

Genetics and Bioinformatics

GBIO0002

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FASTA format

- **The FASTA format is a simple and widely used format for storing biological (DNA or protein) sequences.**
- **It was first used by the FASTA program for sequence alignment.**
- **It begins with a single-line description starting with a “>” character, followed by lines of sequences.**
- **Here is an example of a FASTA file:**

```
> A06852 183 residues  
MPRLFSYLLGVWLLLSQLPREIPGQSTNDFIKACGRELVRLWVEICGSVSWGRTALSLEE  
PQLETGPPAETMPSSITKDAEILKMMLEFVPNLPQELKATLSERQPSLRELQQSASKDSN  
LNFEEFKKIILNRQNEAEDKSLLLELKNLGLDKHSRKKRLFRMTLSEKCCQVGCIRKDIARLC
```

Sequence Database

- The National Centre for Biotechnology Information (NCBI) (www.ncbi.nlm.nih.gov) in the US maintains a huge database of all the DNA and protein sequence data that has been collected, the NCBI Sequence Database
- A similar database in Europe, the European Molecular Biology Laboratory (EMBL) Sequence Database (www.ebi.ac.uk/embl)
- A similar database in Japan, the DNA Data Bank of Japan (DDBJ; www.ddbj.nig.ac.jp).
- These three databases exchange data every night, so at any one point in time, they contain almost identical data.

- **Each sequence in the NCBI Sequence Database is stored in a separate *record*, and is assigned a unique identifier that can be used to refer to that sequence record.**
- **The identifier is known as an *accession*, and consists of a mixture of numbers and letters.**
- **The NCBI accessions for the DNA sequences of the DEN-1, DEN-2, DEN-3, and DEN-4 Dengue viruses are NC_001477, NC_001474, NC_001475 and NC_002640, respectively.**

Retrieving genome sequence data via the NCBI website

- You can easily retrieve DNA or protein sequence data from the NCBI Sequence Database via its website www.ncbi.nlm.nih.gov

The screenshot displays the NCBI website interface. At the top, there is a navigation bar with the NCBI logo and links for 'Resources' and 'How To'. Below this is a search bar with a dropdown menu set to 'All Databases' and the search term 'NC_001477'. On the left side, a vertical menu lists various categories such as 'NCBI Home', 'Resource List (A-Z)', 'All Resources', 'Chemicals & Bioassays', 'Data & Software', 'DNA & RNA', 'Domains & Structures', 'Genes & Expression', 'Genetics & Medicine', 'Genomes & Maps', 'Homology', 'Literature', 'Proteins', 'Sequence Analysis', 'Taxonomy', 'Training & Tutorials', and 'Variation'. The main content area is titled 'Welcome to NCBI' and includes a brief description of the center's mission. Below the welcome message are six service tiles: 'Submit' (Deposit data or manuscripts into NCBI databases), 'Download' (Transfer NCBI data to your computer), 'Learn' (Find help documents, attend a class or watch a tutorial), 'Develop' (Use NCBI APIs and code libraries to build applications), 'Analyze' (Identify an NCBI tool for your data analysis task), and 'Research' (Explore NCBI research and collaborative projects). Each tile features a representative icon.

Dengue virus 1, complete genome

NCBI Reference Sequence: NC_001477.1

[FASTA](#) [Graphics](#)

Go to:

