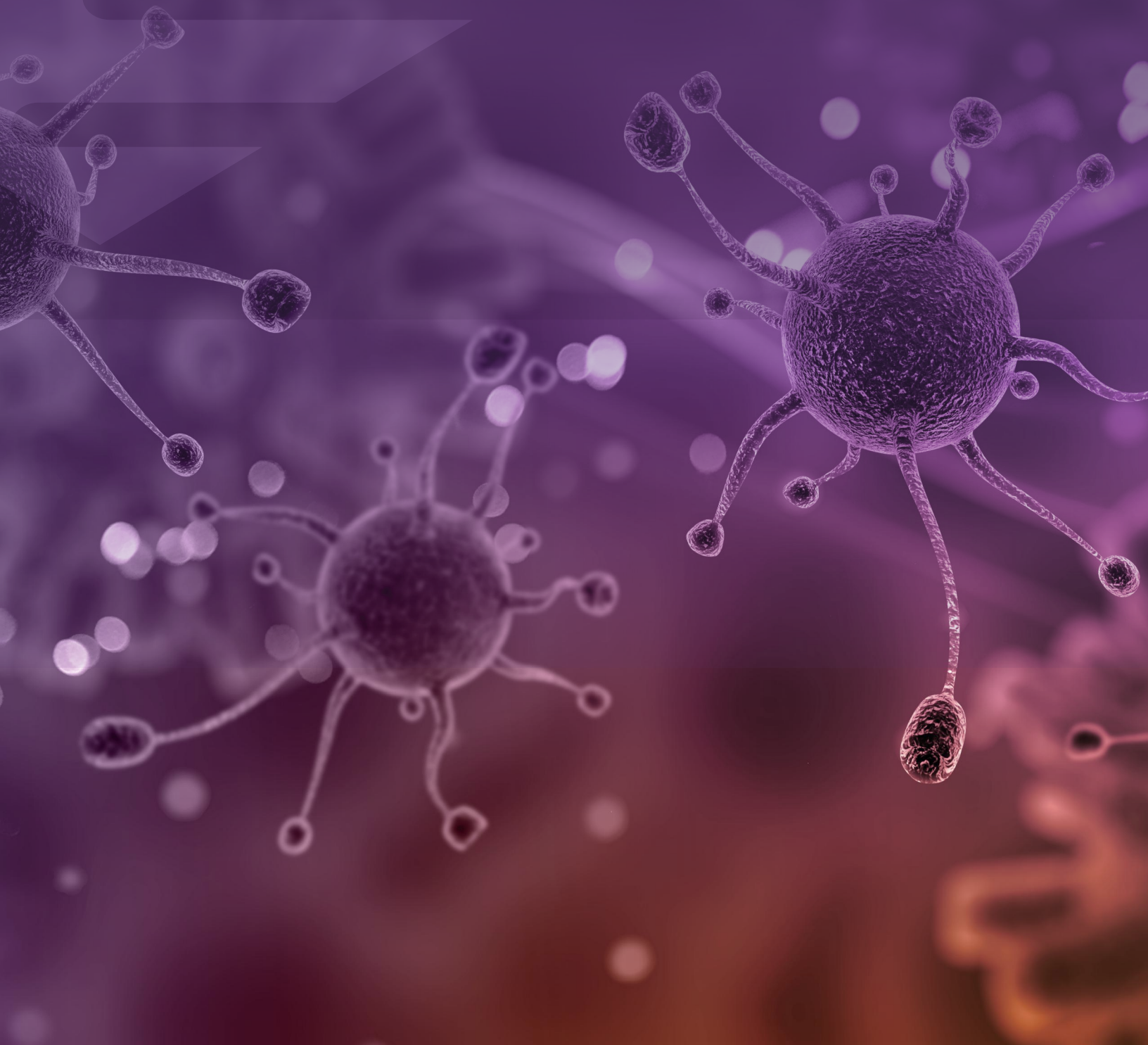
PromptBio

Multi-Omics Analysis of Cystic Fibrosis using Conversation-Based Interactions



Executive Summary

In this white paper, we demonstrate how to leverage the **PromptBio platform** to replicate a **multi-omics analysis** using **conversational-based interactions**. Our case study is based on research published in Genome Medicine, titled "Interactions between the gut microbiome and host gene regulation in cystic fibrosis." This study explores the complex interplay between **host gene expression** and **gut microbiome composition** in individuals with cystic fibrosis.

Key Analytical Components Replicated from the Study

1. Host Transcriptomics Analysis

- Processes RNA-seq data to identify differential gene expression in cystic fibrosis (CF) patients.
- Reveals key pathways associated with disease mechanisms and host response.

2. Metagenomics Analysis

- Utilizes 16S rRNA sequencing to characterize gut microbiome composition in CF patients.
- Highlights shifts in microbial diversity and abundance relevant to disease state.

3. Integrated Multi-Omics Analysis

- Combines transcriptomic and metagenomic data to uncover correlations between host gene activity and microbial taxa.
- Illuminates the molecular interactions shaping the gut environment in CF.

