Bioinformatics Summer Program Report

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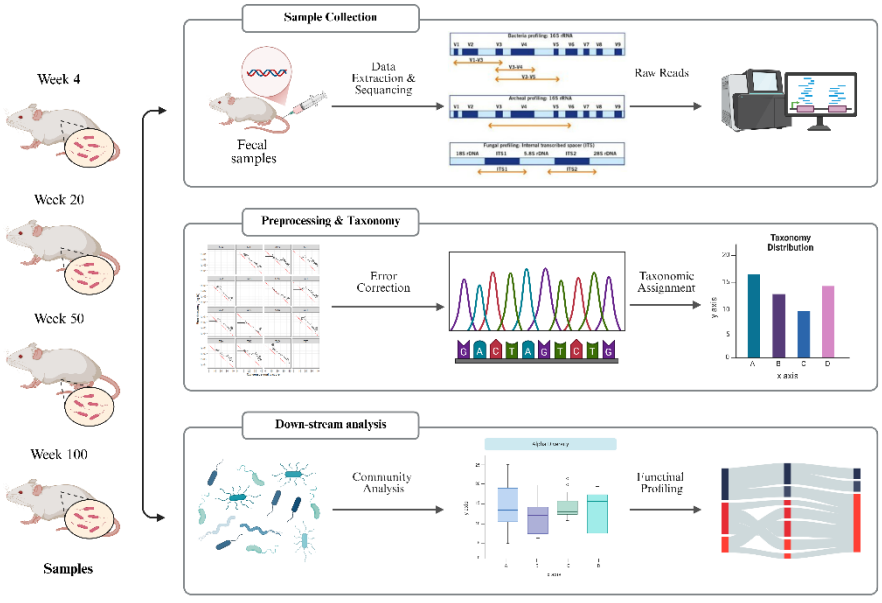
Project title: Integrative Analysis of Gut Microbiome Composition and Diversity to Characterize Aging-Associated Changes in Mice

Introduction

Aging is a complex biological process that is closely linked to alterations in the gut microbiome. Several studies have shown that the composition and diversity of intestinal bacteria change across the lifespan, with specific microbial taxa either enriched or depleted in old age. These shifts are not limited to taxonomic profiles but extend to microbial functions, influencing metabolic pathways, immune regulation, and host physiology. Functional profiling, including KEGG pathway analysis, provides insights into how microbial communities contribute to processes such as inflammation, energy metabolism, and immune homeostasis during aging. Understanding these microbiome–aging interactions is crucial for identifying microbial signatures of healthy aging and potential therapeutic targets.

Material and Methodology

Fecal samples were collected from mice of different ages, representing young, middle, and old groups. This sampling design allowed us to track changes in the gut microbiome across the lifespan. Sequencing data were processed and analyzed in R (https://drive.google.com/drive/folders/11KwHiMgmCs-opqks9MkTipbfXBNpTD0A) using standard microbiome pipelines to generate taxonomic profiles. Community composition was compared across age groups, and functional pathways were explored using KEGG-based analysis to connect microbial shifts with potential biological effects. Statistical analyses and visualizations were also performed to highlight significant patterns and functional trends associated with aging.



Results

We found that the gut microbiome changes noticeably with age. Certain bacteria, like Akkermansia and Muribaculum, were more common in younger and mid-aged mice, while Lactobacillus and Bifidobacterium increased in older mice. We also observed that overall diversity declined with age, suggesting a less balanced microbial community. On the functional side, microbial pathways related to metabolism and transport shifted across age groups. Together, these findings highlight that both the composition and the activity of the gut microbiome are strongly shaped by aging.

Figure 1: Taxonomy Distribution by Genus

This stacked bar plot shows the bacterial composition at the genus level across weeks (4, 20, 50, 100). Each color represents a different genus. Some genera like Akkermansia and Parabacteroides dominate early but decrease over time, while Lactobacillus increases in later weeks.

