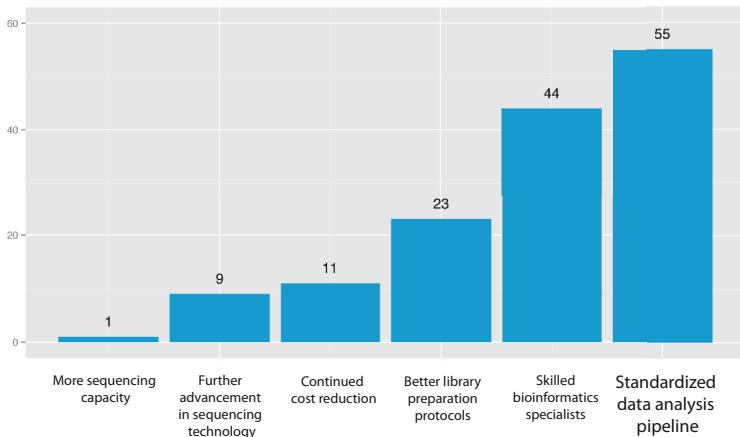


RNA-Seq Blog Poll Results

What is the greatest immediate need facing the RNA Sequencing community?



Reproducible Quantitative Transcriptome Analysis with oqtans

Vipin T. Sreedharan <vipin@cbio.mskcc.org>

Rätsch Laboratory, Computational Biology Center
Memorial Sloan-Kettering Cancer Center, USA
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14th Bioinformatics Open Source Conference, 19-20 July 2013 at Berlin



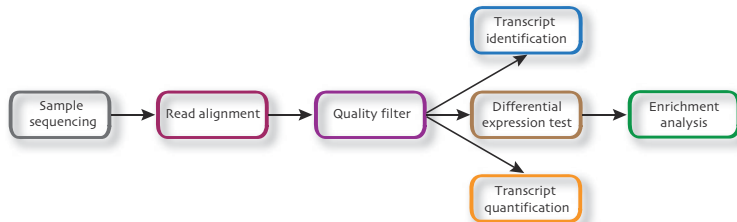
EBERHARD KARLS
UNIVERSITÄT
TÜBINGEN



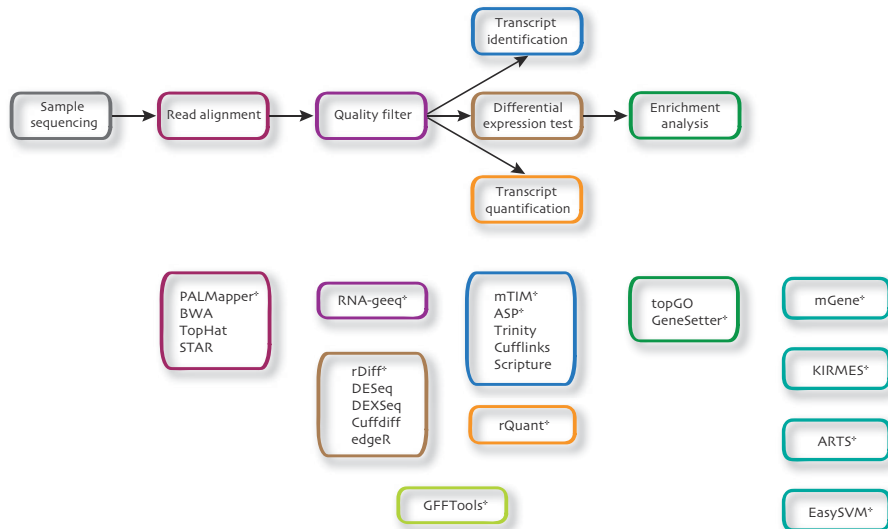
oqtans
online
quantitative
transcriptome
analysis



oqtans: online quantitative transcriptome analysis



oqtans: online quantitative transcriptome analysis



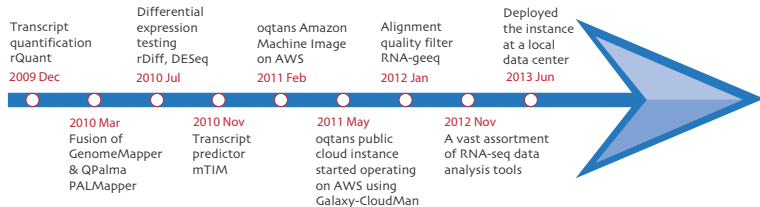
*developed by Rättsch lab members from cBio MSKCC and FML of the Max Planck Society

Timeline: Key events in the history of oqtans

- Online since December 2009.

