

High Performance Bioinformatics - Agenda

December 3-5 / 2025 - CINECA – Online course

Course coordinator: Silvia Gioiosa

Teachers: Silvia Gioiosa, Alessandro Grottesi, Xhulio Dhorì, Bala Chandramouli

3 dicembre

09:45 - 10:00	Welcome & technical check
10:00 - 10:45	Course overview: Big data challenges through HPC (Gioiosa)
10:45 - 11:15	Introduction to CINECA Supercomputing Hardware Architectures and UNIX Environment (Grottesi)
11:15 - 11:30	Coffee Break
11:30 - 12:15	Hands-on I: UNIX basics (terminal, filesystem, working envs) (Grottesi/tutors)
12:15 - 13:00	Introduction to the production environment (Grottesi)
13:00 - 14:15	Lunch Break
14:15 - 15:00	Introduction to SLURM scheduler (Grottesi)
15:00 - 16:30	Hands-on session II: Build your first SLURM scripts for RNA-seq (Gioiosa/tutors)
16:30 - 16:45	Q&A + recap & next steps

4 dicembre

10:00 - 10:30	Introduction to High Throughput Sequencing technology (Gioiosa)
10:30 - 11:15	Hands-on session I: Job concatenation with SLURM dependencies (Gioiosa)
11:15 - 11:30	Coffee Break
11:30 - 12:00	Hands-on session II: working over multiple samples (Gioiosa)
12:00 - 13:00	DGE Analysis on HPC: Remote Coding with VSCode and Jupyter. (Dhorì)
13:00 - 14:15	Lunch
14:15 - 15:15	Containers on HPC and GPU support (Dhorì)
15:15 - 16:15	Mastering High-Speed Genomics: Parabricks Use Cases on the OMICS Analysis Platform (Dhorì/tutors)
16:30 - 16:45	Q&A + recap & next steps

5 dicembre

10:00 – 11:00	Introduction to Snakemake workflow management system (Bala)
11:00 - 12:30	Hands-on session I: Snakemake (Bala/tutors)
12:30 - 13:45	Lunch break
13:45 - 15:15	Hands-on session II: Snakemake (Bala/tutors)
15:15 - 16:00	Snakemake with SLURM (Bala/tutors)
16:00 – 16:30	Closing Session: Summary & Open Discussion