bioSyntax Manual v0.1

April 13th, 2018

Grok your data

The objective of bioSyntax is to bring you closer to your data, giving you an intuitive & empathetic understanding of biology. To appreciate all that bioSyntax has to offer read this short manual (~10 minutes) and go explore.

1. Getting Started
2. Reading bioSyntax
3. Supported Formats
4. Developing New Formats & Themes

Getting Started

See: Installing bioSyntax

bioSyntax integreates seamlessly with **vim** *(Linux / Mac / Win)*, **sublime** *(Linux / Mac / Win)*, **gedit** *(Linux / Win)*, & **less** *(Linux / Mac)*. After installing bioSyntax files will automatically detected by file-extension.

Reading large-data

For very large data sets, it's often slow to open them in a text editor. It's best to use the command-line program **less** which will read your file from a data-stream.

Read your large-data set with less directly

```
# If your file is uncompressed, it can be read directly.
# less will recognize the file extension (.XYZ)

cd ~/myData/

less dbSNP107_common.vcf
less hg19.fa
```

Streaming your data directly into less with pipes |

```
# If your file is compressed, you can 'pipe' the data
# using the "|" operator from decompression, directly into
# less. You must prefix the file extension you want
# as file formats are not recognized within streams.

cd ~/myCompressedData/

samtools view -h NA12878_hg38.bam | sam-less

gzip -dc dbSNP107_rare.vcf.gz | vcf-less

gzip -dc hg38.fa.gz | fa-less
```

Bypassing bioSyntax (data in plain-text)

For **vim** Type `:syntax off` in vim

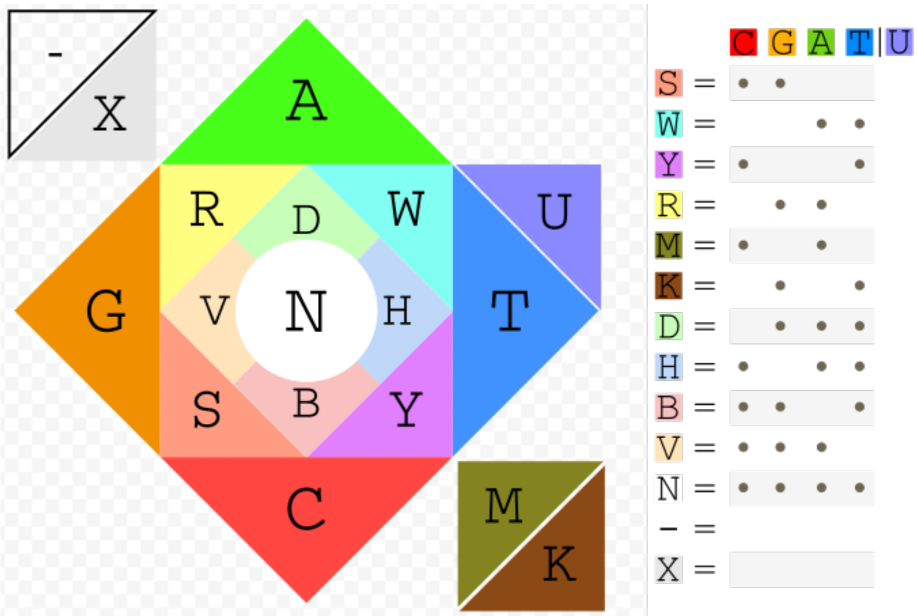
For **less**

```
# You may want to view your data without syntax highlighting
# such as where a file is improperly formatted or very large
# files where syntax highlighting may be slow (i.e. VCF files
# with hundreds of columns).

# 1. Pipe your data through cat
cat snp_1000genomes.vcf | less -

# 2. Within less, switch to a visual editor
less snp_1000genomes.vcf
  # press 'CTRL-C' to stop process
  # press 'v' to switch to visual editor
```

Reading Data

Nucleotides

bioSyntax implements a novel, full IUPAC Nucleotide Code coloring (Figure 1). Ambiguous bases are represented by an ~additive color-mixing of the parent bases. For example, **T**hymine (blue) + **C**ytosine (red) are both p**Y**rimidines (magenta).



