High Performance Bioinformatics - Agenda

December 5-7 / 2022 - CINECA - online course

Teachers
Silvia Gioiosa
Alessandro Grottesi
Bala Chandramouli
Juan Mata Naranjo

5 December

10:00 - 10:20	Registration
10:20-10:50	Introduction: 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 (Gioiosa-Grottesi-Naranjo)
12:15 - 13:00	Introduction to the production environment (Gioiosa)
13:00 - 14:00	Lunch Break
14:00 - 14:45	Introduction to SLURM scheduler (Grottesi)
14:45 - 16:15	Hands-on session II: build your first pipeline for analyzing transcriptomics data (Gioiosa - Grottesi)
16:15 - 16:30	Open questions

6 December

10:00 - 10:45	Introduction to High Throughput Sequencing technology (Gioiosa)
10:45 - 11:30	Hands-on session I: Job concatenation with SLURM dependencies (Gioiosa)
11:30 - 11:45	Coffee Break
11:45 - 12:45	Hands-on session II: working over multiple samples (Gioiosa)
12:45 - 14:00	Lunch
14:00 - 15:00	Gene expression post processing (Bala - Gioiosa)
15:00 - 16:15	Introduction to snakemake Workflow management system pt. I (Bala)
16:15 - 16:30	Open questions

7 December

10:00 - 11:00	Introduction to snakemake Workflow management system pt. II (Bala)
11:00 - 11:15	Coffee break
11:15 - 13:00	Hands-on session I: Snakemake on cloud machines (Bala - Mata)
13:00 - 14:00	Lunch
14:00 - 15:00	Snakemake on cluster machines (Mata)
15:00 - 17:00	Hands-on session II: Snakemake on cluster machines (Mata - Bala)