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FoodMicrobiome Transfert : Web based Metagenomic Analysis

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A large number of micro-organisms are involved in the composition of cheeses[1] : bacteria, yeasts, filamentous fungi, phages. These micro-organisms come from starters used by manufacturers, but also from the environment (milk, maturing cellars, salt). In order to achieve a better understanding of these flora, metagenomic approaches can be used[2]. The FoodMicrobiomes Transfer project brings together industry and academia for the purpose of providing a tool to ease the analysis of metagenomic sequencing data, especially cheese flora samples, via a web interface.

Cheese flora has long been studied, which ensure the availability of several hundred of reference genomes. The partners concerned by the project wish to identify organisms present in the ecosystem with a precise taxonomic assignation, down to the strain level (different strains may have different properties) and also identify micro-organisms present in low abundance. To answer these questions, we chose a shotgun metagenomic sequencing approach, coupled with a tool that aligns the metagenomic reads on the reference genomes. This tool can be used via a web interface, coupled with a database of around 4000 genomes from dairy exosystems and metagenomes. This tool also identifies, for each reference genome, which genes are present into the ecosystem.

The FoodMicrobiome web interface (http ://migale.jouy.inra.fr/foodMicrobiome/) allows users to perform analyses on their own metagenomes on reference sequences (public or not). In order to guide the analyzes, predefined lists of genomes are available. Users can also create their own lists of interest for their own analyzes, or share them with other users.

The FoodMicrobiome application is based on a PostgreSQL relational database. This database allows the management of genomes, genome lists, metagenomes and analytical results. Computations are performed transparently for the user on the Migale platform's calculation cluster via the Bioblend API and the Galaxy portal. The web interface is developed via the Python Django framework as well as web technologies such as HTML and JavaScript.

The FoodMicrobiome application was designed and developed to study cheese ecosystems. It can be adapted to other ecosystems for which we have sequenced genomes, for example food ecosystems. It will be available on the migale plateforme.

1. Marie-Christine Montel, Solange Buchin, Adrien Mallet et al. "Traditional cheeses : Rich and diverse microbiota with associated benefits". In :International Journal of Food Microbiology 177 (2014) pp.136–154

2. Bhagya. R. Yeluri Jonnala, Paul L. H. McSweeney et al. "Sequencing of the Cheese Microbiome and Its Relevance to Industry". In :frontiers in Microbiology, doi : 10.3389/fmicb.2018.01020