

## Introducing Meta<sup>2</sup>genomics: the search for the “micro-bee”

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We will describe what may be called *meta-metagenomics* (or *Meta<sup>2</sup>genomics*), a novel approach to mine metagenomic data and how we apply it to search for microbial sentinels of contamination, the microbial equivalent of bees (or “micro-bee”).

One of the main challenges of Next Generation Sequencing (NGS) is its pervasive use for afterthought research: mining of existing experiments developed with a specific aim for the pursuit of novel, unrelated quests that were not foreseen in advance.

The last years have seen a tremendous increase in the availability of metagenomic data collected from soil samples under a variety of soil textures, locations, circumstances and treatments. All these experiments were carried out with specific aims in mind: understand the variability of the rhizobacterial community under specific environmental conditions.

In parallel with these advances, and partly thanks to some of these studies, society has become increasingly aware of the impact that human activities have on the environment, and is trying to adapt policies and operation procedures to better exploit this newly acquired knowledge. As an example, studies of the impact of herbicide treatments on soil rhizobacteria has been one of the factors considered in the ap-

proval or renewal (or its deny thereof) of the use of herbicidal preparations in the EU and elsewhere.

An orthornormal approach is used in the biological security field. Here, the problem is not knowing and preventing the effect of specific substances, but preventing and detecting the release of biological or toxic agents, and reacting accordingly to minimize their impact on humans and the environment at large. We are interested in the development of cost-effective advisory policies that may help professionals in the detection of potentially harmful spills, specially in developing countries.

Here we describe our quest for a sensitive test that may help detect contamination changes in the soil through the identification of the “micro-bee”, a soil microorganism taxon that may act as a sentinel, developing in the process what can be called *meta-metagenomics* (or *Meta<sup>2</sup>genomics*): mining many unrelated metagenomics experiments to identify a common trend of interest. In effect, this requires to select multiple soil metagenomics experiments from the Sequence Read Archive, re-analyse each of them towards our ends, and compare them for common trends that meet our end criteria, developing new planning, analysis, comparison and statistical technologies in the process.