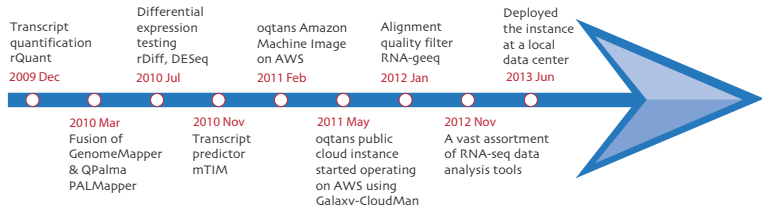
Timeline: Key events in the history of oqtans

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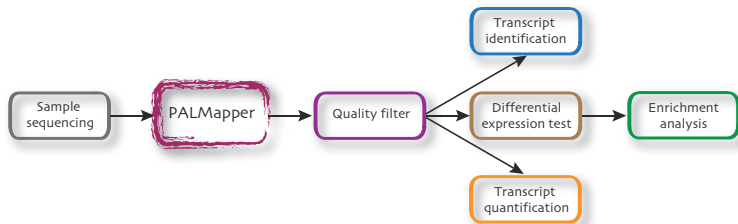
Timeline: Key events in the history of oqtans

- Online since December 2009.



- 593 registered and 336 active users.
- 12 tools developed from our lab.
- 15 tools from other open-source software development community.

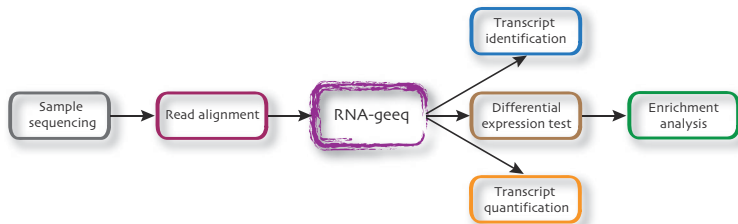
oqtans: Transcriptome analysis toolsuite



- **PALMapper**: highly accurate, variation-aware sequencing read mapper using base quality and splice site predictions.¹

¹G Jean et al. *Curr Protoc Bioinformatics* (2010).

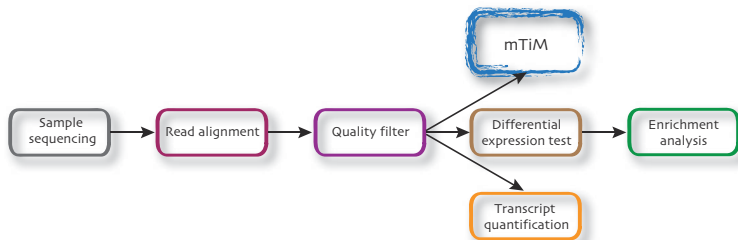
oqtans: Transcriptome analysis toolsuite



- **RNA-geeq**: alignment optimization and postprocessing toolbox.²
 - SPACE - Alignment evaluation and comparison.
 - SAFT - Simple alignment filtering.
 - MMR - Multiple mapper resolution.

²Kahles A, Behr J, and G Rättsch. *In preparation* (2013).

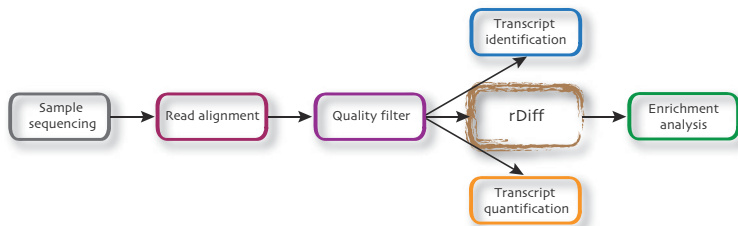
oqtans: Transcriptome analysis toolsuite



- **mTiM**: reconstructs exon-intron structure from read alignments and splice site predictions.³

³Görnitz N et al. *Neural Information Processing Systems* (2011).

