**Supervisor:** Prof. Edoardo Pasolli

**Title:** Transfer learning methodologies for large-scale metagenomic analysis of the human microbiome

**Research project:** The human microbiome, the diverse community of microorganisms residing in the human body, plays a crucial role in health and disease. Its composition varies significantly across individuals, influenced by factors such as genetics, age, diet, lifestyle, and environmental exposures. Dysbiosis, or imbalance in the microbiome, has been linked to a wide range of health conditions, including metabolic, inflammatory, and neurological disorders.

As microbiome research advances, machine learning has emerged as a powerful tool for predictive modeling and biological discovery. However, a major challenge lies in the limited generalizability of models trained on specific datasets. Variability in sample collection, sequencing protocols, and population characteristics often leads to discrepancies in the statistical properties of datasets, hindering model transferability across cohorts.

This project aims to address this challenge by developing and applying transfer learning methodologies to align statistical distributions across datasets. The goal is to enhance the robustness and generalizability of predictive models in metagenomic analysis. The proposed methods will be validated using both in-house datasets and publicly available large-scale metagenomic data, focusing on the gut and oral microbiomes. This research will contribute to more reliable and scalable computational tools for microbiome-based diagnostics and therapeutics.