

**NAME**

vsearch — chimera detection, clustering, dereplication and rereplication, FASTA/FASTQ file processing, masking, pairwise alignment, searching, shuffling, sorting and subsampling of amplicons for metagenomics, genomics, and population genetics.

**SYNOPSIS**

Chimera detection:

**vsearch** --uchime\_denovo *fastafile* (--chimeras | --nonchimeras | --uchimealns | --uchimeout) *outputfile* [*options*]

**vsearch** --uchime\_ref *fastafile* (--chimeras | --nonchimeras | --uchimealns | --uchimeout) *outputfile* --db *fastafile* [*options*]

Clustering:

**vsearch** (--cluster\_fast | --cluster\_size | --cluster\_smallmem) *fastafile* (--alnout | --biomout | --blast6out | --centroids | --clusters | --mothur\_shared\_out | --msaout | --otutabout | --profile | --samout | --uc | --userout) *outputfile* --id *real* [*options*]

Dereplication and rereplication:

**vsearch** (--derep\_fulllength | --derep\_prefix) *fastafile* (--output | --uc) *outputfile* [*options*]

**vsearch** --rereplicate *fastafile* --output *outputfile* [*options*]

FASTA/FASTQ file processing:

**vsearch** --fastq\_chars *fastqfile* [*options*]

**vsearch** --fastq\_convert *fastqfile* --fastqout *outputfile* [*options*]

**vsearch** --fastq\_eestats *fastqfile* --output *outputfile* [*options*]

**vsearch** --fastq\_filter *fastqfile* (--fastaout | --fastaout\_discarded | --fastqout | --fastqout\_discarded) *outputfile* [*options*]

**vsearch** --fastq\_mergepairs *fastqfile* --reverse *fastqfile* (--fastaout | --fastqout | --fastaout\_notmerged\_fwd | --fastaout\_notmerged\_rev | --fastqout\_notmerged\_fwd | --fastqout\_notmerged\_rev | --eetabbedout) *outputfile* [*options*]

**vsearch** --fastq\_stats *fastqfile* [--log *logfile*] [*options*]

**vsearch** --fastx\_revcomp *fastxfile* (--fastaout | --fastqout) *outputfile* [*options*]

Masking:

**vsearch** --fastx\_mask *fastxfile* (--fastaout | --fastqout) *outputfile* [*options*]

**vsearch** --maskfasta *fastafile* --output *outputfile* [*options*]

Pairwise alignment:

**vsearch** --allpairs\_global *fastafile* (--alnout | --blast6out | --matched | --notmatched | --samout | --uc | --userout) *outputfile* (--acceptall | --id *real*) [*options*]

Searching:

**vsearch** --search\_exact *fastafile* --db *fastafile* (--alnout | --biomout | --blast6out | --mothur\_shared\_out | --otutabout | --samout | --uc | --userout) *outputfile* [*options*]

**vsearch** --usearch\_global *fastafile* --db *fastafile* (--alnout | --biomout | --blast6out | --mothur\_shared\_out | --otutabout | --samout | --uc | --userout) *outputfile* --id *real* [*options*]

Shuffling and sorting:

**vsearch** (--shuffle | --sortbylength | --sortbysize) *fastafile* --output *outputfile* [*options*]

Subsampling:

**vsearch** --fastx\_subsample *fastafile* (--fastaout | --fastqout) *outputfile* (--sample\_pct *real* | --sample\_size *positive integer*) [*options*]

## DESCRIPTION

Environmental or clinical molecular diversity studies generate large volumes of amplicons (e.g.; SSU-rRNA sequences) that need to be checked for chimeras, dereplicated, masked, sorted, searched, clustered or compared to reference sequences. The aim of **vsearch** is to offer a all-in-one open source tool to perform these tasks, using optimized algorithm implementations and harvesting the full potential of modern computers, thus providing fast and accurate data processing.

Comparing nucleotide sequences is at the core of **vsearch**. To speed up comparisons, **vsearch** implements an extremely fast Needleman-Wunsch algorithm, making use of the Streaming SIMD Extensions (SSE2) of post-2003 x86-64 CPUs. If SSE2 instructions are not available, **vsearch** exits with an error message. On Power8 CPUs it will use AltiVec/VSX/VMX instructions. Memory usage increases rapidly with sequence length: for example comparing two sequences of length 1 kb requires 8 MB of memory per thread, and comparing two 10 kb sequences requires 800 MB of memory per thread. For comparisons involving sequences with a length product greater than 25 million (for example two sequences of length 5 kb), **vsearch** uses a slower alignment method described by Hirschberg (1975) and Myers and Miller (1988), with much smaller memory requirements.

### Input

**vsearch** accept as input fasta or fastq files containing one or several nucleotidic entries. In fasta files, each nucleotidic entry is made of a header and a sequence. The header is defined as the string comprised between the '>' symbol and the first space, tab or the end of the line, whichever comes first. Additionally, if the header matches *integer* as the number of occurrences (or abundance) of the sequence in the study. That abundance information is used or created during chimera detection, clustering, dereplication, sorting and searching.

The sequence is defined as a string of IUPAC symbols (ACGTURYSWKMDBHVN), starting after the end of the identifier line and ending before the next identifier line, or the file end. **vsearch** silently ignores ascii characters 9 to 13, and exits with an error message if ascii characters 0 to 8, 14 to 31, '.' or '-' are present. All other ascii or non-ascii characters are stripped and complained about in a warning message.

In fastq files, each entry is made of sequence header starting with a symbol '@', a nucleotidic sequence (same rules as for fasta sequences), a quality header starting with a symbol '+' and a string of ASCII characters (offset 33 or 64), each one encoding the quality value of the corresponding position in the nucleotidic sequence.

**vsearch** operations are case insensitive, except when soft masking is activated. Masking is automatically applied during chimera detection, clustering, masking, pairwise alignment and searching. Soft masking is specified with the options '--dbmask soft' (for searching and chimera detection with a reference) or '--qmask soft' (for searching, *de novo* chimera detection, clustering and masking). When using soft masking, lower case letters indicate masked symbols, while upper case letters indicate regular symbols. Masked symbols are never included in the unique index words used for sequence comparisons, otherwise they are treated as normal symbols.

When comparing sequences during chimera detection, dereplication, searching and clustering, T and U are considered identical, regardless of their case. If two symbols are not identical, their alignment result in a negative mismatch score (default -4), except if one or both of the symbols are ambiguous (RYSWKMDBHVN) in which case the score is zero. Alignment of two identical ambiguous symbols (for example, R vs R) also receives a score of zero.

**vsearch** can read data from standard files and write to standard files, but it can also read from pipes and write to pipes! For example, multiple fasta files can be piped into **vsearch** for dereplication. To do so, file names can be replaced with:

- the symbol '-', representing '/dev/stdin' for input files or '/dev/stdout' for output files,
- a named pipe created with the command mkfifo,
- a process substitution '<(command)' as input or '>(command)' as output.

**vsearch** can automatically read compressed gzip or bzip2 files if the appropriate libraries are present during the compilation. **vsearch** can also read pipes streaming compressed gzip or bzip2 data if the options

--gzip\_decompress or --bzip2\_decompress are selected. When reading from a pipe, the progress indicator is not updated.

## Options

**vsearch** recognizes a large number of command-line options. For easier navigation, options are grouped below by theme (chimera detection, clustering, dereplication and rereplication, FASTA/FASTQ file processing, masking, pairwise alignment, searching, shuffling, sorting, and subsampling). We start with the general options that apply to all themes. Options may start with a single (-) or double dash (--). Option names may be shortened as long as they are not ambiguous (e.g. --derep\_f).

General options:

### --bzip2\_decompress

When reading from a pipe streaming bzip2-compressed data, decompress the data. That option is not needed when reading from a standard bzip2-compressed file.

### --fasta\_width *positive integer*

Fasta files produced by **vsearch** are wrapped (sequences are written on lines of *integer* nucleotides, 80 by default). Set that value to zero to eliminate the wrapping.

### --gzip\_decompress

When reading from a pipe streaming gzip-compressed data, decompress the data. That option is not needed when reading from a standard gzip-compressed file.

### --help | -h

Display help text and exit.

### --log *filename*

Write messages to the specified log file. Information written includes program version, amount of memory available, number of cores and command line options, and if need be, informational messages, warnings and fatal errors. The start and finish times are also recorded as well as the elapsed time and the maximum amount of memory consumed. The different **vsearch** commands can also write additional informations to the log file.

### --maxseqlength *positive integer*

All **vsearch** operations discard sequences of length equal or greater than *integer* (50,000 nucleotides by default).

### --minseqlength *positive integer*

All **vsearch** operations discard sequences of length smaller than *integer*: 1 nucleotide by default for sorting or shuffling, 32 nucleotides for clustering, dereplication or searching.

### --notrunclabels

Do not truncate sequence labels at first space or tab, use the full header in output files.

### --quiet

Suppress all messages to stdout and stderr except for warnings and fatal error messages.

### --threads *positive integer*

Number of computation threads to use (1 to 256). The number of threads should be lesser or equal to the number of available CPU cores. The default is to use all available resources and to launch one thread per logical core. The following commands are multi-threaded: allpairs\_global, cluster\_fast, cluster\_size, cluster\_smallmem, fastq\_mergepairs, maskfasta, search\_exact, uchime\_ref, and usearch\_global. Only one thread is used for the other commands.

### --version | -v

Output version information and exit.

Chimera detection options:

Chimera detection is based on a scoring function controlled by five options (`--dn`, `--mindiffs`, `--mindiv`, `--minh`, `--xn`). Sequences are first sorted by decreasing abundance, if available, and compared on their *plus* strand only (case insensitive).

Input sequences are masked as specified with the `--qmask` and `--hardmask` options. Masking of the database for reference based chimera detection is specified with the `--dbmask` option.

In *de novo* mode, input fasta file should present abundance annotations (i.e. a pattern `[:]size=integer[:]` in the fasta header). Input order matters for chimera detection, so we recommend to sort sequences by decreasing abundance (default of `--derep_fulllength` command). If your sequence set needs to be sorted, please see the `--sortbysize` command in the sorting section.

**--abskew** *real*

When using `--uchime_denovo`, the abundance skew is used to distinguish in a three-way alignment which sequence is the chimera and which are the parents. The assumption is that chimeras appear later in the PCR amplification process and are therefore less abundant than their parents. The default value is 2.0, which means that the parents should be at least 2 times more abundant than their chimera. Any positive value equal or greater than 1.0 can be used.

**--alignwidth** *positive integer*

When using `--uchimealns`, set the width of the three-way alignments (80 nucleotides by default). Set to zero to eliminate wrapping.

**--borderline** *filename*

Output borderline chimeric sequences to *filename*, in fasta format. Borderline chimeric sequences are sequences that have a high enough score but which are not sufficiently different from their closest parent.

**--chimeras** *filename*

Output chimeric sequences to *filename*, in fasta format. Output order may vary when using multiple threads.

**--db** *filename*

When using `--uchime_ref`, detect chimeras using the fasta-formatted reference sequences contained in *filename*. Reference sequences are assumed to be chimera-free. Chimeras cannot be detected if their parents, or sufficiently close relatives, are not present in the database.

**--dn** *real* No vote pseudo-count, corresponding to the parameter *n* in the chimera scoring function (default value is 1.4).

**--fasta\_score**

Add the chimera score to the headers in the fasta output files for chimeras, non-chimeras and borderline sequences, using the format

**--mindiffs** *positive integer*

Minimum number of differences per segment (default value is 3).

**--mindiv** *real*

Minimum divergence from closest parent (default value is 0.8).

**--minh** *real*

Minimum score (*h*). Increasing this value tends to reduce the number of false positives and to decrease sensitivity. Default value is 0.28, and values ranging from 0.0 to 1.0 included are accepted.

**--nonchimeras** *filename*

Output non-chimeric sequences to *filename*, in fasta format. Output order may vary when using multiple threads.

**--relabel** *string*

Relabel sequences using the prefix *string* and a ticker (1, 2, 3, etc.) to construct the new headers. Use `--sizeout` to conserve the abundance annotations.

**--relabel\_keep**

When relabelling, keep the old identifier in the header after a space.

**--relabel\_md5**

Relabel sequences using the MD5 message digest algorithm applied to each sequence. Former sequence headers are discarded. The sequence is converted to upper case and each 'U' is replaced by a 'T' before computation of the digest. The MD5 digest is a cryptographic hash function designed to minimize the probability that two different inputs give the same output, even for very similar, but non-identical inputs. Still, there is a very small, but non-zero, probability that two different inputs give the same digest (i.e. a collision). MD5 generates a 128-bit (16-byte) digest that is represented by 16 hexadecimal numbers (using 32 symbols among 0123456789abcdef). Use `--sizeout` to conserve the abundance annotations.