Leveraging PromptBio's Conversational Intelligence

Using intuitive **conversational-based interactions**, we demonstrate how the **PromptBio platform** manages each analytical stage — from **data input** to **result generation** — in a way that mirrors the original study's methodology.

What sets PromptBio apart is its ability to:

- **Plan complex analyses** autonomously based on natural language queries.
- **Generate executable code** dynamically, tailored to the context and tools required.
- **Auto-correct errors** in real time, reducing friction and debugging overhead.
- **Leverage validated tools** natively provided by the platform, including widely accepted frameworks such as **Nextflow**, as well as retrieve and integrate tools from the **public domain** when necessary.
- **Streamline workflows** with smart automation, eliminating the need for manual setup or configuration.
- Offer an **easy-to-use, intelligent**, and **efficient** interface that enables both novice users and advanced bioinformaticians to conduct robust multi-omics analysis effortlessly.

Our results successfully replicate key findings from the original Genome Medicine study — including **differential gene expression patterns, microbial diversity shifts**, and **host-microbe correlation signatures** — affirming the platform's ability to produce **accurate, reproducible**, and **publication-grade insights** with minimal technical overhead.

Background

While some domain expertise is currently required to guide the analysis, we are actively working toward a more **hands-off,** fully guided system designed to support users **without specialized expertise.**

Data Resource

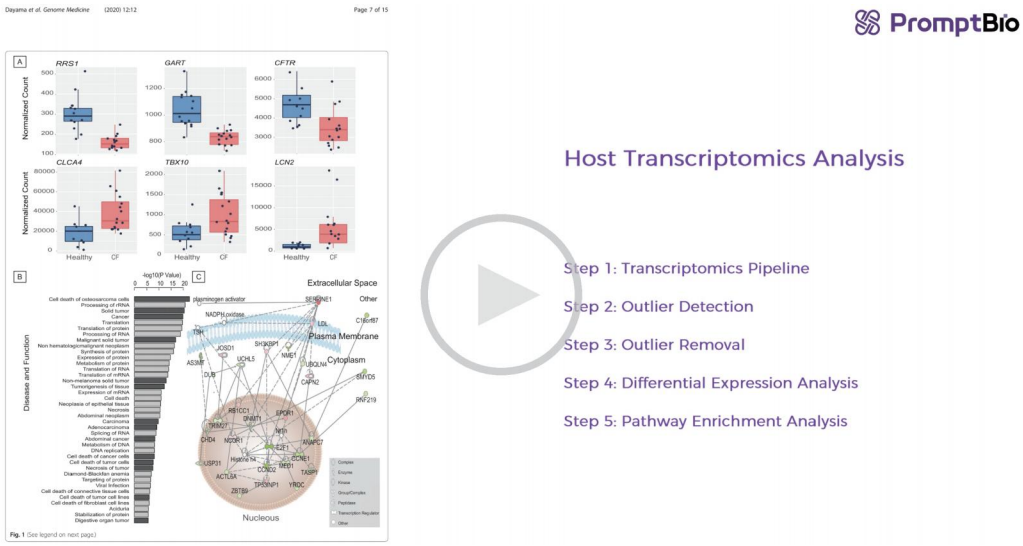
The study analyzes multi-omics data—RNA-seq transcriptomics of colonic mucosa and 16S rRNA-based metagenomics—to investigate host gene expression and gut microbiome composition in cystic fibrosis. It identifies differentially expressed genes, microbial taxa shifts between patients and healthy donors, and explores host-microbe interactions. Raw sequencing data are available in the NCBI SRA under BioProject ID: PRJNA552270.

Analysis Workflow

To replicate the comprehensive multi-omics analysis in the paper, we have divided the workflow into three distinct sections: Host Transcriptomics Analysis, Gut Metagenomics Analysis, and Multi-Omics Integration. Each section corresponds to a critical component of the original study and is demonstrated through a dedicated video. These videos illustrate how the PromptBio platform empowers researchers to conduct sophisticated analyses using intuitive, conversation-based interactions.

