

```
starting to denoise
['--help']

[[1mDisplaying help[[0m
    -h --help display help
[[1mInput file options:[0m
    --csv_input [path] input file path in csv format
    --fasta_input [path] input file path in fasta format
    --fastq_input [path] input file path in fastq format
    --joining_file [path] file path of an info output from DnoisE. This option
allows to use the information of previous runs of DnoisE to return different joining
criteria outputs without running the program again
    -n --count_name [size/reads/count...] count name column 'size' by default
    -p --sep [1/2/3] separator in case of csv input file
        1='      ' (tab)
        2=','
        3=';'

    -q --sequence [sequence/seq...] sequence column name, 'sequence' by default
    -s --start_sample_cols [number] first sample column (1 == 1st col) if not
given, just one column with total read counts expected (see README.md)
    -z --end_sample_cols [number] last sample column (n == nst col) if not given,
just one column with total read counts expected (see README.md)
[[1mOutput file options:[0m
    --csv_output [path] common path for csv format
    --fasta_output [path] common path for fasta format
    -j --joining_criteria [1/2/3/4]
        1-> will join by the lesser [abundance ratio / beta(d)]
(default r_d criterion)
        2-> will join by the lesser abundance ratio (r criterion)
        3-> will join by the lesser distance (d) value (d criterion)
        4-> will provide all joining criteria in three different
outputs (all)
[[1mOther options:[0m
    -a --alpha [number] alpha value, 5 by default
    -c --cores [number] number of cores, 1 by default
    -e --entropy [number,number,number] entropy values (or any user-settable
measure of variability) of the different codon positions. If -y is enabled and no values are
given, default entropy values are computed from the data
    -g --get_entropy get only entropy values from a dataset
    -m --modal_length [number] when running DnoisE with entropy correction,
sequence length expected can be set, if not, modal_length is used and only sequences with
modal_length + or - 3*n are accepted
    -r --min_abund [number] minimum abundance filtering applied at the end of
analysis, 1 by default
    -u --unique_length only modal length is accepted as sequence length when
running with entropy correction
    -w --within_MOTU [MOTU/motu/...] MOTU column name. This option allows to run
DnoisE within MOTU. Is only available for --csv_input and --csv_output
    -x --first_nt_codon_position [number] as DnoisE has been developed for COI
sequences amplified with Leray-XT primers, default value is 3 (i.e., the first nucleotide in
the sequences is a third codon position)
    -y --entropy_correction a distance correction based on entropy is performed
(see https://github.com/adriantich/DnoisE). If not enabled no correction for entropy is
performed (corresponding to the standard Unoise formulation)
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