

## 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 -a [ARGUMENTS]  
\$ python flexidot.py -i <fasta\_file\_name> [ARGUMENTS]

### GENERAL...

-h, --help Help screen

-v, --verbose Verbose

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

-a, --auto\_fas Imports all fasta files from current directory (\*.fasta, \*.fas, \*.fa, \*.fna)  
Y or 1 = ON  
N or 0 = OFF [default]

-i, --in\_file Input fasta file (fasta file name 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 combined in a collage  
Y or 1 = ON [default]  
N or 0 = OFF

-m, --m\_col Number of columns per page (only if --collage\_output=y)  
[default = 4]

-n, --n\_row Number of rows per page (only if --collage\_output=y)  
[default = 5]

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

-s, --alphabetic\_sorting Sort sequences alphabetically according to titles  
Y or 1 = ON  
N or 0 = OFF [default]

### CALCULATION PARAMETERS...

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

-p, --plotting\_mode Mode of FlexiDot dotplotting  
0 = self [default]  
1 = paired  
2 = poly (matrix with all-against-all dotplots)  
> Run multiple plotting modes: Recall -p or provide comma-separated numbers

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

-w, --wobble\_conversion Ambiguity handling for relaxed matching  
Y or 1 = ON  
N or 0 = OFF [default]

-S, --substitution\_count Number of substitutions (mismatches) allowed per window for relaxed matching  
[default = 0]

-r, --rc\_option Find reverse complementary matches (only if type\_nuc=y)  
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 [default = 10]
-F, --spacing	Spacing between all-against-all dotplots (only if --plotting_mode=2) [default = 0.04]
-P, --plot_size	Plotsize [default = 10]
-L, --length_scaling	Scale plot size for pairwise comparison (only if --plotting_mode=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_mode=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)

### LCS 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 (hues) for LCS (-x) and user matrix shading (-u) [default = 5]
-y, --lcs_shading_ref	Reference for LCS shading 0 = maximal LCS length [default] 1 = maximally possible length (length of shorter sequence in pairwise comparison) 2 = given interval sizes - DNA [default 50 bp] or proteins [default 10 aa] - see -Y
-Y, --lcs_shading_interval_len	Length of intervals for LCS shading (only if --lcs_shading_ref=2) [default for nucleotides = 50; 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	Shading above diagonal according to values in matrix file specified by the user (tab-delimited or comma-separated matrix with sequence name in column 1 and numbers in columns 2-n, e.g. identity matrix from sequence multiple alignment - strings are ignored)
-U, --user_matrix_print	Display matrix entries in the fields above diagonal of all-against-all dotplots Y or 1 = ON N or 0 = OFF [default]