**--relabel\_sha1**

Relabel sequences using the SHA1 message digest algorithm applied to each sequence. It is similar to the `--relabel_md5` option but uses the SHA1 algorithm instead of the MD5 algorithm. SHA1 generates a 160-bit (20-byte) digest that is represented by 20 hexadecimal numbers (40 symbols). The probability of a collision (two non-identical sequences resulting in the same digest) is smaller for the SHA1 algorithm than it is for the MD5 algorithm.

**--self**

When using `--uchime_ref`, ignore a reference sequence when its label matches the label of the query sequence (useful to estimate false-positive rate in reference sequences).

**--selfid**

When using `--uchime_ref`, ignore a reference sequence when its nucleotide sequence is strictly identical to the nucleotidic sequence of the query.

**--sizeout**

When relabelling, add abundance annotations to fasta headers (using the format `';size=integer;'`).

**--uchime\_denovo** *filename*

Detect chimeras present in the fasta-formatted *filename*, without external references (i.e. *de novo*). Automatically sort the sequences in *filename* by decreasing abundance beforehand (see the sorting section for details). Multithreading is not supported.

**--uchime\_ref** *filename*

Detect chimeras present in the fasta-formatted *filename* by comparing them with reference sequences (option `--db`). Multithreading is supported.

**--uchimealns** *filename*

Write the three-way global alignments (parentA, parentB, chimera) to *filename* using a human-readable format. Use `--alignwidth` to modify alignment length. Output order may vary when using multiple threads. All sequences are converted to upper case before alignment. Lower case letters indicate disagreement in the alignment.

**--uchimeout** *filename*

Write chimera detection results to *filename* using a 18-field, tab-separated uchime-like format. Use `--uchimeout5` to use a format compatible with usearch v5 and earlier versions. Rows output order may vary when using multiple threads.

1. score: higher score means a more likely chimeric alignment.
2. Q: query sequence label.
3. A: parent A sequence label.
4. B: parent B sequence label.

5. T: top parent sequence label (i.e. parent most similar to the query). That field is removed when using `--uchimeout5`.
6. idQM: percentage of similarity of query (Q) and model (M) constructed as a part of parent A and a part of parent B.
7. idQA: percentage of similarity of query (Q) and parent A.
8. idQB: percentage of similarity of query (Q) and parent B.
9. idAB: percentage of similarity of parent A and parent B.
10. idQT: percentage of similarity of query (Q) and top parent (T).
11. LY: yes votes in the left part of the model.
12. LN: no votes in the left part of the model.
13. LA: abstain votes in the left part of the model.
14. RY: yes votes in the right part of the model.
15. RN: no votes in the right part of the model.
16. RA: abstain votes in the right part of the model.
17. div: divergence, defined as (idQM - idQT).
18. YN: query is chimeric (Y), or not (N), or is a borderline case (?).

#### **--uchimeout5**

When using `--uchimeout`, write chimera detection results using a 17-field, tab-separated uchime-like format (drop the 5th field of `--uchimeout`), compatible with usearch version 5 and earlier versions.

**--xn** *real* No vote weight, corresponding to the parameter *beta* in the scoring function (default value is 8.0).

**--xsize** Strip abundance information from the headers when writing the output file.

Clustering options:

**vsearch** implements a single-pass, greedy star-clustering algorithm, similar to the algorithms implemented in usearch, DNAClust and sumacust for example. Important parameters are the global clustering threshold (`--id`) and the pairwise identity definition (`--iddef`).

Input sequences are masked as specified with the `--qmask` and `--hardmask` options.

#### **--biomout** *filename*

Generate an OTU table in the biom version 1.0 JSON file format as specified at [http://biom-format.org/documentation/format\\_versions/biom-1.0.html](http://biom-format.org/documentation/format_versions/biom-1.0.html). The format describes how to store a sparse matrix containing the abundances of the OTUs in the different samples. This format is much more efficient than the classic and mothur OTU table formats available with the `--otutabout` and `--mothur_shared_out` options, respectively, and is recommended at least for large tables. The OTUs are represented by the cluster centroids. Taxonomy information will be included for the OTUs if available. Sample identifiers will be extracted from the headers of all sequences in the input file. If the header contains `';sample=abc123;'` or `';barcodelabel=abc123;'` or a similar string somewhere, then the given sample identifier (here `'abc123'`) will be used. The semicolon is not mandatory at the beginning or end of the header. The sample identifier may contain any printable character except semicolons. If no such sample label is found, the identifier in the initial part of the header will be used, but only letters, digits and underscores are allowed. OTU identifiers will be extracted from the headers of the cluster centroid sequences. If the header contains `';otu=def789;'` or a similar string somewhere, then the given OTU identifier (here `'def789'`) will be used. The semicolon is not mandatory at the beginning or end of the header. The OTU identifier may contain any

printable character except semicolons. If no such OTU label is found, the identifier in the initial part of the header will be used, and all characters except semicolons are allowed. Alternatively, OTU identifiers can be generated using the relabelling options (`--relabel`, `--relabel_sha1` or `--relabel_md5`). Taxonomy information, if present, will also be extracted from the headers of the centroid sequences. If the header contains `';tax=Homo_sapiens;'` or a similar string somewhere, then the given taxonomy information (here `'Homo_sapiens'`) will be used. The semicolon is not mandatory at the beginning or end of the header. The taxonomy information may contain any printable character except semicolons. If an OTU table in the biom version 2.1 HDF5 file format is required, the biom utility may be used as described at [http://biom-format.org/documentation/biom\\_conversion.html](http://biom-format.org/documentation/biom_conversion.html).

**--centroids** *filename*

Output cluster centroid sequences to *filename*, in fasta format. The centroid is the sequence that seeded the cluster (i.e. the first sequence of the cluster).

**--clusterout\_id**

Add cluster identifier information to the output files when using the `--consout` and `--profile` options.

**--clusterout\_sort**

Sort output files by decreasing abundance when using the `--consout`, `--msaout` and `--profile` options.

**--cluster\_fast** *filename*

Clusterize the fasta sequences in *filename*, automatically sort by decreasing sequence length beforehand.

**--cluster\_size** *filename*

Clusterize the fasta sequences in *filename*, automatically sort by decreasing sequence abundance beforehand.

**--cluster\_smallmem** *filename*

Clusterize the fasta sequences in *filename* without automatically modifying their order beforehand. Sequence are expected to be sorted by decreasing sequence length, unless `--usersort` is used.

**--clusters** *string*

Output each cluster to a separate fasta file using the prefix *string* and a ticker (0, 1, 2, etc.) to construct the path and filenames.

**--consout** *filename*

Output cluster consensus sequences to *filename*. For each cluster, a multiple alignment is computed, and a consensus sequence is constructed by taking the majority symbol (nucleotide or gap) from each column of the alignment. Columns containing a majority of gaps are skipped, except for terminal gaps.

**--cons\_truncate**

This command is ignored. A warning is issued.

**--id** *real* Do not add the target to the cluster if the pairwise identity with the centroid is lower than *real* (value ranging from 0.0 to 1.0 included). The pairwise identity is defined as the number of (matching columns) / (alignment length - terminal gaps). That definition can be modified by `--iddef`.

**--iddef** 0/1/2/3/4

Change the pairwise identity definition used in `--id`. Values accepted are:

0. CD-HIT definition: (matching columns) / (shortest sequence length).
1. edit distance: (matching columns) / (alignment length).

2. edit distance excluding terminal gaps (same as --id).
3. Marine Biological Lab definition counting each gap opening (internal or terminal) as a single mismatch, whether or not the gap was extended:  $1.0 - [(mismatches + gap\ openings) / (longest\ sequence\ length)]$
4. BLAST definition, equivalent to --iddef 1 in a context of global pairwise alignment.

**--msaout** *filename*

Output a multiple sequence alignment and a consensus sequence for each cluster to *filename*, in fasta format. Be warned that vsearch computes center star multiple sequence alignments using a fast method whose accuracy can decrease significantly when using low pairwise identity thresholds. The consensus sequence is constructed by taking the majority symbol (nucleotide or gap) from each column of the alignment. Columns containing a majority of gaps are skipped, except for terminal gaps.

**--mothur\_shared\_out** *filename*

Output an OTU table in the mothur 'shared' tab-separated plain text format as described at [http://www.mothur.org/wiki/Shared\\_file](http://www.mothur.org/wiki/Shared_file). The format describes how a matrix containing the abundances of the OTUs in the different samples is stored. The first line will start with the strings 'label', 'group' and 'numOtus' and is followed by a list of all OTU identifiers. The following lines, one for each sample, starts with the string 'vsearch' followed by the sample identifier, the total number of OTUs, and a list of abundances for each OTU in that sample, in the order given on the first line. The OTU and sample identifiers are extracted from the FASTA headers of the sequences. The OTUs are represented by the cluster centroids. See the --biomout option for further details.

**--otutabout** *filename*

Output an OTU table in the classic tab-separated plain text format as a matrix containing the abundances of the OTUs in the different samples. The first line will start with the string '#OTU ID' and is followed by a tab-separated list of all sample identifiers. The following lines, one for each OTU, starts with the OTU identifier and is followed by a tab-separated list of abundances for that OTU in each sample, in the order given on the first line. The OTU and sample identifiers are extracted from the FASTA headers of the sequences. The OTUs are represented by the cluster centroids. An extra column is added to the right of the table if taxonomy information is available for at least one of the OTUs. This column will be labelled 'taxonomy' and each row will then contain the taxonomy information extracted for that OTU. See the --biomout option for further details.

**--profile** *filename*

Output a sequence profile to a text file with the frequency of each nucleotide in each position in the multiple alignment for each cluster. There is a FASTA-like header line for each cluster, followed by the profile information in a tab-separated format. The eight columns are: position (0-based), consensus nucleotide, number of As, number of Cs, number of Gs, number of Ts or Us, number of gap symbols, and finally the total number of ambiguous nucleotide symbols (B, D, H, K, M, N, R, S, Y, V or W). All numbers are integers.

**--qmask** *none/dust/soft*

Mask regions in sequences using the *dust* or the *soft* methods, or do not mask (*none*). Warning, when using *soft* masking, clustering becomes case sensitive. The default is to mask using *dust*.

**--relabel** *string*

Relabel sequence identifiers in the output files produced by --consout, --profile and --centroids options. Please see the description of the same option under Chimera



detection for details.

**--relabel\_keep**

When relabelling, keep the old identifier in the header after a space.

**--relabel\_md5**

Relabel sequence identifiers in the output files produced by `--consout`, `--profile` and `--centroids` options. Please see the description of the same option under Chimera detection for details.

**--relabel\_sha1**

Relabel sequence identifiers in the output files produced by `--consout`, `--profile` and `--centroids` options. Please see the description of the same option under Chimera detection for details.

**--sizein** Take into account the abundance annotations present in the input fasta file (search for the pattern '`[>]size=integer[:]`' in sequence headers).

**--sizeorder**

When an amplicon is close to 2 or more centroids, both within the distance specified with the `--id` option, resolve the ambiguity by clustering it with the centroid having the highest abundance, not necessarily the closest one. The option only has effect when the value specified with `--maxaccepts` is higher than one. The `--sizeorder` option turns on what is sometimes referred to as abundance-based greedy clustering (AGC), in contrast to the default distance-based greedy clustering (DGC).

**--sizeout** Add abundance annotations to the output fasta files (add the pattern specified, abundance annotations are reported to output files, and each cluster centroid receives a new abundance value corresponding to the total abundance of the amplicons included in the cluster (`--centroids` option). If `--sizein` is not specified, input abundances are set to 1 for amplicons, and to the number of amplicons per cluster for centroids.

**--strand** *plus/both*

When comparing sequences with the cluster seed, check the *plus* strand only (default) or check *both* strands.

**--uc** *filename*

Output clustering results in *filename* using a tab-separated uclust-like format with 10 columns and 3 different type of entries (S, H or C). Each fasta sequence in the input file can be either a cluster centroid (S) or a hit (H) assigned to a cluster. Cluster records (C) summarize information (size, centroid label) for each cluster. In the context of clustering, the option `--uc_allhits` has no effect on the `--uc` output. Column content varies with the type of entry (S, H or C):

1. Record type: S, H, or C.
2. Cluster number (zero-based).
3. Centroid length (S), query length (H), or cluster size (C).
4. Percentage of similarity with the centroid sequence (H), or set to '\*' (S, C).
5. Match orientation + or - (H), or set to '\*' (S, C).
6. Not used, always set to '\*' (S, C) or to zero (H).
7. Not used, always set to '\*' (S, C) or to zero (H).
8. set to '\*' (S, C) or, for H, compact representation of the pairwise alignment using the CIGAR format (Compact Idiosyncratic Gapped Alignment Report): M (match), D (deletion) and I (insertion). The equal sign '=' indicates that the query is identical to the centroid sequence.

9. Label of the query sequence (H), or of the centroid sequence (S, C).
10. Label of the centroid sequence (H), or set to '\*' (S, C).

**--usersort**

When using --cluster\_smallmem, allow any sequence input order, not just a decreasing length ordering.