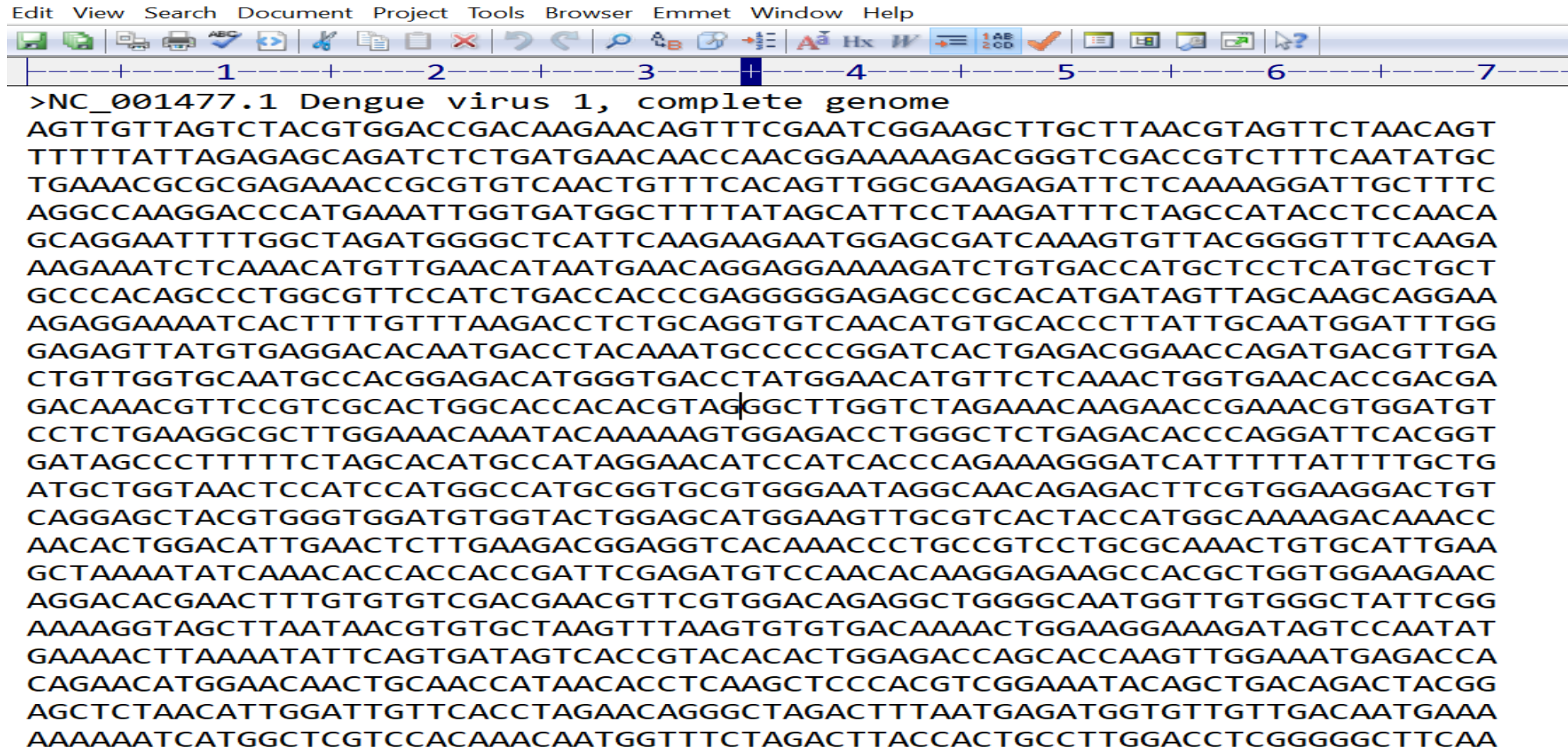
LOCUS NC_001477 10735 bp ss-RNA linear VRL 13-AUG-2018
DEFINITION Dengue virus 1, complete genome.
ACCESSION NC_001477
VERSION NC_001477.1
DBLINK BioProject: [PRJNA485481](#)
KEYWORDS RefSeq.
SOURCE Dengue virus 1
ORGANISM [Dengue virus 1](#)
Viruses; ssRNA viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; Flavivirus.
REFERENCE 1 (bases 1 to 10735)
AUTHORS Puri,B., Nelson,W.M., Henchal,E.A., Hoke,C.H., Eckels,K.H., Dubois,D.R., Porter,K.R. and Hayes,C.G.
TITLE Molecular analysis of dengue virus attenuation after serial passage in primary dog kidney cells
JOURNAL J. Gen. Virol. 78 (PT 9), 2287-2291 (1997)
PUBMED [9292016](#)
REFERENCE 2 (bases 1 to 10735)
AUTHORS McKee,K.T. Jr., Bancroft,W.H., Eckels,K.H., Redfield,R.R., Summers,P.L. and Russell,P.K.
TITLE Lack of attenuation of a candidate dengue 1 vaccine (45AZ5) in human volunteers
JOURNAL Am. J. Trop. Med. Hyg. 36 (2), 435-442 (1987)
PUBMED [3826504](#)
REFERENCE 3 (bases 1 to 10735)
CONSRM NCBI Genome Project
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2000) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

- To retrieve the DNA sequence for the DEN-1 Dengue virus genome sequence as a FASTA format sequence file, click on “Send” at the top right of the NC_001477 sequence record webpage,
- Then choose “File” in the pop-up menu that appears, and then choose FASTA from the “Format” menu that appears, and click on “Create file”

The screenshot shows the NCBI GenBank record for Dengue virus 1, complete genome (NC_001477.1). The 'Send to' pop-up menu is open, showing options for 'Complete Record', 'Coding Sequences', and 'Gene Features'. Under 'Choose Destination', 'File' is selected. The 'Format' dropdown is set to 'FASTA', and the 'Create File' button is visible.

