

Command Line Arguments for sayitwithDNA.py

1. Basic Arguments

Argument	Default value	Options	Description
--help			Help for arguments
--mode		encode, decode	Choose between encode or decode mode
--output_path			Path to output file
--algorithm		YingYang, SimpleCode, HuffCode, FountainCode, GrassCode	Selection algorithm
--time		on	Prints the runtime
--show_log	off	on	Shows coding progress

2. Error Correction & Validation

Argument	Default value	Options	Description
--verify_rs	off	on	Reed-Solomon verification
--verify_hm	off	on	Hamming verification

If used, the argument must be set at encoding as well as at decoding.

Examples:

```
$ python sayitwithDNA.py --mode encode --algorithm GoldmanCode --  
input_path /Users/name/file.gif --output_path /Users/name/file.dna -  
verify_rs on  
  
$ python sayitwithDNA.py --mode decode --algorithm GoldmanCode --  
input_path /Users/name/file.dna --output_path /Users/name/file.gif -  
verify_rs on
```

3. Simple Code

Argument	Default value	Options	Description
--mapping_rule	0 1 2 3	0 1 2 3 (A-00, T-01, C-10, G-11), 0 0 1 1 (A/T-0, C/G-1)	Either each nucleotide corresponds to a number or two nucleotides correspond to one number

Example:

```
$ python sayitwithDNA.py --mode encode --algorithm SimpleCode --  
input_path /Users/name/file.gif --output_path /Users/name/file.dna -  
mapping_rule 0 0 1 1
```

4. Goldman Code

Argument	Default value	Options	Description
--fixed_huff	False	True	Fixing Huffman tree, mapping between binary and ternary

Examples for en- and decoding:

```
$ python sayitwithDNA.py --mode encode --algorithm GoldmanCode --  
input_path /Users/name/file.gif --output_path /Users/name/file.dna -  
fixed_huff True  
  
$ python sayitwithDNA.py --mode decode --algorithm GoldmanCode --  
input_path /Users/name/file.dna --output_path /Users/name/file.gif -  
fixed_huff True
```

5. Grass Code

Argument	Default value	Description
--base_values	48	Base_values is a list of 0 to 47 (total 48 numbers), which is a one-to-one mapping of 47 groups of 3 nucleotides and 47th digit. Different mappings determine the diversity of DNA sequences produces.

Example for en- and decoding:

```
$ python sayitwithDNA.py --mode encode --algorithm GrassCode --  
input_path /Users/name/file.gif --output_path /Users/name/file.dna -  
base_values 48  
  
$ python sayitwithDNA.py --mode decode --algorithm GrassCode --  
input_path /Users/name/file.dna --output_path /Users/name/file.gif -  
base_values 48
```

6. Fountain Code

Argument	Default value	Description
--homopolymer	4	Maximum length of homopolymers
--gc_content	0.2	The fraction of GC content above/below 0.5 (0.1 means 0.4-0.6)
--redundancy	0.5	Artificial redundancy for successfully decoding (0.5 generates 50% more fragments)
--c_dist	0.1	Degree distribution tuning parameter
--delta	0.5	Degree distribution tuning parameter
--recursion_depth	10000000	Adjust the maximum recursion depth in Python
--header_size	4	Number of bytes for the header; default is 4 (32 bits)
--segment_length	120	Is the length of the sequences

Example for en- and decoding:

```
$ python sayitwithDNA.py --mode encode --algorithm FountainCode --  
input_path /Users/name/file.gif --output_path /Users/name/file.dna -  
homopolymer 4 -gc_content 0.2 -redundancy 0.5 -c_dist 0.1 -delta 0.5 -  
recursion_depth 10000000 -header_size 4 -segment_length 120  
  
$ python sayitwithDNA.py --mode decode --algorithm FountainCode --  
input_path /Users/name/file.dna --output_path /Users/name/file.gif
```

7. Yin-Yang Code

Argument	Default value	Description
--base_reference	0 1 0 1	Yang rule, correspondence between base and bit data in the upper bit segment; default is Rule 495 [0,1,0,1]
--current_code_matrix	1 1 1 0 0 1 0 0 1 1 1 0 0 1 1 0 0	"Yin rule, correspondence between base and bit data in the lower bit segment; default is Rule 495 [[1,1,0,0],[1,0,0,1],[1,1,0,0],[1,1,0,0]];write a "1" at begin
--support_bases	A	Base replenishment before official data
--support_spacing	0	Spacing between support base and current base. When support base is in front of the current base, the spacing is 0 (default)
--max_ratio	0.8	When the (count/length) \leq this parameter, the binary sequence is "good"
--search_count	1	Maximum number of queries. If the DNA segment generated by two bit segments obtained in the current query is valid, the query is stopped

Example for en- and decoding:

```
$ python sayitwithDNA.py --mode encode --algorithm YinYang--input_path  
/Users/name/file.gif --output_path /Users/name/file.dna -base_reference  
0 1 0 1 -current_code_matrix 1 1 1 0 0 1 0 0 1 1 1 0 0 1 1 0 0 -  
support_bases A -support_spacing 0 -max_ratio 0.8 -search_count 1  
  
$ python sayitwithDNA.py --mode decode --algorithm YinYang --input_path  
/Users/name/file.dna --output_path /Users/name/file.gif
```