



## Method Course: RNA-seq data analysis with Chipster, September 4-5, 2018

<b>Time:</b>	Day 1: September 4 at 9:15-17:00 Day 2: September 5 at 9:00-13:00
<b>Place:</b>	Computer classroom KT285 (Medical campus, Aapistie 5B, 90220 Oulu)
<b>Organizers:</b>	Health and Biosciences Doctoral Programme and Biocenter Oulu Sequencing Center
<b>Credits:</b>	1.0 ECTS
<b>Contact persons:</b>	Katri Pylkäs and Mirja Peltola, <a href="mailto:firstname.lastname(at)oulu.fi">firstname.lastname(at)oulu.fi</a>
<b>Teachers:</b>	Maria Lehtivaara and Eija Korpelainen, CSC-IT Center for Science
<b>Registration:</b>	<b>Deadline August 28, 2018.</b> Online registration <a href="#">here &gt;&gt;</a> The course is limited to 16 participants.

### Course description:

This hands-on course introduces the participants to RNA-seq data analysis methods, tools and file formats. It covers the whole workflow from quality control and alignment to quantification and differential expression analysis, and also experimental design is discussed. The free and user-friendly Chipster software (<http://chipster.csc.fi/>) is used in the exercises, so no previous knowledge of Unix or R is required, and the course is thus suitable for everybody.

You will learn how to

- check the quality of reads with FastQC and PRINSEQ
- remove bad quality data with Trimmomatic
- infer strandedness with RseQC
- align RNA-seq reads to the reference genome with TopHat2
- visualize aligned reads in genomic context using the Chipster genome browser
- perform alignment level quality control using RseQC and SAMtools
- quantify expression by counting reads per genes using HTSeq
- check the experiment level quality with PCA plots and heatmaps
- analyze differential expression with DESeq2 and edgeR
- take multiple factors (including batch effects) into account in differential expression analysis

Target audience: Life scientists who are planning to apply RNA-seq analysis in their research. This course is suitable also for those researchers who do not plan to analyse data themselves, but who need to understand the concepts in order to discuss with bioinformaticians.

Please note that the course capacity in the computer classroom is 16 participants selected by application. Upon registration, we request you to give a short description of your motivation to participate in the course. A confirmation will be sent on August 29 to all who submitted their registration.

[Apply online here >>](#)

