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usage: perl mkLTG.pl [-options] -in INPUT_FILE -taxonomy TAXONOMY -blast_db BLASTDB
                -outdir OUTDIR -ltg_params PARMETER_FILE
 arguments:
  -in                      name of the input fasta or TSV file containing the sequences to be
assigned; the TSV file must have "sequence" as a heading for one of the columns
  -taxonomy                tsv file with the following tab separated columns:
                           taxid parent_taxid taxlevel taxname merged_taxid taxlevel_index
  -ncbitax_dir             directory of ncbi taxonomy dmp files (https://ftp.ncbi.nih.gov/pub/
taxonomy/new_taxdump/)
                           only necessary if no -taxonomy file is provided
                           taxonomy file can be created from these files if all sequences in the
blast_db have ncbi taxids
  -blast_db                name of the blast database
  -ltg_params              tsv file wih the following tab separated columns:
                           pid pcov phit taxn seqn refres ltgres
  -outdir                  name of the otput directory
  -out_name                alpha-numeric string for naming output files
  -blastout                if empty, run blast; otherwise this file is used to make ltg
  -delete_tmp              0/1; if 1 delete temporary files after the run
  -windows                 0/1, set to one if running on windows
 BLAST parameters
  -task                    megablast/blastn
  -blast_e                 maximum e-value
  -dust                    yes/no
  -max_target_seqs         maximum number of blast hits per query
  -num_threads             number of threads
  -qcov_hsp_perc           minium query coverage in blast
  -batch_size              batch size for blast
```