

A Laboratory Information Management System (L.I.M.S.) to support microbiome analyses

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Background:

Next Generation Sequencing represents a breakthrough in microbiome research, enabling massive genome sequencing. Thus, the management of the huge amount of generated data is a challenge for omics studies. In our case-study, a metagenomic workflow has been managed through a LIMS system, developed by Eusoft Srl (1) with CNR-IBIOM Institute.

Methods and Results:

The entire metagenomic's workflow, from sample collection to data analysis, has been integrated in LIMS using a suite of integrated modules in order to define and control the analytical tests involved, according to user needs and Good Laboratory Practices requirements (2). Moreover, in LIMS data can be processed using PowerBI, a Business Intelligence functionality, to visualize dashboards and to get information about the project. Bioinformatic analyses are managed by exploiting the cluster orchestrator Mesos (3), instantiated in a cloud environment, provided by the INFN Institute, and connected to the LIMS through a RESTAPI.

Conclusions and Significance:

A LIMS represents a valid and innovative instrument to assure the highest levels of reliability, reproducibility and traceability of data in NGS laboratories. In addition, the data elaboration functionality using power BI and business intelligence technology may support the researcher in a successful, accurate and reliable data results interpretation.

Keywords:

Next Generation Sequencing; metagenomics; LIMS; bioinformatics; GLP.

References:

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Thematic Area:

Frontiers in Microbiome Research

Infrastructures:

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