File format

You can now open the FASTA file containing the DEN-1 Dengue virus genome sequence using WordPad on your computer.



The image shows a screenshot of the WordPad application interface. The menu bar includes 'Edit', 'View', 'Search', 'Document', 'Project', 'Tools', 'Browser', 'Emmet', 'Window', and 'Help'. The toolbar contains various icons for file operations and editing. The main text area displays the following FASTA sequence:

```
>NC_001477.1 Dengue virus 1, complete genome
AGTTGTTAGTCTACGTGGACCGACAAGAACAGTTTCGAATCGGAAGCTTGCTTAACGTAGTTCTAACAGT
TTTTTATTAGAGAGCAGATCTCTGATGAACAACCAACGGAAAAAGACGGGTTCGACCGTCTTTCAATATGC
TGAAACGCGCGAGAAACCGCGTGTCAACTGTTTCACAGTTGGCGAAGAGATTCTCAAAGGATTGCTTTC
AGGCCAAGGACCCATGAAATTGGTGATGGCTTTTATAGCATTCCCTAAGATTTCTAGCCATACCTCCAACA
GCAGGAATTTTGGCTAGATGGGGCTCATTCAAGAAGAATGGAGCGATCAAAGTGTTACGGGGTTTCAAGA
AAGAAATCTCAAACATGTTGAACATAATGAACAGGAGGAAAAGATCTGTGACCATGCTCCTCATGCTGCT
GCCACAGCCCTGGCGTTCCATCTGACCACCCGAGGGGGAGAGCCGCACATGATAGTTAGCAAGCAGGAA
AGAGGAAAATCACTTTTGTTTAAGACCTCTGCAGGTGTCAACATGTGCACCCTTATTGCAATGGATTTGG
GAGAGTTATGTGAGGACACAATGACCTACAAATGCCCCCGGATCACTGAGACGGAACCAGATGACGTTGA
CTGTTGGTGCAATGCCACGGAGACATGGGTGACCTATGGAACATGTTCTCAAACCTGGTGAACACCGACGA
GACAAACGTTCCGTCGCACTGGCACCACACGTAGGGCTTGGTCTAGAAACAAGAACCAGAAACGTGGATGT
CCTCTGAAGGCGCTTGGAAACAAATACAAAAAGTGGAGACCTGGGCTCTGAGACACCCAGGATTCACGGT
GATAGCCCTTTTTTCTAGCACATGCCATAGGAACATCCATCACCCAGAAAGGGATCATTTTTTATTTTGCTG
ATGCTGGTAACTCCATCCATGGCCATGCGGTGCGTGGGAATAGGCAACAGAGACTTCGTGGAAGGACTGT
CAGGAGCTACGTGGGTGGATGTGGTACTGGAGCATGGAAGTTGCGTCACTACCATGGCAAAAAGACAAACC
AACACTGGACATTGAACTCTTGAAGACGGAGGTCACAAACCCTGCCGTCCTGCGCAAACCTGTGCATTGAA
GCTAAAATATCAAACACCACCACCGATTTCGAGATGTCCAACACAAGGAGAAGCCACGCTGGTGGGAAGAAC
AGGACACGAACTTTGTGTGTCGACGAACGTTTCGTGGACAGAGGCTGGGGCAATGGTTGTGGGCTATTCGG
AAAAGGTAGCTTAATAACGTGTGCTAAGTTTAAGTGTGTGACAAAACCTGGAAGGAAAGATAGTCCAATAT
GAAAACCTTAAAATATTCAGTGATAGTCACCGTACACACTGGAGACCAGCACCAAGTTGGAAATGAGACCA
CAGAACATGGAACAACCTGCAACCATAACACCTCAAGCTCCCACGTCGGAAATACAGCTGACAGACTACGG
AGCTCTAACATTGGATTGTTACCTAGAACAGGGCTAGACTTTAATGAGATGGTGTGTTGTTGACAATGAAA
AAAAAATCATGGCTCGTCCACAAACAATGGTTTCTAGACTTACCCTGCCTTGGACCTCGGGGGCTTCAA
```


Reading sequence data into R

- **Install seqinr package**

```
if (!requireNamespace("BiocManager", quietly = TRUE))
  install.packages("BiocManager")
BiocManager::install("seqinr")
```