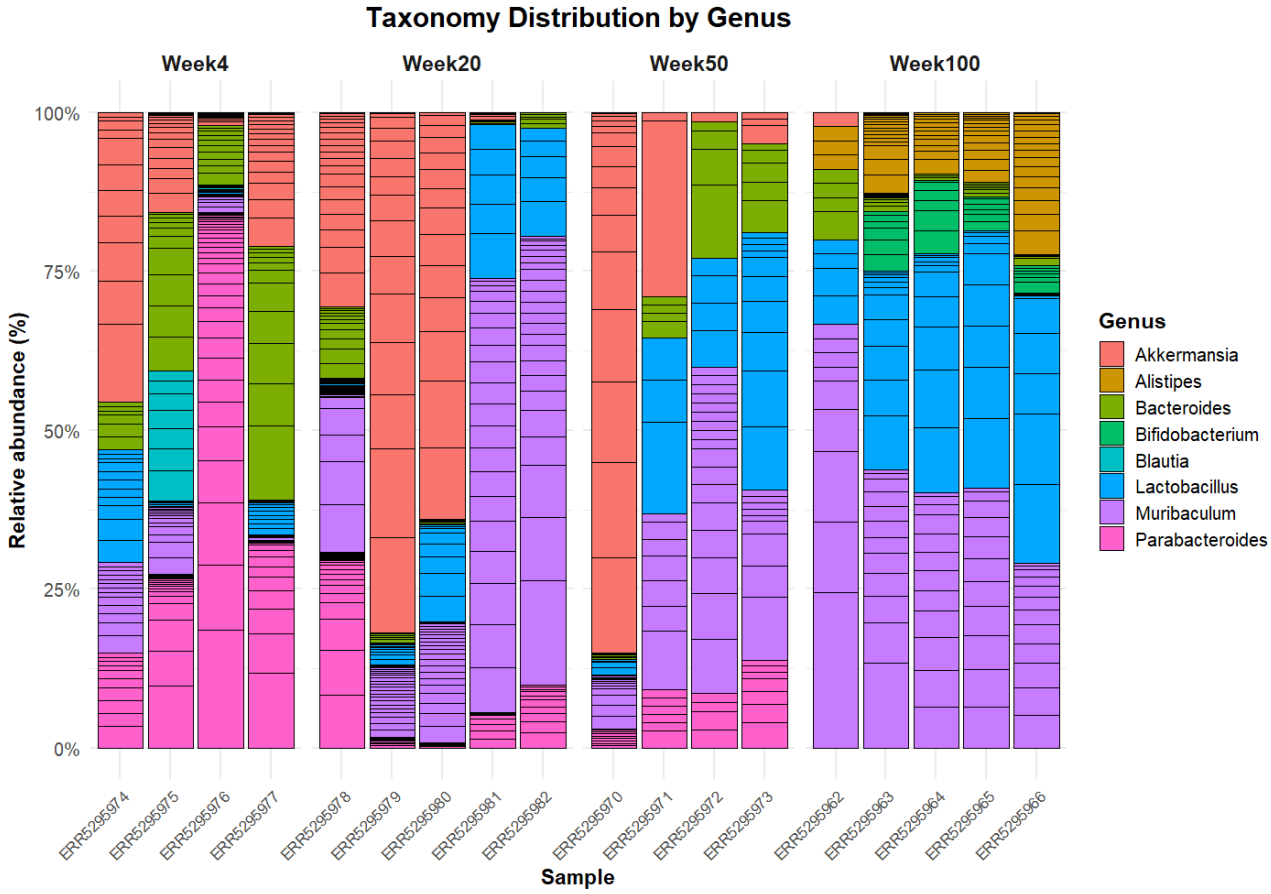


Figure 2: Taxa Heatmap

A heatmap of bacterial abundance across weeks. Red indicates higher abundance, blue lower. Certain taxa are enriched at specific ages (e.g., week 4 or week 100), highlighting age-associated microbial patterns.

