

RADseq to COLONY and beyond!

Sequence data
to sibships

Align | Filter bams | Call genotypes | Select SNPs | Prepare input | Run COLONY

runalign

filter_count

genoget

geno2colony

DAT_maker

colony_runner

COLONY
organizeR

Merge metadata | Exploratory plots | Mapping | Data summaries

colonizeR

sibshipPlots

colony_mapper

summarise_colony

Downstream
data analyses

Separation distances | Colony abundance | Nest locations | Demographics

sib_finder

colony_counter

nest_finder

colony_survivor

Additional scripts: alignment_counts genotype_compare list_maker