- **Load Library**

```
> library("seqinr")
```

- **Read sequence using read.fasta**

```
> dengueseq<- read.fasta(file = "seq.fasta")
```

- The first element of the list object *dengue* contains the the DNA sequence.

```
> dengueseq <- dengueseq[[1]]
```

Length of a DNA sequence

- Once you have retrieved a DNA sequence, we can obtain some simple statistics to describe that sequence, such as the sequence's total length in nucleotides.
- To subsequently obtain the length of the genome sequence, we would use the `length()` function, typing:

```
> length(dengueseq)
```

```
[1] 10735
```

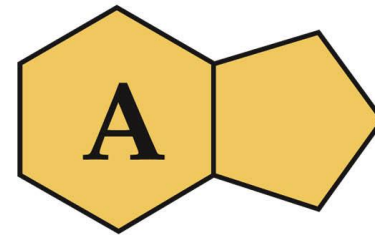
Base composition of a DNA sequence

- To subsequently obtain the composition of the genome sequence, we would use the `table()` function, typing:

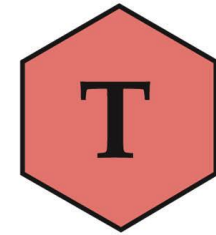
```
> table(dengueseq)
```

```
dengueseq
```

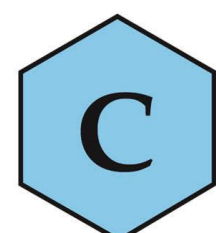
```
a      c      g      t  
3426 2240 2770 2299
```



=



=



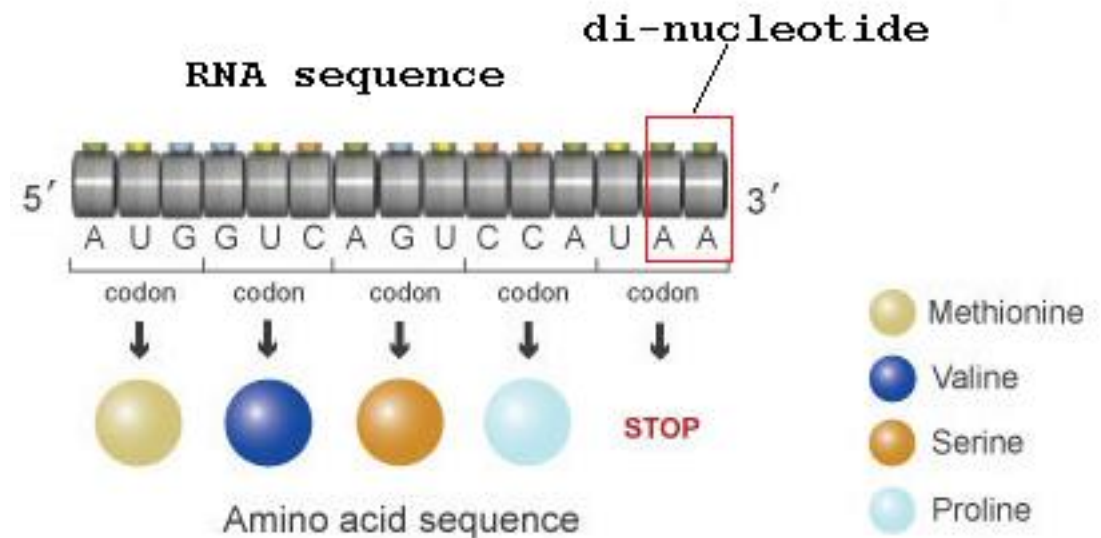
Purines

= Pyrimidines

Words

- Short strings of letters from an alphabet
- A word of length k is called a k -word or k -tuple
- Examples:

- 1-tuple: individual nucleotide
- 2-tuple: dinucleotide
- 3-tuple: codon



2-words: dinucleotides

- **Composed of 2 nucleotides**
 - **Given DNA alphabet {A,T,C,G}**
 - **How many possible dinucleoties?**
 - **Total of 16: AA, AC,AG,AT ... TG,TT**
- **CpG islands are regions of DNA**
 - **Frequent repetition of CpG dinucleotides**
 - **Rich in 'G' and 'C'**
 - **CpG islands appear in some 70% of promoters of human genes**

DNA di-nucleotides words

- if you want to know the frequency of all DNA words that are 2 nucleotides long in the Dengue virus genome sequence, you can type:

