Reproducible Quantitative Transcriptome Analysis with oqtans

online quantitative transcriptome analysis

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Introduction

An open-source workbench integrated in the Galaxy framework that enables researchers to set up a computational pipeline for quantitative transcriptome analysis.

Accessibility

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

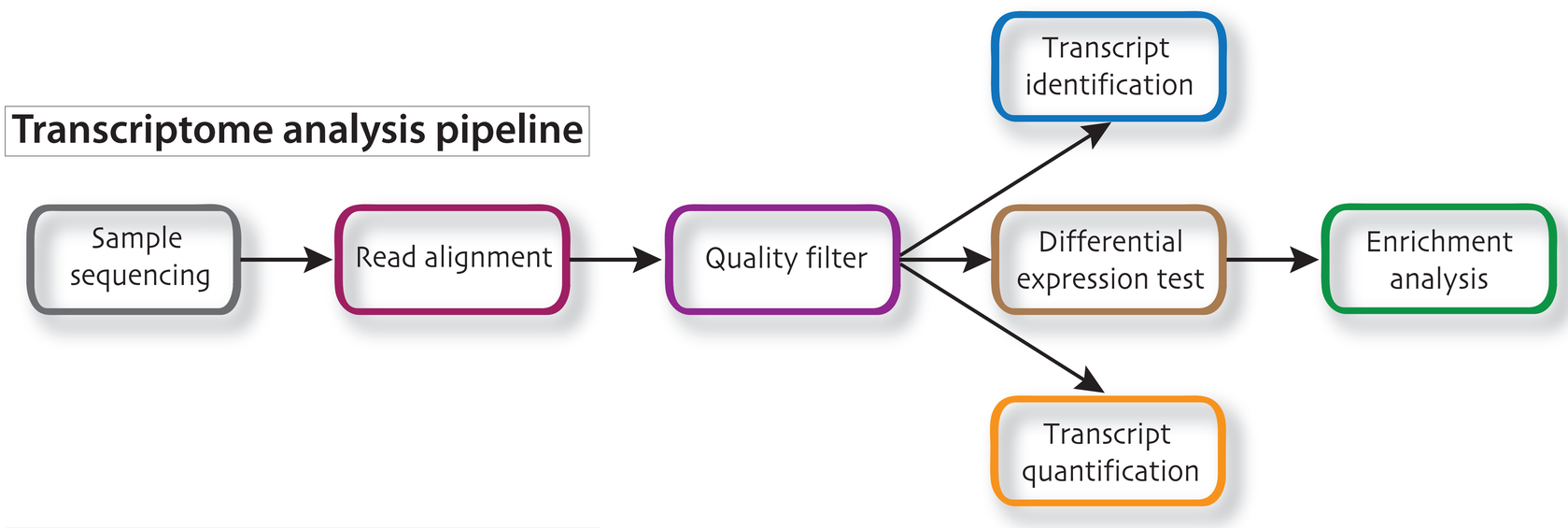
Reproducibility

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

Transparency

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

Transcriptome analysis pipeline



Transcriptome analysis toolsuite

PALMapper*
BWA
TopHat
STAR

RNA-geeq*

rDiff*
DESeq
DEXSeq
Cuffdiff
edgeR

mTIM*
ASP*
Trinity
Cufflinks
Scripture

rQuant*

GFFTools*

topGO
GeneSetter*

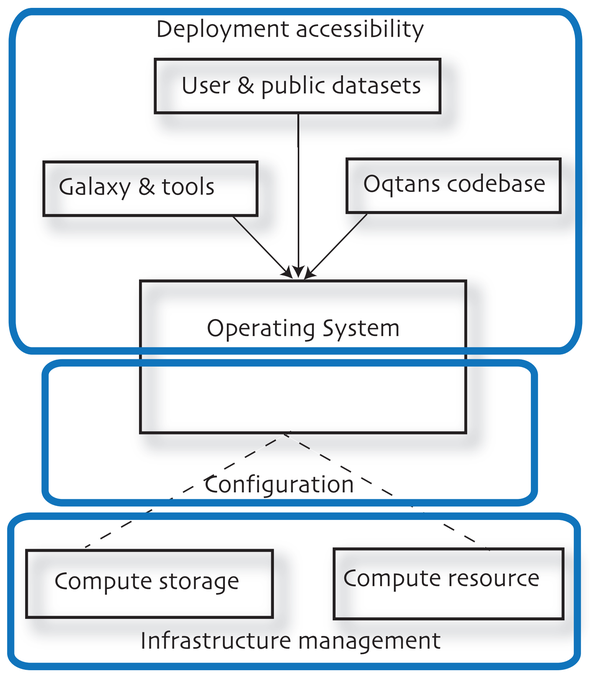
mGene*

KIRMES*

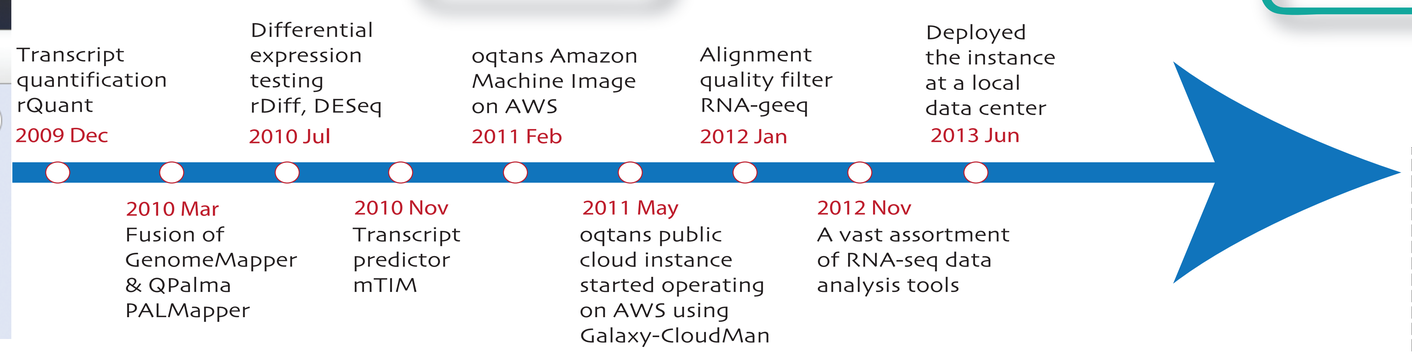
ARTS*

EasySVM*

*developed by Rätsch lab members from cBio MSKCC and FML of the Max Planck Society



oqtans public instance



Support

support@oqtans.org
