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Recommendations for Running Bioinformatics Applications on CHPC

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Running large-scale bioinformatics analyses on high-performance computing (HPC) infrastructure like the CHPC can significantly accelerate research, but comes with technical challenges—especially for researchers aiming to deploy complex workflows such as those built with Nextflow. In this talk, I present practical recommendations and lessons learned from testing and running various bioinformatics applications on the CHPC, with a particular focus on containerised workflows and resource optimisation.

Drawing from real-world use cases and performance benchmarks, I highlight key considerations such as managing limited walltime, dealing with module and environment setup, optimising Singularity containers for reproducibility, and handling input/output bottlenecks. I also reflect on common pitfalls and how to overcome them—especially for researchers with limited systems administration experience.

This presentation aims to equip bioinformatics users with actionable guidance on how to run workflows more efficiently, reproducibly, and with fewer frustrations on the CHPC infrastructure. It is also a call for continued collaboration between HPC support teams and domain researchers to bridge the gap between computational capacity and research usability.

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Registered for the conference?

Yes

CHPC User

Yes

CHPC Research Programme

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