

1. Title:

Comprehensive Profiling of Gut Microbiome Modulation in Response to Polycyclic Aromatic Hydrocarbons (PAH) Exposure.

2. Research Questions:

How is the gut microbiome composition affected by exposure to PAH? What is the difference between modulations to the gut microbiome in response to acute and sub-chronic exposure to PAH?

3. Objectives:

I. To comprehensively profile the gut microbiome's response to PAH using multi-analytical approaches, including diversity analysis, differential abundance testing, and machine learning.

II. Create an R script that supports these methods using the read count output of 16S rRNA-sequencing.

4. Approach:

Using made-up microbiome read count data, I will apply a multi-analytical approach to investigate gut microbiome modulation in response to acute and sub-chronic polycyclic aromatic hydrocarbon (PAH) exposure. Analyses will be performed in R (R Core Team, 2025) using statistical and machine learning techniques to assess microbial diversity, differential abundance, and classification accuracy.

Microbiome read count data will be pre-processed by applying transformations. Diversity metrics will assess richness and compositional shifts and test for significance. Differential abundance analysis will identify bacterial families linked to PAH exposure. Visualization tools like heatmaps and volcano plots will highlight key taxa and, random forest classification will evaluate the ability to predict PAH exposure levels from microbiome data, identifying key distinct taxa (Statnikov et al., 2013). Findings will offer insights into potential microbial biomarkers of PAH exposure and lay the groundwork for future studies on microbiome-mediated xenobiotic metabolism (Yu et al., 2021). This approach integrates traditional ecological metrics with machine learning to comprehensively assess how PAH exposure influences gut microbiome composition.

5. References

- R Core Team. 2025. R: A Language and Environment for Statistical Computing. from <https://www.r-project.org/>
- Statnikov, A., Henaff, M., Narendra, V., Konganti, K., Li, Z., Yang, L., Pei, Z., Blaser, M. J., Aliferis, C. F., & Alekseyenko, A. V. (2013). A comprehensive evaluation of multicategory classification methods for microbiomic data. *Microbiome*, 1(1), 11. <https://doi.org/10.1186/2049-2618-1-11>
- Yu, X., Lv, K., Guan, S., Zhang, X., & Sun, L. (2021). Long-term exposure to phenanthrene at environmental-level induces intestinal dysbiosis and disrupted hepatic lipid metabolism in mice. *Environmental Pollution*, 268, 115738. <https://doi.org/10.1016/j.envpol.2020.115738>
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