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Network-Based Analysis of Gut Microbiome Profiles in Autism Spectrum Disorder

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Professional experience

- Demonstrator at the British University In Egypt.
- B.Sc. In Computer Science and Information Systems.
- Graduate student at The British University in Egypt
- Research interests include:
  - Machine Learning for Biological Data
  - Network Analysis and Graph-Based Methods

Introduction

- Rising prevalence of individuals being diagnosed with Autism Spectrum Disorder escalating over recent decades.
- Almost 1 in every 68 individuals worldwide is diagnosed with ASD.
- Possible relationship with biomarkers that can aid in detecting ASD early in an individual’s life.
- The gut microbiome composition can be influenced by the host genetics, diet, age, or external factors, such as geographical location.

Related work

01. The gut microbiome and hypertension

- short-term diet can temporarily change gut microbiota, while long-term dietary patterns (e.g., Mediterranean vs. Western diets) strongly shape microbial diversity and influence host health.

02. Modulation of Gut Microbiome and Autism Symptoms of ASD Children Supplemented with Biological Response Modifier: A Randomized, Double Blinded, Placebo-Controlled Pilot Study

- A randomized, placebo-controlled pilot study showed that the biological response modifier *Juvenil* helped shift the gut microbiota of children with ASD toward a profile more similar to neurotypical children.

Related work

03. The Gut Microbiome in Autism: StudySite Effects and Longitudinal Analysis of Behavior Change

- Longitudinal analysis found that gut microbiome composition in children with ASD varies by geographic location and changes over time, linking microbial shifts with ASD-related behaviors.

Main Research Aim

- Apply a **network-based similarity and clustering approach to ASD** microbiome datasets.
- Focus on the **structural properties** of microbial communities, not solely on abundance.
- **Early identification of ASD** in younger individuals.
- Improving the overall treatment plan and achieving much better symptom control for individuals.

Network-Based Analysis

- Microbiome samples were modeled as a similarity network, where **nodes represent samples** and **edges represent microbial similarity**.
- Cosine similarity was used to quantify relationships between taxonomic profiles.
- A similarity threshold was applied to retain strong connections and reduce noise.
- Community detection was then used to **identify clusters of samples with shared microbial structure.**

Methodology

Dataset

- **Two datasets** were analyzed: one pediatric ASD dataset (Kang et al.) and a second cohort of 143 ASD subjects with controls.
- Fecal samples were collected and assessed using behavioral scales (ATEC, PDD-BI).
- Microbiome profiling was performed **using 16S rRNA sequencing and analyzed with QIIME.**
- Data preprocessing removed near-zero and low-abundance OTUs to reduce noise.

Methodology

Measures

- **Cosine similarity** Measures similarity between samples based on vector direction (**smaller angle = more similar microbiome profiles**).

$$cos(\theta) = \frac{\sum_{i=1}^{d} x_i \cdot x'_i}{\sqrt{\sum_{i=1}^{d} x_i^2} \cdot \sqrt{\sum_{i=1}^{d} x'^2_i}}$$

