

Microbial Communities and Interactions

Lesson Plan for Five Theoretical Lectures

MSc in Applied Microbiology — Faculty of Sciences, University of Lisbon (FCUL)

Includes suggested bibliography with figures/graphs suitable for in-class discussion

Overview and Session Structure

Each lecture runs for 90 minutes, structured as follows:

- 10 min — grace period / arrival
- ~50–55 min — theoretical content, delivered in two blocks with a short pause or question midway
- 15–20 min — guided exploration of graphs and figures to consolidate concepts
- 5–10 min — synthesis and bridge to the next lecture

The five lectures follow a deliberate progression: from foundational concepts, to interaction typologies, to their evolutionary and ecological consequences, down to the molecular mechanisms that mediate them, and finally to an integrated session combining the methodological toolkit, modelling approaches and a One Health framework — directly preparing students for their group work.

Note on this revision: *The course was reduced from six theoretical lectures to five due to a scheduling change. Rather than dropping a topic entirely, the original Lecture 5 (Tools) and Lecture 6 (Modelling & One Health) were merged into a single, condensed session. See the Summary of Changes table at the end of this document for exactly what was trimmed.*

Lecture 1 – Key Concepts in Microbial Ecology

Objective: Provide students with the vocabulary and conceptual models that will be used throughout the course.

Content

- Introduction: real-world applications of microbial interactions (health, agriculture, climate)
- Definitions: community, population, niche, guild, metacommunity
- Biotic interactions (competition, predation/parasitism, mutualism, commensalism, amensalism) vs. abiotic interactions (pH, temperature, nutrient availability, oxygen)
- Diversity concepts: alpha, beta and gamma diversity
- Classic ecological models applied to microorganisms (Hutchinson's niche concept, r/K selection, community assembly rules)
- Spatial and temporal scales in microbial ecology

Graphs and Figures Exercise (15–20 min)

- Rarefaction and species accumulation curves: how to read them and what they reveal about sampling completeness
- Diversity indices (Shannon, Simpson) applied to a simple dataset
- Venn/UpSet diagrams showing shared OTUs between environments

Suggested Bibliography

- Willis, A. D. (2019). Rarefaction, Alpha Diversity, and Statistics. *Frontiers in Microbiology*, 10, 2407. <https://doi.org/10.3389/fmicb.2019.02407> — excellent for discussing Figure 1, which shows how rarefaction can invert the true ranking of community diversity.
- Pollock, J., Glendinning, L., Wisedchanwet, T., & Watson, M. (2018). The Madness of Microbiome: Attempting To Find Consistency in Amplicon Sequencing Studies. *Applied and Environmental Microbiology*, 84(7). — useful for discussing sampling-to-analysis pipeline figures.

Lecture 2 – Microbial Symbioses and Typologies of Interactions

Objective: Classify and characterise microorganism–microorganism and microorganism–host interactions.

Content

- The symbiotic spectrum: mutualism, commensalism, parasitism — and its context-dependency
- Microorganism–microorganism interactions: cross-feeding, nutrient competition, interference (bacteriocins, antibiotics), syntrophy
- Microorganism–host interactions: colonisation, holobiont, hologenome, microbiome vs. microbiota
- Classic examples: lichens, mycorrhizae, *Rhizobium*–legume symbiosis, *Vibrio fischeri*–squid, human gut microbiota

Graphs and Figures Exercise (15–20 min)

- Interaction (co-occurrence) networks: how to interpret nodes and edges
- Cost–benefit diagrams of symbiosis (host cost vs. benefit axes)
- Life-cycle schematics of symbiotic colonisation (e.g., the *Vibrio fischeri*–squid light organ)

Suggested Bibliography

Visick, K. L., Stabb, E. V., & Ruby, E. G. (2021). A lasting symbiosis: how *Vibrio fischeri* finds a squid partner and persists within its natural host. *Nature Reviews Microbiology*, 19, 654–665. <https://doi.org/10.1038/s41579-021-00557-0> — strong figures illustrating colonisation stages and signalling exchange.

Douglas, A. E., & Werren, J. H. (2016). Holes in the Hologenome: Why Host-Microbe Symbioses Are Not Holobionts. *mBio*, 7(2), e02099-15. <https://doi.org/10.1128/mBio.02099-15> — good for a critical discussion of the holobiont/hologenome concept using its comparative tables of transmission modes.

Lecture 3 – Ecological and Evolutionary Impact of Microbial Interactions

Objective: Connect the interaction types studied in Lecture 2 to their evolutionary consequences at larger scales.

Content

- Coevolution and the Red Queen dynamic; horizontal gene transfer (HGT) as an evolutionary driver
- Speciation and diversification mediated by symbiosis
- The 'keystone species' concept in microbial communities
- Brief introduction to microorganisms as regulators of large-scale ecological processes (expanded further in Lecture 5)

Graphs and Figures Exercise (15–20 min)

- Annotated phylogenetic trees with functional traits, used to discuss coevolutionary patterns
- Time-series plots of community composition (e.g., phytoplankton bloom dynamics)
- Schematic diagrams of host–parasite arms races (Red Queen dynamics)

Suggested Bibliography

Moura de Sousa, J., Lourenço, M., & Gordo, I. (2023). Horizontal gene transfer among host-associated microbes. *Cell Host & Microbe*, 31(4), 513–527.

