

Help & Manual: `-h` | `--help` | `--man` | `perldoc <cmd>`

bioseq: Sequence Utility

FASTA descriptors

<code>-l</code> <code>--length</code>	Length of sequences
<code>-n</code> <code>--num-seq</code>	Number of sequences
<code>-c</code> <code>--composition</code>	Base or aa composition

FASTA filter - Multiple sequences

<code>-r</code> <code>--revcom</code>	Reverse-complement sequence
<code>-p</code> <code>--pick 'tag:x'</code>	Pick seq by tag ("id", "order", or "regex")
<code>-d</code> <code>--delete 'tag:x'</code>	Delete seq by tag ("id", "order", or "regex")
<code>-t</code> <code>--translate 'n'</code>	Translate in 1,3 or 6 reading frames
<code>-g</code> <code>--no-gaps</code>	Remove gaps

FASTA filter - Single sequence

<code>-s</code> <code>--subseq 'x,y'</code>	Sub-sequence from positions <i>x</i> to <i>y</i> (inclusive)
<code>-R</code> <code>--reloop 'x'</code>	re-circularize a bacterial genome at position <i>x</i>

Other options

<code>-B</code> <code>--break</code>	Write a FASTA file for each sequence
<code>-C</code> <code>--count-codons</code>	Count codons for sequence
<code>-F</code> <code>--feat2fas</code>	Extract FASTA sequence from GenBank bacterial genome file
<code>-H</code> <code>--hydroB</code>	Return Kyte-Doolittle hydropathicity (proteins)
<code>-G</code> <code>--lead-gaps</code>	Count and return leading gaps
<code>-X</code> <code>--remove-stop</code>	Remove stop codons
<code>-x</code> <code>--restrict 'RE'</code>	Predict fragments from a restriction enzyme digestion
<code>--restrict-coord 'RE'</code>	Predict fragments from restriction enzyme digestion in BED format
<code>-o</code> <code>--output 'format'</code>	Specify output file format. Default is "fasta". Optional format is "genbank"
<code>-i</code> <code>--input 'format'</code>	Specify Input file format. Default is "fasta". Optional format is "genbank"
<code>-L</code> <code>--linearize</code>	Linearize one sequence per line
<code>--split-cdhit</code>	Parse cdhit output .clstr file and generate a FASTA file for each CDHIT family

biotree: Tree Utility

<code>-i</code> <code>--input 'format'</code>	Specify Input file format
<code>-l</code> <code>--length</code>	Print total tree length
<code>-m</code> <code>--mid-point</code>	Midpoint root a tree
<code>-u</code> <code>--otus-num</code>	List all OTUs
<code>-d</code> <code>--del-otus 'a,b,c'</code>	Delete OTUs
<code>--depth 'n1,n2,n3'</code>	Print depth to root for nodes
<code>--distance 'n1,n2'</code>	Distance between two nodes
<code>-D</code> <code>--del-low-boot '0.9'</code>	Delete low-support (<0.9) branches
<code>-r</code> <code>--reroot 'otu'</code>	Reroot with "otu" as outgroup
<code>-o</code> <code>--output 'format'</code>	Output tree in "nhx" or "tabtree"
<code>-c</code> <code>--ci 'trait-file'</code>	Consistency indices for binary traits
<code>-B</code> <code>--clean-boot</code>	Remove branch support values
<code>-b</code> <code>--clean-br</code>	Remove branch lengths
<code>--ead</code>	Edge-length abundance distribution
<code>--label-nodes</code>	Append IDs to all nodes
<code>--lca 'n1,n2,n3'</code>	Return ID of the last common ancestor
<code>-L</code> <code>--length-all</code>	Print all nodes/branch length
<code>-ltt 'number_of_bins'</code>	Data from Lineage-through-time plot
<code>--multi2bi</code>	Multifurcating tree → bifurcating tree
<code>-U</code> <code>--otus-desc 'n all'</code>	Print all descendant OTUs of a node or all nodes
<code>--random 'n'</code>	Build tree of random subset of <i>n</i> OTUs
<code>--sis-pairs</code>	Print whether or not sisters for all pairs of OTUs
<code>-s</code> <code>--subset 'otu1,otu2,otu3 innode'</code>	Build tree for specified OTUs or a clade defined by an internal node
<code>-t</code> <code>--as-text</code>	Draw tree in ASCII text (for preview)
<code>--tree-shape</code>	Print input for R Package apTreeshape

