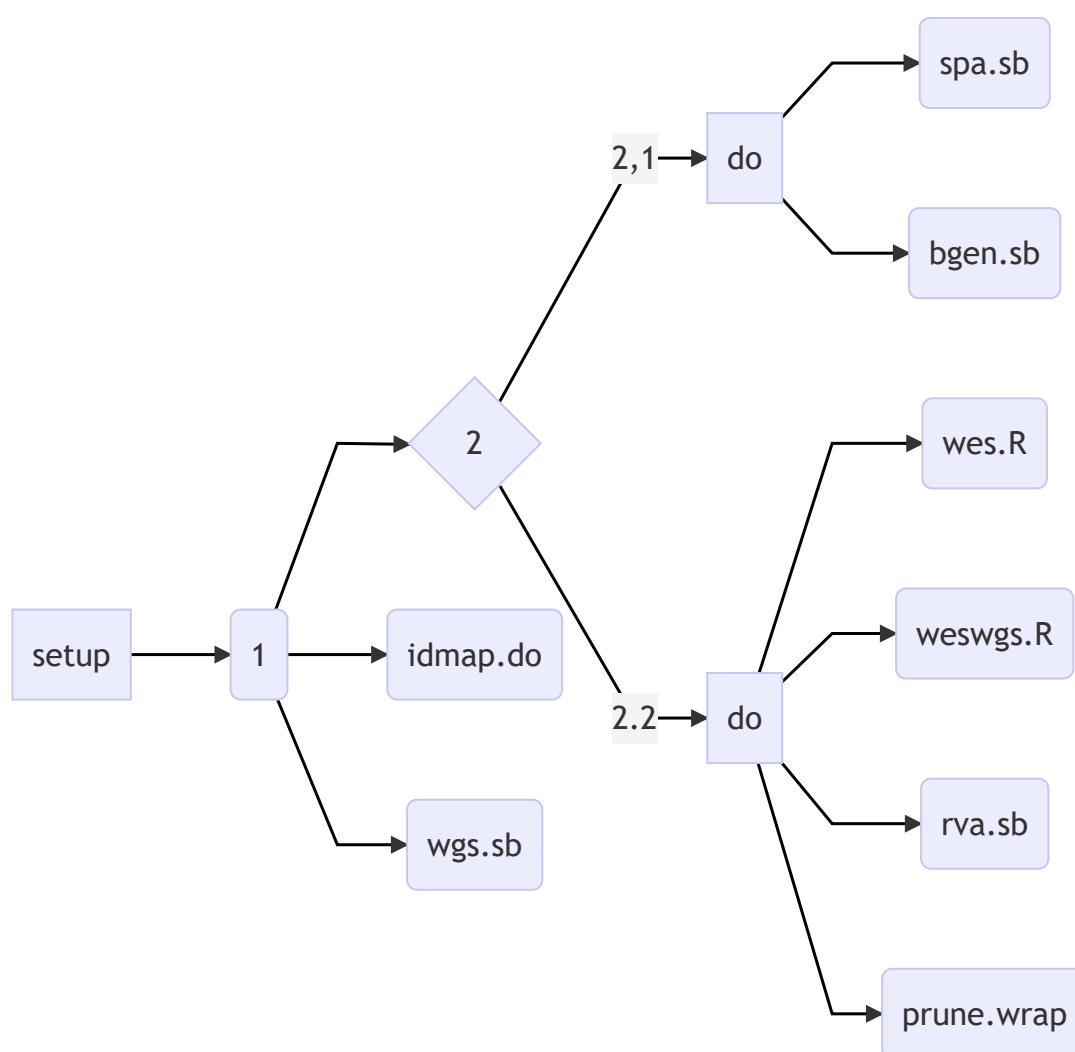


Programs

Sequence	Filename	Description
1	weswgs.sh	WES/WGS preprocessing
2.1	rva.sh	Rare-variant analysis
2.2	spa.sh	Single-point analysis

idmap.do, ngs.wrap, weswgs.R, prune.wrap, rva.sb, spa.sb are subprograms; and remarks on variant lists submitted centrally are described in INTERVAL.md.

The natural order is therefore (see also [README.pdf](#) or <https://jinghuazhao.github.io/SCALLOP-Seq/>)



noting in particular that sbatch implicates the --wait option as the succeeding steps would require its full results.

Contacts

- Grace Png: grace.png@helmholtz-muenchen.de
- Arthur Gilly: arthur.gilly@helmholtz-muenchen.de

Slack channel

- <https://scallop-seq.slack.com>

URLs

- https://github.com/hmgu-itg/burden_testing
- <https://sites.google.com/site/jpopgen/dbNSFP>
- <https://sites.google.com/site/jpopgen/wgsa>
- http://web.corral.tacc.utexas.edu/WGSAdownload/resources/precomputed_hg38/
- http://www.columbia.edu/~ii2135/Eigen_functions_112015.R