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$ python ProgramAB.py -h
usage: ProgramAB.py [-h] [-r REF] [-S [SAM_FILES [SAM_FILES ...]]] [--use_count {0,1}] [--min_abundance1 MIN_ABUNDANCE1]
[--min_abundance2 MIN_ABUNDANCE2] [--ntabund NTABUND] [--max_dist MAX_DIST] [--max_covar MAX_COVAR] [--AAreport {0,1}] [--AAcodonasMNP {0,1}]
[--chim_in_abund CHIM_IN_ABUND] [--alpha ALPHA] [--foldab FOLDAB] [--redist {0,1}] [--max_cycles MAX_CYCLES] [--beta BETA]
[--autopass AUTOPASS] [--colID COLID] [--collect {0,1}] [--sams {0,1}] [--nt_call {0,1}] [--indel {0,1}] [--seq {0,1}] [--covar {0,1}]
[--pass_out {0,1}] [--chim_rm {0,1}] [--deconv {0,1}]

parse Sam files for variant information

optional arguments:
  -h, --help            show this help message and exit
  -r REF, -reference REF
                        reference fasta
  -S [SAM_FILES [SAM_FILES ...]], --Sam_files [SAM_FILES [SAM_FILES ...]]
                        optional .sam files, can use multiple files i.e. "-S Sample1.sam -S Sample2.sam" or "-S Sample1.sam Sample2.sam"
  --use_count {0,1}     Enable/Disable (1/0) use of counts in sequence IDs, default enabled (--use_count 1)
  --min_abundance1 MIN_ABUNDANCE1
                        Minimum observations required to be included in sample reports; >= 1 occurance count; < 1 % observed (.1 = 10%),
                        (default: .001)
  --min_abundance2 MIN_ABUNDANCE2
                        Minimum abundance required for variants to be included in collection reports; must be non-negative and < 1, %
                        observed (.1 = 10%), (default: .01)
  --ntabund NTABUND     Minimum abundance relative to total reads required for a position to be reported in the nt call output; must be non-
                        negative and < 1, % observed (.1 = 10%), (default: .001)
  --max_dist MAX_DIST   Maximum number of variances from the reference a sequence can have to be consider in covars processing (default: 50)
  --max_covar MAX_COVAR
                        Maximum number of variances from the reference to be reported in covars (default: 8)
  --AAreport {0,1}      Enable/Disable (1/0) amino acid reporting, default enabled (--AAreport 1)
  --AAcodonasMNP {0,1}  Enable/Disable (1/0) reporting multiple nt changes in a single codon as one polymorphism, default enabled
                        (--AAcodonasMNP 1), requires AAreport enabled
  --chim_in_abund CHIM_IN_ABUND
                        Minimum abundance a unique sequence must have to be considered in chimera removal / deconvolution (default: .001)
  --alpha ALPHA         Modifier for chim_rm chimera checking, default 1.2. Higher = more sensitive, more false chimeras removed; lower =
                        less sensitive, fewer chimeras removed
  --foldab FOLDAB       Threshold for potential parent / chimera abundance ratio for chim_rm; default is 1.8
  --redist {0,1}        Enable/Disable (1/0) redistribution of chimera counts for chim_rm, default enabled (--redist 1)
  --max_cycles MAX_CYCLES
                        Max number of times chimera removal will be performed for chim_rm; default is 100
  --beta BETA           Modifier for covar pass checking, default 1. Higher = more sensitive, more failed checks; lower = less sensitive,
                        fewer failed checks
  --autopass AUTOPASS   threshold for a sequence to automatically pass the covar pass checking
  --colID COLID         ID to prepend collections
  --collect {0,1}       Enable/Disable (1/0) collection step, default enabled (--collect 1)
  --sams {0,1}          Enable/Disable (1/0) sam processing, default enabled (--sams 1)
  --nt_call {0,1}       Enable/Disable (1/0) nt_call output, default enabled (--nt_call 1)
  --indel {0,1}         Enable/Disable (1/0) indel output, default enabled (--indel 1)
  --seq {0,1}           Enable/Disable (1/0) unique seq output, default enabled (--seq 1)
  --covar {0,1}         Enable/Disable (1/0) covar output, default enabled (--covar 1)
  --pass_out {0,1}      Enable/Disable (1/0) covar_pass output, default disabled (--pass_out 0)
  --chim_rm {0,1}       Enable/Disable (1/0) chim_rm output, default enabled (--chim_rm 1)
  --deconv {0,1}        Enable/Disable (1/0) covar deconv, default enabled (--deconv 1)
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