

Beyond “Who Is There?”: From 16S to Function

Graph-based Machine Learning approaches for predicting microbiome composition

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Motivation

16S sequencing gives us an affordable snapshot of *who is there* — but can we predict *who will be there, with whom, and what they can do*?

WHAT WE HAVE:

- 16S rRNA SEQUENCING
- WHO IS THERE?

DESCRIBE

WHAT WE WANT:

- WHO COEXISTS?
- WHAT CAN THEY DO?

PREDICT

Questions

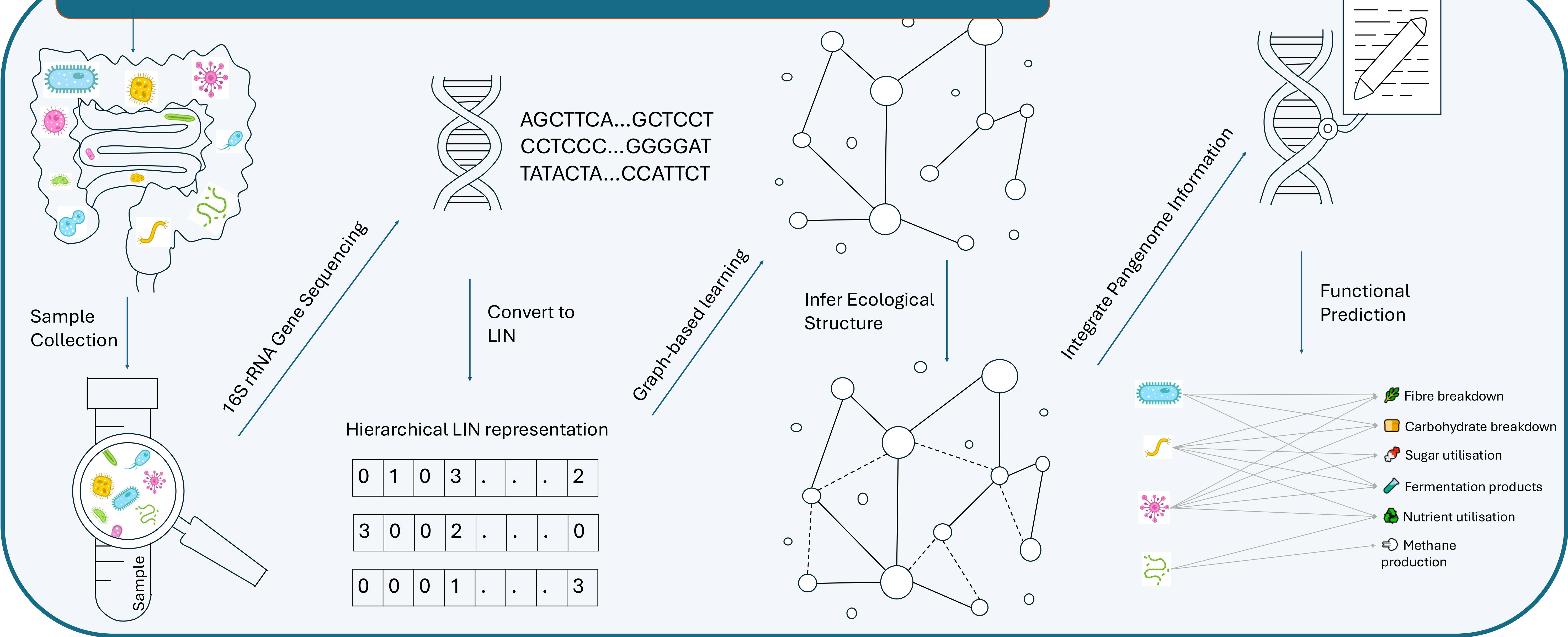
1. Can we predict microbial partners?

Can LIN-based graph learning reveal which microbial lineages are likely to coexist?

2. Can we predict what they can do?

Can LIN-linked pangenome information reveal the functional potential of microbial communities?

PROPOSED PREDICTIVE FRAMEWORK



Expected Output

1. Coexisting Lineages

Predicted microbial community composition

2. Gene Profiles

Estimated gene presence-absence

3. Functional Potential

Predicted metabolic pathways

Take-Home Message

FROM DESCRIBING MICROBIOMES TO PREDICTING THEM

LINs + Graph Learning + Pangenomes could transform widely available 16S data into predictions of microbial composition and functional potential.

16S → Predictive Microbiome Analysis