**--xsize**

Strip abundance information from the headers when writing the output file.

...

Most searching options as well as score filtering, gap penalties and masking also apply to clustering (see the Searching section for definitions): --alnout, --blast6out, --fastapairs, --matched, --notmatched, --maxaccept, --maxreject, --samout, --userout, --userfields

Dereplication and rereplication options:

**--derep\_fulllength** *filename*

Merge strictly identical sequences contained in *filename*. Identical sequences are defined as having the same length and the same string of nucleotides (case insensitive, T and U are considered the same).

**--derep\_prefix** *filename*

Merge sequences with identical prefixes contained in *filename*. A short sequence identical to an initial segment (prefix) of another sequence is considered a replicate of the longer sequence. If a sequence is identical to the prefix of two or more longer sequences, it is clustered with the shortest of them. If they are equally long, it is clustered with the most abundant. Remaining ties are solved using sequence headers and sequence input order. Sequence comparisons are case insensitive, and T and U are considered identical.

**--maxuniquesize** *positive integer*

Discard sequences with a post-dereplication abundance value greater than *integer*.

**--minuniquesize** *positive integer*

Discard sequences with a post-dereplication abundance value smaller than *integer*.

**--output** *filename*

Write the dereplicated sequences to *filename*, in fasta format and sorted by decreasing abundance. Identical sequences receive the header of the first sequence of their group. If --sizeout is used, the number of occurrences (i.e. abundance) of each sequence is indicated at the end of their fasta header using the pattern

**--relabel** *string*

Please see the description of the same option under Chimera detection for details.

**--relabel\_keep**

When relabelling, keep the old identifier in the header after a space.

**--relabel\_md5**

Please see the description of the same option under Chimera detection for details.

**--relabel\_sha1**

Please see the description of the same option under Chimera detection for details.

**--rereplicate** *filename*

Duplicate each sequence the number of times indicated by the abundance of each sequence in the specified file. The sequence labels are identical for the same sequence, unless --relabel, --relabel\_sha1 or --relabel\_md5 is used to create unique labels. Output is written to the file specified with the --output option, in FASTA format. The output file does not contain abundance information unless --sizeout is specified, in which case an abundance of 1 is used.

- sizein** Take into account the abundance annotations present in the input fasta file (search for the pattern '[>]size=*integer*[' in sequence headers).
- sizeout** Add abundance annotations to the output fasta file (add the pattern specified, each unique sequence receives a new abundance value corresponding to its total abundance (sum of the abundances of its occurrences). If **--sizein** is not specified, input abundances are set to 1, and each unique sequence receives a new abundance value corresponding to its number of occurrences in the input file.
- strand** *plus/both*  
When searching for strictly identical sequences, check the *plus* strand only (default) or check *both* strands.
- topn** *positive integer*  
Output only the top *integer* sequences (i.e. the most abundant).
- uc** *filename*  
Output full-length or prefix-dereplication results in *filename* using a tab-separated uclust-like format with 10 columns and 3 different type of entries (S, H or C). Each fasta sequence in the input file can be either a cluster centroid (S) or a hit (H) assigned to a cluster. Cluster records (C) summarize information (size, centroid label) for each cluster. In the context of dereplication, the option **--uc\_allhits** has no effect on the **--uc** output. Column content varies with the type of entry (S, H or C):
1. Record type: S, H, or C.
  2. Cluster number (zero-based).
  3. Sequence length (S, H), or cluster size (C).
  4. Percentage of similarity with the centroid sequence (H), or set to '\*' (S, C).
  5. Match orientation + or - (H), or set to '\*' (S, C).
  6. Not used, always set to '\*' (S, C) or 0 (H).
  7. Not used, always set to '\*' (S, C) or 0 (H).
  8. Not used, always set to '\*'.
  9. Label of the query sequence (H), or of the centroid sequence (S, C).
  10. Label of the centroid sequence (H), or set to '\*' (S, C).
- xsize** Strip abundance information from the headers when writing the output file.

#### FASTA/FASTQ file processing options:

Analyse, shorten, filter, convert or merge sequences in FASTQ files, or reverse complement sequences in FASTA or FASTQ files. The **--fastq\_chars** command can be used to analyse FASTQ files to identify the quality encoding and the range of quality score values used. To convert between different FASTQ file variants, use the **--fastq\_convert** command. Statistical analysis of the quality and length of the sequences in a FASTQ file may be performed with the **--fastq\_stats** and **--fastq\_eestats** commands. Sequences may be shortened, filtered and converted by the **--fastq\_filter** or **--fastx\_filter** commands. Paired-end reads can be merged using the **--fastq\_mergepairs** command. Finally, the **--fastx\_revcomp** command reverse-complements sequences.

- eeout** When using **--fastq\_filter** or **--fastq\_mergepairs**, include the number of expected errors (ee) in the sequence header of FASTQ and FASTA files. This option is a synonym of the **--fastq\_eeout** option.

#### **--eetabbedout** *filename*

When specified with the **--fastq\_mergepairs** command, write statistics with expected errors of each merged read to the given file. The file is a tab separated file with four

columns: The number of errors expected in the forward read, the number of expected errors in the reverse read, the number of observed errors in the forward read, and the number of observed errors in the reverse read. The observed number of errors are the number of differences in the overlap region of the merged sequence relative to each of the reads in the pair.

**--fastaout** *filename*

When using `--fastq_filter`, `--fastq_mergepairs` or `--fastx_filter`, write to the given FASTA-formatted file the sequences passing the filter, or the merged sequences.

**--fastaout\_notmerged\_fwd** *filename*

When using `--fastq_mergepairs`, write forward reads not merged to the specified FASTA file.

**--fastaout\_notmerged\_rev** *filename*

When using `--fastq_mergepairs`, write reverse reads not merged to the specified FASTA file.

**--fastaout\_discarded** *filename*

Write sequences that do not pass the filter of the `--fastq_filter` or `--fastx_filter` command to the given FASTA-formatted file.

**--fastq\_allowmergestagger**

When using `--fastq_mergepairs`, allow to merge staggered read pairs. Staggered pairs are pairs where the 3' end of the reverse read has an overhang to the left of the 5' end of the forward read. This situation can occur when a very short fragment is sequenced. The 3' overhang of the reverse read is not included in the merged sequence. The opposite option is the `--fastq_nostagger` option. The default is to discard staggered pairs.

**--fastq\_ascii** *positive integer*

Define the ASCII character number used as the basis for the FASTQ quality score. The default is 33, which is used by the Sanger / Illumina 1.8+ FASTQ format (phred+33). The value 64 is used by the Solexa, Illumina 1.3+ and Illumina 1.5+ formats (phred+64).

**--fastq\_asciout** *positive integer*

When using `--fastq_convert`, define the ASCII character number used as the basis for the FASTQ quality score when writing FASTQ output files. The default is 33.

**--fastq\_chars** *filename*

Summarize the composition of sequence and quality strings contained in the input FASTQ file. For each of the four DNA letters, `--fastq_chars` gives the number of occurrences of the letter, its relative frequency and the length of the longest run of that letter. For each character present in the quality strings, `--fastq_chars` gives the ASCII value of the character, its relative frequency, and the number of times a *k*-mer of that character appears at the end of quality strings. The length of the *k*-mer can be set using `--fastq_tail` (4 by default). The command `--fastq_chars` tries to automatically detect the quality encoding (Solexa, Illumina 1.3+, Illumina 1.5+ or Illumina 1.8+/Sanger) by analyzing the range of observed quality score values. In case of success, `--fastq_chars` suggests values for the `--fastq_ascii` (33 or 64), `--fastq_qmin` and `--fastq_qmax` options to be used with the other commands that require a FASTQ input file.

**--fastq\_convert** *filename*

Convert between the different variants of the FASTQ file format. The quality encoding of the input file must be specified with the `--fastq_ascii` option (either 33 or 64, the default is 33), and the output quality encoding must be specified with the `--fastq_asciout` option (default 33). The minimum and maximum output quality scores may be limited using the `--fastq_qminout` and `--fastq_qmaxout` options. The output file is specified with the `--fastqout` option.

**--fastq\_eeout**

When using `--fastq_filter` or `--fastq_mergepairs`, include the number of expected errors (ee) in the sequence header of FASTQ and FASTA files. This option is a synonym of the `--eeout` option.

**--fastq\_eestats *filename***

Analyze a FASTQ file and report statistics on the distributions of quality scores, error probabilities and expected accumulated errors. The report, a table of 21 tab-separated columns, is written to the file specified with the `--output` option. The first column corresponds to the position in the reads (Pos). The second and third columns correspond to the number of reads (Reads) and percentage of reads (PctRecs) that include this position. The remaining columns include information about the distribution of quality scores in this position (Q), error probabilities in this position (Pe), and finally the expected number of accumulated errors from the beginning of the reads and until the current position (EE). For each of the Q, Pe and EE distributions, the following statistics are included: minimum value (Min), lower quartile (Low), median (Med), mean (Mean), upper quartile (Hi), and maximum value (Max). The quality encoding and the range of quality values may be specified with `--fastq_ascii` `--fastq_qmin` and `--fastq_qmax`.

**--fastq\_filter *filename***

Shorten and/or filter sequences in the given FASTQ file. Similar to the `--fastx_filter` command, but works only on FASTQ files. See `--fastx_filter` for details.

**--fastq\_maxdiffs *positive integer***

When using `--fastq_mergepairs`, specify the maximum number of non-matching nucleotides allowed in the overlap region. That option has a strong influence on the merging success rate. The default value is 5.

**--fastq\_maxee *real***

When using `--fastq_filter`, `--fastq_mergepairs` or `--fastx_filter`, discard sequences with more than the specified number of expected errors.

**--fastq\_maxee\_rate *real***

When using `--fastq_filter` or `--fastx_filter`, discard sequences with more than the specified number of expected errors per base.

**--fastq\_maxlen *positive integer***

When using `--fastq_filter`, `--fastq_mergepairs` or `--fastx_filter`, discard sequences with more than the specified number of bases.

**--fastq\_maxmergelen *positive integer***

When using `--fastq_mergepairs`, specify the maximum length of the merged sequence. By default there is no limit.

**--fastq\_maxns *positive integer***

When using `--fastq_filter`, `--fastq_mergepairs` or `--fastx_filter`, discard sequences with more than the specified number of N's.

**--fastq\_mergepairs *filename***

Merge paired-end sequence reads into one sequence. The method has some similarities to the PEAR algorithm (Zhang, Kobert, Flouri & Stamatakis, 2014). The forward reads are specified as the argument to this option and the reverse reads are specified with the `--reverse` option. The merged sequences are output to the file(s) specified with the `--fastaout` or `--fastqout` options. The non-merged reads can be output to the files specified with the `--fastaout_notmerged_fwd`, `--fastaout_notmerged_rev`, `--fastqout_notmerged_fwd` and `--fastqout_notmerged_rev` options. Statistics may be output to the file specified with the `--eetabbedout` option. Sequences are truncated as specified with the `--fastq_truncqual` option to remove low-quality bases in the 3' end. Sequences shorter than specified with `--fastq_minlen` (after truncation) are discarded (1 by default).

Sequences with too many ambiguous bases (N's), as specified with the `--fastq_maxns` are also discarded (no limit by default). Staggered reads are not merged unless the `--fastq_allowmergestagger` option is specified. The minimum length of the overlap region between the reads may be specified with the `--fastq_minovlen` option (default 16), and the overlap region may not include more mismatches than specified with the `--fastq_maxdiffs` option (5 by default), otherwise the read pair is discarded. The minimum and maximum length of the merged sequence may be specified with the `--fastq_minmergelen` and `--fastq_maxmergelen` options, respectively. Other relevant options are: `--fastq_ascii`, `--fastq_maxee`, `--fastq_nostagger`, `--fastq_qmax`, `--fastq_qmin`, and `--label_suffix`.

**`--fastq_minlen`** *positive integer*

When using `--fastq_filter`, `--fastq_mergepairs` or `--fastx_filter`, discard sequences with less than the specified number of bases (default 1).

**`--fastq_minmergelen`** *positive integer*

When using `--fastq_mergepairs`, specify the minimum length of the merged sequence. The default is 1.

**`--fastq_minovlen`** *positive integer*

When using `--fastq_mergepairs`, specify the minimum overlap between the merged reads. The default is 16.

**`--fastq_nostagger`**

When using `--fastq_mergepairs`, forbid the merging of staggered read pairs. This is the default behaviour of `--fastq_mergepairs`. To change that behaviour, see the `--fastq_allowmergestagger` option.

**`--fastq_qmax`** *positive integer*

Specify the maximum quality score accepted when reading FASTQ files. The default is 41, which is usual for recent Sanger/Illumina 1.8+ files.

**`--fastq_qmaxout`** *positive integer*

When using `--fastq_convert`, specify the maximum quality score used when writing FASTQ files. The default is 41, which is usual for recent Sanger/Illumina 1.8+ files. Older formats may use a maximum quality score of 40.