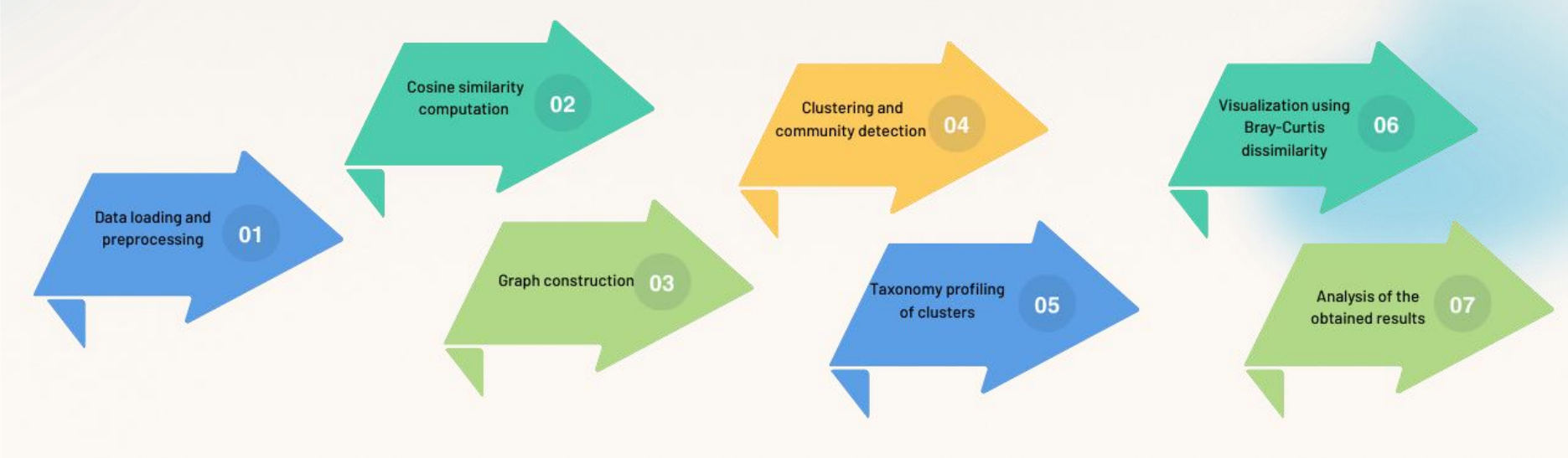
- **Bray–Curtis Dissimilarity** Measures differences in microbial composition between samples (**0 = very similar, 1 = completely different**).

$$BC_{ij} = 1 - \frac{2C_{ij}}{S_i + S_j}$$

- Both metrics were used to compare microbiome profiles between ASD and control groups.

