

Лабораторная работа 3

1. Геномные данные *Banana streak virus* были загружены в формате fasta с портала NCBI (всего 11 образцов)

NCBI - WWW Error Blocked Diagnostic

Your access to the NCBI website at www.ncbi.nlm.nih.gov has been temporarily blocked due to a possible misuse/abuse situation involving your site. This is not an indication of a security issue

<https://www.ncbi.nlm.nih.gov/genomes/GenomesGroup.cgi?taxid=10239&opt=Virus>

2. Геномные файлы были объединены в один командой

```
cat *.fasta > Banana_streak_concat.fasta
```

3. Множественное выравнивание было произведено при помощи онлайн-версии Mafft

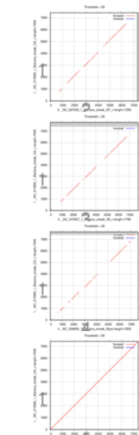
MAFFT alignment and NJ / UPGMA phylogeny

For a large number of short sequences, try an experimental service.

■ <https://mafft.cbrc.jp/alignment/server/index.html>

LAST hits (score>39) between the top sequence and the others.

[Open all plots](#)



Be careful if there are blue lines. By default, MAFFT considers similarities in forward strands (red) only, but ignores similarities in reverse strands (blue). If blue lines are seen around diagonal regions in the plots above, try the "Adjust

[Clustal format](#) | [Fasta format](#) | [MAFFT result](#) | [View](#) | [Tree](#) | [Refine dataset](#) | [Return to home](#)

[View](#)

Reformat to GCG, PHYLIP, MSF, NEXUS, uppercase/lowercase, etc. with Readseq

[GUIDANCE2](#) computes the residue-wise confidence scores and extracts well-aligned residues.

[Refine dataset](#)

[Phylogenetic tree](#)

MAFFT-FFT-NS-i Result for Banana_streak_MSA

CLUSTAL format alignment by MAFFT (v7.511)

```
NC_015506. TGGTATCAGAGCAAGGTTAGTT-----CTTATGGCTTTCATGGGGTAAACCCCTTA
NC_003381. TGGTATCAGAGCAAGGTTTCGTT-----TTTATGGCTTTCATGGGGTAAATCCCTTA
NC_015502. TGGTATCAGAGCAAGGTTAGTT-----CTTATGGCTTTCATGGGGTAAATCCCTAG
NC_015503. TGGTATCAGAGCAAGGTTTCGTTAGTT--TTTATGGCTTTCATGGGGTAAATCCCTTA
NC_007003. TGGTATCAGAGCAAGGTTTCTGTAAGTAA--TTTATGGCTTTCATGGGGTAAACCCCTTA
NC_008018. TGGTATCAGAGCAAGGTTTCTGTAAGTAA--TTTATGGCTTTCATGGGGTAAACCCCTTA
NC_007002. TGGTATCAGAGCAAGGTTAAGA-----TTGATGGCTTTCATGGGGTAAACCCCTAA
NC_006955. TGGTATCAGAGCAAGGTTTCTGTAAGTAA--TTTATGGCTTTCATGGGGTAAATCCCTAG
NC_015503. TGGTATCAGAGCAAGGTTAGTT-----CTTATGGCTTTCATGGGGTAAATCCCTTA
NC_015504. TGGTATCAGAGCAAGGTTATGAT-----TTTATGGCTTTCATGGGGTAAATCCCTTA
NC_015505. TGGTATCAGAGC--AGGTTAGTA-----TCTATGGCTTTCATGGGGTAAACCCCTTA
*****
NC_015506. GGTAGAGCCGAT--GGGCTCTGCTAT--TTTGAATTTGGGTTAATGGTTGTACAAG--
NC_003381. GATAGAGCCGAA--GGGCTCTGCTTT--TCTGAATTTGAGTTACAAGTT-----
NC_015502. GATAGAGCCCTGA--GGGCTCTGCTATGCTTCAATTTGGGAAATAATGTGCAAGTA--
NC_015507. GATAGAGCCCTAA--GGGCTCTGCTATGCTTCAATTTGAGAAATAAGCTGTGAAGTAG-
NC_007003. GATAGAGCCCTGA--GGGCTCTGCTATGTTCTAATTTGAGAAATAAGCTGTGAAGTAG-
NC_008018. GATAGAGCCCTAA--GGGCTCTGCTATGCTTCTG--TTTGAATAATAGTTGTGCAAGTAGA
NC_007002. GATAGAGCCCTGATTGAGTTCTAC--GTTCTGTTAAGTAAAGATTT-----
NC_006955. GATAGAGCCCTAA--GGGCTCTTTTATGCATATTTCTGAATTTCTGTGAAGCTATG--
NC_015503. GATAGAGCCCAAG--AGGCTCTGCAAT--GTTGTTTAAACAACTACCTGTGCAATGT-
NC_015504. GATAGAGCCCTGA--GGGCTCTGCTTT--CTATGTTAAGACAACTACTTGTGCAAGTTT-
NC_015505. GATAGAGCCCAAA--GGGCTCTGAGTTTATGGAAGGCAACTGTTTGACAAATA--
*****
NC_015506. --TTCTATGAT-----AGATAAGTCGAATGGAGCA-----
NC_003381. -----TATGATTT-----AAATGTTTAAATTTGAGCT-----
NC_015503. GATTGCTGTTGAT-----AGCTGCAAGCTTTTAAATTTA
```

4. Филогенетическое дерево было построено при помощи тула Phylo.io 1.0.0 (по ссылке Phylogenetic tree)

