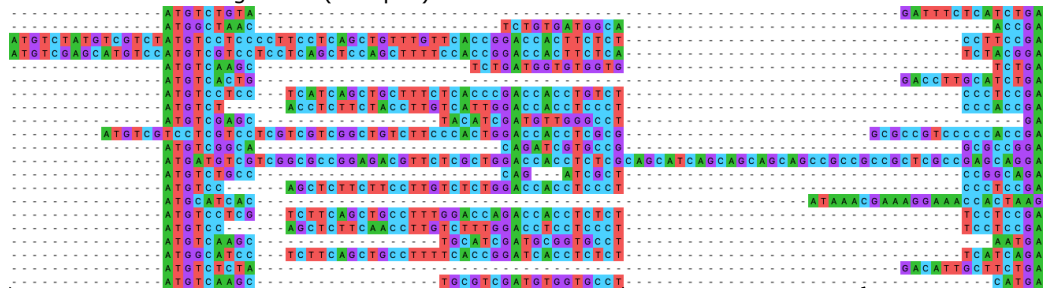


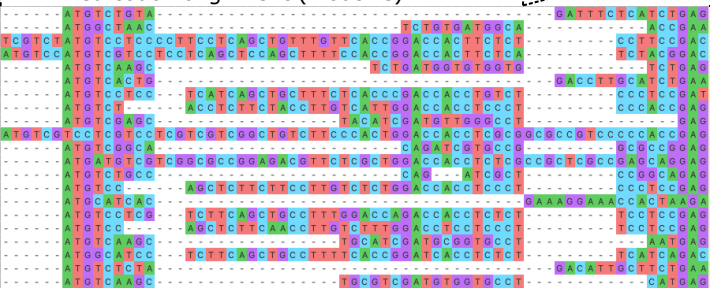
## Untrimmed codon alignment (--seqfile)

Input files



## Trimmed codon alignment (--outfile)

Output file



Translation

## Trimmed amino acid alignment (--trimmed\_aa\_aln)

