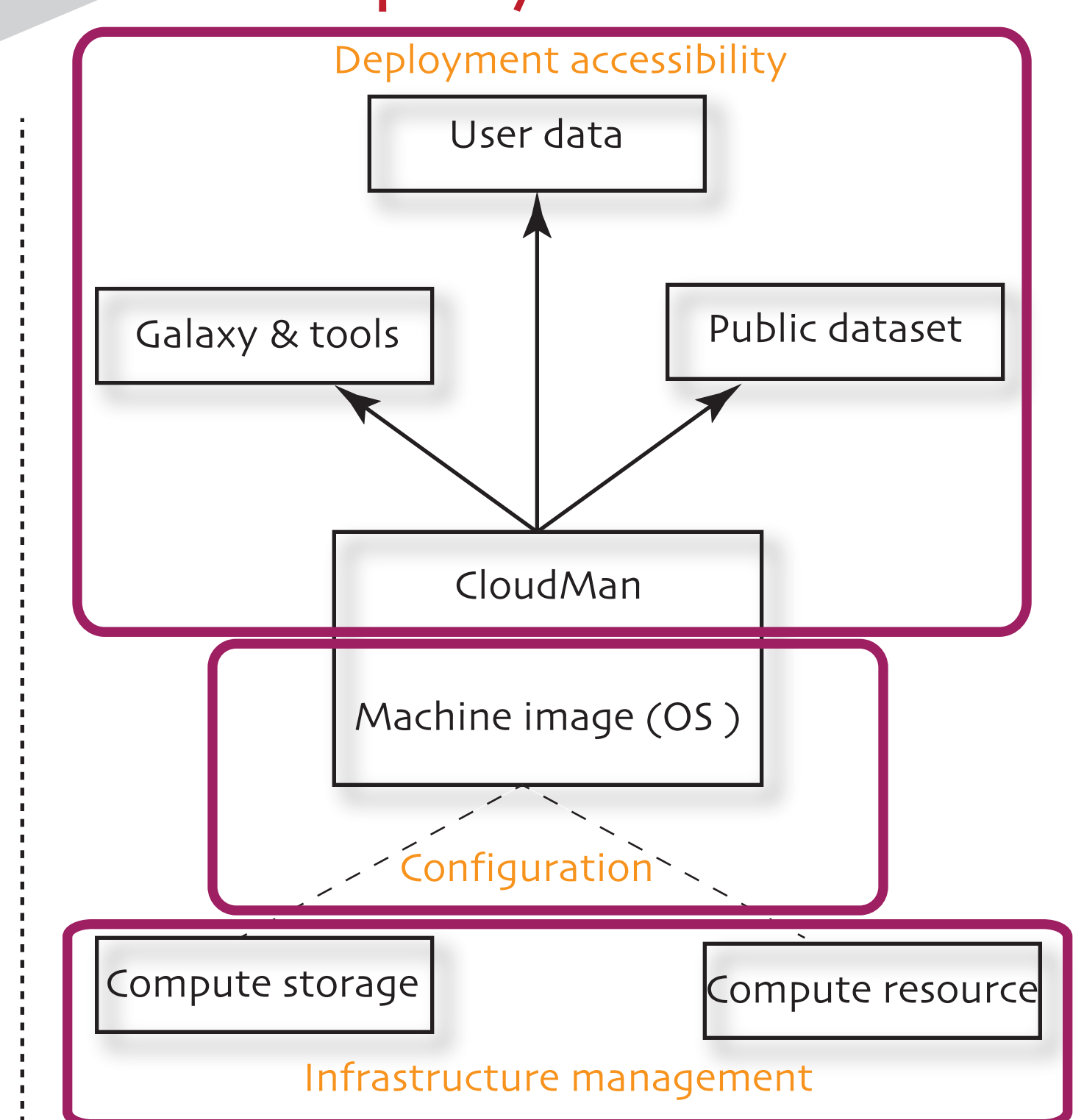
Galaxy CloudMan is a comprehensive manager for running and managing tools on cloud computing infrastructures, primarily Amazon Elastic Compute Cloud (EC2).

CloudMan automatically handles all aspects of resource acquisition, configuration and data persistence, thus entirely insulating a user from the informatics details.

### Components



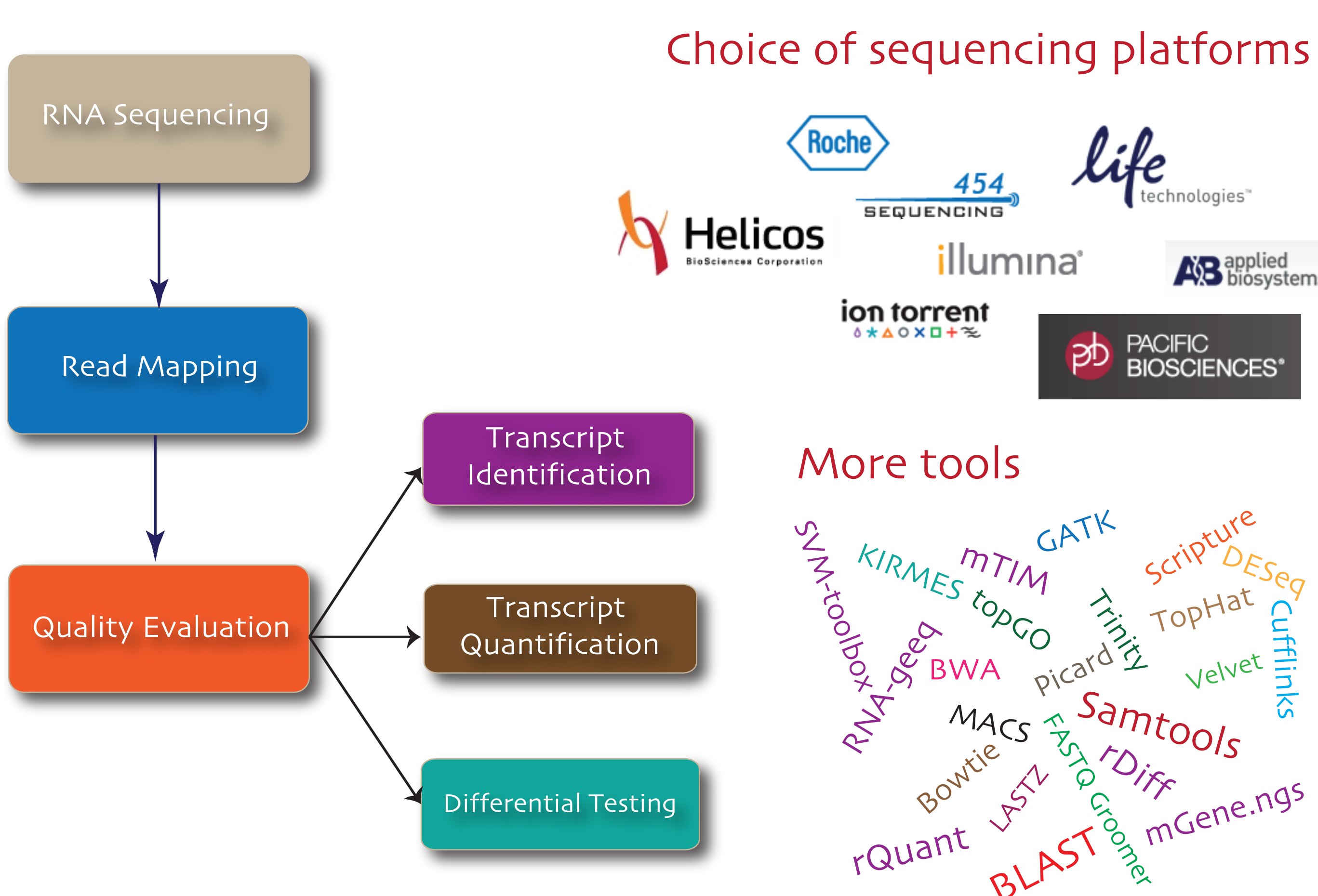
