

Scalepopgen: bioinformatics workflow

resources for population genomics

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Motivation

- Advancement in affordable sequencing technology coupled with easy accessibility to huge computational resources \rightarrow generate and analyse hundreds of WGS in relatively short time **
- Challenges of population genomics analyses \rightarrow 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 **





cattle samples.

PCA plot produced by the workflow

Q-matrix plot produced by the workflow



Github project page

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