Analysis.Rmd

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Link to github (https://github.com/alyssagreen02)

Part I

Image of bacteria



image of Borrelia burgdorferi

Link to Borrelia burgdorferi Wikipedia page

Borrelia burgdorferi Wikipedia page (https://en.wikipedia.org/wiki/Borrelia_burgdorferi)

Import Sequences.csv

Sequences=read.csv("Sequences.csv")

Print out each sequence

print(Sequences\$Sequence)

Count number of each base pair

```
Sequences$Sequence=as.factor(Sequences$Sequence)
A=c()
Th=c()
C=c()
G=c()
ABP=c()
TBP=c()
CBP=c()
GBP=c()
for (i in 1:length(Sequences$Sequence)) {
 A[i]=gsub("T|C|G", "", Sequences$Sequence[i])
 Th[i]=gsub("A|C|G", "", Sequences$Sequence[i])
 C[i]=gsub("A|T|G", "", Sequences$Sequence[i])
 G[i]=gsub("A|T|C", "", Sequences$Sequence[i])
ABP[i]=nchar(A[i])
TBP[i]=nchar(Th[i])
CBP[i]=nchar(C[i])
GBP[i]=nchar(G[i])
 }
```

Table with number of each nucleotide

```
Tab=matrix(nrow=4, ncol = 3)
Tab[1,]=ABP
Tab[2,]=TBP
Tab[3,]=CBP
Tab[4,]=GBP
colnames(Tab)=c("HQ433692.1","HQ433694.1", "HQ433691.1")
rownames(Tab)=c("A","Th","C", "G")
print(Tab)
```

```
##
      HQ433692.1 HQ433694.1 HQ433691.1
## A
             154
                         155
                                     154
## Th
             114
                         114
                                     115
## C
              82
                          81
                                     81
## G
             131
                         131
                                     131
```

GC content of nucleotides

```
BP1=nchar(as.character(Sequences$Sequence[1]))
BP2=nchar(as.character(Sequences$Sequence[2]))
BP3=nchar(as.character(Sequences$Sequence[3]))
GC1=((CBP[1]+GBP[1])/BP1)*100
GC2=((CBP[2]+GBP[2])/BP2)*100
GC3=((CBP[2]+GBP[2])/BP3)*100
Tab=matrix(nrow=3, ncol = 2)
Tab[1,]=c("HQ433692.1", GC1)
Tab[2,]=c("HQ433694.1", GC2)
Tab[3,]=c("HQ433691.1", GC3)
colnames(Tab)=c("Sequence ID", "GC Content")
print(Tab)
##
        Sequence ID GC Content
## [1,] "HQ433692.1" "44.2827442827443"
## [2,] "HQ433694.1" "44.0748440748441"
```

```
## [3,] "HQ433691.1" "44.0748440748441"
```

Part II

Load Library

Loading required package: stats4

Loading required package: BiocGenerics

```
library(BiocManager)
## Warning: package 'BiocManager' was built under R version 4.1.3
## Bioconductor version '3.14' is out-of-date; the current release version '3.16'
    is available with R version '4.2'; see https://bioconductor.org/install
library(annotate)
## Warning: package 'annotate' was built under R version 4.1.1
## Loading required package: AnnotationDbi
## Warning: package 'AnnotationDbi' was built under R version 4.1.1
```

```
## Warning: package 'BiocGenerics' was built under R version 4.1.1
##
## Attaching package: 'BiocGenerics'
## The following objects are masked from 'package:stats':
##
##
       IQR, mad, sd, var, xtabs
## The following objects are masked from 'package:base':
##
##
       anyDuplicated, append, as.data.frame, basename, cbind, colnames,
       dirname, do.call, duplicated, eval, evalq, Filter, Find, get, grep,
##
       grepl, intersect, is.unsorted, lapply, Map, mapply, match, mget,
##
##
       order, paste, pmax, pmax.int, pmin, pmin.int, Position, rank,
       rbind, Reduce, rownames, sapply, setdiff, sort, table, tapply,
##
       union, unique, unsplit, which.max, which.min
##
## Loading required package: Biobase
## Warning: package 'Biobase' was built under R version 4.1.1
## Welcome to Bioconductor
##
##
       Vignettes contain introductory material; view with
       'browseVignettes()'. To cite Bioconductor, see
##
       'citation("Biobase")', and for packages 'citation("pkgname")'.
##
## Loading required package: IRanges
## Warning: package 'IRanges' was built under R version 4.1.1
## Loading required package: S4Vectors
## Warning: package 'S4Vectors' was built under R version 4.1.3
##
## Attaching package: 'S4Vectors'
## The following objects are masked from 'package:base':
##
##
       expand.grid, I, unname
```

```
##
 ## Attaching package: 'IRanges'
 ## The following object is masked from 'package:grDevices':
 ##
 ##
        windows
 ## Loading required package: XML
 ## Warning: package 'XML' was built under R version 4.1.3
Load sequence
 Seq=data.frame(Sequence="> Human isolate, unknown sequence
 GCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATGAC
 CTCGCAAGAGCAAAGTGGGGGACCTTAGGGCCTCACGCCATCGGATGAAC
 CCAGATGGGATTAGCTAGTAGGTGGGGTAATGGCTCACCTAGGCGACGAT
 CCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGAACTGAGACACGGT
 CCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAA")
 Blast=blastSequences(paste(Seq$Sequence), as='data.frame', timeout = 500, hitListSize=10)
 ## estimated response time 59 seconds
```