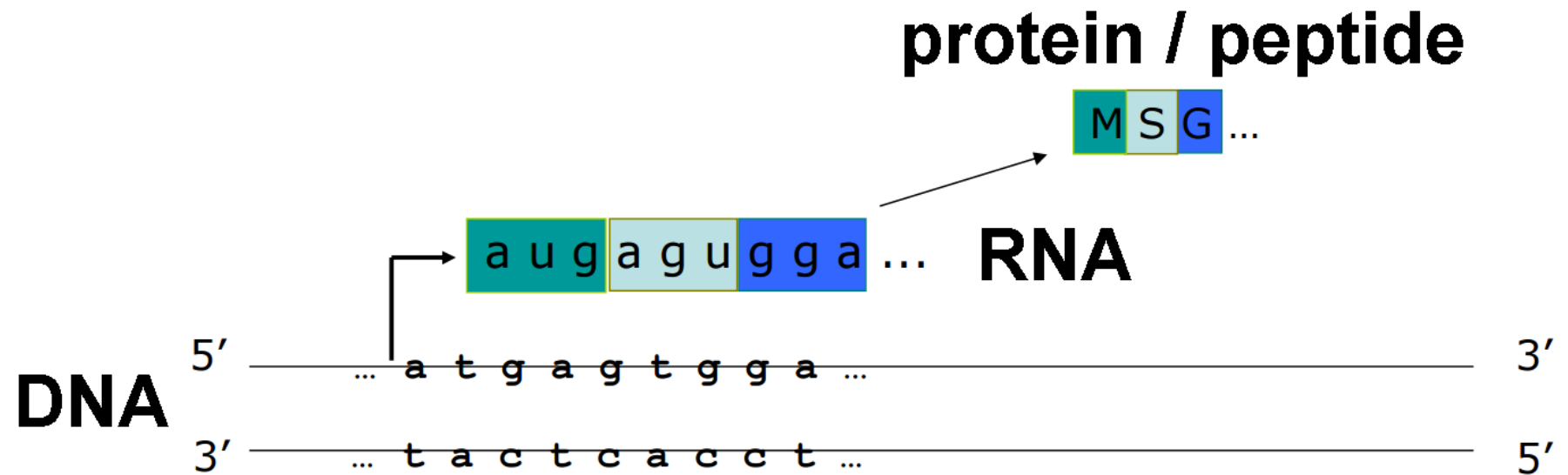
```
> count(dengueseq, 2)
```

```
aa ac ag at ca cc cg ct ga gc gg gt ta tc tg tt
```

```
1108 720 890 708 901 523 261 555 976 500 787 507 440 497 832 529
```

3-words: codons

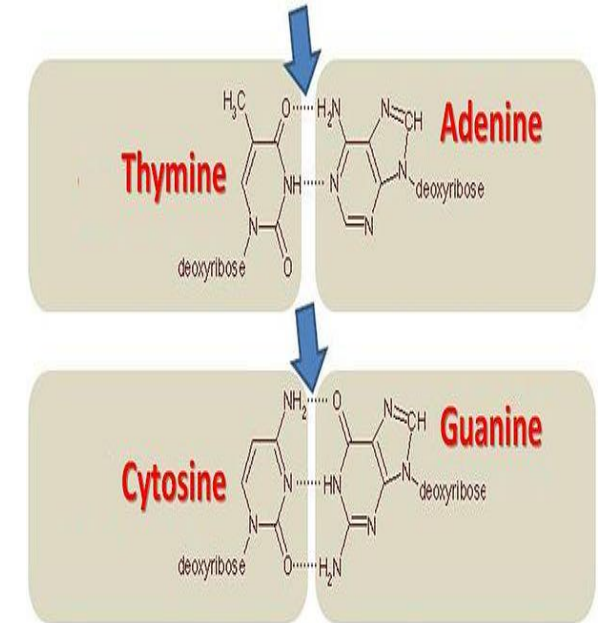
- Important in case of DNA sequences
- Linked to expression
 - DNA → RNA → protein



GC Content of DNA

- One of the most fundamental properties of a genome sequence is its GC content, the fraction of the sequence that consists of Gs and Cs, ie. the $\%(G+C)$.
- You can easily calculate the GC content based on the number of As, Gs, Cs, and Ts in the genome sequence.
- For example, for the DEN-1 Dengue virus genome sequence, we know from using the `table()` function above that the genome contains 3426 As, 2240 Cs, 2770 Gs and 2299 Ts. Therefore, we can calculate the GC content using the command:
> `GC(dengueseq)`

