

# drylab.nl.enabling.translational.research

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## Background

- The Cancer Center Amsterdam (CCA) with 400 cancer researchers is part of the the academic hospital VU University Medical Center
- Given the rise of multiple omics technologies and their clinical potential we are currently establishing a Drylab that empowers both researchers and clinicians with state-of-the-art bioinformatics solutions
- Galaxy-based analysis workflows are implemented usable by non-bioinformatics researchers
- We promote Sustainable Software Development of internal tools and their integration in Galaxy
- We train users in bioinformatics through seminars, tutorials and coaching; give them power to do more analyses themselves



### Galaxy Challenges

- Queuing system
- Distributed computing
- Versioning of different Galaxy instances
- Galaxy workflows should accept dynamic range of input files
- Easy transfer & exchange of new workflows
- Development, Test and Production installations
- Test cases for automated testing of tools

### Own Galaxy Pipelines

- DNaseq analysis:**
- Copy number analysis: QDNAseq<sup>1</sup> (see poster P18)
  - Variant detection in TruSeq Cancer Amplicon Panel (by Daoud Sie, example 1)
- RNAseq analysis:**
- Differential expression analysis (in-house pipeline by Irsan Kooi, example 2)
  - Variant detection (with Star & GATK)
- Proteomics / Proteogenomics:**
- riboSeq, sequencing of protein coding transcripts (example 3)

Workflow TruSeq Cancer Amplicon Panel Variant detection (by Daoud Sie)

Stage	Tools
Grooming	Cutadapt, fastx-toolkit, flash
Alignment	BWA Stampy
Variant Calling	Falco (by Daoud Sie)
Annotation	snpEff, snpSift
Filtering	R / perl / shell
Reporting	MySQL / HTML / PDF

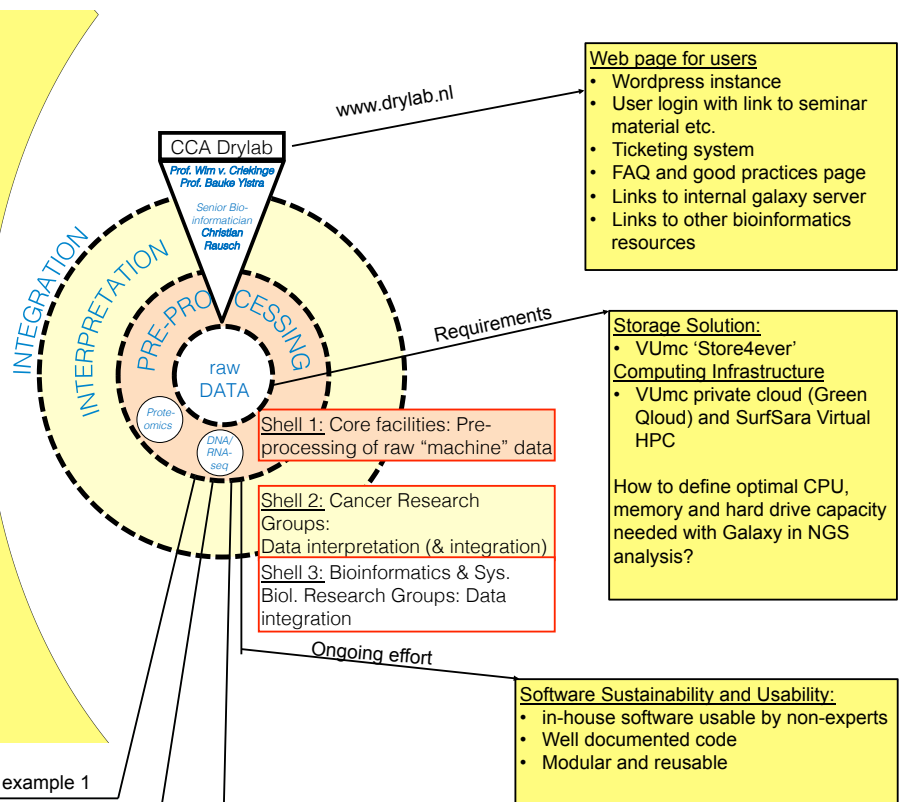
Workflow RNAseq differential expression analysis

Stage	Tools
Local Read Alignment	STAR (alternative Tophat)
Data prep	Picard-tools, Samtools
Quantification	HTSeq
Diff. expr. Test	edgeR
Clustering	Unsupervised hierarchical clustering (R hclust)
Statistical analysis	Principal component analysis (R prcomp)

### References

- www.bioconductor.org package QDNAseq
- www.biobix.be/proteofomer

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example 1

example 2

example 3

Workflow riboSeq proteogenomics<sup>2</sup>

