

Abstract

It was my great pleasure and honor to be invited at INRA, Centre de Clermont Ferrand/Theix, Unite de Nutrition Humaine, to conduct the STSM “Bioinformatic analysis of nutrigenomics data of plant food bioactives extracted from in-vitro and in-vivo studies”. This STSM was related to the upcoming activities of the WG2 of the COST Action POSITIVE, more specifically to the subgroup Cell and Molecular Targets.

During my stay at INRA, I conducted a pilot bioinformatics analysis of nutrigenomic data of plant food bioactives. For in-vitro studies, extracted data were grouped according to the cell type and bioactives used for treatment. Some of the gene symbols were transformed to official gene symbols using the database GeneCards. Differentially expressed genes were analyzed using the software GeneTrail2. Pathways which were significantly associated with these genes ($p < 0.05$) were identified in BioCarta and KEGG databases. Common genes and pathways for different cell types were identified with the software Venny 2.1.0.

During this STSM I tested various approaches for data analysis. In consultation with my host, Dr. Dragan Milenkovic, we were able to identify the workflow and critical points to be addressed in the upcoming analysis of extracted data from in-vitro and in-vivo studies.