[1] 0.4666977



Nucleotide bonds showing AT and GC pairs. **Arrows point to the hydrogen bonds**

Local variation in GC content

- **Although the GC content of the whole DEN-1 Dengue virus genome sequence is about 46.7%, there is probably local variation in GC content within the genome.**
- **That is, some regions of the genome sequence may have GC contents quite a bit higher than 46.7%, while some regions of the genome sequence may have GC contents that are quite a bit lower than 46.7%.**
- **Local fluctuations in GC content within the genome sequence can provide different interesting information, for example, they may reveal cases of horizontal transfer or reveal biases in mutation.**

A sliding window analysis of GC content

- In order to study local variation in GC content within a genome sequence, we could calculate the GC content for small chunks of the genome sequence.

```
> GC(dengueseq[1:2000]) # Calculate the GC content of nucleotides 1-2000 of the Dengue genome
[1] 0.465
> GC(dengueseq[2001:4000]) # Calculate the GC content of nucleotides 2001-4000 of the Dengue genome
[1] 0.4525
> GC(dengueseq[4001:6000]) # Calculate the GC content of nucleotides 4001-6000 of the Dengue genome
[1] 0.4705
> GC(dengueseq[6001:8000]) # Calculate the GC content of nucleotides 6001-8000 of the Dengue genome
[1] 0.479
> GC(dengueseq[8001:10000]) # Calculate the GC content of nucleotides 8001-10000 of the Dengue genome
[1] 0.4545
> GC(dengueseq[10001:10735]) # Calculate the GC content of nucleotides 10001-10735 of the Dengue genome
[1] 0.4993197
```

for loop in R

- In R, it is possible to write a *for loop* to carry out the same command several times.
- For example, if we want to print out the square of each number between 1 and 10, we can write the following for loop:

```
> for (i in 1:10) { print (i*i) }
```

```
[1] 1
```

```
[1] 4
```

```
[1] 9
```

```
[1] 16
```

```
[1] 25
```

```
[1] 36
```

```
[1] 49
```

```
[1] 64
```

```
[1] 81
```

```
[1] 100
```

the variable i is a counter for the number of cycles through the loop

In the first cycle through the loop, the value of i is 1, and so $i * i = 1$ is printed out.

In the second cycle through the loop, the value of i is 2, and so $i * i = 4$ is printed out

Lets us create a new function

- We can also create our own functions in R to do calculations that you want to carry out very often on different input data sets.
- For example, we can create a function to calculate the value of 20 plus the square of some input number:

```
> myfunction <- function(x) { return(20 + (x*x)) }
```

This function will calculate the square of a number (x), and then add 20 to that value. The return() statement returns the calculated value.

- we can use the function for different input numbers (eg. 10, 25):

```
> myfunction(10)
```

```
[1] 120
```

```
> myfunction(25)
```

```
[1] 645
```

For loop - GC content

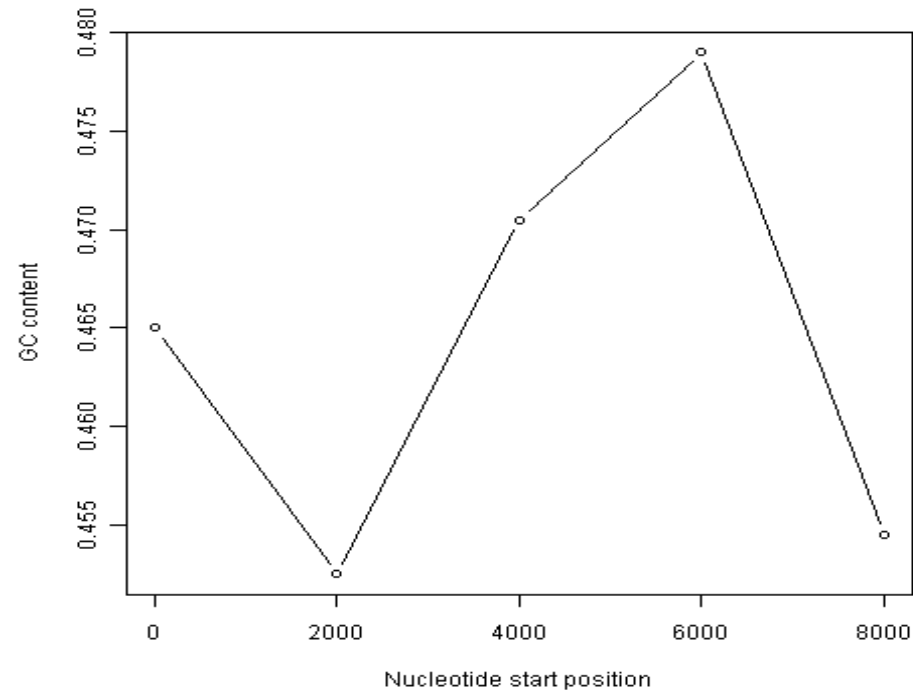
```
> starts <- seq(1, length(dengueseq)-2000, by = 2000)
> n <- length(starts) # Find the length of the vector
"starts"
> chunkGCs <- numeric(n) # Make a vector of the same
length as vector "starts", but just containing zeroes
> for (i in 1:n) {
  chunk <- dengueseq[starts[i]:(starts[i]+1999)]
  chunkGC <- GC(chunk)
  print(chunkGC)
  chunkGCs[i] <- chunkGC
}
> plot(starts,chunkGCs,type="b",xlab="Nucleotide start
position",ylab="GC content")
```

