Bioinformatics Summer School Report

Project Title:

Co-housing Accelerates Exchange of Age-Linked Gut Microbiota with Synchronized Genus-Level Responses

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1. Abstract:

The gut microbiota plays a crucial role in health, and its composition changes significantly with age. In this project, I investigated how co-housing influences the gut microbiota of young and aged mice. By analyzing microbial composition at the genus level, I observed that co-housing accelerated the exchange of microbial communities between age groups. Distinct age-related differences became less marked, suggesting that environmental factors can synchronize microbial profiles. These findings highlight the impact of co-housing on reducing age-associated variation in gut microbiota.

2. Introduction:

The gut microbiota changes with age, and these changes can affect host health. Older individuals usually show lower microbial diversity and enrichment of specific genera compared to younger ones. At the same time, environmental factors, like co-housing, can drive microbial exchange and synchronization between individuals living together.

In this project, I studied how co-housing affects the exchange of age-linked gut microbiota at the genus level. The goal was to see if co-housing leads to synchronized microbial responses between young and aged mice, and which genera are mainly involved in this process.

3. Project Objectives and Goals:

- Assess whether co-housing accelerates exchange of gut microbiota between young and aged mice.
- Identify genus-level taxa showing synchronized responses.
- Evaluate whether a shared environment reduces age-associated differences.

4. Methodology and Approach:

I analyzed 16S rRNA amplicon data in the RStudio environment. The workflow included the following steps (Figure 1):

1. Raw sequencing reads were processed using the DADA2 pipeline, which performs quality filtering, denoising, and chimera removal to infer ASVs.
2. Taxonomy was assigned using the **SILVA** reference database.
3. Downstream analysis and data visualization were performed in R using ggplot2 and related packages.

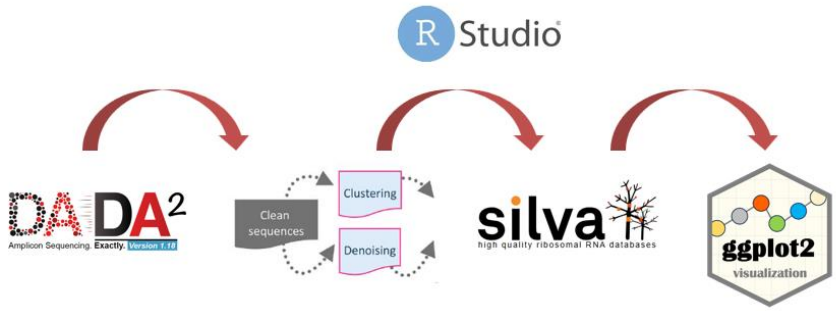


Figure 1 . *Overview of the data processing workflow.*

5. Results:

- Co-housing reduced distinct microbial differences between young and aged groups (Figure 2).
- Several genera that were initially unique to one age group appeared in the opposite group after co-housing, indicating bidirectional transfer.
- Among these transferred taxa, some were recognized as beneficial bacteria, while other genus displayed context-dependent effects (beneficial or harmful depending on host conditions).
- These findings suggest that the shared environment facilitated microbial exchange and synchronized gut microbial composition between age groups.

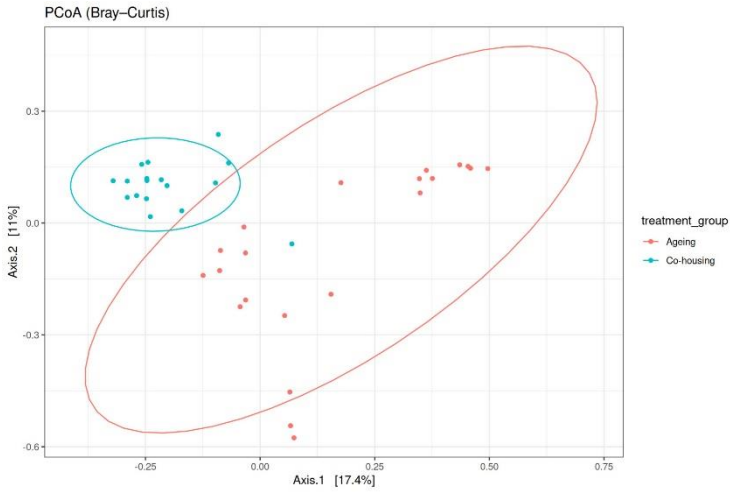


Figure 2 . *PCoA shows the difference between Ageing and Co-housing groups*

6. Discussion:

The results support the hypothesis that co-housing accelerates the exchange of gut microbiota between young and aged mice, reducing age-related differences. This highlights the strong influence of environmental factors in shaping microbial communities, sometimes overriding intrinsic host factors such as age.

However, the analysis was restricted to genus-level composition and did not include functional profiling or longitudinal testing, which limits the ability to interpret biological consequences in detail.

7. Strengths and Limitations:

Strengths:

- Clear genus-level signal of synchronized responses under co-housing.
- Reproducible pipeline using DADA2, SILVA, and R-based visualization tools.

Limitations:

- Restricted to genus-level composition only.
- Did not extend analysis to functional inference or across all experimental methods due to time and computational constraints.

8. Next Steps and Future Work:

- Apply functional prediction tools (e.g., PICRUSt2) to investigate metabolic consequences of microbial exchange.
- Extend the analysis to additional experimental conditions to validate findings.
- Incorporate longitudinal samples to test stability of transferred taxa.

9. Conclusion:

Co-housing accelerates the exchange of age-linked gut microbiota, leading to synchronized genus-level responses between young and aged mice. This project shows how environmental interactions can shape microbial communities and potentially affect host health.

Strength of the approach: The project clearly demonstrated age-related microbial synchronization through co-housing using available sequencing data.
Limitation of the approach: The analysis was restricted to genus-level composition and did not assess functional implications or long-term stability of changes.