

GLIMMER

Use the command line version of Glimmer to analyze CDSs in a partial sequence from *Spiroplasma helicoides* strain TABS-2, whose genome was submitted to GenBank on August 23, 2016 (file: sheliprt.fasta). The training set will be the full genome of *S. helicoides* strain TABS-2 (file: sheli.fasta).

Command to run: `./run_glimmer.sh`

FGENESB

Use FGENESB to identify CDSs in the partial sequence from *S. helicoides* strain TABS-2 (file: sheliprt.fasta). Use 'bacterial generic' as the training set.

← → ↻ ⚠ Not secure softberry.com/cgi-bin/programs/gfindb/fgenesb.pl									
Prediction of potential genes in microbial genomes									
Time: Tue Jan 1 00:00:00 2005									
Seq name: Spiroplasma helicoides strain TABS-2, partial sequence									
Length of sequence - 5500 bp									
Number of predicted genes - 9									
Number of transcription units - 6, operons - 2									
N	Tu/Op	Conserved	S		Start		End	Score	
		pairs (N/Pv)							
1	1 Op	1	.	+	CDS	635 -	991	117	
2	1 Op	2	.	+	CDS	998 -	1141	144	
3	2 Tu	1	.	-	CDS	1126 -	1365	73	
4	3 Tu	1	.	+	CDS	1334 -	1978	381	
5	4 Tu	1	.	+	CDS	2242 -	2463	231	
6	5 Op	1	.	+	CDS	2585 -	4003	998	
7	5 Op	2	.	+	CDS	4010 -	4678	423	
8	5 Op	3	.	+	CDS	4703 -	4768	72	
9	6 Tu	1	.	+	CDS	4880 -	5143	169	

1. How many CDSs are listed?
There are 9 CDSs listed
2. How many mRNAs are predicted to code for those CDSs?
There are 6 mRNAs predicted

SPLIGN

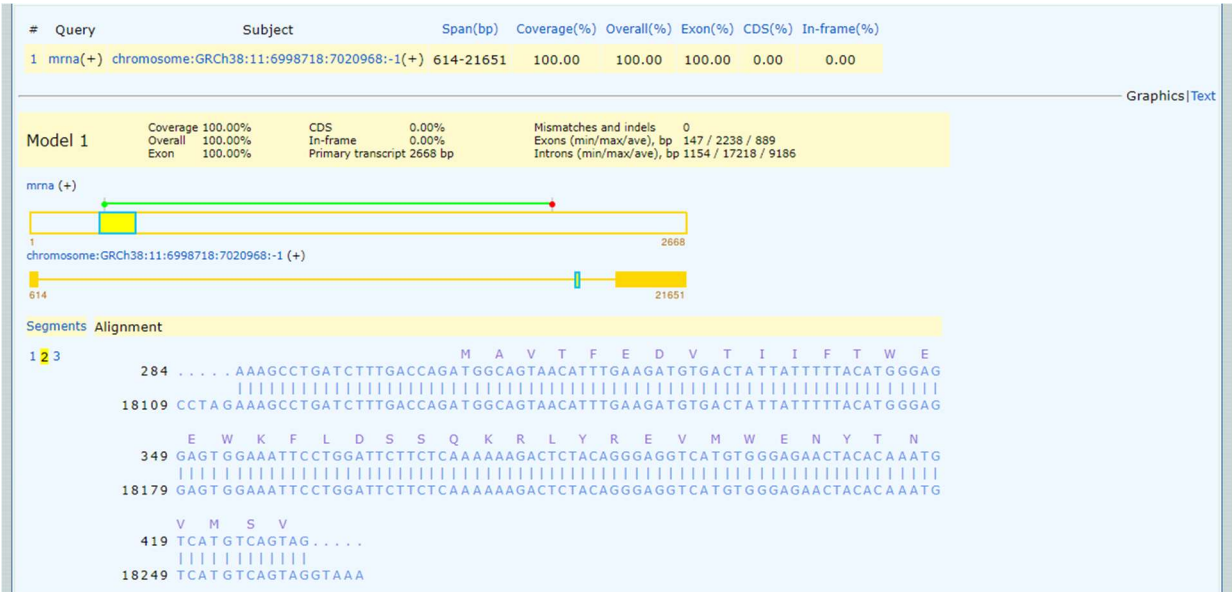
Use SPLIGN to find the mRNA and CDS coordinates in the genomic DNA.

- a. **mRNA locations:** 614~896, 18114~18260, 19414~21651
- b. **CDS locations:** 18134~18260, 19414~21107

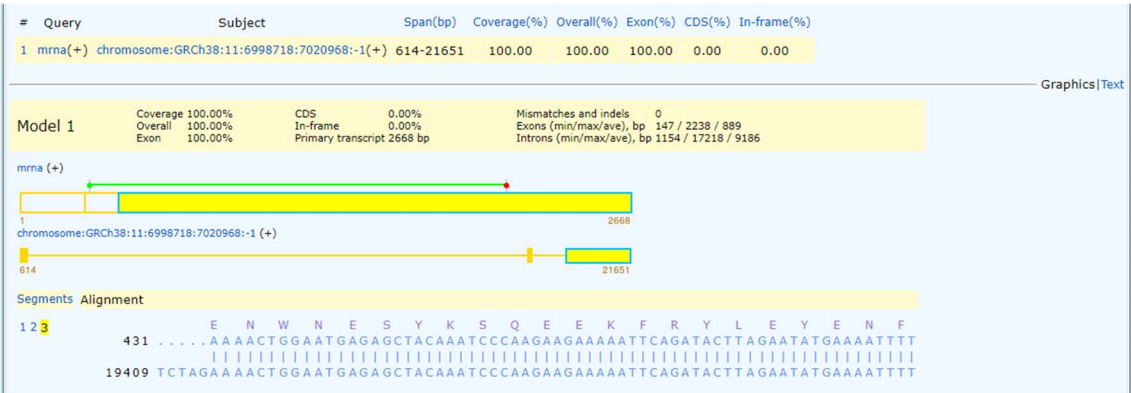
mRNA locations:

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#	Query	Subject	Span(bp)	Coverage(%)	Overall(%)	Exon(%)	CDS(%)	In-frame(%)	
1	mrna(+)	chromosome:GRCh38:11:6998718:7020968:-1(+)	614-21651	100.00	100.00	100.00	0.00	0.00	
Graphics Text									
#	Query	Subject	Idty	Len	Q.Start	Q.Fin	S.Start	S.Fin	Type
+1	mrna	chromosome:GRCh38:11	1	283	1	283	614	896	<exon>GC
+1	mrna	chromosome:GRCh38:11	1	147	284	430	18114	18260	AG<exon>GT
+1	mrna	chromosome:GRCh38:11	1	2238	431	2668	19414	21651	AG<exon>

Segment 2, the first CDS location:



Beginning of segment 3, start of 2nd CDS location:



End of segment 3, end of 2nd CDS location:

