



Center for Translational
Molecular Medicine

Translating science into better healthcare

Building a scalable Galaxy cluster for biomedical research in The Netherlands



David van Enckevort
Galaxy Community Conference 2014, Baltimore



Galaxy adaptation for a clinical setting

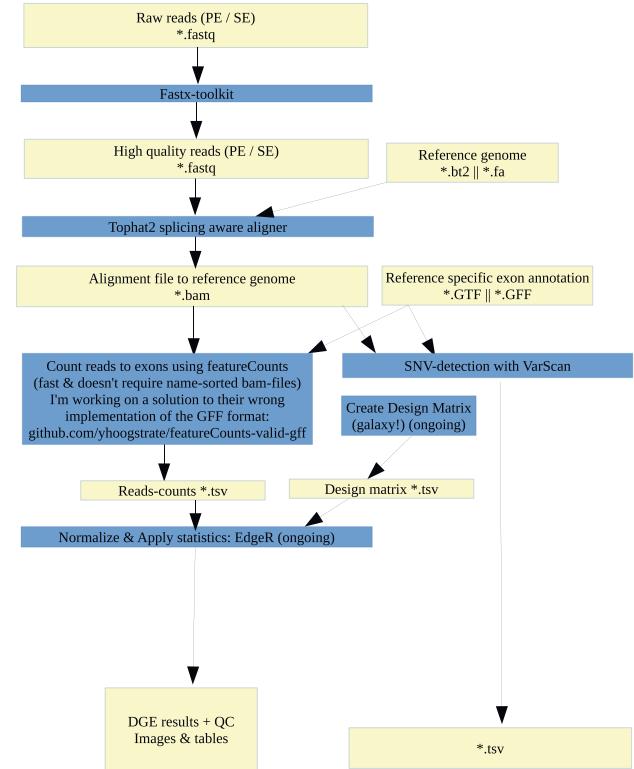
Requirement	Addressed by
Provenance	Galaxy
Ease of administration	Tool Shed / hosting company
Stable system	DTAP instances, Tool Shed, stable releases
Service levels	Hosting company, skilled helpdesk / redundant architecture
Certified security of data	Architecture / hosting company certification
Scalability	Scalable architecture / CloudMan
Performance	HPC architecture
Separation between studies	Multi-tenant Cloud architecture / CloudMan
Resource accounting	Galaxy reporting module, quota & scheduler
Single Sign On	OpenConext (SAML)

Typical Use Cases: NGS, Proteomics

e.g. *RNA-Seq pipeline used for measuring gene expression*

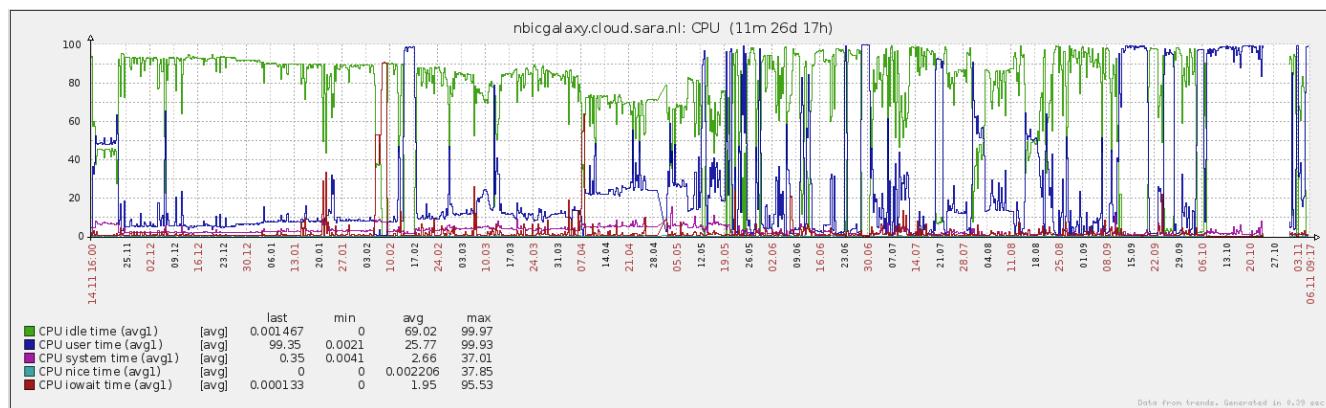
Pipelines are often I/O intensive, because of:

- Input data size typically many gigabytes
- Five-fold increase of the data size in the intermediate files



Bottlenecks for performance

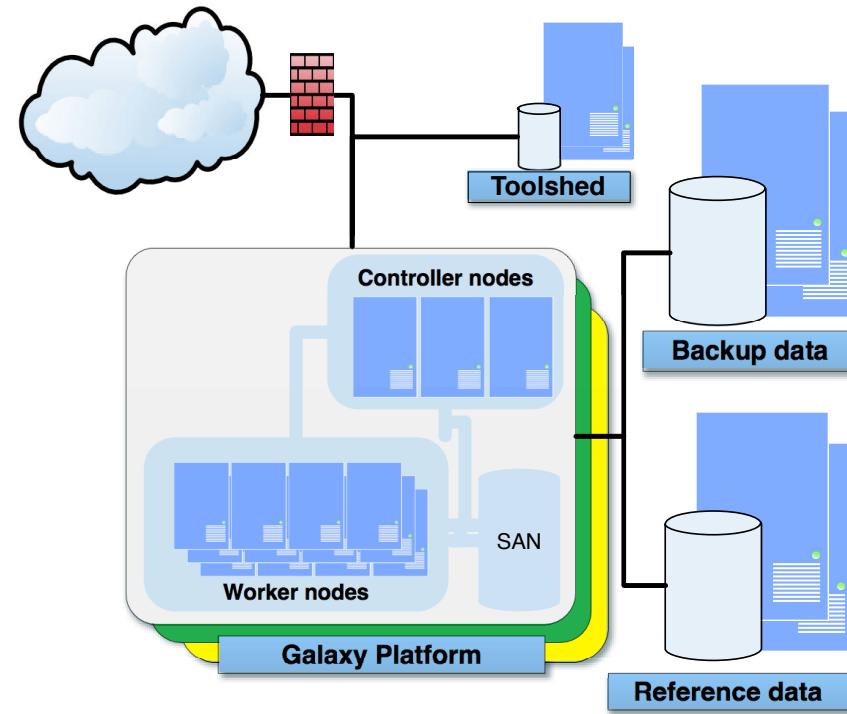
- Based on metrics collected from the NBIC public Galaxy we identified a few key factors:
 1. I/O performance (input/output from storage / hard drive)
 2. Lots of memory
 3. Large storage, allowing for future growth



Architecture

Key design features:

- HPC hardware
- Redundant
- Multi-tenant
- Multi-tiered storage
- Dedicated NFS server
- Elastically scaling through cloud technology



CTMM-TraIT partners

netherlands eScience center



PHILIPS



VU university medical center



nbic



LEIDS UNIVERSITAIR MEDISCH CENTRUM



Vancis



OpenClinica®
Open Source for Clinical Research



Roche
Diagnostics

