

Reproducible Quantitative Transcriptome Analysis with **oqtans**

online
quantitative
transcriptome
analysis



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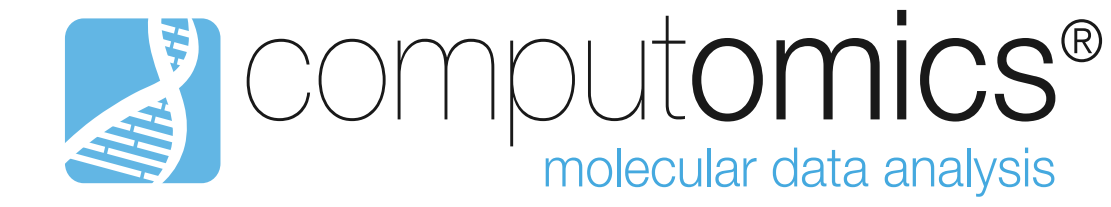
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MAX-PLANCK-GESellschaft



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.

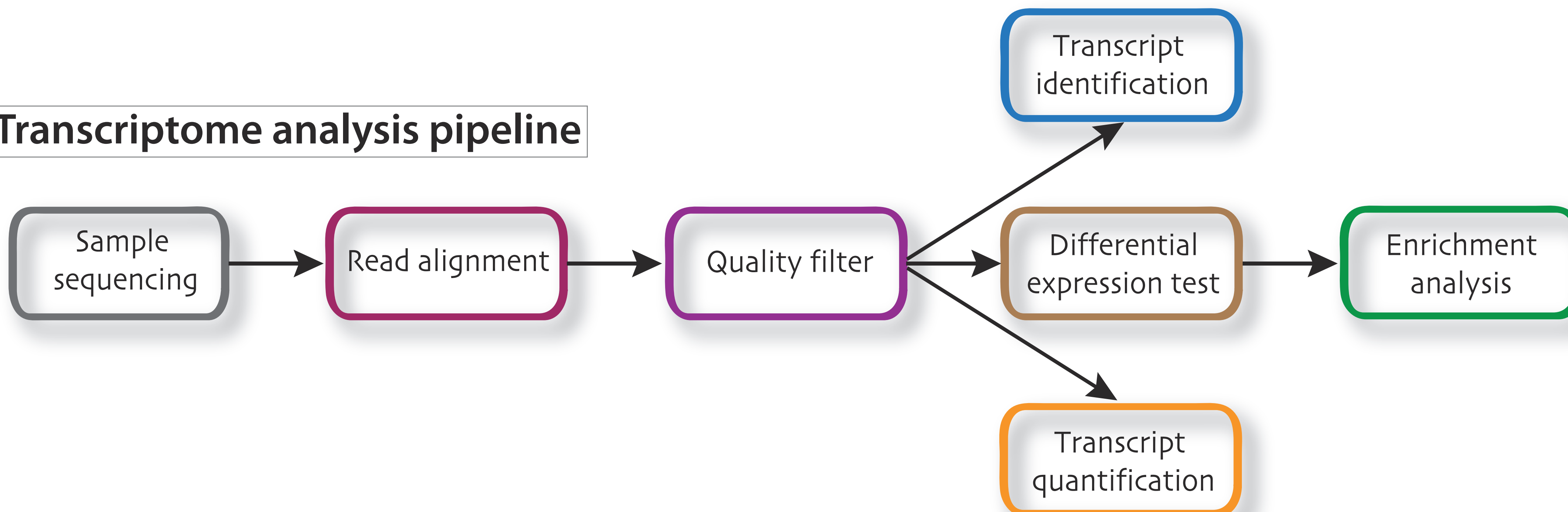
Reproducibility

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*

topGO
GeneSetter*

mGene*

KIRMES*

ARTS*

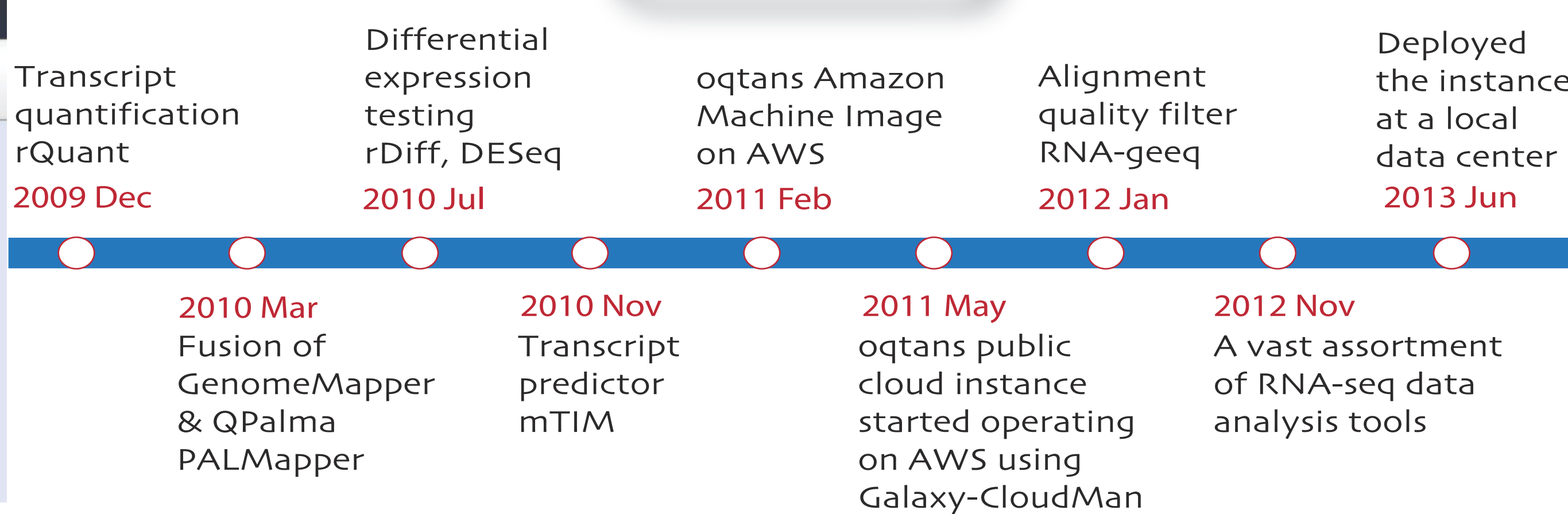
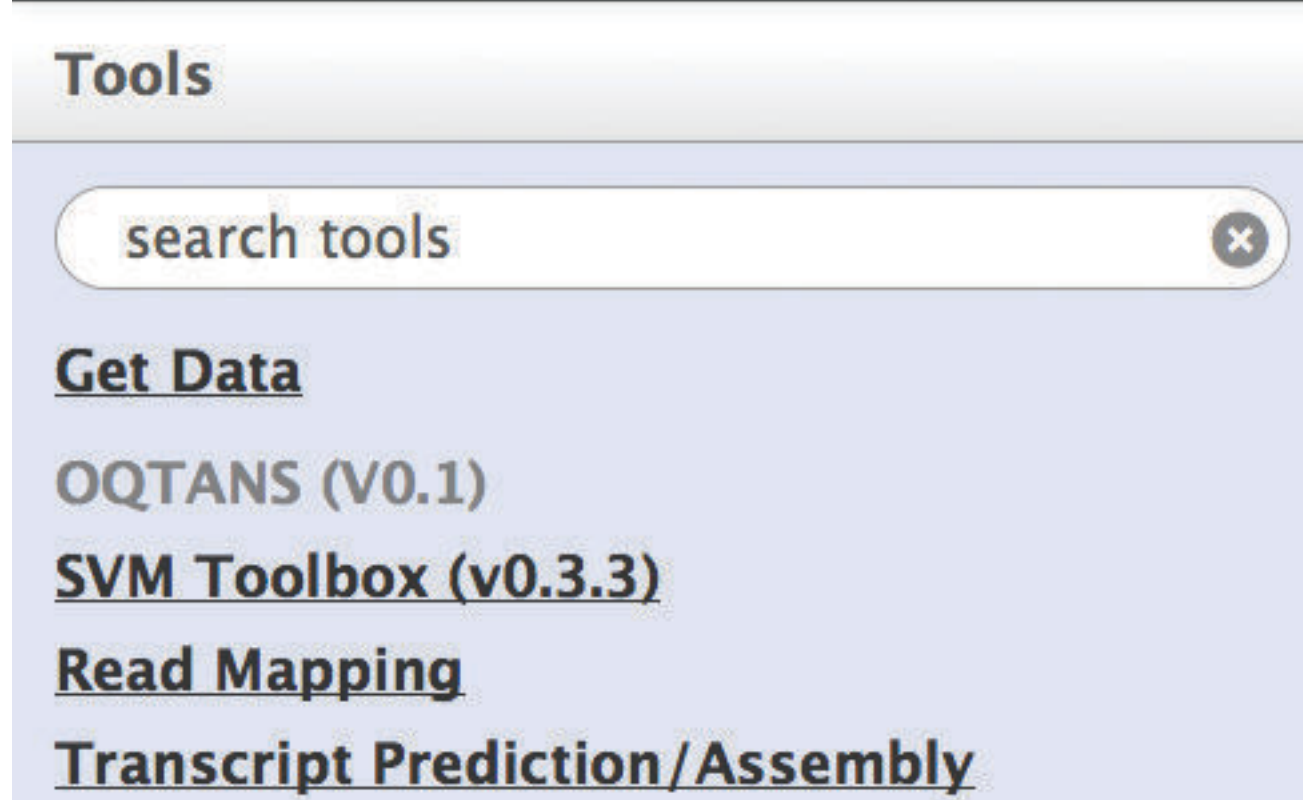
EasySVM*

