

# FoodMicrobiome Transfert

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Quantity of bacteria, fungi and yeast have a role in cheese production processes. They can straight coming from a seeding operation, from elements of the production line or from a farest environment. The FoodMicrobiome-Transfert project is based on the recent metagenomcis shotgun sequencing methodes and is aim is to characterized the cheeses ecosystems. As part of the project, we are developing a tool to facilitate the metagenomics analysis. This tool is especially composed by a data mapping analysis software and by a database.

The database, curently in development, will store (i) some genomics data about microorganisms used in food purposes whom be used for the metagenomics data analysis, (ii) data about the ecology of food microorganisms groups taxonomicaly close and (iii) the metagenomics analysis results. This results will be visualized using a graphical interface allowing to retrieve them in downloadable files and to create illustrating charts. The user will have an access to the information about the species and subspecies present in is studied ecosystem. He also will have access to accurate informations on the genes of this ecosytem, their function and their technological interest. By giving specific metadata about the cheese environment, the user will have the possibility of comparing metagenomes on cheese process characteristics or geographical area.

The developped tool is based on GeDi, a software developped in the team. He will be used on the cluster Migale. GeDi will interact with the database countaining the reference genomes and whom will store the analysis result just as well as the metagenomes metadata. A web graphical user interface based on the Django framework and a Galaxy integrated interface will be developped. Both will allow to access to the users data and to perform reproducible analysis.