**`--fastq_qmin`** *positive integer*

Specify the minimum quality score accepted for FASTQ files. The default is 0, which is usual for recent Sanger/Illumina 1.8+ files. Older formats may use scores between -5 and 2.

**`--fastq_qminout`** *positive integer*

When using `--fastq_convert`, specify the minimum quality score used when writing FASTQ files. The default is 0, which is usual for Sanger/Illumina 1.8+ files. Older versions of the format may use scores between -5 and 2.

**`--fastq_stats`** *filename*

Analyze a FASTQ file and report the number of reads it contains. The quality encoding and the range of quality values may be specified with `--fastq_ascii` `--fastq_qmin` and `--fastq_qmax`. That command requires the `--log` option and outputs the following detailed statistics on read length, quality score, length vs. quality distributions, and length / quality filtering:

Read length distribution:

1. L: read length.
2. N: number of reads.
3. Pct: fraction of reads with this length.

- 4: AccPct: fraction of reads with this length or longer.

Quality score distribution:

1. ASCII: character encoding the quality score.
2. Q: Phred quality score.
3. Pe: probability of error associated with the quality score.
4. N: number of bases with this quality score.
5. Pct: fraction of bases with this quality score.
6. AccPct: fraction of bases with this quality score or higher.

Length vs. quality distribution:

1. L: position in reads (starting from position 2).
2. PctRecs: fraction of reads with at least this length.
3. AvgQ: average quality score over all reads up to this position.
4. P(AvgQ): error probability corresponding to AvgQ.
5. AvgP: average error probability.
6. AvgEE: average expected error over all reads up to this position.
7. Rate: growth rate of AvgEE between this position and position - 1.
8. RatePct: Rate (as explained above) expressed as a percentage.

Effect of expected error and length filtering:

The first column indicates read lengths ( $L$ ). The next four columns indicate the number of reads that would be retained by the `--fastq_filter` command if the reads were truncated at length  $L$  (option `--fastq_truncLen  $L$` ) and filtered to have a maximum expected error of 1.0, 0.5, 0.25 or 0.1 (with the option `--fastq_maxEE  $float$` ). The last four columns indicate the fraction of reads that would be retained by the `--fastq_filter` command using the same length and maximum expected error parameters.

Effect of minimum quality and length filtering:

The first column indicates read lengths ( $Len$ ). The next four columns indicate the fraction of reads that would be retained by the `--fastq_filter` command if the reads were truncated at length  $Len$  (option `--fastq_truncLen  $Len$` ) or at the first position with a quality  $Q$  below 5, 10, 15 or 20 (option `--fastq_truncQual  $Q$` ).

**`--fastq_stripLeft`** *positive integer*

When using `--fastq_filter` or `--fastx_filter`, strip the specified number of bases from the beginning of the reads.

**`--fastq_tail`** *positive integer*

When using `--fastq_chars`, count the number of times a series of characters of length  $k$  appears at the end of quality strings. By default,  $k = 4$ .

**`--fastq_truncEE`** *real*

When using `--fastq_filter` or `--fastx_filter`, truncate sequences so that their total expected error is not higher than the specified value.

**`--fastq_truncLen`** *positive integer*

When using `--fastq_filter` or `--fastx_filter`, truncate sequences to the specified length. Shorter sequences are discarded.

**--fastq\_truncclen\_keep** *positive integer*

When using `--fastq_filter` or `--fastx_filter`, truncate sequences to the specified length. Shorter sequences are not discarded.

**--fastq\_truncqual** *positive integer*

When using `--fastq_filter` or `--fastx_filter`, truncate sequences starting from the first base with the specified base quality score value or lower.

**--fastqout** *filename*

When using `--fastq_filter`, `--fastq_mergepairs` or `--fastx_filter`, write to the given FASTQ-formatted file the sequences passing the filter, or the merged sequences.

**--fastqout\_discarded** *filename*

When using `--fastq_filter` or `--fastx_filter`, write sequences that do not pass the filter to the given FASTQ-formatted file.

**--fastqout\_notmerged\_fwd** *filename*

When using `--fastq_mergepairs`, write forward reads not merged to the specified FASTQ file.

**--fastqout\_notmerged\_rev** *filename*

When using `--fastq_mergepairs`, write reverse reads not merged to the specified FASTQ file.

**--fastx\_filter** *filename*

Shorten and/or filter the sequences in the given FASTA or FASTQ file and output the remaining sequences to the FASTQ file specified with the `--fastqout` option and to the FASTA file specified with the `--fastaout` option. The discarded sequences are written to the files specified with the `--fastaout_discarded` and `--fastqout_discarded` options. The input format (FASTA or FASTQ) is automatically detected. Output can not be written to FASTQ files if the input is in FASTA format. Sequences may be shortened using the options `--fastq_stripleft`, `--fastq_trunclee`, `--fastq_truncclen` and `--fastq_truncqual`. The sequences may be filtered using the options `--fastq_maxee`, `--fastq_maxee_rate`, `--fastq_maxlen`, `--fastq_maxns`, `--fastq_minlen` and `--fastq_truncclen`. If shortening results in an empty sequence, it is discarded. The sequences are first shortened and then filtered based on the remaining bases. If no shortening or filtering options are given, all sequences are written to the output files, possibly after conversion from FASTQ to FASTA format. The `--relabel` option may be used to relabel the output sequences. The `--eeout` may be used to output the expected number of errors in each sequence.

**--fastx\_revcomp** *filename*

Reverse-complement the sequences in the given FASTA or FASTQ file to a file specified with the `--fastaout` and/or `--fastqout` options. If the input file is in FASTA format, the output can not be written back to a FASTQ file due to missing base quality scores.

**--label\_suffix** *string*

When using `--fastx_revcomp` or `--fastq_mergepairs`, add the suffix *string* to sequence headers.

**--output** *filename*

When using `--fastq_eestats`, write tabulated results to *filename*. See `--fastq_eestats`'s documentation for a complete description of the table.

**--relabel\_keep**

When using `--relabel`, keep the old identifier in the header after a space.

**--relabel** *string*

Please see the description of the same option under Chimera detection for details.

**--relabel\_md5**

Please see the description of the same option under Chimera detection for details.



**--relabel\_shal**

Please see the description of the same option under Chimera detection for details.

**--reverse** *filename*

When using `--fastq_mergepairs`, specify the FASTQ file containing the reverse reads.

**--xsize** Strip abundance information from the headers when writing the output file.

## Masking options:

An input sequence can be composed of lower- or uppercase letters. When soft masking is specified, lower case letters are treated as symbols that should be masked. Otherwise the case of the input sequences is ignored.

Masking is performed by the commands for chimera detection (`uchime_denovo`, `uchime_ref`), clustering (`cluster_fast`, `cluster_smallmem`, `cluster_size`), masking (`maskfasta`, `fastx_mask`), pairwise alignment (`allpairs_global`) and searching (`search_exact`, `usearch_global`).

Masking is usually specified with the `--qmask` option, while the `--dbmask` option is used for the database sequences specified with the `--db` option with the `--usearch_global`, `--search_exact` and `--uchime_ref` commands.

The argument to the `--qmask` and `--dbmask` option may be none, soft or dust. If the argument is none, the no masking is performed. If the argument is soft the lower case symbols are masked. Finally, if the argument is dust, the sequence is masked using the DUST algorithm by Tatusov and Lipman to mask low-complexity regions.

If the `--hardmask` option is specified, all masked regions are converted to N's, otherwise masked regions are indicated by lower case letters.

If any sequence is masked, the masked version of the sequence (with lower case letters or N's) is used in all output files. Otherwise the sequence is unmodified. The exception is the sequences in the output file specified with the `--uchimealn` option, where the input sequences are converted to upper case first and lower case letters indicate disagreement between the aligned sequences.

When a sequence region is masked, words in the region are not included in the indices used in the heuristic search algorithm. In all other aspects, the region is treated as other regions.

Regions in sequences that are hardmasked (with N's) have a zero alignment score and do not contribute to an alignment.

Here are the results of combined masking options `--qmask` (or `--dbmask` for database sequences) and `--hardmask`, assuming each input sequence contains both lower and uppercase nucleotides:

<u>qmask</u>	<u>hardmask</u>	<u>action</u>
none	off	no masking, all symbols used, no change
none	on	no masking, all symbols used, no change
dust	off	masked symbols lowercased, rest uppercased
dust	on	masked symbols changed to Ns, rest unchanged
soft	off	lowercase symbols masked, no case changes
soft	on	lowercase symbols masked and changed to Ns

**--fastaout** *filename*

Write the masked sequences to *filename*, in fasta format. Applies only to the `--fastx_mask` command.

**--fastqout** *filename*

Write the masked sequences to *filename*, in fastq format. Applies only to the `--fastx_mask` command.

**--fastx\_mask** *filename*

Mask regions in sequences contained in the specified fasta or fastq file. The default is to mask using DUST (use `--qmask` to modify that behavior). The output files are specified with the `--fastaout` and `--fastqout` options. The minimum and maximum percentage of unmasked residues may be specified with the `--min_unmasked_pct` and `--max_unmasked_pct` options, respectively.

**--hardmask**

Symbols in masked regions are replaced by N's. The default is to replace the masked regions by lower case letters.

**--maskfasta** *filename*

Mask regions in sequences contained in the fasta file *filename*. The default is to mask using *dust* (use *--qmask* to modify that behavior). The output file is specified with the *--output* option. This command is depreciated, please use *--fastx\_mask* instead.

**--max\_unmasked\_pct** *real*

Discard sequences with more than the specified maximum percentage of unmasked residues. Works only with *--fastx\_mask*.

**--min\_unmasked\_pct** *real*

Discard sequences with less than the specified minimum percentage of unmasked residues. Works only with *--fastx\_mask*.

**--output** *filename*

Write the masked sequences to *filename*, in fasta format. Applies only to the *--mask\_fasta* command.

**--qmask** *none|dust|soft*

If the argument is *dust*, mask regions in sequences using the *DUST* algorithm that detects simple repeats and low-complexity regions. This is the default. If the argument is *soft*, mask the lower case letters in the input sequence. If the argument is *none*, do not mask.

## Pairwise alignment options:

The results of the  $n * (n - 1) / 2$  pairwise alignments are written to the result files specified with *--alnout*, *--blast6out*, *--fastapairs* *--matched*, *--notmatched*, *--samout*, *--uc* or *--userout* (see Searching section below). Specify either the *--acceptall* option to output all pairwise alignments, or specify an identity level with *--id* to discard weak alignments. Most other accept/reject options (see Searching options below) may also be used. Sequences are aligned on their *plus* strand only. Masking is performed as usual and specified with *--qmask* and *--hardmask*.

**--acceptall**

Write the results of all alignments to output files. This option overrides all other accept/reject options (including *--id*).

**--allpairs** *global filename*

Perform optimal global pairwise alignments of all vs. all fasta sequences contained in *filename*. This command is multi-threaded.

**--id** *real*

Reject the sequence match if the pairwise identity is lower than *real* (value ranging from 0.0 to 1.0 included).

**--threads** *positive integer*

Number of computation threads to use (1 to 256). The number of threads should be lesser or equal to the number of available CPU cores. The default is to use all available resources and to launch one thread per logical core.

**--uc** *filename*

Output pairwise alignment results in *filename* using a tab-separated uclust-like format with 10 columns. Each sequence is compared to all other sequences, and all hits (*--acceptall*) or only some hits (*--id float*) are reported, with one pairwise comparison per line:

1. Record type, always set to 'H'.
2. Ordinal number of the target sequence (based on input order, starting from zero).

3. Sequence length.
4. Percentage of similarity with the target sequence.
5. Match orientation, always set to '+'.
  6. Not used, always set to zero.
  7. Not used, always set to zero.
8. Compact representation of the pairwise alignment using the CIGAR format (Compact Idiosyncratic Gapped Alignment Report): M (match), D (deletion) and I (insertion). The equal sign '=' indicates that the query is identical to the centroid sequence.
9. Label of the query sequence.
10. Label of the target sequence.

Searching options:

**--alnout** *filename*

Write pairwise global alignments to *filename* using a human-readable format. Use --rowlen to modify alignment length. Output order may vary when using multiple threads.

**--biomout** *filename*

Write search results to an OTU table in the biom version 1.0 file format. The query file contains the samples, while the database file contains the OTUs. Sample and OTU identifiers are extracted from the header of these sequences. See the --biomout option in the Clustering section for further details.

**--blast6out** *filename*

Write search results to *filename* using a blast-like tab-separated format of twelve fields (listed below), with one line per query-target matching (or lack of matching if --output\_no\_hits is used). Warning, vsearch uses global pairwise alignments, not blast's seed-and-extend algorithm. Therefore, some common blast output values (alignment start and end, evalue, bit score) are reported differently. Output order may vary when using multiple threads. A similar output can be obtain with --userout *filename* and --userfields query+target+id+alnlen+mism+opens+qlo+qhi+tlo+thi+evalue+bits. A complete list and description is available in the section 'Userfields' of this manual.

