# A metagenomic tool for cheese ecosystems

**Anne-Laure Abraham[1], Quentin Cavaillé[1], Thibaut Guirimand[2], Sandra Derozier[1], Charlie Pauvert[2],Mahendra Mariadassou[1], Bedis Dridi[2], Valentin Loux[1], Pierre Renault[2]**

[1]INRA, UR1404 MaIAGE - Domaine de Vilvert 78350 Jouy en Josas Cedex, France

[2]INRA, UMR1319 MICALIS - Domaine de Vilvert 78350 Jouy en Josas Cedex, France

anne-laure.abraham@inra.fr

A large number of micro-organisms are involved in the composition of cheeses: bacteria, yeasts, filamentous fungi, phages. These micro-organisms come from starters used by manufacturers, but also from the environment (milk, maturing cellars, salt). The exact composition of most cheeses is not completely known. A better understanding of cheese ecosystems would give insight into micro-organisms involved, their functions during cheese manufacturing, strain diversity and evolution, and would help manufacturer to maintain a constant quality of the cheese products. The FoodMicrobiomes Transfer project brings together industry and academia for the purpose of providing a tool to ease the analysis of metagenomic sequencing data of cheese samples, via a web interface. This tool should give a precise taxonomical assignation of present micro-organisms, detect species present in low abundance, and give informations about genes present in the ecosystem.

Cheese flora has long been studied, which ensure the availability of several hundred of reference genomes. We developped a method based on the mapping of metagenomics reads on reference genomes. It gives informations on present strains based on the genome coverage and mismatches between metagenomic reads and reference genomes. It also provides the list of CDS that are present (coverage and mismatches) as well as their annotations. This tool is based on a specific database of about 4000 reference genomes isolated from dairy products and can be used via a web interface. Computations are performed transparently for the user on the Migale platform's calculation cluster. This tool is still in development and will be improved. It will soon be used in the project '1350 cheeses', in order to caracterize strains of 44 French AOP cheeses.