

## Seamless Genomics Pipeline via Open OnDemand Computing

### Genomics

**Ayush Chaturvedi** (ayushchatur@vt.edu), Virginia Polytechnic Institute and State University (Virginia Tech), **Robert Settlege**, Virginia Polytechnic Institute and State University (Virginia Tech)

HPC centers across the globe still provide a command line interface (CLI) due to many reasons, which converts to an open issue of accessibility for a major proportion of researchers and scientists that originate from a non computer science background. Open OnDemand is one panacea to HPC users and administrators, is an innovative, open-source, secure, web-based portal for accessing HPC services that removes many pre-requisites of computer sciences and intricacies of similar tools such as SSH, FTP and batch job submission by providing more familiar browser based access to the HPC clusters. Through OnDemand, HPC users can benefit from custom workflow creation and seamless integration of multiple dissociated and/or interdependent tasks in a genomics application. In this Flash Talk we will present how scientists and researchers from non computer engineering background can reduce the iterative and “technical” steps involved in processing data and setting up of workflow in a genomics via use of Open-OnDemand’s facilitation of custom interactive apps. Also benefiting from the open source licensing these apps can then be shared and deployed on any instance of Open OnDemand with 0 prerequisite and installation steps. The talk will also present a demo for one such genomics processing workflow and showcase how easy it is for any scientist/research with no experience in computer engineering to benefit from such OOD (open ondemand) apps which are open source, idempotent and mitigate the need of computer engineering prerequisites of bash scripting, tarballing, cross cluster copy and archiving.