1. *query*: query label.
2. *target*: target (database sequence) label. The field is set to
3. *id*: percentage of identity (real value ranging from 0.0 to 100.0). The percentage identity is defined as  $100 * (\text{matching columns}) / (\text{alignment length} - \text{terminal gaps})$ . See fields id0 to id4 for other definitions.
4. *alnlen*: length of the query-target alignment (number of columns). The field is set to 0 if there is no alignment.
5. *mism*: number of mismatches in the alignment (zero or positive integer value).
6. *opens*: number of columns containing a gap opening (zero or positive integer value).
7. *qlo*: first nucleotide of the query aligned with the target. Always equal to 1 if there is an alignment, 0 otherwise (see *qilo* to ignore initial gaps).
8. *qhi*: last nucleotide of the query aligned with the target. Always equal to the length of the pairwise alignment, 0 otherwise (see *qihl* to ignore terminal gaps).

9. *tlo*: first nucleotide of the target aligned with the query. Always equal to 1 if there is an alignment, 0 otherwise (see *tilo* to ignore initial gaps).
10. *thi*: last nucleotide of the target aligned with the query. Always equal to the length of the pairwise alignment, 0 otherwise (see *tithi* to ignore terminal gaps).
11. *eval*: expectancy-value (not computed for nucleotide alignments). Always set to -1.
12. *bits*: bit score (not computed for nucleotide alignments). Always set to 0.

**--db** *filename*

Compare query sequences (specified with `--usearch_global`) to the fasta-formatted target sequences contained in *filename*, using global pairwise alignment.

**--dbmask** *none|dust|soft*

Mask regions in the target database sequences using the dust method or the soft method, or do not mask (*none*). Warning, when using soft masking search commands become case sensitive. The default is to mask using dust.

**--dbmatched** *filename*

Write database target sequences matching at least one query sequence to *filename*, in fasta format. If the option `--sizeout` is used, the number of queries that matched each target sequence is indicated using the pattern `";size=integer;"`.

**--dbnotmatched** *filename*

Write database target sequences not matching query sequences to *filename*, in fasta format.

**--fastapairs** *filename*

Write pairwise alignments of query and target sequences to *filename*, in fasta format.

**--fulldp**

Dummy option for compatibility with usearch. To maximize search sensitivity, **vsearch** uses a 8-way 16-bit SIMD vectorized full dynamic programming algorithm (Needleman-Wunsch), whether or not `--fulldp` is specified.

**--gapext** *string*

Set penalties for a gap extension. See `--gapopen` for a complete description of the penalty declaration system. The default is to initialize the six gap extending penalties using a penalty of 2 for extending internal gaps and a penalty of 1 for extending terminal gaps, in both query and target sequences (i.e. 2I/1E).

**--gapopen** *string*

Set penalties for a gap opening. A gap opening can occur in six different contexts: in the query (Q) or in the target (T) sequence, at the left (L) or right (R) extremity of the sequence, or inside the sequence (I). Sequence symbols (Q and T) can be combined with location symbols (L, I, and R), and numerical values to declare penalties for all possible contexts: aQL/bQI/cQR/dTL/eTI/fTR, where abcdef are zero or positive integers, and `'/'` is used as a separator. To simplify declarations, the location symbols (L, I, and R) can be combined, the symbol (E) can be used to treat both extremities (L and R) equally, and the symbols Q and T can be omitted to treat query and target sequences equally. For instance, the default is to declare a penalty of 20 for opening internal gaps and a penalty of 2 for opening terminal gaps (left or right), in both query and target sequences (i.e. 20I/2E). If only a numerical value is given, without any sequence or location symbol, then the penalty applies to all gap openings. To forbid gap-opening, an infinite penalty value can be declared with the symbol `'*'`. To use **vsearch** as a semi-global aligner, a null-penalty can be applied to the left (L) or right (R) gaps.

**vsearch** always initializes the six gap opening penalties using the default parameters (20I/2E). The user is then free to declare only the values he/she wants to modify. The

*string* is scanned from left to right, accepted symbols are (0123456789/LIREQT\*), and later values override previous values.

Please note that **vsearch**, in contrast to **usearch**, only allows integer gap penalties. Because the lowest gap penalties are 0.5 by default in **usearch**, all default scores and gap penalties in **vsearch** have been doubled to maintain equivalent penalties and to produce identical alignments.

**--hardmask**

Mask sequence regions by replacing them with Ns instead of setting them to lower case as is the default. For more information, please see the Masking section.

**--id** *real* Reject the sequence match if the pairwise identity is lower than *real* (value ranging from 0.0 to 1.0 included). The search process sorts target sequences by decreasing number of *k*-mers they have in common with the query sequence, using that information as a proxy for sequence similarity. That efficient pre-filtering also prevents pairwise alignments with weakly matching targets, as there needs to be at least 6 shared *k*-mers to start the pairwise alignment, and at least one out of every 16 *k*-mers from the query needs to match the target. Consequently, using values lower than **--id** 0.5 is not likely to capture more weakly matching targets. The pairwise identity is by default defined as the number of (matching columns) / (alignment length - terminal gaps). That definition can be modified by **--iddef**.

**--iddef** 0/1/2/3/4

Change the pairwise identity definition used in **--id**. Values accepted are:

0. CD-HIT definition: (matching columns) / (shortest sequence length).
1. edit distance: (matching columns) / (alignment length).
2. edit distance excluding terminal gaps (default definition for **--id**).
3. Marine Biological Lab definition counting each gap opening (internal or terminal) as a single mismatch, whether or not the gap was extended:  $1.0 - [(mismatches + gap\ openings) / (longest\ sequence\ length)]$
4. BLAST definition, equivalent to **--iddef** 1 for global pairwise alignments.

The option **--userfields** accepts the fields **id0** to **id4**, in addition to the field **id**, to report the pairwise identity values corresponding to the different definitions.

**--idprefix** *positive integer*

Reject the sequence match if the first *integer* nucleotides of the target do not match the query.

**--idsuffix** *positive integer*

Reject the sequence match if the last *integer* nucleotides of the target do not match the query.

**--leftjust** Reject the sequence match if the pairwise alignment begins with gaps.

**--match** *integer*

Score assigned to a match (i.e. identical nucleotides) in the pairwise alignment. The default value is 2.

**--matched** *filename*

Write query sequences matching database target sequences to *filename*, in fasta format.

**--maxaccepts** *positive integer*

Maximum number of hits to accept before stopping the search. The default value is 1. This option works in pair with **--maxrejects**. The search process sorts target sequences by decreasing number of *k*-mers they have in common with the query sequence, using that information as a proxy for sequence similarity. After pairwise alignments, if the first target sequence passes the acceptance criteria, it is accepted as best hit and the

search process stops for that query. If `--maxaccepts` is set to a higher value, more hits are accepted. If `--maxaccepts` and `--maxrejects` are both set to 0, the complete database is searched.

**--maxdiffs** *positive integer*

Reject the sequence match if the alignment contains at least *integer* substitutions, insertions or deletions.

**--maxgaps** *positive integer*

Reject the sequence match if the alignment contains at least *integer* insertions or deletions.

**--maxhits** *positive integer*

Maximum number of hits to show once the search is terminated (hits are sorted by decreasing identity). Unlimited by default. That option applies to `--alnout`, `--blast6out`, `--fastapairs`, `--samout`, `--uc`, or `--userout` output files.

**--maxid** *real*

Reject the sequence match if the percentage of identity between the two sequences is greater than *real*.

**--maxqsize** *positive integer*

Reject query sequences with an abundance greater than *integer*.

**--maxqt** *real*

Reject if the query/target sequence length ratio is greater than *real*.

**--maxrejects** *positive integer*

Maximum number of non-matching target sequences to consider before stopping the search. The default value is 32. This option works in pair with `--maxaccepts`. The search process sorts target sequences by decreasing number of *k*-mers they have in common with the query sequence, using that information as a proxy for sequence similarity. After pairwise alignments, if none of the first 32 examined target sequences pass the acceptance criteria, the search process stops for that query (no hit). If `--maxrejects` is set to a higher value, more target sequences are considered. If `--maxaccepts` and `--maxrejects` are both set to 0, the complete database is searched.

**--maxsizeratio** *real*

Reject if the query/target abundance ratio is greater than *real*.

**--maxsl** *real*

Reject if the shorter/longer sequence length ratio is greater than *real*.

**--maxsubs** *positive integer*

Reject the sequence match if the pairwise alignment contains more than *integer* substitutions.

**--mid** *real*

Reject the sequence match if the percentage of identity is lower than *real* (ignoring all gaps, internal and terminal).

**--mincols** *positive integer*

Reject the sequence match if the alignment length is shorter than *integer*.

**--minqt** *real*

Reject if the query/target sequence length ratio is lower than *real*.

**--minsizeratio** *real*

Reject if the query/target abundance ratio is lower than *real*.

**--minsl** *real*

Reject if the shorter/longer sequence length ratio is lower than *real*.

- mintsize** *positive integer*  
Reject target sequences with an abundance lower than *integer*.
- minwordmatches** *non-negative integer*  
Minimum number of word matches required for a sequence to be considered further. Default value is 12 for the default word length 8. For word lengths 3-15, the default minimum word matches are 18, 17, 16, 15, 14, 12, 11, 10, 9, 8, 7, 5 and 3, respectively. If the query sequence has fewer unique words than the number specified, all words in the query must match. If the argument is 0, no word matches are required.
- mismatch** *integer*  
Score assigned to a mismatch (i.e. different nucleotides) in the pairwise alignment. The default value is -4.
- mothur\_shared\_out** *filename*  
Write search results to an OTU table in the mothur 'shared' tab-separated plain text file format. The query file contains the samples, while the database file contains the OTUs. Sample and OTU identifiers are extracted from the header of these sequences. See the `--otutabout` option in the Clustering section for further details.
- notmatched** *filename*  
Write query sequences not matching database target sequences to *filename*, in fasta format.
- otutabout** *filename*  
Write search results to an OTU table in the classic tab-separated plain text format. The query file contains the samples, while the database file contains the OTUs. Sample and OTU identifiers are extracted from the header of these sequences. See the `--mothur_shared_out` option in the Clustering section for further details.
- output\_no\_hits**  
Write both matching and non-matching queries to `--alnout`, `--blast6out`, `--samout` or `--userout` output files. Non-matching queries are labelled 'No hits' in `--alnout` files.
- pattern** *string*  
This option is ignored. It is provided for compatibility with `usearch`.
- qmask** *none/dust/soft*  
Mask regions in the query sequences using the `dust` or the `soft` algorithms, or do not mask (`none`). Warning, when using soft masking search commands become case sensitive. The default is to mask using `dust`.
- query\_cov** *real*  
Reject if the fraction of the query aligned to the target sequence is lower than *real*. The query coverage is computed as (matches + mismatches) / query sequence length. Internal or terminal gaps are not taken into account.
- rightjust**  
Reject the sequence match if the pairwise alignment ends with gaps.
- rowlen** *positive integer*  
Width of alignment lines in `--alnout` output. The default value is 64. Set to 0 to eliminate wrapping.
- samheader**  
Include header lines to the SAM file when `--samout` is specified. The header includes lines starting with `@HD`, `@SQ` and `@PG`, but no `@RG` lines (see <https://github.com/samtools/hts-specs>). By default no header line is written.
- samout** *filename*  
Write alignment results to *filename* using the SAM format (a tab-separated text file). When using the `--samheader` option, the SAM file starts with header lines. Each non-

header line is a SAM record, which represents either a query-target alignment or the absence of match for a query (output order may vary when using multiple threads). Each record contains 11 mandatory fields and optional fields (see <<https://github.com/samtools/hts-specs>> for a complete description of the format):

1. query sequence label.
2. combination of bitwise flags. Possible values are: 0 (top hit), 4 (no hit), 16 (reverse-complemented hit), 256 (secondary hit, i.e. all hits except the top hit).
3. target sequence label.
4. first position of a target aligned with the query (always 1 for global pairwise alignments, 0 if there is no match).
5. mapping quality (ignored, always set to '\*').
6. CIGAR string (set to '\*' if there is no match).
7. name of the target sequence matching with the next read of the query (for mate reads only, ignored and always set to '\*').
8. position of the primary alignment of the next read of the query (for mate reads only, ignored and always set to 0).
9. target sequence length (for multi-segment targets, ignored and always set to 0).
10. query sequence (complete, not only the segment aligned to the target as usearch does).
11. quality string (ignored, always set to '\*').

Optional fields for query-target matches (number and order of fields may vary):

12. AS:i:? alignment score (i.e. percentage of identity).
13. XN:i:? next best alignment score (always set to 0).
14. XM:i:? number of mismatches.
15. XO:i:? number of gap openings (excluding terminal gaps).
16. XG:i:? number of gap extensions (excluding terminal gaps).
17. NM:i:? edit distance to the target (sum of XM and XG).
18. MD:Z:? string for mismatching positions.
19. YT:Z:UU string representing the alignment type.

