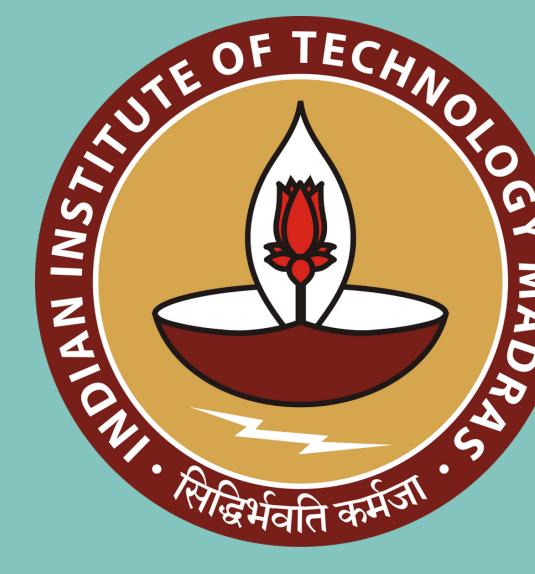


Identification of optimal intervention strategies for manipulating Home Microbiome

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MOTIVATION

- With humans spending most of their time indoors, the indoor microbiome of homes has become a major influencer of health, especially for children whose personal microbiome is still developing.
- The cleaning practices and other environmental conditions in cities have greatly altered the indoor microbiome to create a unique signature.
- These signature urban home microbiomes are significantly different from rural home microbiomes. Several studies have now shown that children growing in rural/farm homes are less prone to develop allergies.
- We wish to find the key organisms and their interactions in each microbiome and identify key differences between rural and urban microbiomes.

DATASET

- Dataset consisted of the abundance table of species found in floor dust samples from different locations - some rural and some urban
- The samples were obtained from four places - Checherta (a remote village in the Amazon rainforest), Puerto Almendra (a rural village), Iquitos (a large town), Manaus (metropolis)
- Microbial composition was found by sequencing of 16S(bacteria), 18S(micro-eukaryotes) and ITS1(fungi) extracted DNA.