<https://doi.org/10.1016/j.chom.2023.03.017> — Figure 1 clearly diagrams the main HGT mechanisms (transformation, conjugation, transduction, lysogeny) for in-class discussion.

Pike, V. L., Ford, S. A., & King, K. C. (2022). Host–parasite coevolution: Backseat drivers take the wheel at the Red Queen's race. *Current Biology*, 32(7), R320–R323. — a short, figure-driven piece (Figure 1) showing how defensive microbial symbionts reshape host–parasite coevolutionary dynamics.

Lecture 4 – Quorum Sensing, Biofilms and Adaptive Mechanisms

Objective: Move to the molecular scale to explain how microbial interactions are physically mediated.

Content

- Brief refresher: gene expression in response to environmental cues, two-component signalling systems
- Quorum sensing: autoinducers (AHLs, peptides, AI-2), density-dependent gene regulation
- Biofilm formation: attachment, maturation, dispersion, extracellular matrix
- Adaptive and developmental mechanisms (sporulation, persister cells, multicellular phenotypes)

Graphs and Figures Exercise (15–20 min)

- Dose–response curves for quorum sensing (autoinducer concentration vs. gene expression)
- Microscopy images illustrating the stages of biofilm formation
- Gene-expression heatmaps / induction curves over time

Suggested Bibliography

Rabin, N., Zheng, Y., Opoku-Temeng, C., Du, Y., Bonsu, E., & Sintim, H. O. (2015). Biofilm formation mechanisms and targets for developing antibiofilm agents. *Future Medicinal Chemistry*, 7(4), 493–512. — companion overview of biofilm stages, useful alongside a schematic figure of the biofilm life cycle.

PMC6328408 — Biofilms: Architecture, Resistance, Quorum Sensing and Control Mechanisms. A review with a clear summary figure (Fig. 1) of AHL/AI-2/quinolone quorum-sensing molecules and their role across biofilm stages — well suited for guided figure discussion.

Lecture 5 – Tools, Modelling & One Health: From Data to Critical Thinking

Objective: Present the essential methodological toolkit for studying microbial communities, and integrate modelling approaches and a One Health perspective — connecting back to concepts from Lectures 1–4 and preparing students for their group projects.

Note: This lecture merges what were originally planned as two separate sessions (Tools, and Modelling & One Health) into one, following a reduction in the number of available teaching lectures. Content has been condensed accordingly: imaging methods, a detailed breakdown of each 'omics layer, and two of the three original One Health case studies have been cut, and the ecosystem-services opening and modelling content are treated at a conceptual level rather than in methodological depth.

Content

- Essential toolkit: culture-dependent vs. culture-independent methods; metabarcoding (16S/18S/ITS) vs. shotgun metagenomics; metatranscriptomics, metaproteomics and metabolomics named briefly as further layers covered in more depth in other course units
- Statistics essentials: ordination (PCoA, NMDS) and PERMANOVA; a brief worked example of pseudo-replication for students to spot the flaw
- Modelling: brief recap of microbial-based ecosystem services (biogeochemical cycles, nitrogen fixation, climate regulation); generalized Lotka-Volterra (gLV) models and statistically inferred interaction networks, presented conceptually with emphasis on their limitations (equilibrium assumptions, correlation vs. true interaction)
- One Health: the One Health concept (human–animal–environment interconnection); one case study — resistance gene circulation across soil–water–animal–human compartments
- Current challenges: the 'unculturable majority' and its historical limitations; causation vs. correlation in microbiome studies; reproducibility and methodological standardisation

Graphs and Figures Exercise (15–20 min)

- Reading ordination plots (PCoA/NMDS): what the axes and point proximity represent
- A microbiome–environment–host interaction network in a One Health context (e.g., a resistome circulation figure) — reading nodes, edge direction, and compartments
- Side-by-side comparison of two published figures, one showing correlation and one showing causal inference in microbiome research — students identify what each does (and does not) allow one to conclude

Suggested Bibliography

Xia, Y. (2020). Correlation and association analyses in microbiome study integrating multiomics in health and disease. *Progress in Molecular Biology and Translational Science*, 171, 309–491. — includes accessible figures on ordination methods (PCoA/NMDS) and PERMANOVA logic.

Stein, R. R., Bucci, V., Toussaint, N. C., et al. (2013). Ecological Modeling from Time-Series Inference: Insight into Dynamics and Stability of Intestinal Microbiota. *PLoS Computational Biology*, 9(12), e1003388. — a foundational application of the generalized Lotka-Volterra model to gut microbiota dynamics, with clear network and stability figures.

- Punch, R., Azani, R., Ellison, C., Majury, A., Hynds, P. D., Payne, S. J., & Brown, R. S. (2025). The surveillance of antimicrobial resistance in wastewater from a One Health perspective: a global scoping and temporal review (2014–2024). *One Health*, 21, 101139. <https://doi.org/10.1016/j.onehlt.2025.101139> — contains a strong schematic figure of AMR transmission across the One Health framework, directly usable for the resistome case study.
- Sze, M. A., & Schloss, P. D. (2016). Looking for a Signal in the Noise: Revisiting Obesity and the Microbiome. *mBio*, 7(4), e01018-16. — a clear cautionary case study for the correlation-vs-causation discussion, showing how a widely cited association weakened substantially under rigorous re-analysis.

Lecture 6 – Group Project Presentations

Each group presents the lecture summary they were responsible for, as part of the course's collaborative study-notes ('sebenta') exercise.