

## 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)

-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]

-M, --mask\_Nstretch Mask hits for N-stretches (DNA) or X-stretching (proteins), if exceeding wordsize  
Y or 1 = ON [default]  
N or 0 = OFF

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### 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)

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

-u, --input_user_matrix_file	Shade top triangle according to values in matrix file  (tab-delimited matrix with sequence name in column 1 and numbers in columns 2-n, e.g. identity matrix from MEGA)
-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]