**Introduction**

The desire to understand the factors that influence human health and cause diseases has always been one of the major driving forces of biological research. Modern high-throughput sequencing and bioinformatics tools provide a powerful means of understanding how the human microbiome contributes to health and its potential as a target for therapeutic interventions. High throughput methods for microbial 16S ribosomal RNA gene and WGS have now begun to reveal the composition of archaeal, bacterial, fungal and viral communities located both, in and on the human body. Biology has recently acquired new technological and conceptual tools to investigate, model and understand living organisms at the system level, thanks to the spectacular progress in quantitative techniques, large-scale measurement methods and the integration of experimental and computational approaches. Systems Biology has mostly been devoted to the study of well-characterized model organisms but, since the early days of the Human Genome Project it has become clear that applications of system-wide approaches to Human Biology would bring huge opportunities in Medicine.

We have seen that the relative changes over time of the microbial composition follows a Taylor’s law, which relates the variance with the mean of the population. This law is ubiquitous in the natural world, and can be found in several systems as cosmic rays [ref1], stock markets [ref2,3], animal populations [ref4, 5, 6], gene expression [ref7], or in the human genome [ref8].

Here we present the imprints of disease in macroscopic properties of the system, by studying the temporal variability in the microbiome. []

We have analyzed more than 35000 time series of taxa from the gut microbiome of 97 individuals (sampling from three up to 332 time points), obtained from publicly available high throughput sequencing data on different conditions: diseases, diets, obese status, antibiotic perturbation and healthy individuals. We engineered a complete software framework, ComplexCruncher, to support the analysis of the dynamics of ranking processes in complex systems, and it is ready to be implemented by other users. [mejorar]

**New References**

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