



Strategies of analysis of metagenomic and metatranscriptomic data

October 14 and 15



Congress participants : \$ 50

No members: \$ 100

With the development of technologies, the ability to obtain data has increased significantly over the past 10 years. The structure and functioning of living beings can be characterized with high precision and increasingly low cost, by using platforms that can generate large amounts of data for genes, proteins and metabolites.

This course aims to cover the most important strategies of massive data analysis for studies of metagenomics and metatranscriptómica. actual data from model systems which can then be extrapolated to other studies will be used.

INSTRUCTOR



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Sunny is a postdoctoral fellow in the area of Metatranscriptomics at Duke University. Her researches are highlighted by the use of bioinformatic tools in genetic studies of mycorrhizae.