		C	G	A	T	U
S	=	●	●			
W	=			●	●	
Y	=	●			●	
R	=		●	●		
M	=	●		●		
K	=		●		●	
D	=		●	●	●	
H	=	●		●	●	
B	=	●	●		●	
V	=	●	●	●		
N	=	●	●	●	●	
–	=					
X	=					

Figure 1: bioSyntax IUPAC nucleotide colouring

An intuitive feature of the bioSyntax color scheme is that the 'GC-content' of a sequence can be quickly approximated by how warm (high GC, red-orange) or cool (low GC, blue-green) a sequence looks (Figure 2).

PHRED Scores

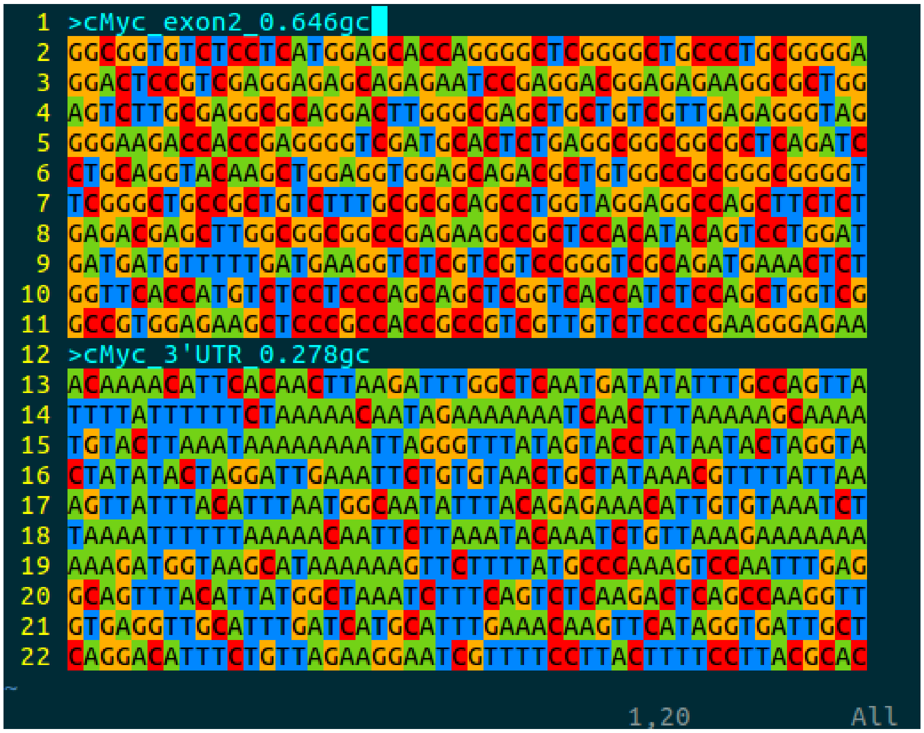
When available, bioSyntax will highlight PHRED quality scores in a step-gradient of blacks (PHRED = 0-10) to whites (PHRED = 40+) (Figure 3).

CIGAR Strings

In `.sam` files the Query:Reference alignment is summarized efficiently but illegibly as a CIGAR String. With a little bit of highlighting these become much easier to read (Figure 4).