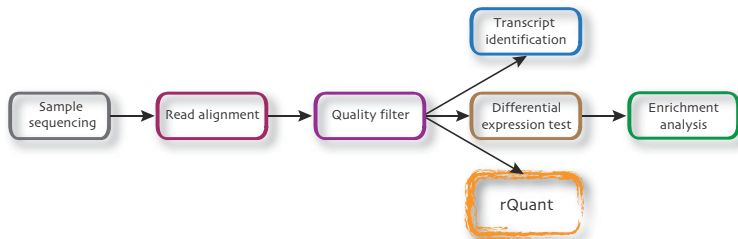
oqtans: Transcriptome analysis toolsuite



- **rDiff**: accurate detection of differential RNA processing from RNA-seq data.⁴
 - Parametric test (complete genome annotation).
 - Non Parametric test (incomplete genome annotation).

⁴P Drewe et al. *Nucleic Acids Res* (2013).

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- **rQuant**: estimates bias in library preparations, sequencing and read mapping; accurately determines the abundance of transcripts.⁵

⁵R Bohnert and G Rättsch. *Nucleic Acids Res* (2010).

Sequencing experiments to biological insight

- Compute the fraction of unexpressed, expressed and differentially expressed family of genes from two strains of *A. thaliana*.



- Illumina, 78 nt RNA-seq reads
 - Columbia accession (Col-0) 13 million reads.
 - Canary Island accession (Can-0) 11.8 million reads.
- Two replicates per accession.⁶

⁶X Gan et al. *Nature* (2011).

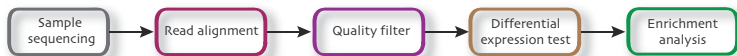
oqtans on Amazon cloud platform



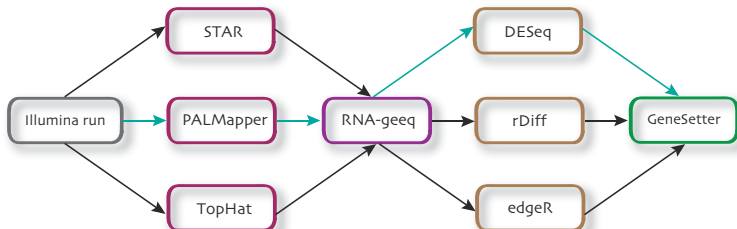
- Compute resources: m3.2xlarge.
 - Alignments: 20 minutes.
 - Quantitative analysis: 10 minutes.
- Cost on Amazon EC2: \$3.82

oqtans: Tool exchangeability

- General steps:



- Different paths in workflow:



oqtans Availability

- Our public Galaxy instance.
 - <http://galaxy.cbio.mskcc.org>
- Public git repository.
 - <http://github.com/ratschlab/oqtans>
- Machine Image on Amazon Web Service.
 - <http://aws.amazon.com/amis/>
Search for "**ami-5e389a37**"
- Galaxy Tool Shed.
 - <http://toolshed.g2.bx.psu.edu/>

Galaxy / Ratsch Lab

Tools

search tools

Get Data

- OQTANS (V0.1)
- SVM_Toolbox (v0.3.3)
- Read Mapping
- Transcript Prediction/Assembly

GitHub This repository

PUBLIC ratschlab / oqtans



Summary

- oqtans **simplifies** the RNA-seq data analysis workflow.
- Easy to **instantiate** in
 - Cloud service platforms
 - Existing Galaxy installation
 - Command line interface



Windows Azure



Google Compute Engine

```
CentOS release 6.2 (Final)
Kernel 2.6.32-228.23.1.el6.x86_64 on an x86_64

CentOS login: _
```

oqtans Team



Jonas Behr



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David Kuo



Sebastian Schultheiss



Georg Zeller



Gunnar Rättsch

<http://oqtans.org>

oqtans
online
quantitative
transcriptome
analysis



Would love to hear your experience!