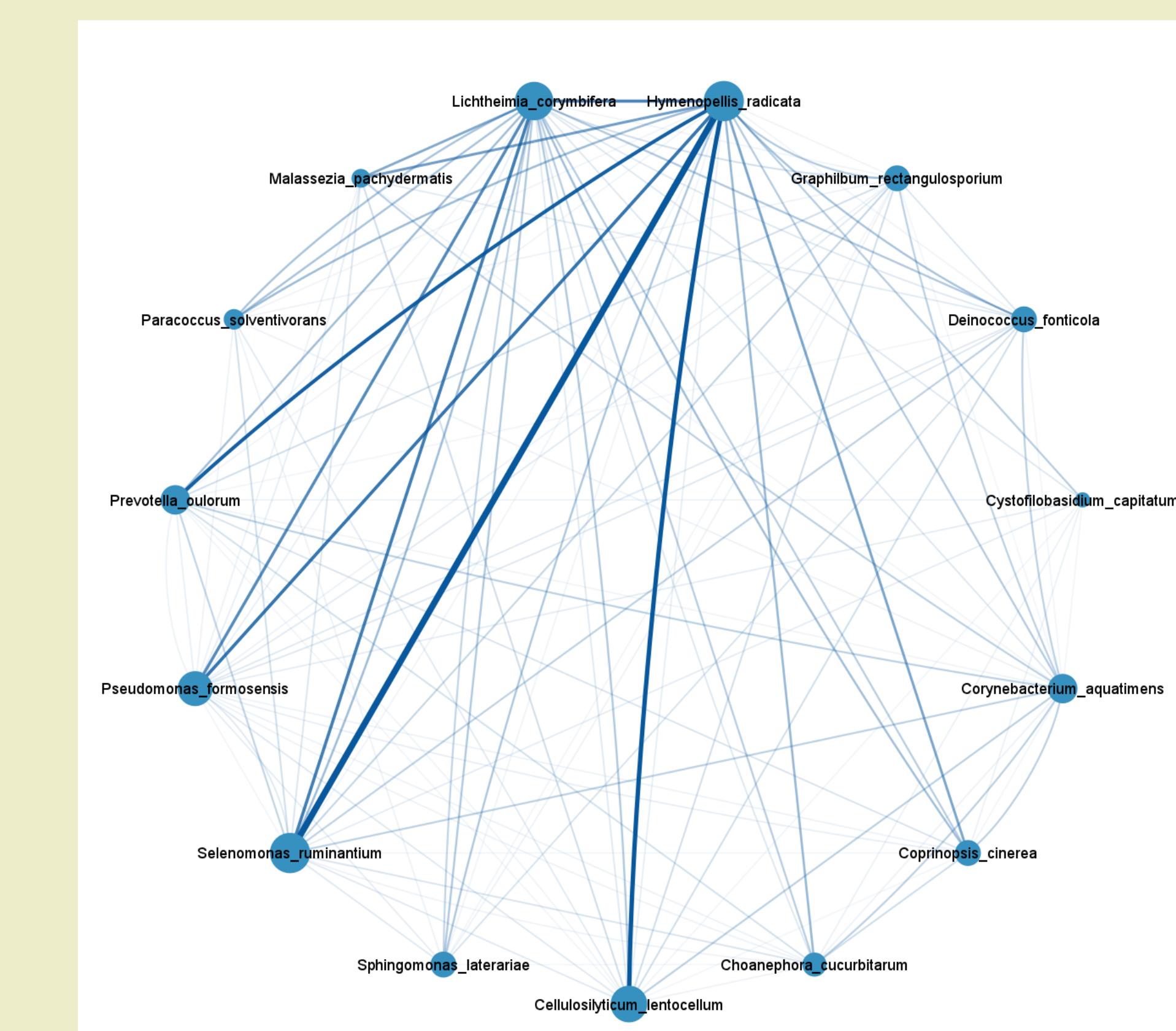


METHODS

- The metabolic model is a mathematical model of the reactions and the metabolites involved in the cell
- Reference genomes for the top 20 species (based on connectivity) in both rural and urban microbiomes were obtained and modelled in KBase and ModelSEED
- The metabolic support index (MSI) quantifies the benefits derived by organisms in a community.
- MSI is computed as the fractions of reactions stuck in the metabolic network of a certain organism in the presence of another organism
- MSI values were found for each of the pairwise interactions between the species.

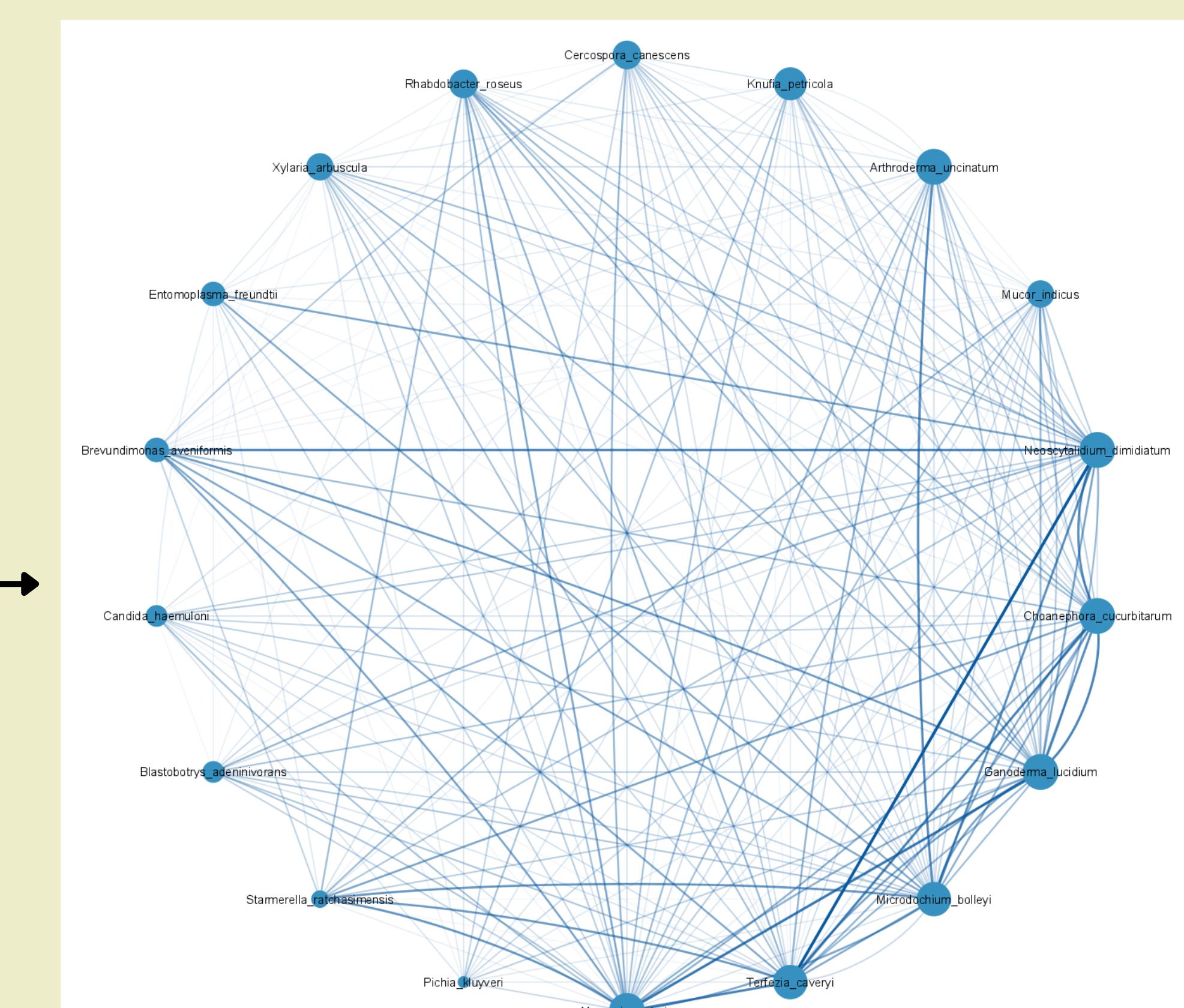
RESULTS

Microbial association networks for pairs of species, Color and thickness of each edge are mapped to the MSI value between the two species
Organisms most benefitted were inferred from the MSI values



← Rural
Urban →

Organisms most benefitted	
Rural	Urban
Entomoplasma freundtii	Selenomonas ruminantium
Terfezia cavyrei	Pseudomonas formosensis
Ganoderma lucidum	Lichtheimia corymbifera
Choanephora cucurbitarum	Prevotella oulorum
Microdochium bolleyi	Malassezia pachydermatis



FUTURE WORK

- Broader comparative analysis of the rural and urban microbiome
- Understand the organization of different microbiomes from datasets
- Understand perturbations to these microbiomes and how these can be used to manipulate the microbiome

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