

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/waldrondlab/curatedMetagenomicData> and my conversations with ChatGPT to build functional code that selects microbial consortia.

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.