**--search\_exact** *filename*

Search for exact full-length matches to the query sequences contained in *filename* in the database of target sequences (--db). Only 100% exact matches are reported and this command is much faster than --usearch\_global. The --id, --maxaccepts and --maxrejects options are ignored, but the rest of the searching options may be specified.

**--self** Reject the sequence match if the query and target labels are identical.

**--selfid** Reject the sequence match if the query and target sequences are strictly identical.

**--sizeout** Add abundance annotations to the output of the option --dbmatched (using the pattern ';size=*integer*;',), to report the number of queries that matched each target.

**--strand** *plus/both*

When searching for similar sequences, check the *plus* strand only (default) or check *both* strands.



**--target\_cov** *real*

Reject the sequence match if the fraction of the target sequence aligned to the query sequence is lower than *real*. The target coverage is computed as (matches + mismatches) / target sequence length. Internal or terminal gaps are not taken into account.

**--top\_hits\_only**

Only the top hits between the query and database sequence sets are written to the output specified with the options --alnout, --samout, --userout, --blast6out, --uc, --fastapairs, --matched or --notmatched (but not --dbmatched and --dbnotmatched). For each query, the top hit is the one presenting the highest percentage of identity (see the --iddef option to change the way identity is measured). For a given query, if several top hits present exactly the same percentage of identity, the number of hits reported is controlled by the --maxaccepts value (1 by default).

**--uc** *filename*

Output searching results in *filename* using a tab-separated uclust-like format with 10 columns. When using the --search\_exact command, the table layout is the same than with the --allpairs\_global. When using the --usearch\_global command, the table present two different type of entries: hit (H) or no hit (N). Each query sequence is compared to all other sequences, and the best hit (--maxaccept 1) or several hits (--maxaccept > 1) are reported (H). Output order may vary when using multiple threads. Column content varies with the type of entry (H or N):

1. Record type: H, or N ('hit' or 'no hit').
2. Ordinal number of the target sequence (based on input order, starting from zero). Set to '\*' for N.
3. Sequence length. Set to '\*' for N.
4. Percentage of similarity with the target sequence. Set to '\*' for N.
5. Match orientation + or -. Set to '.' for N.
6. Not used, always set to zero for H, or '\*' for N.
7. Not used, always set to zero for H, or '\*' for N.
8. Compact representation of the pairwise alignment using the CIGAR format (Compact Idiosyncratic Gapped Alignment Report): M (match), D (deletion) and I (insertion). The equal sign '=' indicates that the query is identical to the centroid sequence. Set to '\*' for N.
9. Label of the query sequence.
10. Label of the target centroid sequence. Set to '\*' for N.

**--uc\_allhits**

When using the --uc option, show all hits, not just the top hit for each query.

**--usearch\_global** *filename*

Compare target sequences (--db) to the fasta-formatted query sequences contained in *filename*, using global pairwise alignment.

**--userfields** *string*

When using --userout, select and order the fields written to the output file. Fields are separated by '+' (e.g. query+target+id). See the 'Userfields' section for a complete list of fields.

**--userout** *filename*

Write user-defined tab-separated output to *filename*. Select the fields with the option --userfields. Output order may vary when using multiple threads. If --userfields is empty or not present, *filename* is empty.

**--weak\_id** *real*

Show hits with percentage of identity of at least *real*, without terminating the search. A normal search stops as soon as enough hits are found (as defined by --maxaccepts, --maxrejects, and --id). As --weak\_id reports weak hits that are not deduced from --maxaccepts, high --id values can be used, hence preserving both speed and sensitivity. Logically, *real* must be smaller than the value indicated by --id.

**--wordlength** *positive integer*

Length of words (i.e. *k*-mers) for database indexing. The range of possible values goes from 3 to 15, but values near 8 or 9 are generally recommended. Longer words may reduce the sensitivity/recall for weak similarities, but can increase precision. On the other hand, shorter words may increase sensitivity or recall, but may reduce precision. Computation time generally increases with shorter words and decreases with longer words, but it increases again for very long words. Memory requirements for a part of the index increase with a factor of 4 each time word length increases by one nucleotide, and this generally becomes significant for long words (12 or more). The default value is 8.

## Shuffling options:

Fasta entries in the input file are outputted in a pseudo-random order.

**--output** *filename*

Write the shuffled sequences to *filename*, in fasta format.

**--randseed** *positive integer*

When shuffling sequence order, use *integer* as seed. A given seed always produces the same output order (useful for replicability). Set to 0 to use a pseudo-random seed (default behavior).

**--relabel** *string*

Relabel sequences using the prefix *string* and a ticker (1, 2, 3, etc.) to construct the new headers. Use --sizeout to conserve the abundance annotations.

**--relabel\_keep**

When relabelling, keep the old identifier in the header after a space.

**--relabel\_md5**

Relabel sequences using the MD5 message digest algorithm applied to each sequence. Former sequence headers are discarded. The sequence is converted to upper case and U is replaced by T before the digest is computed. The MD5 digest is a cryptographic hash function designed to minimize the probability that two different inputs gives the same output, even for very similar, but non-identical inputs. Still, there is always a very small, but non-zero probability that two different inputs give the same result. The MD5 digest generates a 128-bit (16-byte) digest that is represented by 16 hexadecimal numbers (using 32 symbols among 0123456789abcdef). Use --sizeout to conserve the abundance annotations.

**--relabel\_sha1**

Relabel sequences using the SHA1 message digest algorithm applied to each sequence. It is similar to the --relabel\_md5 option but uses the SHA1 algorithm instead of the MD5 algorithm. The SHA1 digest generates a 160-bit (20-byte) result that is represented by 20 hexadecimal numbers (40 symbols). The probability of a collision (two non-identical sequences having the same digest) is smaller for the SHA1 algorithm than it is for the MD5 algorithm. Use --sizeout to conserve the abundance annotations.

**--sizeout** When using --relabel, --relabel\_md5 or --relabel\_sha1, preserve and report abundance annotations to the output fasta file (using the pattern ';size=*integer*;').

**--shuffle** *filename*

Pseudo-randomly shuffle the order of sequences contained in *filename*.

**--topn** *positive integer*

Output only the first *integer* sequences after pseudo-random reordering.

**--xsize**

Strip abundance information from the headers when writing the output file.

#### Sorting options:

Fasta entries are sorted by decreasing abundance (**--sortbysize**) or sequence length (**--sortbylength**). To obtain a stable sorting order, ties are sorted by decreasing abundance and label increasing alpha-numerical order (**--sortbylength**), or just by label increasing alpha-numerical order (**--sortbysize**). Label sorting assumes that all sequences have unique labels. The same applies to the automatic sorting performed during chimera checking (**--uchime\_denovo**), dereplication (**--derep\_fulllength**), and clustering (**--cluster\_fast** and **--cluster\_size**).

**--maxsize** *positive integer*

When using **--sortbysize**, discard sequences with an abundance value greater than *integer*.

**--minsize** *positive integer*

When using **--sortbysize**, discard sequences with an abundance value smaller than *integer*.

**--output** *filename*

Write the sorted sequences to *filename*, in fasta format.

**--relabel** *string*

Please see the description of the same option under Chimera detection for details.

**--relabel\_keep**

When relabelling, keep the old identifier in the header after a space.

**--relabel\_md5**

Please see the description of the same option under Chimera detection for details.

**--relabel\_sha1**

Please see the description of the same option under Chimera detection for details.

**--sizeout** When using **--relabel**, report abundance annotations to the output fasta file (using the pattern `';size=integer;'`).

**--sortbylength** *filename*

Sort by decreasing length the sequences contained in *filename*. See the general options **--minseqlength** and **--maxseqlength** to eliminate short and long sequences.

**--sortbysize** *filename*

Sort by decreasing abundance the sequences contained in *filename* (missing abundance values are assumed to be `';size=1'`). See the options **--minsize** and **--maxsize** to eliminate rare and dominant sequences.

**--topn** *positive integer*

Output only the top *integer* sequences (i.e. the longest or the most abundant).

**--xsize**

Strip abundance information from the headers when writing the output file.

#### Subsampling options:

Subsampling randomly extracts a certain number or a certain percentage of the sequences in the input file. If the **--sizein** option is in effect, the abundances of the input sequences is taken into account and the sampling is performed as if the input sequences were rereplicated, subsampled and dereplicated before being written to the output file. The extraction is performed as a random sampling with a uniform distribution among the input sequences and is performed without replacement. The input file is specified with **--fastx\_subsample** option, the output files are specified with the **--fastaout** and **--fastqout** options and the amount of sequences to be sampled is specified with

the `--sample_pct` or `--sample_size` options. The sequences not sampled may be written to files specified with the options `--fasta_discarded` and `--fastq_discarded`. The `--fastq_ascii`, `--fastq_qmin` and `--fastq_qmax` options are also available.

**--fastaout** *filename*

Write the sampled sequences to *filename*, in fasta format.

**--fastaout\_discarded** *filename*

Write the sequences not sampled to *filename*, in fasta format.

**--fastq\_ascii** *positive integer*

Define the ASCII character number used as the basis for the FASTQ quality score. The default is 33, which is used by the Sanger / Illumina 1.8+ FASTQ format (phred+33). The value 64 is used by the Solexa, Illumina 1.3+ and Illumina 1.5+ formats (phred+64).

**--fastq\_qmax** *positive integer*

Specify the maximum quality score accepted when reading FASTQ files. The default is 41, which is usual for recent Sanger/Illumina 1.8+ files.

**--fastq\_qmin** *positive integer*

Specify the minimum quality score accepted for FASTQ files. The default is 0, which is usual for recent Sanger/Illumina 1.8+ files. Older formats may use scores between -5 and 2.

**--fastqout** *filename*

Write the sampled sequences to *filename*, in fastq format. Requires input in fastq format.

**--fastqout\_discarded** *filename*

Write the sequences not sampled to *filename*, in fastq format. Requires input in fastq format.

**--fastx\_subsample** *filename*

Perform subsampling from the sequences in the specified input file that is in FASTA or FASTQ format.

**--randseed** *positive integer*

Use *integer* as a seed for the pseudo-random generator. A given seed always produces the same output, which is useful for replicability. Set to 0 to use a pseudo-random seed (default behavior).

**--relabel** *string*

Relabel sequences using the prefix *string* and a ticker (1, 2, 3, etc.) to construct the new headers. Use `--sizeout` to conserve the abundance annotations.

**--relabel\_keep**

When relabelling, keep the old identifier in the header after a space.

**--relabel\_md5**

Relabel sequences using the MD5 message digest algorithm applied to each sequence. Former sequence headers are discarded. The sequence is converted to upper case and U is replaced by T before the digest is computed. The MD5 digest is a cryptographic hash function designed to minimize the probability that two different inputs give the same output, even for very similar, but non-identical inputs. Still, there is always a very small, but non-zero probability that two different inputs give the same result. The MD5 digest generates a 128-bit (16-byte) digest that is represented by 16 hexadecimal numbers (using 32 symbols among 0123456789abcdef). Use `--sizeout` to conserve the abundance annotations.

**--relabel\_sha1**

Relabel sequences using the SHA1 message digest algorithm applied to each sequence. It is similar to the `--relabel_md5` option but uses the SHA1 algorithm instead of the MD5 algorithm. The SHA1 digest generates a 160-bit (20-byte) result that is represented by 20 hexadecimal numbers (40 symbols). The probability of a collision (two non-identical sequences having the same digest) is smaller for the SHA1 algorithm than it is for the MD5 algorithm. Use `--sizeout` to conserve the abundance annotations.

**--sample\_pct** *real*

Subsample the given percentage of the input sequences. Accepted values range from 0.0 to 100.0.

**--sample\_size** *positive integer*

Extract the given number of sequences.

**--sizein** Take the abundance information of the input file into account, otherwise the abundance of each sequence is considered to be 1.