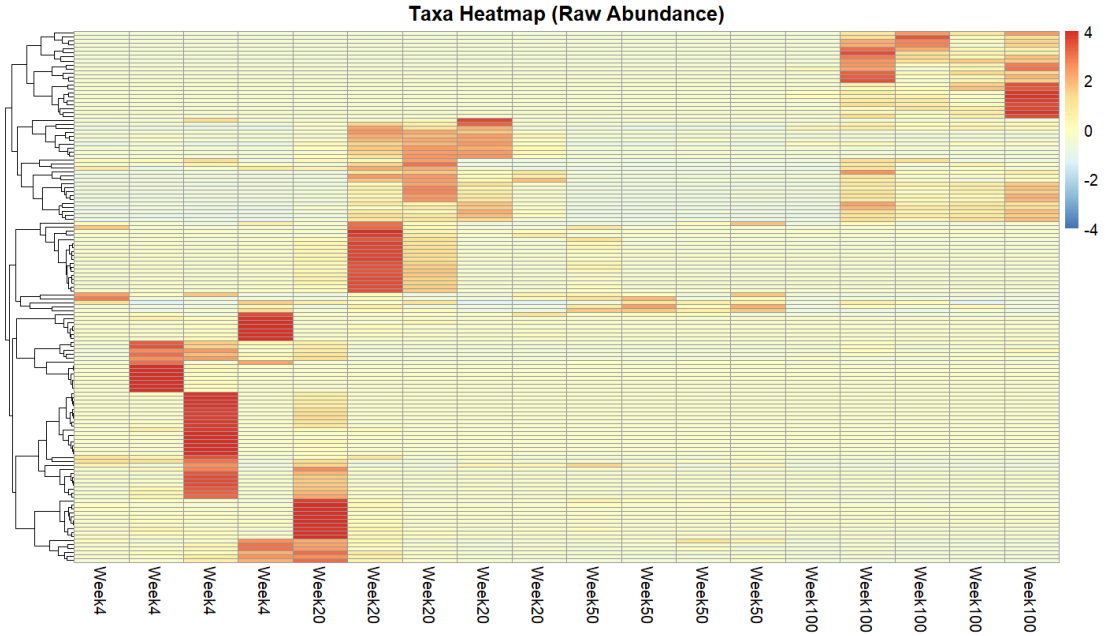


Figure 3: Alpha Diversity

Alpha diversity measures within each sample.

- Observed richness: higher in weeks 4 and 20, but drops significantly at weeks 50 and 100.
- Shannon index: similar trend, showing reduced diversity with aging.

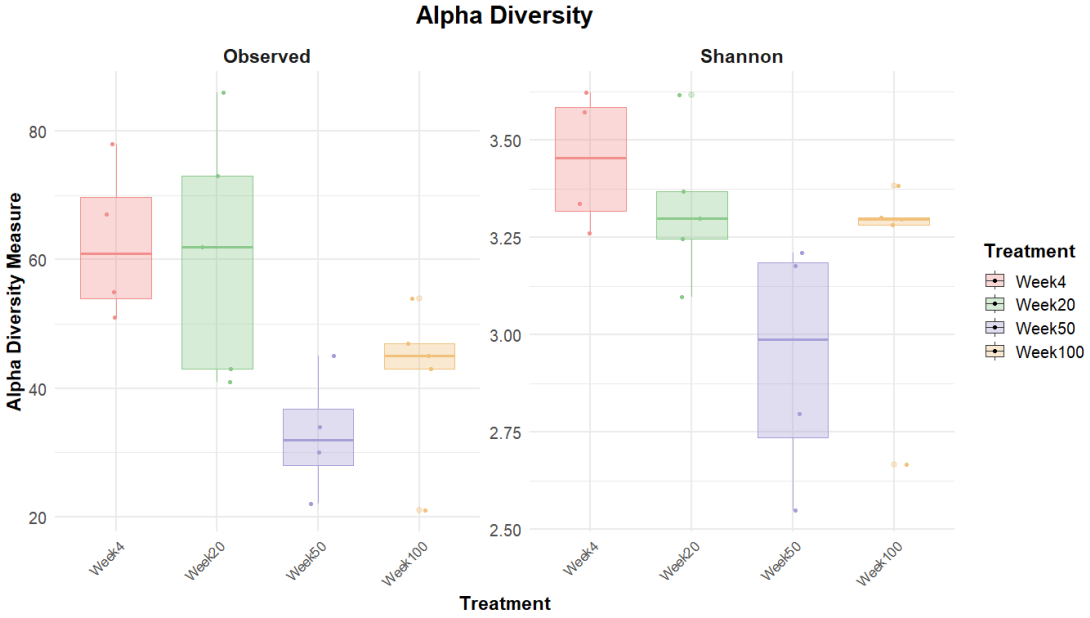


Figure 4: Genus-level Across Weeks

Boxplots comparing the relative abundance of key genera across weeks. Certain genera rise with age (Lactobacillus, Bifidobacterium), while others decline (Akkermansia, Parabacteroides).

