FLEXIDOT USAGE

Version:	1.0
Citation:	Kathrin M. Seibt, Thomas Schmidt, Tony Heitkam (in prep.) "FlexiDot: Highly customizable, ambiguity-aware dotplots for visual sequence analyses"
General usage:	$ python flexidot.py [ARGUMENTS]

GENERAL...

-h, --help	Help screen
-v, --verbose	Verbose

INPUT/OUTPUT OPTIONS... required are [-a] OR [-i]

-a, --auto_fas	Imports all fasta from current directory
	    Y or 1 = ON
	    N or 0 = OFF [default]

-i, --in_file	Input fasta file (fasta file or comma-separated file list) (provide multiple files: Recall -i or provide comma-separated file names)
-o, --output_file_prefix	File prefix to be added to the generated filenames [default = NONE]

-c, --collage_output	Multiple dotplots are printed as a collage
	    Y or 1 = ON [default]
	    N or 0 = OFF

-m, --m_col	Number of columns per page [default = 4] (only if --collage_output is ON)
-n, --n_row	Number of rows per page [default = 5] (only if --collage_output is ON)

-f, --filetype	Output file format
	    0 = PNG [default]
	    1 = PDF
	    2 = SVG

-t, --type_nuc	Type of residue is nucleotide
	    Y or 1 = nucleotide [default]
	    N or 0 = amino acid

CALCULATION PARAMETERS...

-k, --wordsize	Wordsize (kmer length) for dotplot comparison (default = 7)

-p, --plotting_mode	Plotting modes
	    0 = self [default]
	    1 = paired
	    2 = poly (matrix with all-against-all dotplots)

-w, --wobble_conversion	Ambiguity handling
	    Y or 1 = ON
	    N or 0 = OFF [default]

-S, --substitution_count	Number of substitutions (mismatch mutations) allowed in fuzzy matching [default = 0]

-r, --rc_option	Find reverse complementary matches
	    Y or 1 = ON [default]
	    N or 0 = OFF

-s, --alphabetic_sorting	Sort sequence identifiers alphabetically
	    Y or 1 = ON
	    N or 0 = OFF [default]

GRAPHIC FORMATTING...

-A, --line_width	Line width [default = 1]
-B, --line_col_for	Line color [default = black]
-C, --line_col_rev	Reverse line color [default = green]
-D, --x_label_pos	Position of the X-label Y or 1 = top [default] N or 0 = bottom
-E, --label_size	Font size
-F, --spacing	Spacing between subdotplots (only if --collage_output is ON))
-P, --plot_size	Plotsize [default = 10]
-L, --length_scaling	Scale plot size for pairwise comparison (only if --plotting_modes=1) Y or 1 = Scaling ON (axes scaled according to sequence length) N or 0 = Scaling OFF (squared plots) [default]
-T, --title_length	Limit title length for dotplot comparison (only if --plotting_modes=0) [default = infinite]

ANNOTATION SHADING (for -p/--plotting mode 0 only)…

-g, --input_gff_files	GFF3 file used for markup in self-dotplots (provide multiple files: Recall -g or provide comma-separated file names)
-G, --gff_color_config_file	Tab-delimited config file for custom gff shading column 1: feature type column 2: color column 3: alpha column 4: zoom factor (for small regions)

GFF SHADING (for -p/--plotting mode 2 only)…

-x, --lcs_shading	Shade subdotplot based on the length of the longest common substring (LCS) Y or 1 = ON N or 0 = OFF [default]
-X, --lcs_shading_num	Number of shading intervals (number of grey shades besides standard white background) [default = 5]
-y, --lcs_shading_ref	Choose reference for LCS shading 0 = maximal LCS length [default] 1 = maximally possible length (length of shorter sequence in pairwise comparison) 2 = given interval sizes (length in bp)
-Y, --lcs_shading_interval_len	Length of intervals for LCS shading (only if --lcs_shading_ref=2) [default for nucleotides = 100; default for amino acids = 10]
-z, --lcs_shading_ori	Shade subdotplots according to LCS on 0 = forward [default], 1 = reverse, or 2 = both strands (forward shading above diagonal, reverse shading on diagonal and below; if --input_user_matrix_file used, best LCS is used below diagonal)

USER MATRIX SHADING (for -p/--plotting mode 2 only)...

-u, --input_user_matrix_file	Shade top right triangle according to values in matrix file (tab-delimited or comma-separated matrix with sequence name in column 1 and numbers in columns 2-n, e.g. identity matrix from MEGA - strings are ignored)
-U, --user_matrix_print	Print matrix entries in the upper right section of all-against-all dotplots Y or 1 = ON N or 0 = OFF [default]