**--sizeout** Write abundance information to the output file.

**--xsize** Strip abundance information from the headers when writing the output file.

Userfields (fields accepted by the `--userfields` option):

<b>aln</b>	Print a string of M (match), D (delete, i.e. a gap in the query) and I (insert, i.e. a gap in the target) representing the pairwise alignment. Empty field if there is no alignment.
<b>alnl</b>	Print the length of the query-target alignment (number of columns). The field is set to 0 if there is no alignment.
<b>bits</b>	Bit score (not computed for nucleotide alignments). Always set to 0.
<b>caln</b>	Compact representation of the pairwise alignment using the CIGAR format (Compact Idiosyncratic Gapped Alignment Report): M (match), D (deletion) and I (insertion). Empty field if there is no alignment.
<b>evaluate</b>	E-value (not computed for nucleotide alignments). Always set to -1.
<b>exts</b>	Number of columns containing a gap extension (zero or positive integer value).
<b>gaps</b>	Number of columns containing a gap (zero or positive integer value).
<b>id</b>	Percentage of identity (real value ranging from 0.0 to 100.0). The percentage identity is defined as $100 * (\text{matching columns}) / (\text{alignment length} - \text{terminal gaps})$ .
<b>id0</b>	CD-HIT definition of the percentage of identity (real value ranging from 0.0 to 100.0) using the length of the shortest sequence in the pairwise alignment as denominator: $100 * (\text{matching columns}) / (\text{shortest sequence length})$ .
<b>id1</b>	The percentage of identity (real value ranging from 0.0 to 100.0) is defined as the edit distance: $100 * (\text{matching columns}) / (\text{alignment length})$ .
<b>id2</b>	The percentage of identity (real value ranging from 0.0 to 100.0) is defined as the edit distance, excluding terminal gaps. The field <code>id2</code> is an alias for the field <code>id</code> .
<b>id3</b>	Marine Biological Lab definition of the percentage of identity (real value ranging from 0.0 to 100.0), counting each gap opening (internal or terminal) as a single mismatch, whether or not the gap was extended, and using the length of the longest sequence in the pairwise alignment as denominator: $100 * (1.0 - [(\text{mismatches} + \text{gaps}) / (\text{longest sequence length})])$ .
<b>id4</b>	BLAST definition of the percentage of identity (real value ranging from 0.0 to 100.0), equivalent to <code>--iddef 1</code> in a context of global pairwise alignment. The field <code>id4</code> is always equal to the field <code>id1</code> .

<b>ids</b>	Number of matches in the alignment (zero or positive integer value).
<b>mism</b>	Number of mismatches in the alignment (zero or positive integer value).
<b>opens</b>	Number of columns containing a gap opening (zero or positive integer value).
<b>pairs</b>	Number of columns containing only nucleotides. That value corresponds to the length of the alignment minus the gap-containing columns (zero or positive integer value).
<b>pctgaps</b>	Number of columns containing gaps expressed as a percentage of the alignment length (real value ranging from 0.0 to 100.0).
<b>pctpv</b>	Percentage of positive columns. When working with nucleotide sequences, this is equivalent to the percentage of matches (real value ranging from 0.0 to 100.0).
<b>pv</b>	Number of positive columns. When working with nucleotide sequences, this is equivalent to the number of matches (zero or positive integer value).
<b>qcov</b>	Fraction of the query sequence that is aligned with the target sequence (real value ranging from 0.0 to 100.0). The query coverage is computed as $100.0 * (\text{matches} + \text{mismatches}) / \text{query sequence length}$ . Internal or terminal gaps are not taken into account. The field is set to 0.0 if there is no alignment.
<b>qframe</b>	Query frame (-3 to +3). That field only concerns coding sequences and is not computed by <b>vsearch</b> . Always set to +0.
<b>qhi</b>	Last nucleotide of the query aligned with the target. Always equal to the length of the pairwise alignment, 0 otherwise (see <i>qihi</i> to ignore terminal gaps).
<b>qihi</b>	Last nucleotide of the query aligned with the target (ignoring terminal gaps). Nucleotide numbering starts from 1. The field is set to 0 if there is no alignment.
<b>qilo</b>	First nucleotide of the query aligned with the target (ignoring initial gaps). Nucleotide numbering starts from 1. The field is set to 0 if there is no alignment.
<b>ql</b>	Query sequence length (positive integer value). The field is set to 0 if there is no alignment.
<b>qlo</b>	First nucleotide of the query aligned with the target. Always equal to 1 if there is an alignment, 0 otherwise (see <i>qilo</i> to ignore initial gaps).
<b>qrow</b>	Print the sequence of the query segment as seen in the pairwise alignment (i.e. with gap insertions if need be). Empty field if there is no alignment.
<b>qs</b>	Query segment length. Always equal to query sequence length.
<b>qstrand</b>	Query strand orientation (+ or - for nucleotide sequences). Empty field if there is no alignment.
<b>query</b>	Query label.
<b>raw</b>	Raw alignment score (negative, null or positive integer value). The score is the sum of match rewards minus mismatch penalties, gap openings and gap extensions. The field is set to 0 if there is no alignment.
<b>target</b>	Target label. The field is set to '*' if there is no alignment.
<b>tcov</b>	Fraction of the target sequence that is aligned with the query sequence (real value ranging from 0.0 to 100.0). The target coverage is computed as $100.0 * (\text{matches} + \text{mismatches}) / \text{target sequence length}$ . Internal or terminal gaps are not taken into account. The field is set to 0.0 if there is no alignment.
<b>tframe</b>	Target frame (-3 to +3). That field only concerns coding sequences and is not computed by <b>vsearch</b> . Always set to +0.
<b>thi</b>	Last nucleotide of the target aligned with the query. Always equal to the length of the pairwise alignment, 0 otherwise (see <i>tihi</i> to ignore terminal gaps).

<b>tihi</b>	Last nucleotide of the target aligned with the query (ignoring terminal gaps). Nucleotide numbering starts from 1. The field is set to 0 if there is no alignment.
<b>tilo</b>	First nucleotide of the target aligned with the query (ignoring initial gaps). Nucleotide numbering starts from 1. The field is set to 0 if there is no alignment.
<b>tl</b>	Target sequence length (positive integer value). The field is set to 0 if there is no alignment.
<b>tlo</b>	First nucleotide of the target aligned with the query. Always equal to 1 if there is an alignment, 0 otherwise (see <i>tilo</i> to ignore initial gaps).
<b>trow</b>	Print the sequence of the target segment as seen in the pairwise alignment (i.e. with gap insertions if need be). Empty field if there is no alignment.
<b>ts</b>	Target segment length. Always equal to target sequence length. The field is set to 0 if there is no alignment.
<b>tstrand</b>	Target strand orientation (+ or - for nucleotide sequences). Always set to '+', so reverse strand matches have tstrand '+' and qstrand

## DELIBERATE CHANGES

If you are a usearch user, our objective is to make you feel at home. That's why **vsearch** was designed to behave like usearch, to some extent. Like any complex software, usearch is not free from quirks and inconsistencies. We decided not to reproduce some of them, and for complete transparency, to document here the deliberate changes we made.

During a search with usearch, when using the options `--blast6out` and `--output_no_hits`, for queries with no match the number of fields reported is 13, where it should be 12. This is corrected in **vsearch**.

The field raw of the `--userfields` option is not informative in usearch. This is corrected in **vsearch**.

The fields `qlo`, `qhi`, `tlo`, `thi` now have counterparts (`qilo`, `qihi`, `tilo`, `tihi`) reporting alignment coordinates ignoring terminal gaps.

In usearch, when using the option `--output_no_hits`, queries that receive no match are reported in `--blast6out` file, but not in the alignment output file. This is corrected in **vsearch**.

**vsearch** introduces a new `--cluster_size` command that sorts sequences by decreasing abundance before clustering.

**vsearch** reintroduces `--iddef` alternative pairwise identity definitions that were removed from usearch.

**vsearch** extends the `--topn` option to sorting commands.

**vsearch** extends the `--sizein` option to dereplication (`--derep_fulllength`) and clustering (`--cluster_fast`).

**vsearch** treats T and U as identical nucleotides during dereplication.

**vsearch** sorting is stabilized by using sequence abundances or sequences labels as secondary or tertiary keys.

**vsearch** by default uses the DUST algorithm for masking low-complexity regions. Masking behavior is also slightly changed to be more consistent.

## NOVELTIES

**vsearch** introduces new commands and new options not present in usearch 7. They are described in the 'Options' section of this manual. Here is a short list:

- `alignwidth`, `borderline`, `fasta_score` (chimera checking)
- `cluster_size`, `clusterout_id`, `clusterout_sort`, `profile` (clustering)
- `fasta_width`, `gzip_decompress`, `bzip2_decompress` (general option)
- `iddef` (clustering, pairwise alignment, searching)

- maxuniquesize (dereplication)
- relabel\_md5 and relabel\_sha1 (chimera detection, dereplication, FASTQ processing, shuffling, sorting)
- shuffle (shuffling)
- fastq\_eestats, fastq\_maxlen, fastq\_truncree (FASTQ processing)
- fastaout\_discarded, fastqout\_discarded (subsampling)
- rereplicate (dereplication/rereplication)

## EXAMPLES

Align all sequences in a database with each other and output all pairwise alignments:

```
vsearch --allpairs_global database.fas --alnout results.aln --acceptall
```

Check for the presence of chimeras (*de novo*); parents should be at least 1.5 times more abundant than chimeras. Output non-chimeric sequences in fasta format (no wrapping):

```
vsearch --uchime_denovo queries.fas --abskew 1.5 --nonchimeras results.fas --fasta_width 0
```

Cluster with a 97% similarity threshold, collect cluster centroids, and write cluster descriptions using a uclust-like format:

```
vsearch --cluster_fast queries.fas --id 0.97 --centroids centroids.fas --uc clusters.uc
```

Dereplicate the sequences contained in *queries.fas*, take into account the abundance information already present, write unwrapped fasta sequences to *queries\_unique.fas* with the new abundance information, discard all sequences with an abundance of 1:

```
vsearch --derep_fulllength queries.fas --sizein --fasta_width 0 --sizeout --output queries_unique.fas --minuniquesize 2
```

Mask simple repeats and low complexity regions in the input fasta file with the DUST algorithm (masked regions are lowercased), and write the results to the output file:

```
vsearch --maskfasta queries.fas --qmask dust --output queries_masked.fas
```

Search queries in a reference database, with a 80%-similarity threshold, take terminal gaps into account when calculating pairwise similarities, output pairwise alignments:

```
vsearch --usearch_global queries.fas --db references.fas --id 0.8 --iddef 1 --alnout results.aln
```

Search a sequence dataset against itself (ignore self hits), get all matches with at least 60% similarity, and collect results in a blast-like tab-separated format. Accept an unlimited number of hits (--maxaccepts 0), and compare each query to all other sequences, including unlikely candidates (--maxrejects 0):

```
vsearch --usearch_global queries.fas --db queries.fas --self --id 0.6 --blast6out results.blast6 --maxaccepts 0 --maxrejects 0
```

Shuffle the input fasta file (change the order of sequences) in a repeatable fashion (fixed seed), and write unwrapped fasta sequences to the output file:

```
vsearch --shuffle queries.fas --output queries_shuffled.fas --randseed 13 --fasta_width 0
```

Sort by decreasing abundance the sequences contained in *queries.fas* (using the 'size=integer' information), relabel the sequences while preserving the abundance information (with --sizeout), keep only sequences with an abundance equal to or greater than 2:

```
vsearch --sortbysize queries.fas --output queries_sorted.fas --relabel sampleA_ --sizeout --min-size 2
```

## AUTHORS

Implementation by Torbj rn Rognes and Tom s Flouri, documentation by Fr d ric Mah .



## CITATION

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## REPORTING BUGS

Submit suggestions and bug-reports at <<https://github.com/torognes/vsearch/issues>>, send a pull request on <<https://github.com/torognes/vsearch>>, or compose a friendly or curmudgeont e-mail to TorbjÃrn Rognes <[torognes@ifi.uio.no](mailto:torognes@ifi.uio.no)>.

## AVAILABILITY

Source code and binaries are available at <<https://github.com/torognes/vsearch>>.

## COPYRIGHT

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We would like to thank the authors of the following projects for making their source code available:

- **vsearch** includes code from Google's CityHash project by Geoff Pike and Jyrki Alakuijala, providing some excellent hash functions available under a MIT license.

- **vsearch** includes code derived from Tatusov and Lipman's DUST program that is in the public domain.
- **vsearch** includes public domain code written by Alexander Peslyak for the MD5 message digest algorithm.
- **vsearch** includes public domain code written by Steve Reid and others for the SHA1 message digest algorithm.
- **vsearch** binaries may include code from the zlib library, copyright Jean-Loup Gailly and Mark Adler.
- **vsearch** binaries may include code from the bzip2 library, copyright Julian R. Seward.

## SEE ALSO

**swipe**, an extremely fast pairwise local (Smith-Waterman) database search tool by Torbj rn Rognes, available at <<https://github.com/torognes/swipe>>.

**swarm**, a fast and accurate amplicon clustering method by Fr  d  ric Mah   and Torbj rn Rognes, available at <<https://github.com/torognes/swarm>>.

