Building an open, collaborative, online infrastructure for bioinformatics training



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33rd TBI Winterseminar Februar 2018

Why caring about bioinformatics

training?

Need for bioinformatic training

Bioinformatics has become too central to biology to be left to specialist bioinformaticians

- Explosion of data to analyze
- Access to computational power
- Thousand of possible tools for specialized analyses

An increasing demand for learning bioinformatics



Graphs of Brazas et al, 2017

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- Web interface for numerous bioinformatics tools
- Scalable
- No issue with computer configuration during training



Building a new **open**, **collaborative** and **FAIR** model for bioinformatics training

Requirements

- Easy to use
- Support for effective training for
 - Individual users
 - Instructors
- Definition of technological infrastructure
- Limited redundancy







Separation between content and format

Here treatment is the primary factor which we are interested in. The sequencing type is some further information that we know about the data that might affect the analysis. This particular multi-factor analysis allows us to assess the effect of the treatment, while taking the sequencing type into account, too.

> ### {% icon comment %} Comment

>

> We recommend you to add as many factors as you think may affect gene expression in your experiment. It can be the sequencing type like here, but it can also be the manipulation (if different persons are involved in the library preparation), ... {: .comment}

> ### {% icon hands_on %} Hands-on: Analysis of the differential gene expression
(1)

>

- > 1. Create a new history
- > 2. Import the seven count files from [Zenodo]
- (https://dx.doi.org/10.5281/zenodo.290221)
- > `GSM461176_untreat_single.deseq.counts`
- > `GSM461177 untreat paired.deseq.counts`
- > `GSM461178 untreat paired.deseq.counts`
- > `GSM461179_treat_single.deseq.counts`
- > `GSM461180 treat paired.deseq.counts`
- > `GSM461181 treat paired.deseq.counts`
- > `GSM461182 untreat single.deseq.counts`

>

> 3. **DESeq2** {% icon tool %}: Run **DESeq2** with:

> - "Treatment" as first factor with "treated" and "untreated" as levels and selection of count files corresponding to both levels >

```
> > ### {% icon tip %} Tip
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>
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> > You can select several files by keeping the CTRL (or COMMAND) key pressed and clicking on the interesting files

- > {: .tip}
- >

Markdown

Here treatment is the primary factor which we are interested in. The sequencing type is some further information that we know about the data that might affect the analysis. This particular multi-factor analysis allows us to assess the effect of the treatment, while taking the sequencing type into account, too.

💬 Comment

We recommend you to add as many factors as you think may affect gene expression in your experiment. It can be the sequencing type like here, but it can also be the manipulation (if different persons are involved in the library preparation), ...

Hands-on: Analysis of the differential gene expression (1)

1. Create a new history

- 2. Import the seven count files from Zenodo
 - GSM461176_untreat_single.deseq.counts
 - GSM461177_untreat_paired.deseq.counts
 - GSM461178_untreat_paired.deseq.counts
 - GSM461179_treat_single.deseq.counts
 - GSM461180_treat_paired.deseq.counts
 - GSM461181_treat_paired.deseq.counts
 - o GSM461182_untreat_single.deseq.counts

3. DESeq2 &: Run DESeq2 with:

 "Treatment" as first factor with "treated" and "untreated" as levels and selection of count files corresponding to both levels

🖓 Tip

You can select several files by keeping the CTRL (or COMMAND) key pressed and clicking on the interesting files

User-friendly HTML





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Transcriptomics - Reference-based RNA-Seq data analysis	
Training material for all kinds of transcriptomics analysis. Questions of the tutorial: - What are alyze RNA sequencing data using a reference genome? Objectives of the tutorial: - Analysis of	the effects of Pasilla (PS) gene depletion on splicing events? - How to an RNA sequencing data using
	Strange E
ChIP-seq analysis using R - Mapping and file formats	
This lecture introduces the principles behind alignment, different tools and de-novo assembly.	It also covers post mapping data format and quality control
Scientific topics: Sequence assembly, RNA-Seq	
Keywords: ChIP-Seq, RNA-Seq, Alignment, Data-format, Assembly, QC	

https://tess.elixir-europe.org/





Storage of training datasets on Zenodo

Zenodo

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February 10, 2017

Dataset Open Access

Reference-based RNA-seq data analysis (training data)

Batut, Bérénice; Videm, Pavankumar; Erxleben, Anika; Houwaart, Torsten; Grüning, Björn

RNA-seq (RNA sequencing) uses high-throughput (HTS) data to reveal the presence and quantity of RNA in a biological sample at a given moment in time.

Q

In the training available at http://galaxyproject.github.io/RNA-Seq/tutorials/ref_based, we introduce the bioinformatics methods to analyze RNA-seq data using a reference genome. The toy datasets were extracted from the study of Brooks *et al.* 2011.

Files (246.0 MB)		~
Name	Size	
dexseq.gtf	61.7 kB	📥 Download
md5:51df689fc40c62fe062f6338f1e1c0f6 @		
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md5:e07b8dcbd4f4f7602feeba0d5ed1698e @		
GSM461176_untreat_single.deseq.counts	231.3 kB	A Download
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Publication date: February 10, 2017 DOI: DOI 10.5281/zenodo.290221 Communities: Galaxy training network License (for files):

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Batut, Bérénice, Videm, Pavankumar, Erxleben, Anika, Houwaart, Torsten, & Grüning, Björn. (2017). Reference-based RNA-seq data analysis (training data) [Data set]. Zenodo. http://doi.org/10.5281/zenodo.290221











Galaxy Training materials

裬 Galaxy Training!

O Fork me on GitHub D Help -

Welcome to Galaxy Training!

Collection of tutorials developed and maintained by the worldwide Galaxy community.

Galaxy for Scientists

Торіс	Tutorials
Introduction to Galaxy	13
Assembly	3
ChIP-Seq data analysis	2
Epigenetics	1
Metagenomics	2
Proteomics	8
Sequence analysis	6
Transcriptomics	5
Variant Analysis	5

Galaxy for Developers and Admins

Торіс	Tutorials
Galaxy Server administration	8
Development in Galaxy	13
Train the trainers	6

http://training.galaxyproject.org



Thank you!



An open, collaborative, FAIR, online infrastructure training.galaxyproject.org github.com/galaxyproject/training-material