

Contratto di Filiera Stalla Modello

WP2 – OF 2.2 Computing and data analysis cluster
implemented and operational to meet the project's needs

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OF2.2 Description

A computing infrastructure dedicated to the data analysis and bioinformatics activities planned within the Stalla Modello project has been implemented and made operational. The computing cluster was designed to support the processing of data generated by genomic sequencing platforms, enabling the execution of the pipelines required for the analysis of biological samples, milk, and environmental matrices. The infrastructure allows the efficient management of workflows associated with whole-genome sequencing, shotgun metagenomics, and 16S metataxonomic analyses.

The system is based on high-performance servers equipped with multi-core AMD EPYC 9224 processors, providing a total of 96 logical CPUs and 377 GB of RAM. This configuration enables the simultaneous execution of multiple bioinformatics pipelines and the parallel analysis of large volumes of data, significantly reducing processing times compared with conventional systems. The availability of substantial computational resources also supports complex activities such as sequence quality control, genome assembly, taxonomic classification, microbiome analysis, genomic variant identification, and the interpretation of biological data generated through NGS analyses.

The computing infrastructure is closely integrated with the project's centralised storage system, enabling direct access to datasets and efficient management of analysis processes. The implemented configuration ensures high operational reliability and continuity of processing activities, even under heavy computational workloads. The cluster also supports the execution of open-source and customised bioinformatics software and pipelines used to analyse the genomic and metagenomic data generated within the project.

The infrastructure therefore represents a strategic asset for achieving the scientific objectives of the VeLaSeq project, providing a stable, scalable computing environment suited to the requirements of genomic research applied to the dairy sector. The availability of dedicated computational resources increases the laboratory's analytical capacity and supports the development of new methods for analysing biological and microbiological data.

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