Contribution ID: **21** Type: **not specified**

A framework for Large NGS data analysis: Metagenomics

Wednesday, 23 November 2016 11:20 (20 minutes)

Next-Generation Sequencing (NGS) provides a lot of platforms to sequence DNA and samples at a cheaper and faster rate. Genomic research is benefiting from this, thus making various analysis and interpretations possible. Despite the benefits of NGS, large data handling is a challenge in the area of whole genome/exome sequencing. The analysis of this large data is complex and requires high performance computing (HPC) to remote users. Here, were describe a framework that uses HPC to address large NGS data processing, incomplete data (no sample metadata information) and reduce the task complexity. We use technologies from Sci-GaIA Open Science Platform to make this analysis available for remote users. This framework proposes to ease research in metagenomics and microbial diversity analysis.

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Session Classification: Presentation of use cases and their implementation stategies continued