

CCR – Impromptu Seminar

Monday, February 19th 2024, 09:30

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Oncology Data Science

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Computational Tools for Inferring Genetic Parameters from Noisy Sequencing Data

Involvement in diverse interdisciplinary projects can be significantly streamlined through the implementation of autonomous Snakemake bioinformatic pipelines. These pipelines serve as robust frameworks, integrating the processing of raw genomic data with more complex downstream population genetic analyses. Nonetheless, challenges arise from sequencing data, including noise resulting from contamination and low sequencing depth. Thus, the development of novel statistical models and the implementation of intuitive software tools become crucial. One way is to effectively account for genotype uncertainty in noisy data, which then enables accurate deciphering of population genetic patterns such as heterozygosity and helps reveal evolutionary processes like introgression. By using these tools, researchers can explore not only human populations but also non-model organisms and even ancient DNA, thereby enhancing our understanding of evolutionary history across a diverse spectrum of species and into the complex mechanisms shaping biodiversity and genetic variation.

Venue: CCR Lecture Hall

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Host: Thomas Vogl