### Deployment



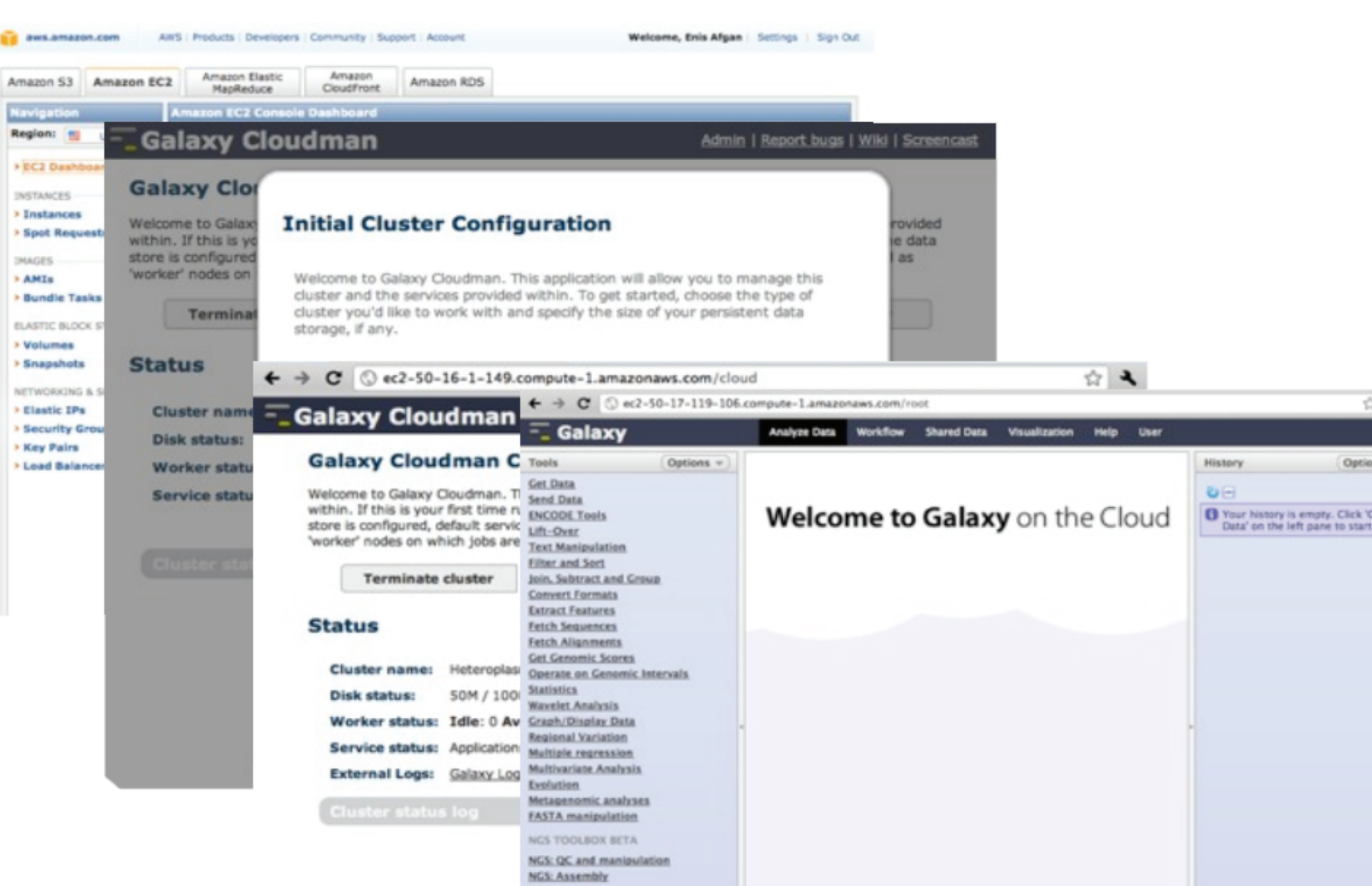
