**CCDI Jamboree Abstract**

**VCF Table Viewer: Flexible Visualization of Variants Called from the Nextflow Sarek Pipeline**

Michael Sierk, CGBB/CBIIT/NCI

Variant calling pipelines produce variant caller format (VCF) files. VCF files have large amounts of information about called variants, especially if they are annotated by tools such as VEP, but are difficult to read and interpret directly, particularly for non-computational biologists. Thus, there are many tools available to extract information from VCF files for visualization and analysis. We present here a new Shiny app, VCF Table Viewer, that extracts information from annotated VCF files produced by the sarek variant calling pipeline from Nextflow Core and displays them in an interactive table. The table provides the ability to flexibly sort through a list of called variants while visualizing desired annotations, including color highlighting of various annotations. It also allows easy visualization of the bam file pileups in an embedded IGV tab for variants selected in the table, as well as plots of somatic allele frequencies from mutect2 calls over multiple samples. VCF Table Viewer provides a novel interface that facilitates the examination of variant calls by non-computational biologists. We provide examples from an ongoing clinical study of patients with familial platelet disorder. The code is freely available on Github. We propose integrating this app into the Cancer Genomics Cloud with easy selection of CCDI datasets for visualization, as well as making it easy to add on to the end of a variant calling pipeline. If there is enough interest we can add visualization features to the app. We do not have a pre-assembled team to work on this project.