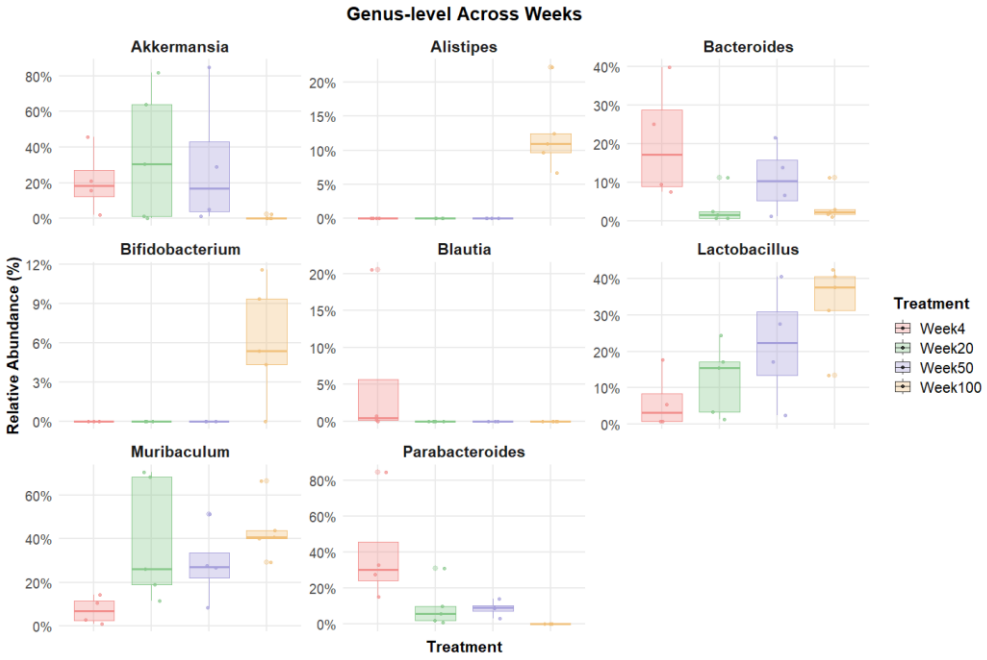


Figure 5: KEGG Enzymes

Relative abundance of KEGG enzymes across ageing weeks shows overall functional shifts, with some decrease around mid-age and recovery later.

