



## *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](mailto:ehud.elnekave@mail.huji.ac.il)*

*Coordinator Office Hours: By appointment*

*Teaching Staff:*

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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*

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- 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 %

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*Other 0 %*

*Additional information:*

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