We set the variable *n* to be equal to the number of elements in the vector *starts*,

The line “for (i in 1:n)” means that the counter *i* will take values of 1-5 in subsequent cycles of the *for loop*.

A sliding window plot of GC content

```
> plot(starts,chunkGC,type="b",xlab="Nucleotide start position",ylab="GC content")
```

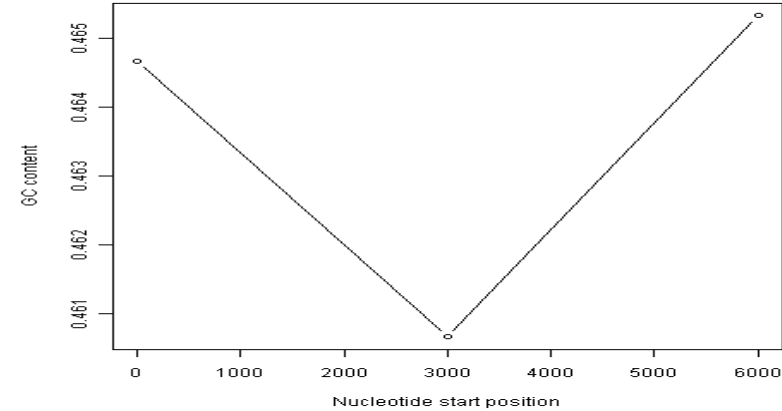


Create a new Function to plot slidingwindowplot

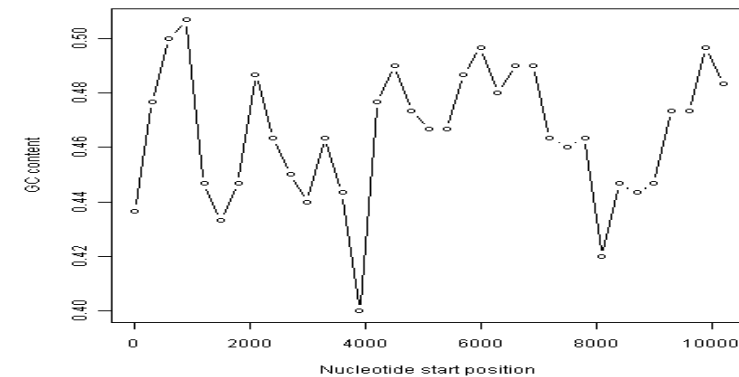
```
> slidingwindowplot <- function(windowsize, inputseq)
{
  starts <- seq(1, length(inputseq)-windowsize, by = windowsize)
  n <- length(starts) # Find the length of the vector "starts"
  chunkGCs <- numeric(n) # Make a vector of the same length as vector "starts", but just containing zeroes
  for (i in 1:n) {
    chunk <- inputseq[starts[i):(starts[i]+windowsize-1)]
    chunkGC <- GC(chunk)
    print(chunkGC)
    chunkGCs[i] <- chunkGC
  }
  plot(starts,chunkGCs,type="b",xlab="Nucleotide start position",ylab="GC content")
}
```

Let us plot GC content in different window size

```
> slidingwindowplot(3000, dengueseq)
```



```
> slidingwindowplot(300, dengueseq)
```



Over and under represented words (1)

- It is interesting to identify DNA words that are two nucleotides long (“dinucleotides”, ie. “AT”, “AC”, etc.) that are over-represented or under-represented in a DNA sequence.
- If a particular DNA word is *over-represented* in a sequence, it means that it occurs many more times in the sequence than you would have expected by chance.
- Similarly, if a particular DNA word is *under-represented* in a sequence, it means it occurs far fewer times in the sequence than you would have expected.

