RNA-Seq data analysis with Galaxy for clinical applications

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www.sbi.uni-rostock.de

▶ Who are we?

▶ Course outline

▶ RNA Sequencing (RNA-Seq)

▶ Next Generation Sequencing (NGS)

▶ Tools and materials

SYSTEMS BIOLOGY
BIOINFORMATICS
ROSTOCK

- ▶ Data Management and standardisation

- ▶ Computational Modeling and Machine Learning

- ▶ Omics analysis and data integration

- ▶ Clinical trials

- ▶ Training courses

- ▶ eHealth

https://denbi.de

de.STAIR: Structured Analysis and Integration of RNA-Seq experiments (de.STAIR)

Our aim is to provide and enable comprehensive analyses of RNA-Seq experiments as a service. To bring ease of use, reproducibility, and accessibility for the developed approaches and services, we provide dedicated workshops, training programs and screen casts for bioinformaticians and other life scientists.
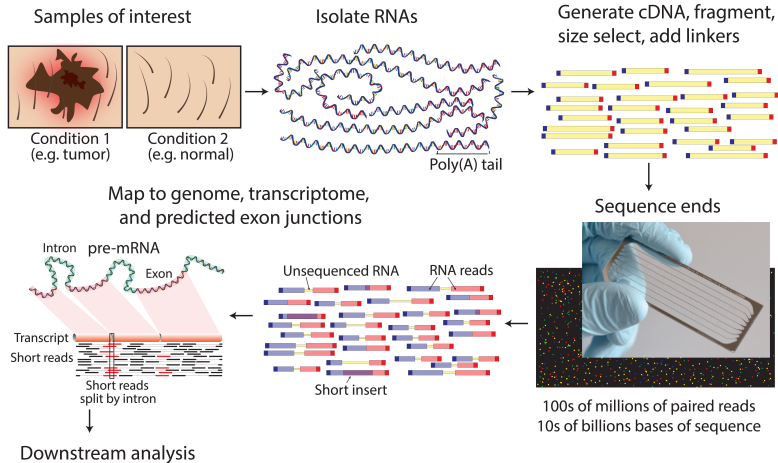
Who are you? :)

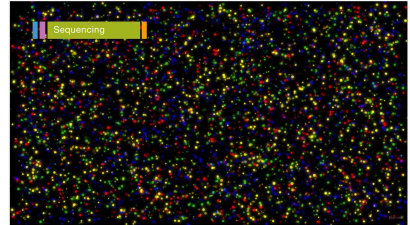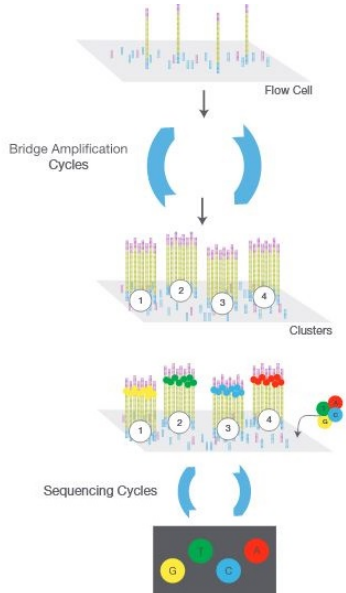https://github.com/destairdenbi/trainings

RNA-Seq is able to identify thousands of differentially expressed genes, tens of thousands of differentially expressed gene isoforms and can detect mutations and germline variations for hundreds to thousands of expressed genetic variants, as well as detecting chimeric gene fusions, transcript isoforms and splice variants.

Wang, Nature 2009

RNA Sequencing (RNA-Seq)

Samples of interest

Condition 1 (e.g. tumor) Condition 2 (e.g. normal)

Isolate RNAs

Poly(A) tail

Generate cDNA, fragment, size select, add linkers

Sequence ends

100s of millions of paired reads
10s of billions bases of sequence

Map to genome, transcriptome, and predicted exon junctions

Intron pre-mRNA
Exon
Transcript
Short reads
Short reads split by intron

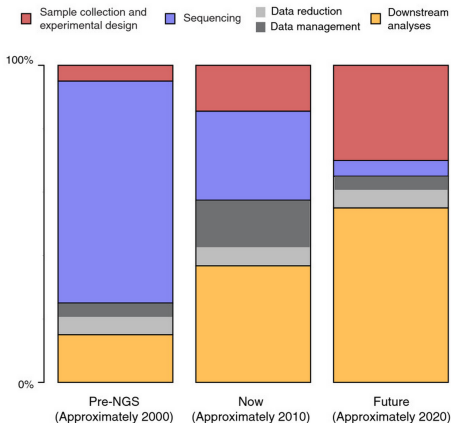Unsequenced RNA RNA reads
Short insert

Downstream analysis

Griffith et al., PLOS 2015

Oxford Genomics Centre, 2017
Illumina, 2015

The decrease of sequencing costs is met with an increased effort in data processing $\implies$ Increased need of Bioinformatics expertise.

Sboner et al., Genome Biology 2011

Galaxy
P R O J E C T

https://usegalaxy.eu

https://galaxyproject.github.io/training-material/