Formulaire de stage (sur une page maximum)

Parcours M2 GGBS 2019-2020

**Laboratoire:** LS2N – UMR 6004 **Équipe:** COMBI

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**Candidat pressenti:** -

**Titre du stage:** Inferring co-activity networks to model the nature of microbial symbioses in the human gut microbiome

**Résumé du projet proposé:**

Microbial communities inhabiting our intestinal tract impact and influence our nutrition, immunity and development. Today, High-Throughput Sequencing and functional genomics are revealing the under-explored diversity and complexity of these microbial ecosystems. Limited by the fact that most microbes can hardly be isolated and cultivated in lab-controlled environments, we are just starting to grasp the complexity and diversity of microbial interactions. Even when successful, laboratory experiments inherently lose valuable information about the richness and diversity of community functioning and interactions in situ. Today, large scale environmental surveys of microbial communities across Earth's ecosystems (e.g. Tara Oceans expeditions, Human Microbiome Project) gathered large volumes of meta-omic and contextual data that are enabling the reconstruction of genomes of uncultivated microbial species or Metagenome-Assembled Genomes (MAGs). While classical co-occurrence analyses enable to predict interactions between newly identified microbes, these approaches are inherently limited since true biotic interactions can hardly be disentangle from abiotic (environmental) effects. Here, we propose to develop a trait-based approach to enrich co-occurring information and uncover putative biotic interactions among human gut MAGs. Genomic and growth traits can directly be inferred from MAGs and meta-omics data. Here, co-growth signals across individuals will be used to reveal positive or negative interactions between co-occurring microbes. In addition, the functional content of MAGs and the reconstruction of their metabolism will be used to predict and model potential microorganisms’ dependencies. Inferring and combining (meta-)genomic traits in a global approach can help to identify consortia of microbes and pave the way towards the functional understanding and the metabolic modeling of their interactions.