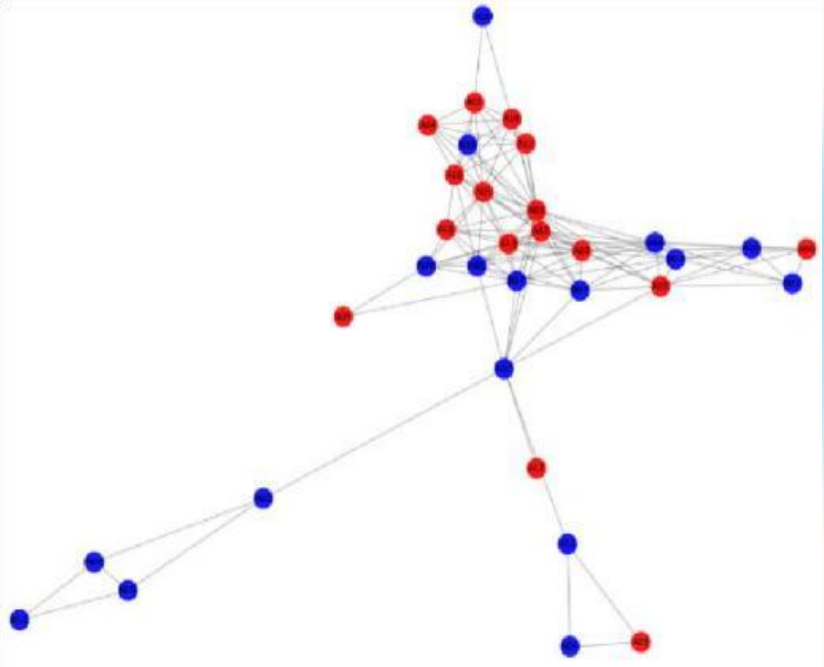
Methodology

Proposed pipeline



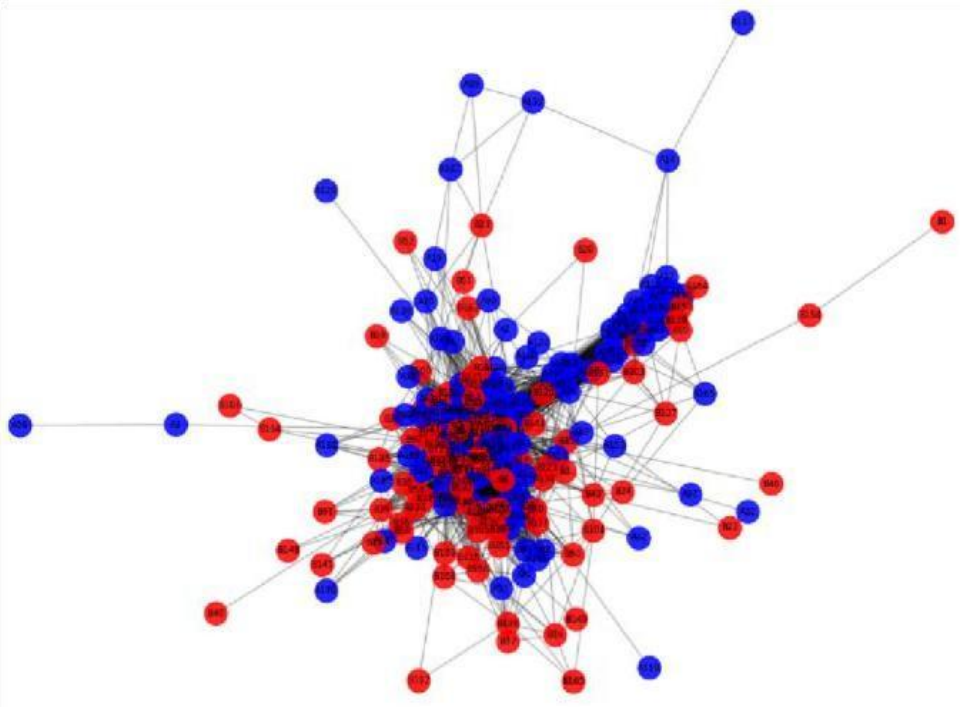
Results

- **Dataset 1 (Kang et al.)** showed several microbiome clusters with **both mixed and diagnosis-dominated** groups.
- Cosine similarity analysis revealed **partial clustering patterns** rather than full separation between ASD and controls.



Results

- **Dataset 2 (GSE113690)** showed **less clear separation between ASD and control samples**, suggesting more overlap in microbial structure.



Discussions

Dataset 1 (Kang et al.)

- **Cluster 1:** Mixed ASD and controls (21 each), dominated by Bacteroidota/Bacteroidaceae/Phocaeicola, suggesting a generally balanced gut profile.

- **Cluster 2:** Mostly one ASD sample, dominated by Firmicutes/Lachnospiraceae/Hungatella, indicating a diverse gut but with potential disease-associated taxa.

- **Cluster 3:** One ASD sample, dominated by Verrucomicrobiota/Akkermansia, which may be linked to reduced gut inflammation.

Discussions

Dataset 2 (GSE113690)

- **Six genus–level clusters were identified** using cosine similarity.
- Several clusters showed mixed ASD and control samples, mainly dominated by Firmicutes and Ruminococcaceae.
- Some clusters contained potentially pathogenic taxa (e.g., Rickettsiales) or uncommon gut residents (e.g., Perlucidibaca).
- Microbial distributions were **mixed and uneven**, with no clear separation between ASD and controls.

Conclusion

- Different profiles were identified.
- The current datasets were not able to provide us with severity indication.
- Most of the profiles detected are normal occurrences in a healthy gut microbial structure.
- Limited metadata and descriptive attributes in the current datasets restricted deeper analysis and reduced result clarity.
- Future work will use richer datasets to enable more comprehensive enrichment analysis.

Future Work

- A larger sample of individuals will need to be studied over a long period to determine the environmental impact on the gut microbiome.
- Autism Spectrum Disorder is not only related to the physical symptoms, but the attitude and the behavior of the diagnosed individual can act as an indicator that can help diagnose ASD earlier, so a dataset with more metadata is needed.
- Future work will include additional datasets with richer attributes and individual-level features to support deeper analysis and more robust enrichment studies along with pathway analysis to enrich the results.

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