galaxy@raetschlab.org

Useful links

http://oqtans.org/
http://galaxy.cbio.mskcc.org/
http://github.com/ratschlab/
http://toolshed.g2.bx.psu.edu/

oqtans Availability

Compute and visualize the differential expressed gene familes

Alignment optimization and postprocessing toolbox

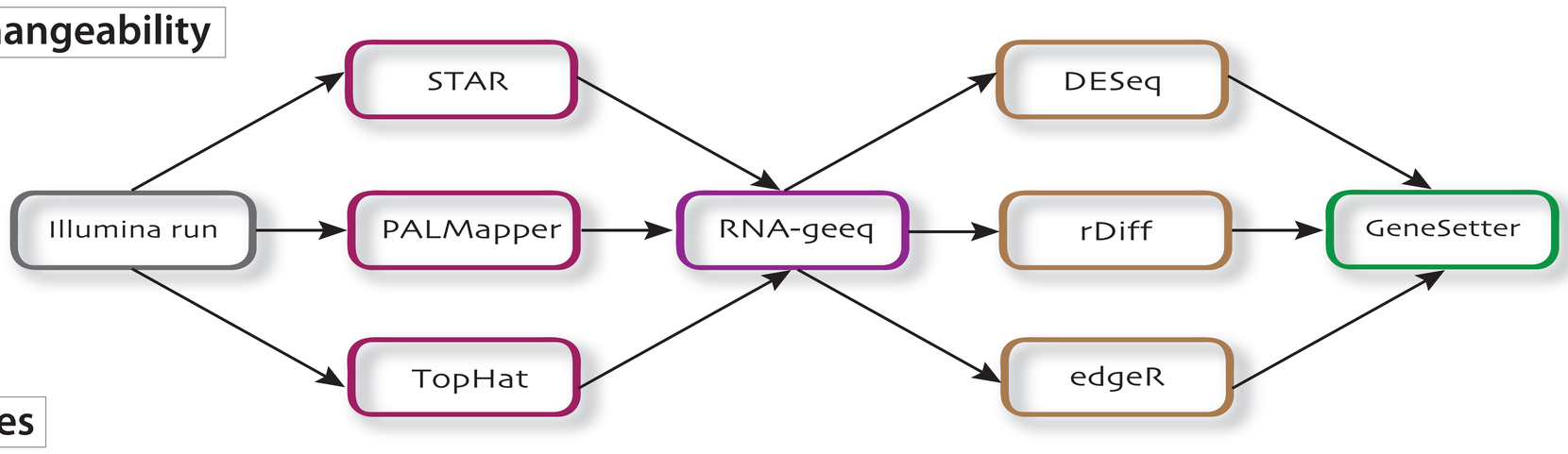
Highly accurate variation aware sequencing read mapper

Accurately determine the abundance of transcripts

Margin based transcript reconstruction from read alignments

Differential RNA-processing program

Tool exchangeability



References

[1] Blankenberg, D. et al., Galaxy: a web-based genome analysis tool for experimentalists, Curr Protoc Mol Biol, 2010.

[2] Schultheiss, S. et.al., Oqtans: a Galaxy-integrated workflow for quantitative transcriptome analysis from NGS Data, BMC Bioinformatics, 2011.

[3] Afgan E et. al., Harnessing cloud computing with Galaxy Cloud, Nature Biotechnology, 2011.

[4] Sreedharan V et. al., Oqtans:The RNA-seq Workbench in the Cloud for Complete and Reproducible Quantitative Transcriptome Analysis, (in revision), 2013.