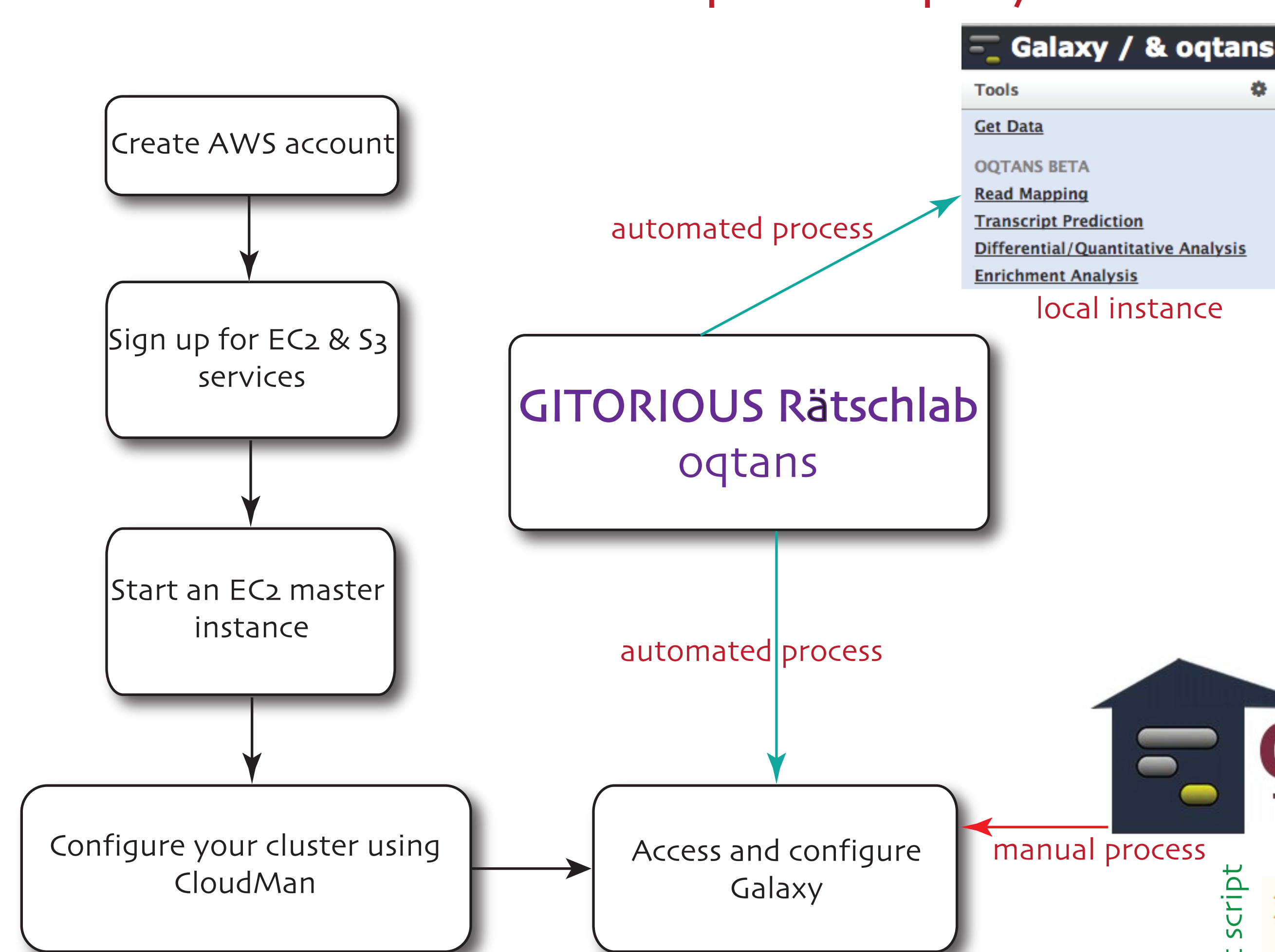
High CPU, less waiting and pay-as-you-go!