nrow(Blast)

[1] 67

head(Blast)

```
##
   Iteration_iter-num Iteration_query-ID
                                    Iteration query-def
## 1
                    Query 28231 Human isolate, unknown sequence
              1
## 2
              1
                    Query 28231 Human isolate, unknown sequence
## 3
              1
                    Query 28231 Human isolate, unknown sequence
              1
                    Query 28231 Human isolate, unknown sequence
## 4
## 5
                    Query 28231 Human isolate, unknown sequence
              1
                    Query_28231 Human isolate, unknown sequence
## 6
              1
##
   Iteration_query-len
## 1
              250
## 2
              250
## 3
              250
## 4
              250
## 5
              250
## 6
              250
##
Iteration hits
## 1 1gi|2290367315|gb|CP096666.1|Yersinia pestis EV76-CN chromosome, complete genomeCP096666455
36851452.1295001.69196e-1221250230190230439112502500250GCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATA
CCGCATGACCTCGCAAGAGCAAAGTGGGGGACCTTAGGGCCTCACGCCATCGGATGAACCCAGATGGGATTAGCTAGTAGGTGGGGTAATGGCTCA
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||||||||4452.1295001.69196e-1221250450729045070411-12502500250GCCTGATGGAGGGGGATAACTACTGGAAACGG
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```

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2gi 2279781810 gb CP084343.1 Yersinia pestis strain 20 chromosome, complete genomeCP
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7.1944e-1211250967464967713112492490250GCCTGATGGAGGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATGACCTCGCAA
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genomeCP08433946476101452.1295001.69196e-1221250322877323126112502500250GCCTGATGGAGGGGGATAACTACT
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6447.624957.1944e-1211250561091561340112492490250GCCTGATGGAGGGGGGATAACTACTGGAAACGGTAGCTAATACCG
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${\tt CACAATGGGCGCAAGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCGTGACCTCGCAAGAGCAAAGTGGGGGACCTTAGGGCC}\\$
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- SANNO I SANTADUDUNDU I CONCENCIO I ACCUCACIO DE LA LANDO DE LA LACENCIO DE LA LACENCIO I CONCENCIO I CONCENCIO I CONCENCIO DE LA LACENCIO DEL LACENCIO DE LA LACENCIO DE LA LACENCIO DEL LACENCIO DE LA LACENCIO DE LA LACENCIO DE LA LACENCIO DE LACENCIO DE LA LACENCIO DEL LACENCIO DE LACENCIO DEL LACENCIO DE LA LACENCIO DEL LACENCIO DELLA LA

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$ome, \ complete \ genome CP06412546365451452.1295001.69196e-1221250175544175793112502500250GCCTGATGGAB and the complete \ genome \$
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731 gb CP064119.2 Yersinia pestis strain C-792 chromosome, complete genomeCP06411944815421452.12
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$\verb gi 1948828809 gb CP065918.1 Yersinia pestis EV NIIEG chromosome, complete genome CP06591845536871 Persinia CP06591845536871 Persinia Pestis EV NIIEG chromosome, complete genome CP06591845536871 Pestis EV NIIEG chromosome, complete genome CP0659184553687 Pestis EV NIIEG chromosome, complete genome CP0659184553687 Pestis EV NIIEG chromosome, complete genome CP065918455368 Pestis EV NIIEG chromosome, complete genome CP06591845536 Pestis EV NIIEG chromosome, complete genome CP06591845 Pestis EV NIIEG chromosome CP0659184 Pestis EV NIIEG chromosome CP0659184 Pestis EV NIIEG c$
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${\tt TGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAAGCCTGATGGAGGGGGATAACTACTGGAAAAAAAA$
${\tt CGGTAGCTAATACCGCATGACCTCGCAAGAGCAAAGTGGGGGACCTTAGGGCCTCACGCCATCGGATGAACCCAGATGGGATTAGCTAGTAGGTGGCATGGGATGAACCCAGATGGGATTAGCTAGTAGGTGGATGGGATGAACCCAGATGGGATTAGCTAGTAGGTGGATGAACCCAGATGGGATTAGCTAGTAGGTGGATGAACCCAGATGGGATGAACCCAGATGGGATTAGCTAGTAGGTGGATGAACCCAGATGGGATTAGCTAGTAGGTGGATGAACCCAGATGGGATTAGCTAGTAGGTGGATGAACCCAGATGGGATTAGCTAGTAGGTGGATGAACCCAGATGGGATTAGCTAGTAGGTGGATGAACCCAGATGGGATTAGCTAGTAGGTGGATGAACCCAGATGGGATTAGCTAGTAGGTGGATGAACCCAGATGGGATTAGCTAGTAGGTGGATGAACCCAGATGGGATTAGCTAGTAGGTGGATGAACCCAGATGGGATTAGCTAGTAGGTGGATGAACCCAGATGGGATTAGCTAGTAGGTGGATGAACCCAGATGAGATGAACCCAGATGGGATGAACCCAGATGAGATGAACCCAGATGAGATGAACCCAGATGAGAACCCAGATGAGATGAACCCAGATGAGATGAACCCAGATGAGATGAACCCAGATGAGATGAACCCAGATGAACCCAGATGAACCCAGATGAACCCAGATGAACCCAGATGAACACAACAACAACAACAACAACAACAACAACAACAACA$
