Question 1. Compare Dengue (NC_001477) with Zika virus (NC_012532.1).
They are both mosquito borne viruses spread especially by the Aedes Aegypti
mosquito. Both have similar symptoms, including:
conjunctivitis, muscle and joint pain, rashes, headaches and fever.

Use all the techniques explained in the lectures that you consider suitable.

In order to see Question 1. results, please look at the plots produced

Question 2 - Download Zika virus (NC_012532.1).
Fit its genome sequence to a Markov chain model
estimating its transition probability matrix

Transition probability matrix - Zika virus genome

	a	c	g	t
a	0.2664661	0.2129723	0.3119358	0.2086259
c	0.3611700	0.2467147	0.1242052	0.2679101
g	0.3195285	0.1994266	0.3029627	0.1780822
t	0.1467014	0.2230903	0.4175347	0.2126736

Question 3 - Take the sequence of Dengue virus (NC_001477) from position 101 to 200
Suppose now that you don't know whether this sequence
belongs to Zica or Dengue virus (of course, you know it!).
Decide using the log likelihood method to which virus this sequence belongs.

Transition probability matrix - Dengue virus genome

	a	c	g	t
a	0.3234092	0.2101576	0.2597782	0.2066550
c	0.4022321	0.2334821	0.1165179	0.2477679
g	0.3523466	0.1805054	0.2841155	0.1830325
t	0.1914708	0.2162750	0.3620540	0.2302002

Create slice of sequence of length 100 from dengue genome,
fit it into the probability matrix using log likelihood method.

  [1] "a" "a" "c" "c" "a" "a" "c" "g" "g" "a" "a" "a" "a" "a" "g" "a" "c" "g" "g"
"g" "t" "c" "g" "a" "c" "c"
 [27] "g" "t" "c" "t" "t" "t" "c" "a" "a" "t" "a" "t" "g" "c" "t" "g" "a" "a" "a"
"c" "g" "c" "g" "c" "g" "a"
 [53] "g" "a" "a" "a" "c" "c" "g" "c" "g" "t" "g" "t" "c" "a" "a" "c" "t" "g" "t"
"t" "t" "c" "a" "c" "a" "g"
 [79] "t" "t" "g" "g" "c" "g" "a" "a" "g" "a" "g" "a" "t" "t" "c" "t" "c" "a" "a"
"a" "a" "g"

 Log likelihood method:
      If score > 0 the sequence belongs to dengue, if score < 0 then to zika

[1] 1.495699

 Question 4. Fit the Zica virus sequence to a two second order Markov chain model.
          Compare the results with respect a simple Markov chain model.

Comparing results = multinomial, classical markov chain model and
a second order markov chain model

BIC multinomial:
[1] 29751.26
BIC classical Markov Chain:
[1] 29115.85
BIC k=2:
[1] 29241.58
Min BIC: 29115.85
Min BIC (best model): Classical Markov Chain