High Performance Bioinformatics - Agenda

December 4-6 / 2024 - CINECA

Teachers

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4 December

09:30 - 10:00	Registration
10:00 - 10:50	Course overview: Big data challenges through HPC (Gioiosa)
10:50 - 11:15	Introduction to Cineca Supercomputing Hardware Architectures and UNIX Environment (Grottesi)
11:15 - 11:30	Coffee Break
11:30 - 12:15	Hand-on session I: UNIX environment (Grottesi/tutors)
12:15 - 13:00	Introduction to the production environment (Gioiosa)
13:00 - 14:30	Lunch Break
14:30 – 15:15	Introduction to SLURM scheduler (Grottesi)
15:15 - 16:30	Hands-on session II: build your first pipeline for analyzing transcriptomics data (Gioiosa/tutors)
16:30 - 17:00	Open questions

5 December

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 - 12:30	Hands-on session II: working over multiple samples (Gioiosa)
12:30 – 13:00	Gene expression post processing (Mata)
13:00 - 14:30	Lunch
14:30 - 15:30	Containers on HPC (Dhori)
15:30 - 16:30	Parabricks use case in pangenomics (Dhori)

6 December

09:30 – 10:45	Introduction to Snakemake workflow management system (Bala)
10:45 - 11:30	Hands-on session I: Snakemake on cloud machines (Bala/tutors)
11:30 - 11:45	Coffee break
11:45 - 13:00	Hands-on session II: Snakemake on cloud machines (Bala/tutors)
13:00 - 14:30	Lunch
14:30 - 15:30	Snakemake on cluster machines (Mata)
15:30 - 16:30	Hands-on session III: Snakemake on cluster machines (Mata/tutors)
16:30 – 17:00	Concluding remarks