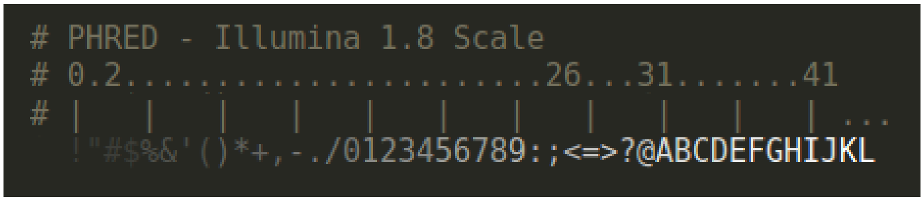
Amino Acid Color Schemes

You can choose from several color-schemes for amino-acid fasta files. The `Fasta Clustal` (Default) syntax colors amino acids based on their physiochemical properties, so does `Fasta Hydrophobicity`, or you may prefer better discrimination of each amino acids with `Fasta Zappo` or `Fasta Taylor`.



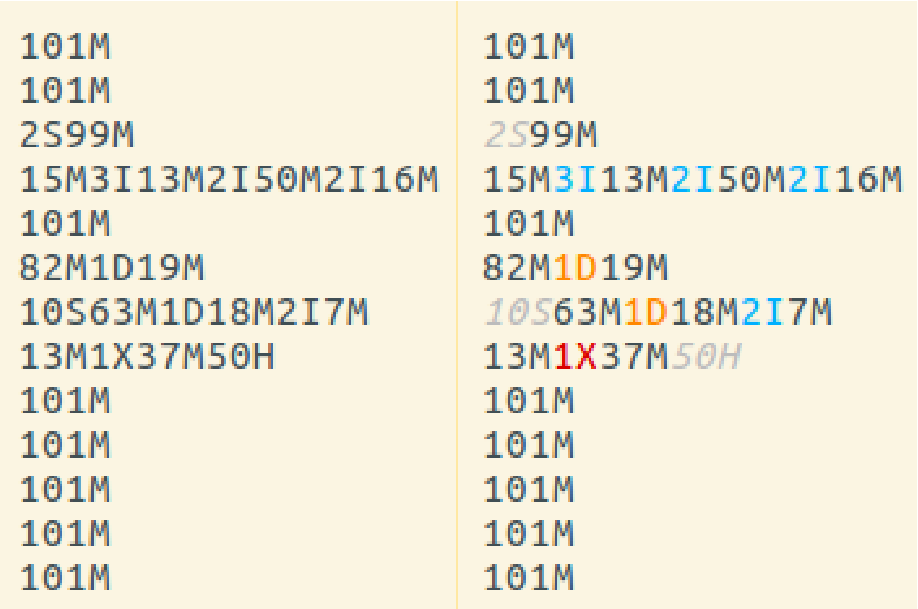
```
>cMyc_exon2_0.646gc
GGCGGTGTCTCCTCATGGAGCACCAGGGGCTCGGGGCTGCCCTGCGGGGA
GGACTCCGTCGAGGAGAGCAGAGAATCCGAGGACGGAGAGAAGGCGCTGG
AGTCTTGCGAGGCGCAGGACTTGGGCGAGCTGCTGTCGTTGAGAGGGTAG
GGGAAGACCACCGAGGGGTCGATGCACTCTGAGGCGGCGGCGCTCAGATC
CTGCAGGTACAAGCTGGAGGTGGAGCAGACGCTGTGGCCGCGGGCGGGGT
TCGGGCTGCCGCTGTCTTTGCGCGCAGCCTGGTAGGAGGCCAGCTTCTCT
GAGACGAGCTTGGCGGCGGCCGAGAAGCCGCTCCACATACAGTCCTGGAT
GATGATGTTTTTGATGAAGGTCTCGTCGTCCGGGTCGCAGATGAAACTCT
GGTTCACCATGTCTCCTCCCAGCAGCTCGGTCACCATCTCCAGCTGGTCG
GCCGTGGAGAAGCTCCCGCCACCGCCGTCGTTGTCTCCCCGAAGGGAGAA
>cMyc_3'UTR_0.278gc
ACAAAACATTCACAACTTAAGATTTGGCTCAATGATATATTTGCCAGTTA
TTTTATTTTTTCTAAAAACAATAGAAAAAAATCAACTTTAAAAAGCAAAA
TGTACTTAAATAAAAAAAATTAGGGTTTATAGTACCTATAATACTAGGTA
CTATATACTAGGATTGAAATTCTGTGTAACTGCTATAAACGTTTTATTAA
AGTTATTTACATTTAATGGCAATATTTACAGAGAAACATTGTGTAAATCT
TAAAATTTTTTAAAAACAATTCTTAAATACAAATCTGTTAAAGAAAAAAA
AAAGATGGTAAGCATAAAAAAGTTCTTTTATGCCCAAAGTCCAATTTGAG
GCAGTTTACATTATGGCTAAATCTTTCAGTCTCAAGACTCAGCCAAGGTT
GTGAGGTTGCATTTGATCATGCATTTGAAACAAGTTCATAGGTGATTGCT
CAGGACATTTCTGTTAGAAGGAATCGTTTTCCTTACTTTTCCTTACGCAC
~
                                        1,20          All
```

