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Computation and the future of biological research

Wednesday, 6 December 2017 13:30 (30 minutes)

Classic biological research where individual molecules or organisms are studied in isolation, is rapidly being complemented by high-throughput highly-parallel research approaches. The implications are profound for established researchers, but even more so for new post-graduate students entering nearly all fields of biology.

This is particularly true for the high impact that massive scale genomic studies are having on work in organisms ranging from viruses and bacteria, up to mammals and humans. Highlights of bioinformatics-related work performed at the CHPC will be shown, including the Forest Molecular Biology programme, the Tree Pathology Co-operative programme, the Maize Fungal Pathogen programme, the HIV Computational Immunology programme, the Malaria Transcriptomics programme and the Cancer Genomics programme.

This will be combined with some speculation around the future needs of all biological researcher to be able to operate in a computational and particularly a high-performance computational environment.

HPC content

Not included

Primary author: Prof. JOUBERT, Fourie (University of Pretoria)

Presenter: Prof. JOUBERT, Fourie (University of Pretoria)

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