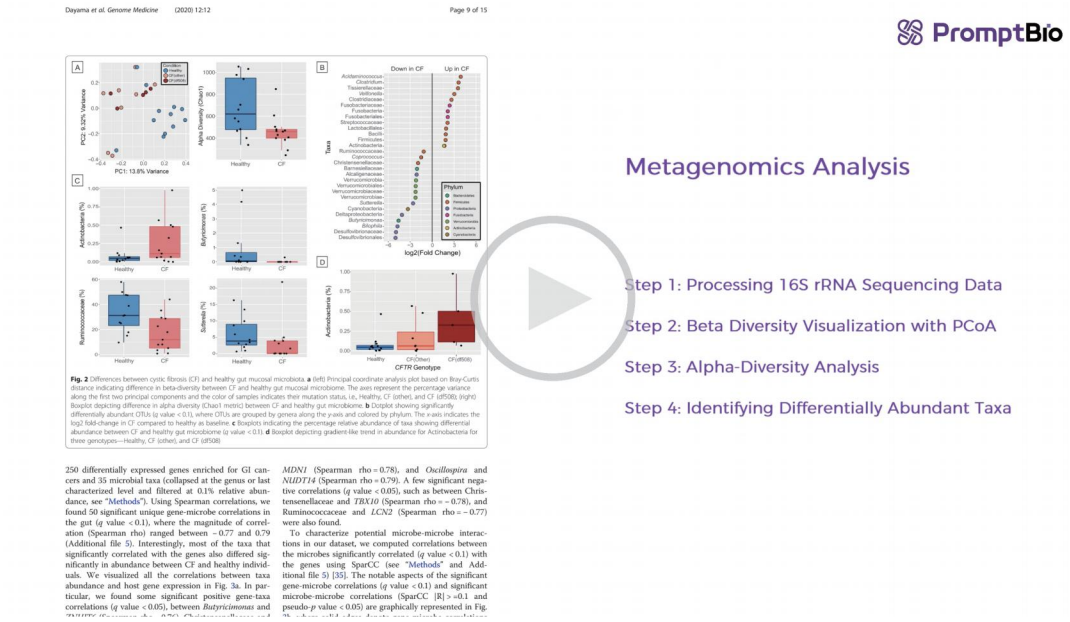
Video 1: Host Transcriptomics Analysis

This video shows RNA-seq analysis on the PromptBio platform using dataset PRJNA552270. It processes data to measure gene expression, removes outliers with PCA, performs differential expression analysis using DESeq2, and conducts functional enrichment. Outputs include PCA plots, cleaned matrices, differentially expressed genes, and enriched pathways.



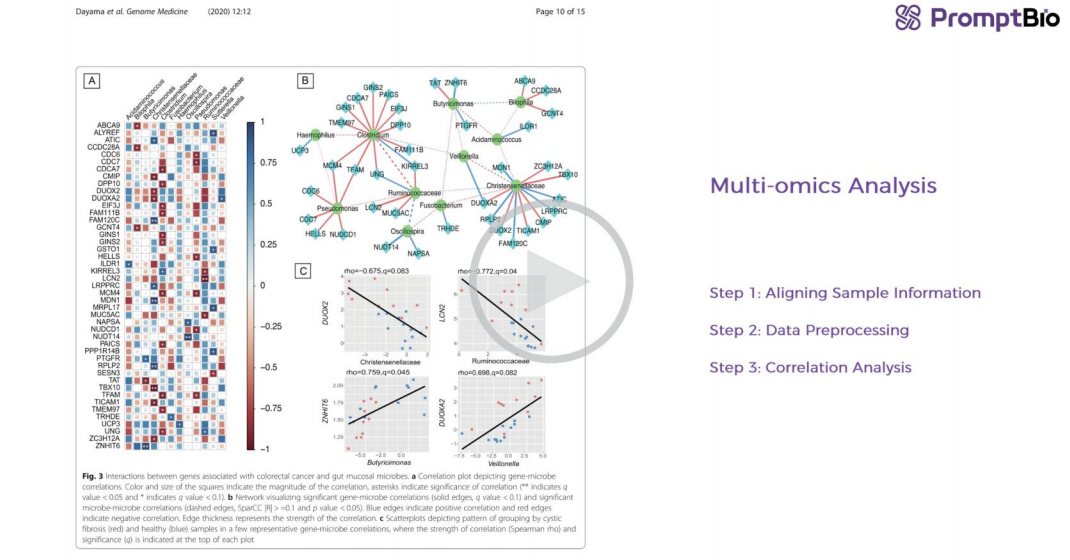
Video 2: Metagenomics Analysis

This video demonstrates metagenomics analysis on PromptBio with 16S rRNA sequencing data. It uses an nf-core pipeline to process amplicons, analyzes beta diversity with PCoA, measures alpha diversity with Chao1, and finds differentially abundant taxa with phyloseq and DESeq2. Outputs include OTU tables, PCoA plots, differentially abundant taxa, and diversity charts.



Video 3: Multi-Omics Analysis

This video covers multi-omics integration, combining RNA-seq and 16S-seq data. It normalizes datasets, aligns sample IDs, applies CLR transformations, and uses Spearman correlation to link genes and taxa. Outputs include normalized tables and correlation results.



Conclusion: Empowering Research with PromptBio

Through these three videos, we have demonstrated how the PromptBio platform replicates the multi-omics workflow from the Genome Medicine study using conversation-based interactions. Covering transcriptomics, metagenomics, and integrative analysis, each section showcases the platform's precision, reproducibility, and user-friendly design. By removing the need for coding expertise, PromptBio accelerates scientific discovery in the life sciences, making advanced analytical tools accessible to all researchers. This case study exemplifies how PromptBio transforms research workflows, allowing scientists to focus on generating insights rather than overcoming technical challenges.

Reference

Dayama G, Priya S, Niccum DE, et al. Interactions between the gut microbiome and host gene regulation in cystic fibrosis. Genome Med. 2020 Jan 28;12(1):12. doi: 10.1186/s13073-020-0710-2.

Appendix

Screenshots and corresponding input/output files for each step in all three sections:
https://drive.google.com/drive/folders/1iyELZfENG55NSchQpVxTFhnWXHLe81KS?usp=sharing

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