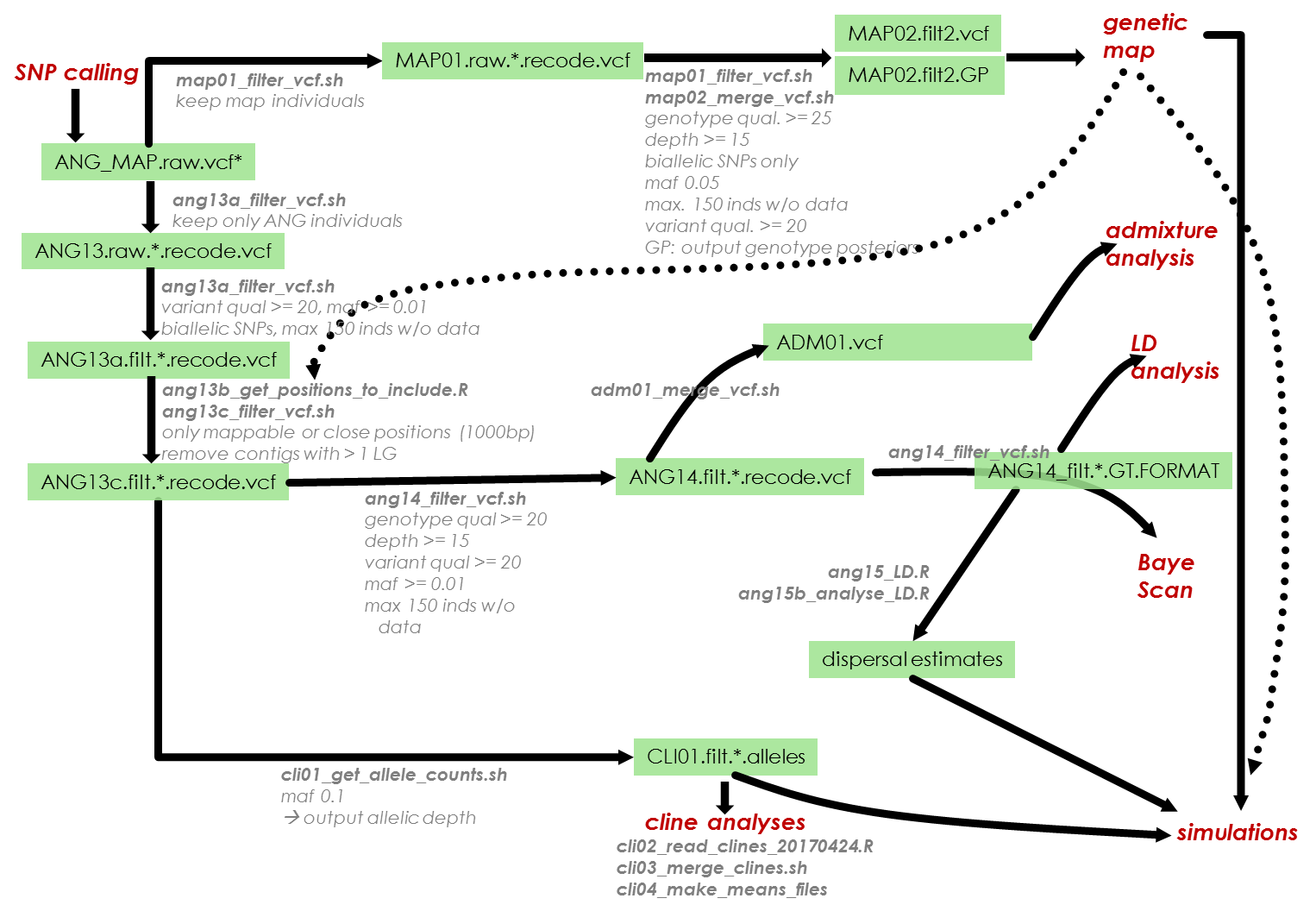
This repository contains scripts used to analyse capture sequencing data from a single Swedish *Littorina saxatilis* hybrid zone (Anglavebukten / “ANG”), and a family resulting from a lab cross of Crab ecotype individuals (“MAP”).

Bioinformatic steps performed on all sequencing data files (ANG and MAP):

|  |  |
| --- | --- |
| ang05\_trim\_PE.sh |  |
| ang05\_trim\_SE.sh |  |
| ang06\_map\_paired\_reads.sh |  |
| ang06\_map\_single\_reads.sh |  |
| ang06\_map\_unpaired\_reads.sh |  |
| ang06a\_index\_ref.sh |  |
| ang07\_get\_contigs1.sh |  |
| ang07\_get\_contigs2.sh |  |
| ang07\_make\_bed.sh |  |
| ang08\_bam\_sort\_filter\_index.sh |  |
| ang09\_dedup.sh |  |
| ang10\_clip\_overlap.sh |  |
| ang11\_merge.sh |  |
| ang11b\_merge\_parents.sh |  |
| ang12a\_prep\_calling.sh |  |
| ang12b\_call.sh |  |

After the SNP calling step, processing and filtering varied between different downstream analyses. An overview is given in the following scheme.



Scripts for downstream analyses (red) are in separate folders.