

Settings

NCBI email (required for Entrez/BLAST)

Optional outputs (toggle on to compute)

- ☐ Show ORFs (6-frame, M->stop)
- ☐ Show codon usage (frame 1)
- ☐ Show annotated CDS (GenBank)

GeneScope

Simple Biopython pipeline — fetch an accession or upload a FASTA. All sequence ops use Biopython.

Input

NCBI accession (e.g. NC_005816)

NM_001256799

Fetch from NCBI

Or upload FASTA

Drag and drop file here

Load uploaded FASTA

Browse files

Summary

Length (nt)	GC %	AT %	Ambiguous %	Mol weight (Da)
1386	56.566	43.434	0.0	427...

Base counts

A	C	G	T	N
311	412	372	291	0

FASTA

```
>NM_001256799.3 Homo sapiens glyceraldehyde-3-phosphate dehydrogenase  
GTCCGGATGCTGCGCCTGCGGTAGAGCGGCCGCCATGTTGCAACCGGGAAGGAAATGAAT  
GGGCAGCCGTTAGGAAAGCCTGCCGGTGACTAACCTGCGCTCCTGCCTCGATGGGTGGA  
GTCGCGTGTGGCGGGGAAGTCAGGTGGAGCGAGGCTAGCTGGCCCGATTCTCTCCGGG  
TGATGCTTTTCCTAGATTATTCTCTGATTTGGTCGTATTGGGCGCCTGGTCACCAGGGCT  
GCTTTTAACTCTGGTAAAGTGGATATTGTTGCCATCAATGACCCCTTCATTGACCTCAAC  
TACATGGTTTACATGTTCCAATATGATTCCACCCATGGCAAATTCCATGGCACCGTCAAG  
GCTGAGAACGGGAAGCTTGTCAATGGAATCCCATCACCATCTTCCAGGAGCGAGAT  
CCCTCCAAAATCAAGTGGGGCGATGCTGGCGCTGAGTACGTCGTGGAGTCCACTGGCGTC  
TTCACCACCATGGAGAAGGCTGGGGCTCATTTGCAGGGGGGAGCCAAAAGGGTCATCATC  
TCTGCCCCCTCTGCTGATGCCCCCATGTTTCGTCATGGGTGTGAACCATGAGAAGTATGAC  
AACAGCCTCAAGATCATCAGCAATGCCTCCTGCACCACCAACTGCTTAGCACCCCTGGCC  
AAGGTCATCCATGACAACTTTGGTATCGTGGAAGGACTCATGACCACAGTCCATGCCATC  
ACTGCCACCCAGAAGACTGTGGATGGCCCCTCCGGGAAACTGTGGCGTGATGGCCGCGGG  
GCTCTCCAGAACATCATCCCTGCCTCTACTGGCGCTGCCAAGGCTGTGGGCAAGGTCATC  
CCTGAGCTGAACGGGAAGCTCACTGGCATGGCCTTCCGTGTCCCCACTGCCAACGTGTCA  
GTGGTGGACCTGACCTGCCGTCTAGAAAAACCTGCCAAATATGATGACATCAAGAAGGTG
```

```
GTGAAGCAGGCGTCGGAGGGCCCCCTCAAGGGCATCCTGGGCTACACTGAGCACCAGGTG
GTCTCCTCTGACTTCAACAGCGACACCCACTCCTCCACCTTTGACGCTGGGGCTGGCATT
GCCCTCAACGACCACTTTGTCAAGCTCATTTCTGGTATGACAACGAATTTGGCTACAGC
AACAGGGTGGTGGACCTCATGGCCACATGGCCTCCAAGGAGTAAGACCCCTGGACCACC
AGCCCCAGCAAGAGCACAAGAGGAAGAGAGAGACCCTCACTGCTGGGGAGTCCCTGCCAC
ACTCAGTCCCCCACCACACTGAATCTCCCCTCCTCACAGTTGCCATGTAGACCCCTTGAA
GAGGGGAGGGGCCTAGGGAGCCGCACCTTGTCATGTACCATCAATAAAGTACCCTGTGCT
CAACCA
```

