

Integrating ecological analysis into massive sequencing studies

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Researchers at the joint CSIC-University of Valencia Institute for Integrative Systems Biology, Cristina Vilanova and Manuel Porcar, have proposed a change in the way massive sequencing studies into the microbial composition of biological samples are carried out. Their article, published in *Nature Microbiology*, posits that the data should be crossed with innovative culture criteria and interpreted from the ecological viewpoint.

It is the first time that such a holistic approach has been proposed for microbiome studies, which analyse the microbial composition of an ecosystem (earth, water, faeces, etc.) using DNA sequencing on the kind of [massive scale](#) permitted by technology today. Indeed, sequencing techniques are currently so powerful that they provide more information than research teams are able to analyse.

"More and more data is being stored in databases that are just not being interpreted", Vilanova tells us, in the article stating that "the challenge is to reduce complexity to improve understanding". The idea behind their approach, then, is to make sense of the masses of data recorded in a way that goes beyond having infinite lists of species present in a given sample, extracting relevant conclusions of ecological interest.

It is known, for instance, that microorganisms do not live in isolation. The application of ecological parameters to the data makes it possible to detect and study these natural associations or microbial consortia. By doing so, these microbiome studies become much more useful for

environmental studies and even studies related to human health.

More information: Cristina Vilanova et al. Are multi-omics enough?, *Nature Microbiology* (2016). [DOI: 10.1038/nmicrobiol.2016.101](https://doi.org/10.1038/nmicrobiol.2016.101)

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