## VERSION HISTORY

New features and important modifications of **vsearch** (short lived or minor bug releases may not be mentioned):

- v1.0.0** released November 28th, 2014  
First public release.
- v1.0.1** released December 1st, 2014  
Bug fixes (sortbysize, semicolon after size annotation in headers) and minor changes (labels as secondary sort key for most sorts, treat T and U as identical for dereplication, only output size in --dbmatched file if --sizeout specified).
- v1.0.2** released December 6th, 2014  
Bug fixes (ssse3/sse4.1 requirement, memory leak).
- v1.0.3** released December 6th, 2014  
Bug fix (now writes help to stdout instead of stderr).
- v1.0.4** released December 8th, 2014  
Added --allpairs\_global option. Reduce memory requirements slightly and eliminate memory leaks.
- v1.0.5** released December 9th, 2014  
Fixes a minor bug with --allpairs\_global and --acceptall options.
- v1.0.6** released December 14th, 2014  
Fixes a memory allocation bug in chimera detection (--uchime\_ref option).
- v1.0.7** released December 19th, 2014  
Fixes a bug in the output from chimera detection with the --uchimeout option.
- v1.0.8** released January 22nd, 2015  
Introduces several changes and bug fixes:
  - a new linear memory aligner for alignment of sequences longer than 5,000 nucleotides,
  - a new --cluster\_size command that sorts sequences by decreasing abundance before clustering,
  - meaning of userfields qlo, qhi, tlo, thi changed for compatibility with usearch,
  - new userfields qilo, qihi, tilo, tihi give alignment coordinates ignoring terminal gaps,
  - in --uc output files, a perfect alignment is indicated with a '=' sign,

- the option `--cluster_fast` now sorts sequences by decreasing length, then by decreasing abundance and finally by sequence identifier,
- default `--maxseqlength` value set to 50,000 nucleotides,
- fix for bug in alignment in rare cases,
- fix for lack of detection of under- or overflow in SIMD aligner.

**v1.0.9** released January 22nd, 2015

Fixes a bug in the function sorting sequences by decreasing abundance (`--sortbysize`).

**v1.0.10** released January 23rd, 2015

Fixes a bug where the `--sizein` option was ignored and always treated as on, affecting clustering and dereplication commands.

**v1.0.11** released February 5th, 2015

Introduces the possibility to output results in SAM format (for clustering, pairwise alignment and searching).

**v1.0.12** released February 6th, 2015

Temporarily fixes a problem with long headers in FASTA files.

**v1.0.13** released February 17th, 2015

Fix a memory allocation problem when computing multiple sequence alignments with the `--msaout` and `--consout` options, as well as a memory leak. Also increased line buffer for reading FASTA files to 4MB.

**v1.0.14** released February 17th, 2015

Fix a bug where the multiple alignment and consensus sequence computed after clustering ignored the strand of the sequences. Also decreased size of line buffer for reading FASTA files to 1MB again due to excessive stack memory usage.

**v1.0.15** released February 18th, 2015

Fix bug in calculation of identity metric between sequences when using the MBL definition (`--iddef 3`).

**v1.0.16** released February 19th, 2015

Integrated patches from Debian for increased compatibility with various architectures.

**v1.1.0** released February 20th, 2015

Added the `--quiet` option to suppress all output to stdout and stderr except for warnings and fatal errors. Added the `--log` option to write messages to a log file.

**v1.1.1** released February 20th, 2015

Added info about `--log` and `--quiet` options to help text.

**v1.1.2** released March 18th, 2015

Fix bug with large datasets. Fix format of help info.

**v1.1.3** released March 18th, 2015

Fix more bugs with large datasets.

**v1.2.0-1.2.19** released July 6th to September 8th, 2015

Several new commands and options added. Bugs fixed. Documentation updated.

**v1.3.0** released September 9th, 2015

Changed to autotools build system.

**v1.3.1** released September 14th, 2015

Several new commands and options. Bug fixes.

**v1.3.2** released September 15th, 2015

Fixed memory leaks. Added `-h` shortcut for help. Removed extra `'v'` in version number.

- v1.3.3** released September 15th, 2015  
Fixed bug in hexadecimal digits of MD5 and SHA1 digests. Added --samheader option.
- v1.3.4** released September 16th, 2015  
Fixed compilation problems with zlib and bzip2lib.
- v1.3.5** released September 17th, 2015  
Minor configuration/makefile changes to compile to native CPU and simplify makefile.
- v1.4.0** released September 25th, 2015  
Added --sizeorder option.
- v1.4.1** released September 29th, 2015  
Inserted public domain MD5 and SHA1 code to eliminate dependency on crypto and openssl libraries and their licensing issues.
- v1.4.2** released October 2nd, 2015  
Dynamic loading of libraries for reading gzip and bzip2 compressed files if available. Circumvention of missing gzoffset function in zlib 1.2.3 and earlier.
- v1.4.3** released October 3rd, 2015  
Fix a bug with determining amount of memory on some versions of Apple OS X.
- v1.4.4** released October 3rd, 2015  
Remove debug message.
- v1.4.5** released October 6th, 2015  
Fix memory allocation bug when reading long FASTA sequences.
- v1.4.6** released October 6th, 2015  
Fix subtle bug in SIMD alignment code that reduced accuracy.
- v1.4.7** released October 7th, 2015  
Fixes a problem with searching for or clustering sequences with repeats. In this new version, vsearch looks at all words occurring at least once in the sequences in the initial step. Previously only words occurring exactly once were considered. In addition, vsearch now requires at least 10 words to be shared by the sequences, previously only 6 were required. If the query contains less than 10 words, all words must be present for a match. This change seems to lead to slightly reduced recall, but somewhat increased precision, ending up with slightly improved overall accuracy.
- v1.5.0** released October 7th, 2015  
This version introduces the new option --minwordmatches that allows the user to specify the minimum number of matching unique words before a sequence is considered further. New default values for different word lengths are also set. The minimum word length is increased to 7.
- v1.6.0** released October 9th, 2015  
This version adds the relabeling options (--relabel, --relabel\_md5 and --relabel\_sha1) to the shuffle command. It also adds the --xsize option to the clustering, dereplication, shuffling and sorting commands.
- v1.6.1** released October 14th, 2015  
Fix bugs and update manual and help text regarding relabelling. Add all relabelling options to the subsampling command. Add the --xsize option to chimera detection, dereplication and fastq filtering commands. Refactoring of code.
- v1.7.0** released October 14th, 2015  
Add --relabel\_keep option.
- v1.8.0** released October 19th, 2015  
Added --search\_exact, --fastx\_mask and --fastq\_convert commands. Changed most commands to read FASTQ input files as well as FASTA files. Modified --fastx\_revcomp and

--fastx\_subsample to write FASTQ files.

**v1.8.1** released November 2nd, 2015

Fixes for compatibility with QIIME and older OS X versions.

**v1.9.0** released November 12th, 2015

Added the --fastq\_mergepairs command and associated options. This command has not been tested well yet. Included additional files to avoid dependency of autoconf for compilation. Fixed an error where identifiers in fasta headers were not truncated at tabs, just spaces. Fixed a bug in detection of the file format (FASTA/FASTQ) of a gzip compressed input file.

**v1.9.1** released November 13th, 2015

Fixed memory leak and a bug in score computation in --fastq\_mergepairs, and improved speed.

**v1.9.2** released November 17th, 2015

Fixed a bug in the computation of some values with --fastq\_stats.

**v1.9.3** released November 19th, 2015

Workaround for missing x86intrin.h with old compilers.

**v1.9.4** released December 3rd, 2015

Fixed incrementation of counter when relabeling dereplicated sequences.

**v1.9.5** released December 3rd, 2015

Fixed bug resulting in inferior chimera detection performance.

**v1.9.6** released January 8th, 2016

Fixed bug in aligned sequences produced with --fastapairs and --userout (qrow, trow) options.

**v1.9.7** released January 12th, 2016

Masking behavior is changed somewhat to keep the letter case of the input sequences unchanged when no masking is performed. Masking is now performed also during chimera detection. Documentation updated.

**v1.9.8** released January 22nd, 2016

Fixed bug causing segfault when chimera detection is performed on extremely short sequences.

**v1.9.9** released January 22nd, 2016

Adjusted default minimum number of word matches during searches for improved performance.

**v1.9.10** released January 25th, 2016

Fixed bug related to masking and lower case database sequences.

**v1.10.0** released February 11th, 2016

Parallelized and improved merging of paired-end reads and adjusted some defaults. Removed progress indicator when stderr is not a terminal. Added --fasta\_score option to report chimera scores in FASTA files. Added --rereplicate and --fastq\_eestats commands. Fixed typos. Added relabelling to files produced with --consout and --profile options.

**v1.10.1** released February 23rd, 2016

Fixed a bug affecting the --fastq\_mergepairs command causing FASTQ headers to be truncated at first space (despite the bug fix release 1.9.0 of November 12th, 2015). Full headers are now included in the output (no matter if --notrunclabels is in effect or not).

**v1.10.2** released March 18th, 2016

Fixed a bug causing a segmentation fault when running --usearch\_global with an empty query sequence. Also fixed a bug causing imperfect alignments to be reported with an alignment string of '=' in uc output files. Fixed typos in man file. Fixed fasta/fastq

processing code regarding presence or absence of compression library header files.

**v1.11.1** released April 13th, 2016

Added strand information in UC file for `--derep_fulllength` and `--derep_prefix`. Added expected errors (ee) to header of FASTA files specified with `--fastaout` and `--fastaout_discarded` when `--eeout` or `--fastq_eeout` option is in effect for `fastq_filter` and `fastq_mergepairs`. The options `--eeout` and `--fastq_eeout` are now equivalent.

**v1.11.2** released June 21st, 2016

Two bugs were fixed. The first issue was related to the `--query_cov` option that used a different coverage definition than the `qcov` userfield. The coverage is now defined as the fraction of the whole query sequence length that is aligned with matching or mismatching residues in the target. All gaps are ignored. The other issue was related to the consensus sequences produced during clustering when only N's were present in some positions. Previously these would be converted to A's in the consensus. The behaviour is changed so that N's are produced in the consensus, and it should now be more compatible with `usearch`.

**v2.0.0** released June 24th, 2016

This major new version supports reading from pipes. Two new options are added: `--gzip_decompress` and `--bzip2_decompress`. One of these options must be specified if reading compressed input from a pipe, but are not required when reading from ordinary files. The `vsearch` header that was previously written to `stdout` is now written to `stderr`. This enables piping of results for further processing. The file name '-' now represent standard input (`/dev/stdin`) or standard output (`/dev/stdout`) when reading or writing files, respectively. Code for reading FASTA and FASTQ files has been refactored.

**v2.0.1** released June 30th, 2016

Avoid segmentation fault when masking very long sequences.

**v2.0.2** released July 5th, 2016

Avoid warnings when compiling with GCC 6.

**v2.0.3** released August 2nd, 2016

Fixed bad compiler options resulting in Illegal instruction errors when running precompiled binaries.

**v2.0.4** released September 1st, 2016

Improved error message for bad FASTQ quality values. Improved manual.

**v2.0.5** released September 9th, 2016

Add options `--fastaout_discarded` and `--fastqout_discarded` to output discarded sequences from subsampling to separate files. Updated manual.

**v2.1.0** released September 16th, 2016

New command: `--fastx_filter`. New options: `--fastq_maxlen`, `--fastq_truncate`. Allow `--min_wordmatches` down to 3.

**v2.1.1** released September 23rd, 2016

Fixed bugs in output to UC-files. Improved help text and manual.

**v2.1.2** released September 28th, 2016

Fixed incorrect abundance output from `fastx_filter` and `fastq_filter` when relabelling.

**v2.2.0** released October 7th, 2016

Added OTU table generation options `--biomout`, `--mothur_shared_out` and `--otutabout` to the clustering and searching commands.

**v2.3.0** released October 10th, 2016

Allowed zero-length sequences in FASTA and FASTQ files. Added `--fastq_trunc_len_keep` option. Fixed bug with output of OTU tables to pipes.

**v2.3.1** released November 16th, 2016

Fixed bug where `--minwordmatches 0` was interpreted as the default minimum word matches for the given word length instead of zero. When used in combination with `--maxaccepts 0` and `--maxrejects 0` it will allow complete bypass of kmer-based heuristics.

**v2.3.2** released November 18th, 2016

Fixed bug where vsearch reported the ordinal number of the target sequence instead of the cluster number in column 2 on H-lines in the uc output file after clustering. For search and alignment commands both usearch and vsearch reports the target sequence number here.

**v2.3.3** released December 5th, 2016

A minor speed improvement.

**v2.3.4** released December 9th, 2016

Fixed bug in output of sequence profiles and updated documentation.

**v2.4.0** released February 8th, 2017

Added support for Linux on Power8 systems (ppc64le) and Windows on x86\_64. Improved detection of pipes when reading FASTA and FASTQ files. Corrected option for specifying output from `fastq_eestats` command in help text.

**v2.4.1** released March 1st, 2017

Fixed an overflow bug in `fastq_stats` and `fastq_eestats` affecting analysis of very large FASTQ files. Fixed maximum memory usage reporting on Windows.

**v2.4.2** released March 10th, 2017

Default value for `fastq_minovlen` increased to 16 in accordance with help text and for compatibility with usearch. Minor changes for improved accuracy of paired-end read merging.

**v2.4.3** released April 6th, 2017

Fixed bug with progress bar for shuffling. Fixed missing N-lines in UC files with `usearch_global`, `search_exact` and `allpairs_global` when the `output_no_hits` option was not specified.

**v2.4.4** released August 28th, 2017

Fixed a few minor bugs, improved error messages and updated documentation.