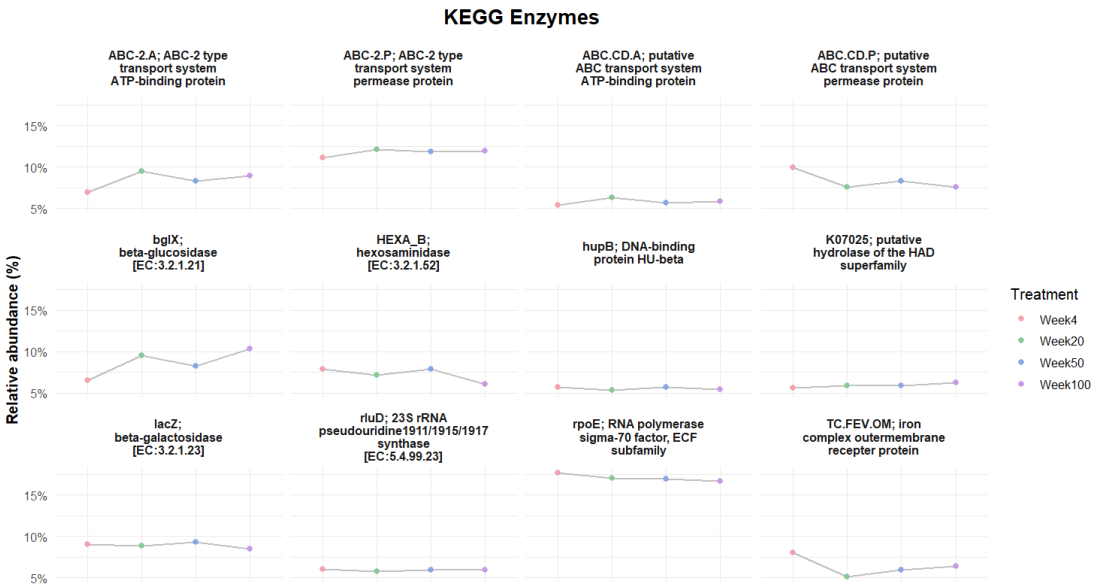
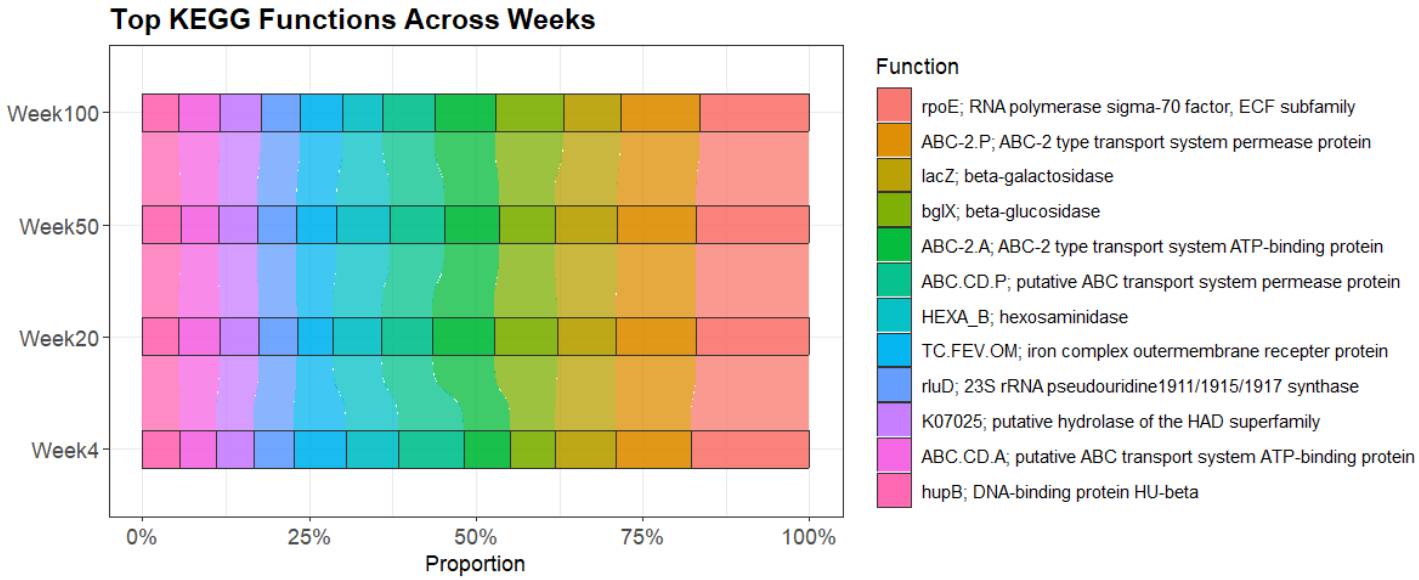


Figure X. Top KEGG Functions Across Weeks
The plot shows the relative distribution of the top KEGG functions across ageing weeks. Overall, the functional composition remains broadly stable, with slight shifts observed between mid-age and late-age groups.



Conclusion:

Our study highlights how gut microbiome composition changes across different stages of aging. By applying advanced bioinformatics pipelines and statistical analyses, we were able to identify key bacterial taxa and functional pathways that shift significantly with age. These findings suggest that aging is strongly associated with alterations in microbial diversity and functionality, which may play a role in age-related health outcomes. Moreover, network and KEGG pathway analyses provided deeper biological interpretation, linking microbial changes to potential mechanisms underlying aging. Overall, our results emphasize the importance of considering the gut microbiome as a dynamic factor in aging biology and open opportunities for further studies exploring microbiome-targeted interventions.

Link of the R scripts: https://drive.google.com/drive/folders/11KwHiMgmCs-opqks9MkTipbfXBNpTD0A

Reference: https://microbiomejournal.biomedcentral.com/articles/10.1186/s40168-021-01189-5