

Analysis pipeline code
TOPMed data
Analysts work directories

TOPMed NFS
Volume

User specified
analysis

Analysis Pipeline

- get cluster config
- read analysis config
- process each job in analysis

- get task options
- get mem spec
- get thread spec
- find slurm partition
- create sbatch script args
- submit job (sbatch)

slurm head node
(e.g., g2-login)

docker container

analysis_pipeline / R
Code
(e.g., assoc_single.R)

runRscript.sh

runDocker.py

sbatch_python.sh

slurm partition/compute node

slurm
controller

