

# Bioinformatics Applied to Microbiota-based Science

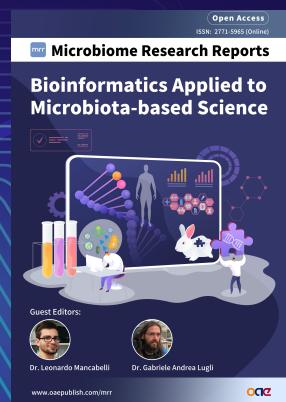
## Guest Editors:



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## Special Issue Introduction:

During the past two decades, the evolution of DNA sequencing technologies has allowed the gathering of a vast amount of metagenomic data, laying the foundation to study complex microbial communities, also called microbiomes. At the dawn of the metagenomic classification era, DNA sequences were mainly used to unveil the composition of the bacterial communities inhabiting specific environments through analysis based on the amplification of microbial marker genes. Recently, the more informative shotgun metagenomics approach allowed the reconstruction of the functional contribution of the bacteria harbored in the biological samples without the necessity to compromise data during sample preparation. To date, the interest of the scientific community is rapidly moving to a complete overview of the microbiomes, involving multiple bioinformatic pipelines aiming at understanding complex dynamics between members of the same environmental niche and their host.

This special issue aims to gather projects that rely on bioinformatics strategies to investigate bacteria, archaea, protists, and fungi in the frame of microbiome research, highlighting applications in the field of the human microbiome as well as more unexplored microbiomes, such as non-human animals.

We welcome original or review manuscripts, perspectives, opinions, and commentary on different aspects of this special issue, including but not limited to:

### Microbiota investigation by using bioinformatic approaches:

- Microbial profiling of human and animal, microbiomes.
- Genome reconstruction of microorganisms from complex environments.
- DNA enrichment studies of microbiomes.
- Investigation of the microbial dark matter among microbiomes.
- Functional profiling of host-related microbiomes.
- Host-microbiome and microbiome-microbiome relationships.

### Bioinformatic pipelines and microbiomes:

- Development of bioinformatic pipeline in the field.
- Comparisons between bioinformatic pipeline.
- Innovative approaches to microbiome data management.

### Keywords or key topics of the SI:

Bioinformatics, metagenomic data, DNA sequences, Genome reconstruction, microbiomes, host-related microbiomes

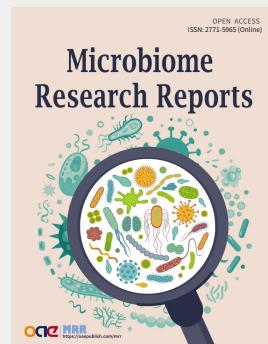
**Submission Deadline: March 31, 2023**

## Benefits to Authors:

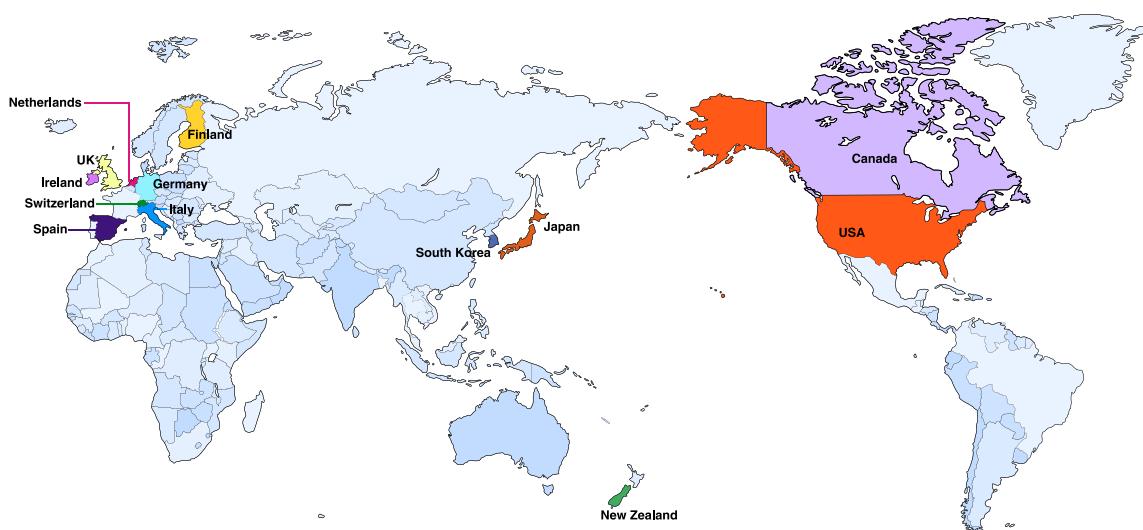
- The APCs (\$600) will be WAIVED;
- Enjoy faster publication than regular submissions;
- Authors will be invited as Guest Speakers to our journal webinars. The webinar will be held via Zoom and it will also be broadcast live on YouTube and the Chinese WeChat Official Account, Video Account, Bilibili;
- A special interview will be provided to authors and will be promoted on the journal homepage and all media promotion platforms of both via the journal and publisher.

## Journal Introduction:

*Microbiome Research Reports (MRR)* is an international peer-reviewed, open access journal. The overall aim of MRR is to publish high quality researches from scientists with a common interest in microbiome/microbiota research in all its multidisciplinary aspects. The journal is founded by OAE Publishing Inc., under the guidance of our Editor-in-Chief Professor Marco Ventura (University of Parma, Italy). MRR was officially launched on July 26 2021. Looking forward to your attention and cooperation! Welcome to contact the editorial office for details, [editorialoffice@mrrjournal.net](mailto:editorialoffice@mrrjournal.net).



## Editorial Board team:



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