The Hebrew University of Jerusalem

Syllabus

Bacterial molecular epidemiology - 73557

Last update 28-07-2021

HU Credits: 2

Degree/Cycle: 2nd degree (Master)

Responsible Department: Animal and Veterinary Science

Academic year: 0

Semester: 1st Semester

Teaching Languages: English

Campus: Rehovot

Course/Module Coordinator: Dr. Ehud Elnekave

Coordinator Email: ehud.elnekave@mail.huji.ac.il

Coordinator Office Hours: By appointment

Teaching Staff:

Dr. Ehud Elnekave

Course/Module description:
Molecular epidemiology of Bacterial pathogens of livestock origin– Genetic Data Analysis of whole genome sequences of bacteria - Phylogenies, Evolution and Antimicrobial Resistance. Theory and practice.

Course/Module aims:
1. Presenting molecular epidemiology as a tool for analyzing genetic data of bacteria of livestock origin
2. How to interpret phylogeny trees
3. Basic genetic analysis on different modules – hands on
4. Analyzing big datasets using R – hands on
5. Bayesian analysis to determine the evolution of bacteria – hands on using BEAST software

Learning outcomes - On successful completion of this module, students should be able to:
As part of the course, students will learn and experience using different tools such as R and BEAST.

Attendance requirements(%):
100%

Teaching arrangement and method of instruction: The course includes frontal lectures and hands on computational work

Course/Module Content:
1. Introduction to molecular epidemiology – lecture (week 1)
2. Introduction to phylogenetic analysis – lecture (week 2)
3. Whole genome sequencing of bacterial genomes – lecture (week 3)
- The sequencing processes
- Sequencing methods
- Sequencing outputs
- Quality control
- …
4. Phylogenetic trees – lecture and hands on (weeks 4-6)
- Trees reconstruction methods
- Bootstrapping

- Reference based vs. core genome
- Rooted vs. unrooted trees (outgroup selection)
- …
5. Genome Assembly – lecture and hands on (week 7)
- Why and how to assemble genomes
- Genome annotation
- Antimicrobial resistance genes detection
- Genotypic characterization – MLST, in silico serotyping
- …
6. Large databases analysis using R – lecture and hands on (weeks 8-9)
- Data wrangling
- Basic presentation of data in R – scatterplots, histograms, etc.
- 'for' and 'while' loops
- …
7. Bacterial evolution – using BEAST– lecture and hands on (weeks 10-11)
- Time scaled phylogenies
- Transmission of pathogens (who gave it to whom?)
8. Summary/literature review (weeks 12-13)

Required Reading:

Scientific papers will be provided.

Additional Reading Material:

- *David A Baum; Stacey D Smith. “Tree thinking: an introduction to phylogenetic biology”. Greenwood Village, Colo.; 2013*
- *Barry G. Hall. “Phylogenetic trees made easy: a how-to manual for molecular biologists”. Sunderland, Mass.; 2001*
- *Paul G. Higgs; Teresa K. Attwood. "Bioinformatics and molecular evolution". Blackwell science ltd.; 2005*
- *Alexei J. Drummond and Remco R. Bouckaert. “Bayesian Evolutionary Analysis with BEAST” (2). Cambridge University Press; 2015 (1st edition)*

Course/Module evaluation:

End of year written/oral examination 0 %
Presentation 0 %
Participation in Tutorials 60 %
Project work 0 %
Assignments 40 %
Reports 0 %
Research project 0 %
Quizzes 0 %

Other 0 %

Additional information:

- *The course will be n English unless all students are Hebrew speaking*
- *A laptop with windows 10 system is required*
- *No need to bring your own set of data*