

# 3<sup>rd</sup> International Conference and Exhibition on **Nutrition & Food Sciences**

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## Statistical analysis for the gut microbiome-diet association: An overview

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In this talk we present several statistical approaches applied until now in the study of the gut microbiome-diet association and deploy them to analyze the PopGen cohort (see (1)). Taxa abundances and phylogenetic tree deduced out of the microbial metagenomics data are used to characterize the microbiome diversity, while nutritional data consists of the habitual dietary intake. High-dimensionality, sparsity, heterogeneity and dependency of the data enforces the use of the regularization methods to identify taxon-diet intake associations (see (2)). On the other hand, food pattern-gut microbial enterotype relationship could be identified with the help of ordination and classification methods (see (3), (4)). Finally, these statistical methods serve to detect microbiome-food intake connections after taking in consideration different lifestyle and demographics data from the PopGen cohort.

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