Association between oral microbiota and close-range proximity of children in primary school

Keywords: Oral microbiome; Social networks;
Close-range proximity; Human health; Children's interactions

Extended Abstract

The human microbiota is a complex ecosystem of microorganisms inhabiting the human body, and it influences human health and well-being. Recent studies showed its interplay with social behavior, suggesting that part of the microbiota might be socially transmissible [1–3]. One of the main challenges encountered in these studies is accurately measuring the network of social interactions, typically estimated from known, long-standing relations. While information on these associations is readily available, using such relationships does not allow the study of the microbiota's similarities among individuals with social contacts reaching beyond their closest social circle.

We investigate the association between social interactions and oral microbiota composition in 35 primary school children. This cohort comprises individuals from different families, allowing us to consider interactions beyond the familiar social circle. We characterized the participants' oral microbiota with saliva sampling during class hours and 16S rRNA gene sequencing at the ASV (amplicon sequence variant) level. In parallel, we objectively measured a close-range proximity network among children with wearable sensors, developed by the `SocioPatterns` collaboration [4].

Our results evidence a strong association between social interactions and microbiota formation. Figure 1A shows that prolonged interactions are associated with a significantly higher microbiota similarity, compared with a null model randomizing the association between the proximity interaction duration and the microbiota distance. Figure 1B shows that it is possible to predict the proximity network using the oral microbiota information alone. We train a binary classifier that predicts, given the microbiota compositions of two individuals i and j, whether they interacted for a duration longer than a threshold τ^*. We cross-validate the classifier on 100 randomization of the training and test sets. We then identify a set of ASVs whose distribution across children correlates more closely with the structure of the proximity network. For these ASVs, the edges formed by pairs of nodes harboring ASV a ($y_a = 1$) have a significantly longer duration than all others ($y_a = 0$). Figure 1C shows the interaction distribution durations of the edges $y_a = 0$ and $y_a = 1$ for one of the 13, with a significant difference between the two distributions. Finally, Figure 1D shows that the most central children in the proximity network have a higher number of these taxa in their microbiota.

In conclusion, our study shows a strong association between oral microbiota and close-range proximity of non-cohabiting children in a primary school setting, complementing the results on cohabiting individuals. This suggests that microbiota might be transmitted in social settings, and it motivates further research on the interplay between the social network structure and the microbiota composition.

The research protocol was reviewed by the Regional Committee for Medical and Health Research Ethics (REK East Norway), and it received approval from the Data Protection Officer at Molde University College (September 2022). All re-identifiable data were stored at Molde University College, and only de-identified data files were shared with research group members.

References

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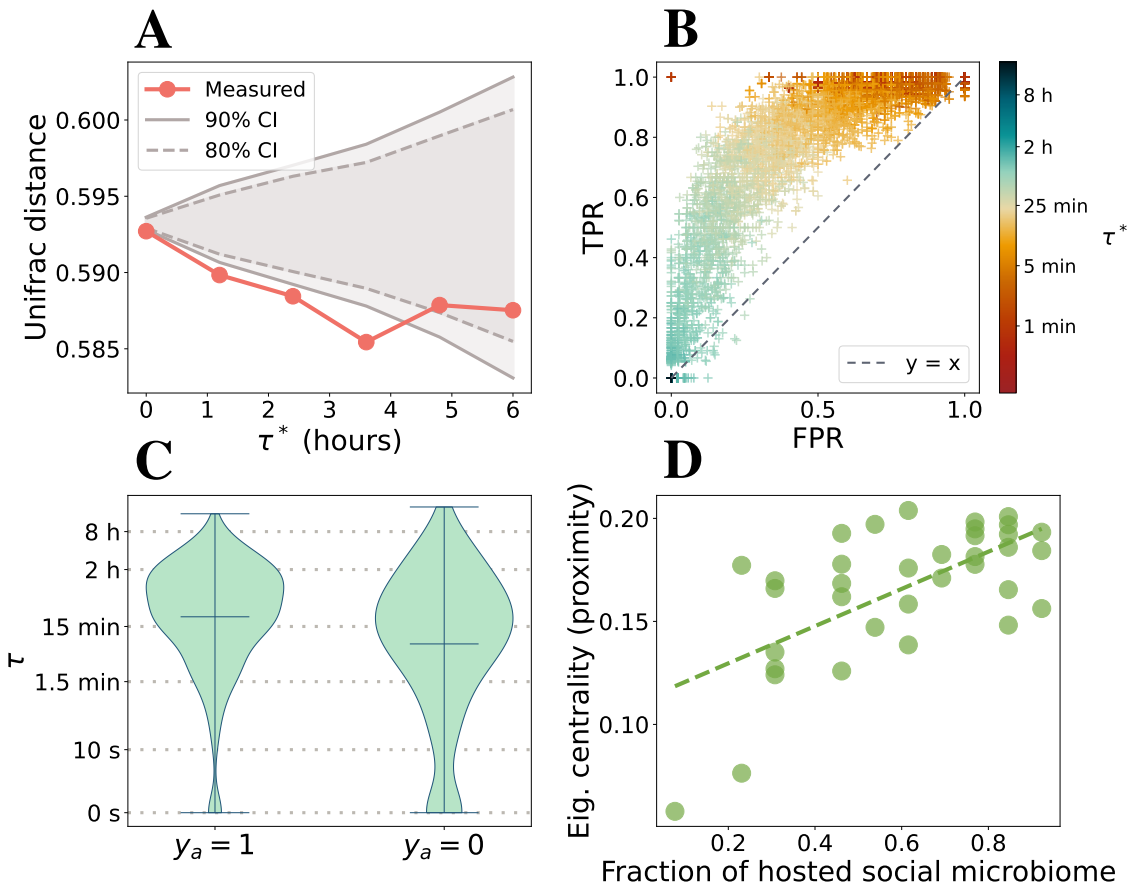

Figure 1: **Panel A**. Average Unifrac distance between children pairs with cumulative interaction time exceeding τ as a function of τ. The 95% confidence interval shown in dashed lines is obtained by randomizing the association between edge weights and microbiota similarity. **Panel B.** ROC curve for the binary classifier used to infer the proximity links based with interaction duration exceeding τ^* on microbiota profiles. Every cross in the plot corresponds to one realization of the training and test sets. Markers are color-coded according to the value of the threshold τ^*. **Panel C**. Histogram of the cumulative interaction times for one of the 13 taxa in which the edges formed by pairs of nodes harboring taxon a ($y_a = 1$) have a significantly longer duration than all others ($y_a = 0$). **Panel D**. Scatter plot of the eigenvector centrality in the proximity network against the number of taxa harbored by the child, out of the 13 (*Capnocytophaga leadbetteri*) identified in the previous step.