Transcription & Translation

RNA

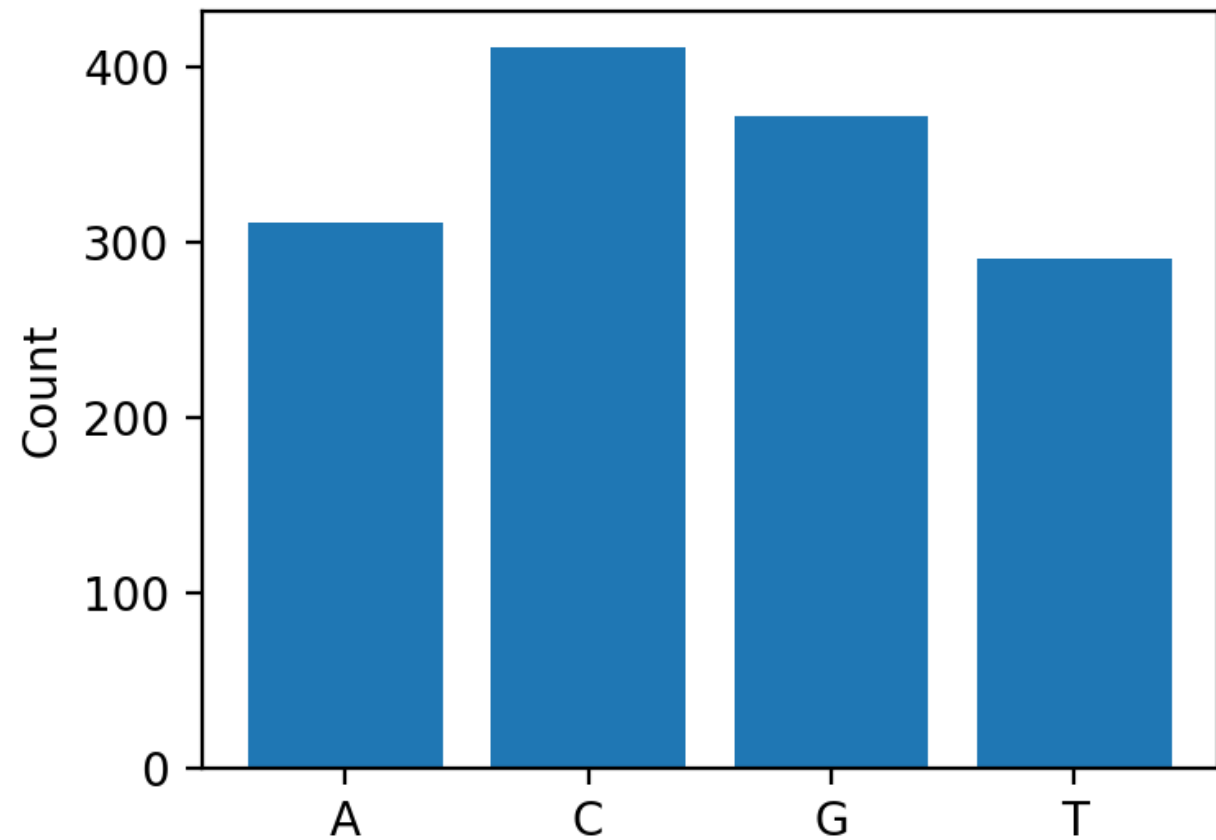
```
GUCCGGAUGCUGCGCCUGCGGUAGAGCGGCCGCAUGUUGCAACCGGGAAGGAAAUGAAUGGGCAGCC
```

Protein

```
VRMLRLR★SGRHVATGKEMNGQPLGKPAGD★PCAPASMGGVACGGGEVRWSEASWPDFSSG★CFS★IIL★
```

Plots

Base composition



Pairwise alignment (optional)

Upload FASTA with targets for pairwise alignment



Drag and drop file here

Limit 200MB per file • FA, FASTA, TXT

Browse files

Run pairwise alignment

Protein structure lookup

Find PDB (BLASTp top hit)

BLASTn (top 5 hits)

Run BLASTn (top 5)