

Motivation

- ❖ Advancement in affordable sequencing technology coupled with easy accessibility to huge computational resources → generate and analyse hundreds of WGS in relatively short time
- ❖ Challenges of population genomics analyses → plethora of tools and its dependencies, series of data transformation in a particular order
- ❖ Potential solution → usage of container-based technologies such as conda, singularity and docker with workflow management system such as Nextflow, Snakemake