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ATGGGCGCAA
Yersinia pestis strain R chromosome, complete genomeCP08433646488241452.1295001.69196e-12212503
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4452.1295001.69196e-12
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ACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAA
$ 5 {\rm gi} 2152215862 {\rm gb} {\rm CP071944.1} {\rm Yersinia} \ pseudotuberculosis \ strain \ 598 \ chromosom \ pseudotuberculosis \ p$
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$\verb CTACTGGAAACGGTAGCTAATACCGCATGACCTCGCAAGAGCAAAGTGGGGGACCTTAGGGCCTCACGCCATCGGATGAACCCAGATGGGATTAGC $
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303.2 Yersinia pestis strain 14D chromosome, complete genomeCP06330346017121452.1295001.69196e-1
303.2 Yersinia pestis strain 14D chromosome, complete genomeCP06330346017121452.1295001.69196e-1 221250320046320295112502500250GCCTGATGGAGGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATGACCTCGCAAGAGCAAAGT
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ACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAA	Ш
	 I I I
	som
eCP07194447319091452.1295001.69196e-1221250316075316324112502500250GCCTGATGGAGGGGGATAACTACTGG	
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${\sf GAGAGGATGACCAGCCACACTGGAACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAA }$	
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                            500 1.69196e-122
## 3
         3
                452.129
                                                       1
                                                                250
                                                       1
## 4
         4
                452.129
                            500 1.69196e-122
                                                                250
## 5
         5
                            495 7.1944e-121
                 447.62
                                                       1
                                                                250
## 6
                 447.62
                            495 7.1944e-121
                                                       1
                                                                250
    Hsp hit-from Hsp hit-to Hsp query-frame Hsp hit-frame Hsp identity
##
## 1
         230190
                   230439
                                     1
                                                 1
                                                           250
         439523
## 2
                   439772
                                     1
                                                 1
                                                           250
                                     1
## 3
        3254685
                  3254436
                                                 -1
                                                           250
## 4
        4507290
                  4507041
                                     1
                                                 -1
                                                           250
## 5
         396659
                   396908
                                     1
                                                 1
                                                           249
## 6
         917598
                   917847
                                     1
                                                 1
                                                           249
    Hsp positive Hsp gaps Hsp align-len
##
## 1
            250
                     0
                                250
            250
                                250
## 2
                      0
            250
                                250
## 3
                      0
## 4
            250
                      0
                                250
## 5
                                250
            249
                      0
                                250
## 6
            249
                      0
##
Hsp qseq
```