Figure 2: `vim myc_gcContent.fa`



```
# PHRED - Illumina 1.8 Scale
# 0.2......................26...31.......41
# |   |   |   |   |   |   |   |   |   |   | ...
   !"#$%&'()*+,-./0123456789:;<=>?@ABCDEFGHIJKL
```

Figure 3: PHRED score scale



```
101M                  101M
101M                  101M
2S99M                 2S99M
15M3I13M2I50M2I16M    15M3I13M2I50M2I16M
101M                  101M
82M1D19M              82M1D19M
10S63M1D18M2I7M       10S63M1D18M2I7M
13M1X37M50H           13M1X37M50H
101M                  101M
101M                  101M
101M                  101M
101M                  101M
101M                  101M
```

Figure 4: CIGAR strings colouring

Support

Report a bug / Ask a question

The fastest way to get an answer is to:

1) Search / Open an issue on the bioSyntax Repo.

Please Include: - A detailed and descriptive title. - Enough information about what did for someone else to replicate the problem. - Information about the operating system / software you're using (`uname -a`) - If it's a syntax highlighting issue: a screenshot of the error and a small bit of the input file you used.

2) If you really don't want to make a (fake) github account. Email info@bioSyntax.org and we'll open the issue, but it will be slower.

Collaborating on bioSyntax

bioSyntax is a community-oriented project for scientific syntax highlighting. We encourage you to change and customize it to suit your needs.

Check out the Development page to create syntax-highlighting for custom file-formats and for other ways to help out.

Supported File Formats

File format and software compatibility matrix for bioSyntax.

Core bioSyntax

File Format	Description	sublime	vim	gedit	less
.fasta	Generic nt/aa sequence	X	X	X	X
.fastq	Fasta + PHRED quality	X	X	X	X
.clustal	Multiple Sequence Alignment	X	X	X	X
.bed	Genomic Ranges	X	X	X	X
.gtf	Genomic Annotation	X	X	X	X
.pdb	Protein Structure	X	X	X	X
.vcf	Variant Call Format	X	X	X	X
.sam	NGS Sequence Data	X	X	X	X

Auxillary Syntaxes

File Format	Description	sublime	vim	gedit	less
.fasta	fasta alternative AA colors				
-	Clustal	X	-	X	-
-	Taylor	X	-	X	-
-	Zappo	X	-	X	-
-	Hydrophobicity	X	-	X	-
.fai	Fasta Index (faidx)	X	X	X	X
.flagstat	samtools flag summary	X	X	X	X
.wig	Wiggle data	-	-	X	-
.pdbx	Protein Structure (large)	-	-	-	-
.phylip	Multiple Sequence Alignment	-	-	-	-
.newick	Tree Format	-	-	-	-
.nexus	Phylogenetics data	-	X	-	-
.cwl	Common Workflow Language	-	-	-	-

See Also: Alternative/User Syntax Definitions