Analysis Tutorial Prospectus
Okpe Uchenna

1. Title
Selection of microbial consortia based on their function versus abundance in the human gut

2. Research Question
What are the top 10 bacteria in the human gut-based functional degradation of complex sugars?
What is the abundance of bacteria that degrade complex sugars in the human gut?
How does this population of complex fiber degraders vary with their abundance in the human gut?

3. Objectives
i.   Design a gut bacteria consortium based on function while considering bacteria abundance.
ii.   I will utilize the bacteria consortia to characterize the role of bacteria in the digestion of prebiotics and how this improves gut health.

4. Approach
Microbial consortia are a subset of the gut microbiome that can be used as models to study aspects of gut-microbe interactions. I will use a curated database from https://github.com/waldronlab/curatedMetagenomicData and my conversations with ChatGPT to build functional code that selects microbial consortia and classifies them based on their functions and abundance in the gut. Our function of interest will be the presence of glycoside hydrolase genes. I will generate a scatter plot to evaluate the relationship between function and abundance. Our index for function is the presence of glycoside hydrolase genes. This project will help inform our selection of bacteria to be included in the consortia that make up our synthetic community.

5. Selected References:

(Anon 2025; Esmail et al. 2025; Shetty, Kostopoulos, et al. 2022; Shetty, Kuipers, et al. 2022)
Anon. 2025. *Package 'curatedMetagenomicData' Title Curated Metagenomic Data of the Human Microbiome*.

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Shetty, Sudarshan A., Ioannis Kostopoulos, Sharon Y. Geerlings, Hauke Smidt, Willem M. de Vos, and Clara Belzer. 2022. 'Dynamic Metabolic Interactions and Trophic Roles of Human Gut Microbes Identified Using a Minimal Microbiome Exhibiting Ecological Properties'. *ISME Journal* 16(9):2144–59. doi: 10.1038/s41396-022-01255-2.

Shetty, Sudarshan A., Ben Kuipers, Siavash Atashgahi, Steven Aalvink, Hauke Smidt, and Willem M. de Vos. 2022. 'Inter-Species Metabolic Interactions in an In-Vitro Minimal Human Gut Microbiome of Core Bacteria'. *Npj Biofilms and Microbiomes* 8(1). doi: 10.1038/s41522-022-00275-2.