## oqtans:online quantitative transcriptome analysis

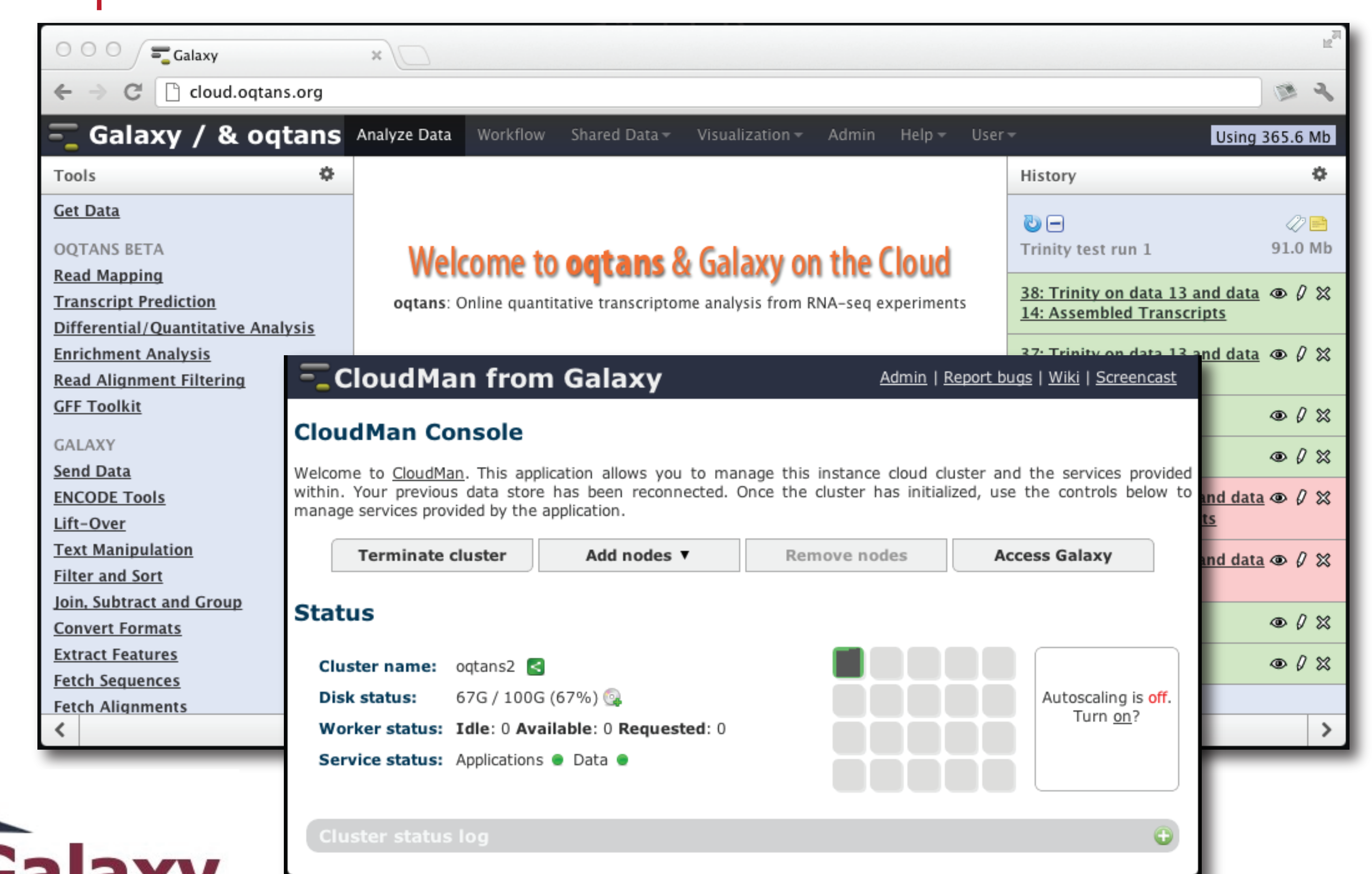
An open-source workbench integrated in the Galaxy framework to perform comparative quantitative transcriptome analysis.



## Local and Cloud based oqtans deployment



## oqtans test instance



## Support

support@oqtans.org  
galaxy@tuebingen.mpg.de

## References

- [1] Blankenberg, D. et al., Galaxy: a web-based genome analysis tool for experimentalists, Curr Protoc Mol Biol, 2010.
- [2] Enis Afgan et. al., Harnessing cloud computing with Galaxy Cloud, Nature Biotechnology, 2011.
- [3] Schultheiss, S. et al., Oqtans: a Galaxy-integrated workflow for quantitative transcriptome analysis from NGS Data, BMC Bioinformatics, 2011.

- PALMapper**: Fast and accurate spliced alignments of sequence reads
  - RNA-geeq**: Read alignment optimization and postprocessing
  - mTIM**: Margin based transcript mapping from RNA-Seq read alignments
  - rQuant**: Quantitative detection of alternative transcripts with RNA-Seq
  - rDiff**: Detecting differential RNA-transcript expression
  - mGene.ngs**: Eukaryotic gene finding system with RNA-Seq features
  - KIRMES**: Promoter analysis from Chip-chip or Chip-Seq data
  - EasySVM**: Generic interface for classification of sequences with SVMs
- More tools at <http://galaxy.fml.mpg.de/>

## Useful links

- <http://cloud.oqtans.org/>
- <http://oqtans.org/>
- <https://git.ratschlab.org/>
- <http://galaxy.fml.mpg.de/>
- <https://usegalaxy.org/>
- <http://toolshed.g2.bx.psu.edu/>