SWEDISH UNIVERSITY OF AGRICULTURAL SCIENCES
Department of Plant Biology
Syllabus

Analysis of High Throughput Sequencing RNA-Seq Data II - apply to your ow
1,5 Credits

Finalized by: Research school Organism Biology, Mattias Thelander chair, 2023-10-13

Valid from: Second half-year 2023 (2023-07-01)
Level within study regulation: Third cycle

Subject

Bioinformatics

Entry requirements

Enrolled as a PhD student in Biology or with equivalent competence. This course is an exten
the course "Analysis of High Throughput Sequencing RNA-Seq Data I" Course code P000057
which is a required prerequisite. We strongly recommend taking these two courses in consec
order. The course is primarily for SLU PhD students but will be open also for researchers if sp
allows.

Examination formats

Pass / Failed. The requirements for passing are described in the course assessment criteria v
are contained in a supplement to the course syllabus.

Objectives

The aims of this course are to:

- apply the knowledge of course "Analysis of High Throughput Sequencing RNA-Seq Data I" student's own data (in lieu of the exemplary dataset otherwise available)

- deepen the understanding of concepts taught in course "Analysis of High Throughput Sequ RNA-Seq Data I"

- give the students the possibility to do RNA-seq analyses on their own data in a supervised

- expose the participants to modern computing technologies, as the hands-on analyses will b performed using cloud computing resources

- develop the participants' awareness to critically reflect onto RNA-Seq analysis strengths an weaknesses

The corresponding Learning Outcomes are:

- strengthen the skills to navigate and interact with the Unix Command Line Interface (CLI) an RStudio Integrated Development Environment (IDE)

- perform data analyses (quality control, pre-processing, pseudo-alignment, differential expre etc) independently on a real world data set

- interpret and reflect on the results

- present the results to a scientific audience

Content

High Throughput Sequencing (HTS) and, in particular, Next Generation Sequencing (NGS) ha revolutionized the way we conduct gene expression analysis. In comparison to micro-array-b methods, NGS has unleashed an almost unlimited power to perform gene expression analysi similar price and with faster, more comprehensive, more efficient, and more reproducible characteristics. Rapidly, the data generation rate has exceeded the analytical capabilities and analysis has become the major bottleneck in gene expression studies. This course, aimed at advanced students, has the objective to help addressing this problem by (i) helping participar critically assess the challenges faced in the HTS field, (ii) developing efficient communication with bioinformatician, and (iii) training students in analyzing HTS data.

The course is a follow up to course "Analysis of High Throughput Sequencing RNA-Seq Data where students are taught the principles and basics of RNAseq analyses. Here, the students apply the knowledge gained from that course to their own data. The course will provide one I and will run over one week.

The students will analyze their own data by applying the methods learned in "Analysis of High Throughput Sequencing RNA-Seq Data I" with some guidance from the teachers (synchronou asynchronous). Students will need to organize their access to the high-performance computi facility (probably their PI / supervisor will need to do so), with the help of SLUBI if needed. Fir asynchronous support from SLUBI, the students will perform the pre-processing and initial ar of their data. Then they will meet with the trainers to address issues, discuss the data interpre and prepare a presentation about their project and results. The last day of the course will be i form of an online mini-symposium, where the students will present their work to the other

participants and trainers.

The course will mix independent and supervised hands-on analyses, literature review, data interpretation, visualization and presentation. The course will offer the participants the possib review and deepen their understanding of the course material at their own pace and to discus among peers.

Other information

Teaching on this course will be provided by the SLU Bioinformatics Infrastructure (SLUBI), na Nicolas Delhomme, Iryna Shutava, Adnan Niazi, Abu Bakar Siddique, Lizel Potgieter and Amr Binzer-Panchal. The course is organized on behalf of the SLU research school Organism Biol There is no tuition fee. Participants are expected to bring their own laptop for the practical co exercises.

The course will be conducted online only. However, if students wish so, they can organise themselves in groups and join using one of the teaching facilities available at SLU.

The maximum number of participants is 20. SLU-registered PhD students are prioritized over researchers but otherwise admission will be on a first come, first serve basis, provided that th minimal requirements are met.

If you have any question, please contact the course leader or the slack channel #organism-bi research-school-rna-seq-course of the slubi-workspace.slack.com workspace.