GFFTools*

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

oqtans public instance

Galaxy / Rätsch Lab



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

GitHub This repository

PUBLIC ratschlab / oqtans



Alignment optimization and postprocessing toolbox

PALMapper

Highly accurate variation aware sequencing read mapper

RNA-geeq

Margin based transcript reconstruction from read alignments

mTIM

Accurately determine the abundance of transcripts

rQuant

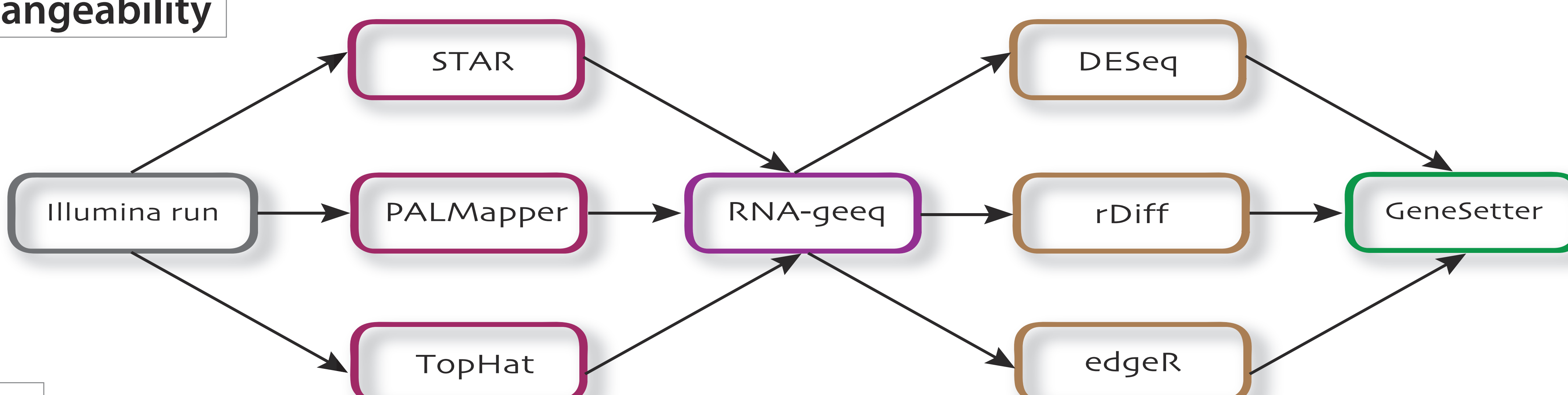
rDiff

Differential RNA-processing program

Compute and visualize the differential expressed gene families

GeneSetter

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.