

What did we cover?

- Experimental design
- Sample preparation
- Generating sequencing data
- Read quality assessment
- Read quantification
- Assembly/Mapping
- Transcript reconstruction
- Differential expression analysis (GO enrichment)
- Alternative splicing, RNA editing, eQTL, Allelic expression
- Biological application/interpretation

What tools did we use?

- FASTQC
- R
- Galaxy
- Trinity
- Tophat/Cufflinks/Cuffdiff
- Tablet/IGV
- CLC
- Pileup

http://www.nbic.nl/education/nbic-phd-school/nbic-phd-school-course-portfolio/wurpowerofrnaseq/

The screenshot shows the NBIC (Netherlands Bioinformatics Centre) website. The top navigation bar includes links for Home, Contact, Sitemap, Software Repository, Data Resources, Wiki, Videos, Login, and RSS. A search bar is located on the right. The main navigation menu features Research, Support, Education (highlighted), About NBIC, and NBIC Showcase. Below the navigation is a banner image of people in a meeting. A breadcrumb trail reads: Home → Education → NBIC PhD School → NBIC PhD School Course Portfolio → The Power of RNA-seq.

Left Sidebar:

- > BioWise
- > Course overview
- Education News
- > E-learning
- ▼ NBIC PhD School
 - About NBIC PhD School
 - ▼ NBIC PhD School Course Portfolio
 - Managing and Integrating Information in the Life Sciences
 - Optimisation Techniques
 - Pattern Recognition
 - Algorithms for Biological Networks
 - Comparative Genomics: from evolution to function
 - Protein structures: production, prowess, power, promises, and problems
 - Advanced NGS: RNA-seq Data Analysis
 - Advanced NGS: De novo Assembly
 - Advanced NGS: Metagenomics Data Analysis

Main Content:

the Power of RNA-seq

day 1 - Wednesday, June 5th, 2013

- 📄 [day1_SanchezPerez_PowerRNA-seq_2013.pdf](#)
Intro - the Power of RNA-seq - Gabino Sanchez-Perez
- 📄 [day1_Schijlen_RNAseqDataMachines_2013_Elio.pdf](#)
Next-gen insights into transcriptomes - Elio Schijlen
- 📄 [day1_Severing_RNAseqBasics_2013.pdf](#)
RNA-seq data analysis Basics - Edouard Severing
- 📄 [day1_Eilers_StateComputerLab_2013.pdf](#)
RNA-seq reads statistics - Paul Eilers
- 📄 [day1_vDriel_IntroGalaxy_2013.pdf](#)
Introduction to Galaxy - Marc van Driel
- 📄 [day1_vDriel_GalaxyExercises_2013.pdf](#)
tutorial for working with Galaxy - Marc van Driel
- 📄 [day1_Smit_RNAseqQC_2013.pdf](#)
Quality Control - Sandra Smit

Right Sidebar: Highlights

- Register now for 3rd edition Life Science Information course
The amount of Life Science data available in the public domain is a vast and growing resource for bioinfo...
- Photo impression NBIC2013
- International Chemical Discovery and Design Course 2013
- Dutch Computers in Chemistry Symposium
- Small molecules, gene products and their interaction - registration open!
- ISMB/ECCB 2013

Monday?

- Design the experiment
 - Talk to a statistician (Marco)
- Sequence your RNA
 - Talk to Elio
- Analyse your data:
 - Use Galaxy
 - Use CLC
 - Learn Linux/scripting, use command line tools (*)
 - Talk to a bioinformatician
 - Resident bioinformatician (edouard.severing@wur.nl)
 - Chair of Bioinformatics (harm.nijveen@wur.nl)
 - Bioscience (gabino.sanchezperez@wur.nl)

Next course

What can we improve?

Thank you

- Edouard
- Elio
- Gabino
- Sandra
- Richard
- Basten
- Paul
- Marco
- Aalt-Jan
- Ole
- Henri
- Mateusz
- Marc
- Patrick

Special thanks

Leon (Hailiang) Mei – 24/7 NBIC Galaxy support



And thank you!

