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# Metagenomic data analysis and integration in a functional population model of fiber degradation by the human intestinal microbiota

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► **To cite this version:**

Béatrice Laroche. Metagenomic data analysis and integration in a functional population model of fiber degradation by the human intestinal microbiota. ECMTB14 - 9. European Conference on Mathematical and Theoretical Biology, Jun 2014, Göteborg, Sweden. 1 p. hal-02799054

**HAL Id: hal-02799054**

**<https://hal.inrae.fr/hal-02799054>**

Submitted on 5 Jun 2020

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Proposed Minisymposium Title:  
**Modeling Microbial ecosystem using Meta-Omic data**

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**Session Description:**

Technologies make it now possible to obtain a large number of data concerning microbial ecosystems, such as a set of genes (genomics), RNA (transcriptomics), proteins (proteomics), metabolites (metabolomics), etc. “Meta”-omic approaches are used to understand microbial communities as a whole. These communities can be composed of a small number of microorganisms or a huge crowd, depending on the type of ecosystem considered, but in all cases the complexity of these data is a challenge to achieving their integration, analysis and modelling.

This session therefore focuses on modelling and model-based applications in microbial ecology using various modelling techniques ranging from statistical to mechanistic models, with meta-omic data to support the modelling and model analysis research presented.

A secondary goal of the session is to provide a broad cross section of the area, rather than focusing on specific application areas, leading to fruitful comparison and discussions.

The proposed presentations illustrate the use of meta-genomic and meta-transcriptomic data for the modelling of

- Environmental Microbial Ecosystem and Microbial Bioprocesses
- Animal or human microbiome
- Food Microbial Ecosystem.

**Schedule:** 6x (25 min + 5 min for questions and discussion) = 3h min

**List of presentations:**

Dominant Species are Specialists. (Dr. Mahendra Mariadassou)

A survey of very heterogeneous microbiotes reveals that abundant species are more likely to be specialist than expected under a null model of neutral microbiote assembly. We first present the null model of microbiote assembly and then discuss some mechanisms that could lead to the specificity - abundance relationship.

Predicting microbial community assembly. (Pr. William Sloan)

The functioning of complex and diverse communities of microorganisms is critical in agriculture, engineering and medicine. Yet the coming together, or assembly, of these communities is poorly understood. When the microbial communities fail to function as we hoped they might it is often attributed to the 'wrong' community microbes having assembled. But we currently have no means of ensuring that the 'right' community assembles. Thus many economically important bio technologies are engineered by a process of trial and error. The ability to predict and hence manage the process of community assembly would thus have wide set applications. We use high resolution time series pyrosequenced amplicons from multiple bioreactors to show that a simple birth-death-immigration process can capture much of the variance in community assembly and that by controlling immigration the probability that key species form part of the community can potentially be controlled.

Energy and Rates of Evolution in Bacteria. (Pr. Thomas Curtis)

The talk will present data to suggest that the rates of evolution are shaped by energetic constraints. It will show how these concepts are very relevant to contemporary challenges in microbial ecology in general and Engineering Biology in particular, with a special nod to the challenges of the calibration of multi-scale models of microbial systems.

Metagenomics data analysis using a latent block model: application to plant-microbial communities interactions in the rhizosphere. (Dr Julie Aubert and Sophie Schbath)

Metagenomics is the study of microbial communities directly from environmental samples. We will propose a model and the tools of inference associated for a simultaneous clustering: the one on the populations of bacteria constituting the metagenome, and the other one on the samples. We will apply this model on the plant-microbial communities interactions in the rhizosphere.

Metagenomic data analysis and integration in a functional population model of fiber degradation by the human intestinal microbiota. (Dr Beatrice Laroche)

The human intestinal microbiota is a complex microbial ecosystem that plays a crucial role in several aspects of human health. It is particularly involved in the metabolism of residual fibers, through anaerobic digestion, thus providing significant energy (Short Chain Fatty Acids, simple sugars) and vitamins to the host. Whole Genome Sequencing (WGS) data from metagenomic analyses give an insight of the content in

terms of genes of an entire microbial community, even if the organisms that compose it cannot be cultivated. In addition to the potential of conventional molecular inventory techniques (such as targeting ADNr16s), which allows an analysis of diversity, WGS approaches provide an access to the functions.

We show how these data can be used to analyse the structure of carbohydrates degradation-related functions. We show how the information obtained can be integrated in a high level mechanistic in silico model of the microbiota carbohydrate trophic chain.

Study of the stability and functional redundancy of a food microbial ecosystem using physico-chemical and transcriptomics data. (Dr Julie Aubert)

The resilience is the capacity of an ecosystem to return to a steady or cyclic state following a perturbation. To study this phenomenon, we have developed an RNA-seq based approach on a model cheese reduced ecosystem composed of nine species. We propose a method to integrate, analyse and link diverse data in order to understand the microbial ecosystem resilience.