<code>-w</code> <code>--walk 'out'</code>	Print distances to all other OTUs from an OTU
---	---

biopop: PopGen Utility

<code>-s</code> <code>--seg-sites</code>	Print number of segregating sites
<code>-p</code> <code>--pi</code>	Print average pairwise nucleotide difference
<code>-f</code> <code>--four-gametes</code>	Perform four-gamete tests for each SNP pair
<code>-c</code> <code>--snp-coding</code>	Print SNP statistics for coding sequences
<code>-C</code> <code>--snp-coding-long</code>	Print the above in long format
<code>-n</code> <code>--snp-noncoding</code>	Print SNP statistics for coding or non-coding seqs
<code>-m</code> <code>--mis-match</code>	Output data for mis-match distribution
<code>-b</code> <code>--bi-sites</code>	Retain binary informative sites
<code>-H</code> <code>--heterozygosity</code>	Print heterozygosity for each SNP site
<code>--bi-part</code>	Print binary Newick trees for all SNPs
<code>-b</code> <code>--bi-sites</code>	Print alignment for binary-informative SNPs
<code>--bi-sites-for-r</code>	Print above to be read by R package "genetics"
<code>-t</code> <code>--stats 'tag'</code>	Statistics ('pi', 'theda', 'tajima_d', per-site values)

bioaln: Alignment Utility

Alignment descriptors

<code>-l</code> <code>--length</code>	Length of alignment
<code>-L</code> <code>--list-ids</code>	List sequence IDs
<code>-n</code> <code>--num-seq</code>	Number of aligned sequences
<code>-a</code> <code>--avg-pid</code>	Average percent identity
<code>-w</code> <code>--window 'n'</code>	Average difference by sliding window of size <i>n</i> .

Alignment viewers

<code>-c</code> <code>--codon-view</code>	Codon view (in groups of 3 nucleotides)
<code>-m</code> <code>--match</code>	Match view (highlight variable sites)

Alignment filters

<code>-d</code> <code>--delete 's1,s2,s3'</code>	Delete sequence(s)
<code>-p</code> <code>--pick 's1,s2,s3'</code>	Pick sequence(s)
<code>-i</code> <code>--input 'format'</code>	Specify input format. ClutstalW is default.
<code>-o</code> <code>--output 'format'</code>	Specify output format. ClutstalW is default.
<code>-g</code> <code>--no-gaps</code>	Remove gapped sites
<code>-r</code> <code>--ref-seq 'seq_id'</code>	Use <i>seq_id</i> as reference sequence
<code>-s</code> <code>--slice 'x,y'</code>	Return an alignment slice from <i>x</i> to <i>y</i> (inclusive)
<code>-u</code> <code>--uniq</code>	Remove redundant sequences
<code>-v</code> <code>--var-sites</code>	Show only variable sites
<code>-P</code> <code>--pep2dna 'cds.fas'</code>	Back align CDS to peptide alignment
<code>-D</code> <code>--dna2pep</code>	DNA alignment to protein alignment

Evolutionary analysis

<code>-A</code> <code>--concat *.aln</code>	Concatenate multiple alignments
<code>-B</code> <code>--con-blocks 'n'</code>	Extract conserved blocks of size <i>n</i>
<code>-S</code> <code>--shuffle_sites</code>	Make a column-permuted alignment
<code>-R</code> <code>--resample 'n'</code>	Resample <i>n</i> aligned sequences
<code>-b</code> <code>--boot</code>	Bootstrap an alignment
<code>-M</code> <code>--permute-states</code>	Permute within columns (to test tree-ness)
<code>--remove-third</code>	Remove third site
<code>-I</code> <code>--aln-index 'id,n'</code>	Return unaligned position for a sequence at <i>n</i>
<code>--binary</code>	Transform sequences into binary format
<code>--bin-inform</code>	Print only binary informative sites
<code>-C</code> <code>--consensus 'n'</code>	Add an <i>n</i> % consensus sequences
<code>--gap-states, --gap-states2</code>	Print gap statistics per column
<code>-F</code> <code>--no-flat</code>	Turns on 'begin-end' naming
<code>--phy-nonint</code>	Generate non-interleaved PHYLIP output
<code>-E</code> <code>--rm-col 'id'</code>	Remove columns with gap in sequence
<code>--select-third</code>	Generate alignment of every-third base
<code>--trim-ends</code>	Remove 5' and 3' gapped columns
<code>--upper</code>	Make uppercase alignment