^{## 1} GCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATGACCTCGCAAGAGCAAAGTGGGGGACCTTAGGGCCTCACGCCAT
CGGATGAACCCAGATGGGATTAGCTAGTAGGTGGGGTAATGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGA
ACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAA

^{## 2} GCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATGACCTCGCAAGAGCAAAGTGGGGGACCTTAGGGCCTCACGCCAT
CGGATGAACCCAGATGGGATTAGCTAGTAGGTGGGGTAATGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGA
ACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAA

- ## 3 GCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATGACCTCGCAAGAGCAAAGTGGGGGACCTTAGGGCCTCACGCCAT
 CGGATGAACCCAGATGGGATTAGCTAGTAGGTGGGGTAATGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGA
 ACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAA
- ## 4 GCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATGACCTCGCAAGAGCAAAGTGGGGGACCTTAGGGCCTCACGCCAT
 CGGATGAACCCAGATGGGATTAGCTAGTAGGTGGGGTAATGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGA
 ACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAA
- ## 5 GCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATGACCTCGCAAGAGCAAAGTGGGGGACCTTAGGGCCTCACGCCAT
 CGGATGAACCCAGATGGGATTAGCTAGTAGGTGGGGTAATGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGA
 ACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAA
- ## 6 GCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATGACCTCGCAAGAGCAAAGTGGGGGACCTTAGGGCCTCACGCCAT CGGATGAACCCAGATGGGATTAGCTAGTAGGTGGGGTAATGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGA ACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAA

##

Hsp_hseq

- ## 1 GCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATGACCTCGCAAGAGCAAAGTGGGGGACCTTAGGGCCTCACGCCAT
 CGGATGAACCCAGATGGGATTAGCTAGTAGGTGGGGTAATGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGA
 ACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAA
- ## 2 GCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATGACCTCGCAAGAGCAAAGTGGGGGACCTTAGGGCCTCACGCCAT
 CGGATGAACCCAGATGGGATTAGCTAGTAGGTGGGGTAATGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGA
 ACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAA
- ## 3 GCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATGACCTCGCAAGAGCAAAGTGGGGGACCTTAGGGCCTCACGCCAT CGGATGAACCCAGATGGGATTAGCTAGTAGGTGGGGTAATGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGA ACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAA
- ## 4 GCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATGACCTCGCAAGAGCAAAGTGGGGGACCTTAGGGCCTCACGCCAT
 CGGATGAACCCAGATGGGATTAGCTAGTAGGTGGGGTAATGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGA
 ACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAA
- ## 5 GCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCGTGACCTCGCAAGAGCAAAGTGGGGGACCTTAGGGCCTCACGCCAT
 CGGATGAACCCAGATGGGATTAGCTAGTAGGTGGGGTAATGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGA
 ACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAA
- ## 6 GCCTGATGGAGGGGGATAACTACTGGAAACGGTGGCTAATACCGCATGACCTCGCAAGAGCAAAGTGGGGGACCTTAGGGCCTCACGCCAT CGGATGAACCCAGATGGGATTAGCTAGTAGGTGGGGTAATGGCTCACCTAGGCGACGATCCCTAGCTGGTCTGAGAGGATGACCAGCCACACTGGA ACTGAGACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGCAA

Hsp_midline



Warning: package 'ggplot2' was built under R version 4.1.3

Report

In our analysis, we searched for the closest matching DNA sequence on Genbank. The analyses found that the outlier sequence comes from *Yersinia pestis*, a zoonotic bacteria usually found in small mammals and their fleas (Plague, n.d.). The accuracy of this finding was tested by looking at Hsp score (Figure 1) and evalue (Figure 2) for each of the hits obtained. All Hsp scores are either 495 or 500, which are very high values, indicating that the hits are accurate. All the evalues are either 7.24e-121 or 1.7e-122, which are extremely small values, indicating that the hits are accurate. Because of the accuracy of the findings, the fact that the sequence comes from *Yersinia pestis* is very concerning. Infection by *Yersinia pestis* is known to cause the plague (Plague (yersinia pestis), 2022). The plague is a life-threatening condition that has historically caused widespread pandemics with high mortality (Plague, n.d.). The finding of the plague in a human sequence is particularly troubling as it has a case fatality ratio of 30% to 100% if left untreated (Plague, n.d.). Currently, up to 3000 cases of the plague are reported to the World Health Organization each year, and it must be closely monitored and the spread mitigated to prevent another pandemic (Plague (yersinia pestis), 2022).

ggplot(aes(x=Hit_accession, y=Hsp_score), data=Blast)+geom_point()+theme_bw()+theme(axis.text.x
= element_text(angle = 90, vjust = 0.5, hjust=1))+labs(x="Hit accession", y="Hsp score")

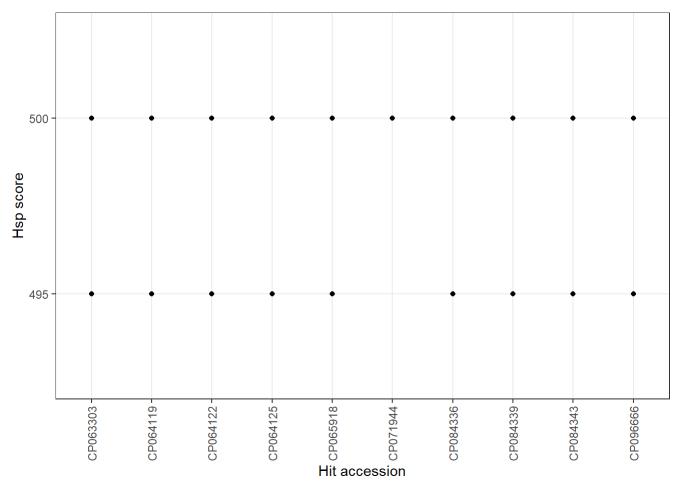


Figure 1: Hsp scores from Blast search. The Hsp scores are all either 495 or 500, which are very high values, indicating that the hits from the blast search are accurate.

```
ggplot(aes(x=Hit_accession, y=Hsp_evalue), data=Blast)+geom_point()+theme_bw()+theme(axis.text.x
= element_text(angle = 90, vjust = 0.5, hjust=1))+labs(x="Hit accession", y="evalue")
```





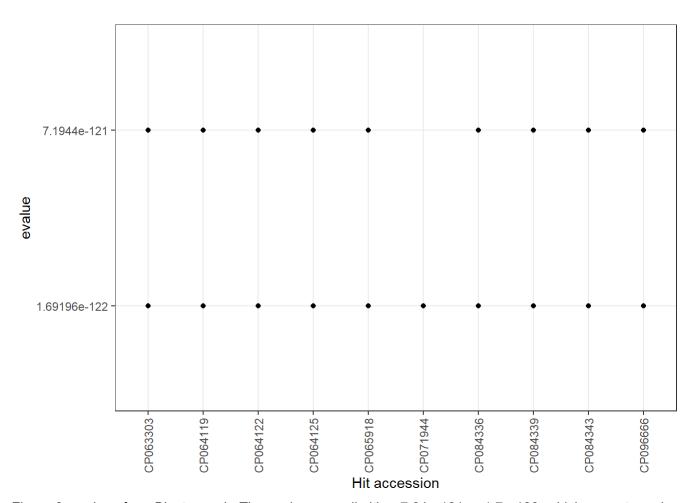


Figure 2: evalues from Blast search. The evalues are all either 7.24e-121 or 1.7e-122, which are extremely small values, indicating that the hits from the blast search are accurate.

References:

Plague. World Health Organization. (n.d.) Retrieved February 15, 2023, from https://www.who.int/news-room/fact-sheets/detail/plague (https://www.who.int/news-room/fact-sheets/detail/plague)

Plague (yersinia pestis). Harvard Health. (2022, February 28). Retrieved February 15, 2023, from https://www.health.harvard.edu/a_to_z/plague-yersinia-pestis-a-to-z (https://www.health.harvard.edu/a_to_z/plague-yersinia-pestis-a-to-z)