Over and under represented words (2)

- A statistic called ρ (Rho) is used to measure how over- or under-represented a particular DNA word is. For a 2-nucleotide (dinucleotide) DNA word ρ is calculated as:

$$\rho(xy) = f_{xy} / (f_x * f_y),$$

where f_{xy} and f_x are the frequencies of the DNA words xy and x in the DNA sequence under study.

- For example, the value of ρ for the DNA word “TA” can be calculated as: $\rho(TA) = f_{TA} / (f_T * f_A)$, where f_{TA} , f_T and f_A are the frequencies of the DNA words “TA”, “T” and “A” in the DNA sequence.

Over and under represented words (3)

- The frequencies of the 2-nucleotide DNA words in a sequence are expected to be equal the products of the specific frequencies of the two nucleotides that compose them.
- If this were true, then ρ would be equal to 1.
- If we find that ρ is much greater than 1 for a particular 2-nucleotide word in a sequence, it indicates that that 2-nucleotide word is much more common in that sequence than expected (ie. it is *over-represented*).
- If ρ is much less than 1, for a particular 2-nucleotide word in a sequence, indicates under represented

Let us calculate Rho (ρ) for GC

```
> count(dengueseq, 1) # Get the number of occurrences of 1-nucleotide DNA words
  a   c   g   t
3426 2240 2770 2299
> 2770/(3426+2240+2770+2299) # Get fG
[1] 0.2580345
> 2240/(3426+2240+2770+2299) # Get fC
[1] 0.2086633
> count(dengueseq, 2) # Get the number of occurrences of 2-nucleotide DNA words
  aa  ac  ag  at  ca  cc  cg  ct  ga  gc  gg  gt  ta  tc  tg  tt
1108 720 890 708 901 523 261 555 976 500 787 507 440 497 832 529
> 500/(1108+720+890+708+901+523+261+555+976+500+787+507+440+497+832+529)
# Get fGC
[1] 0.04658096
> 0.04658096/(0.2580345*0.2086633) # Get rho(GC)
[1] 0.8651364
```

Exercise

Check how many of these are over and under represented sequences in dengue sequence

- TA
- GA
- CT

What is Sequence Alignment ?

A sequence alignment is a way of arranging the sequences of DNA , RNA, or protein to identify regions of similarity.

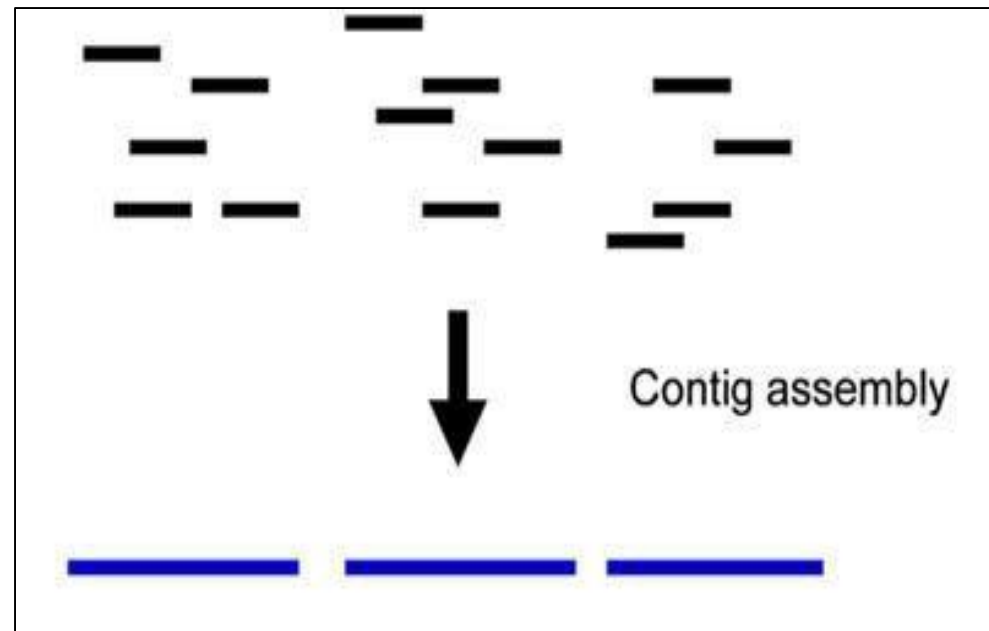


Comparable ?



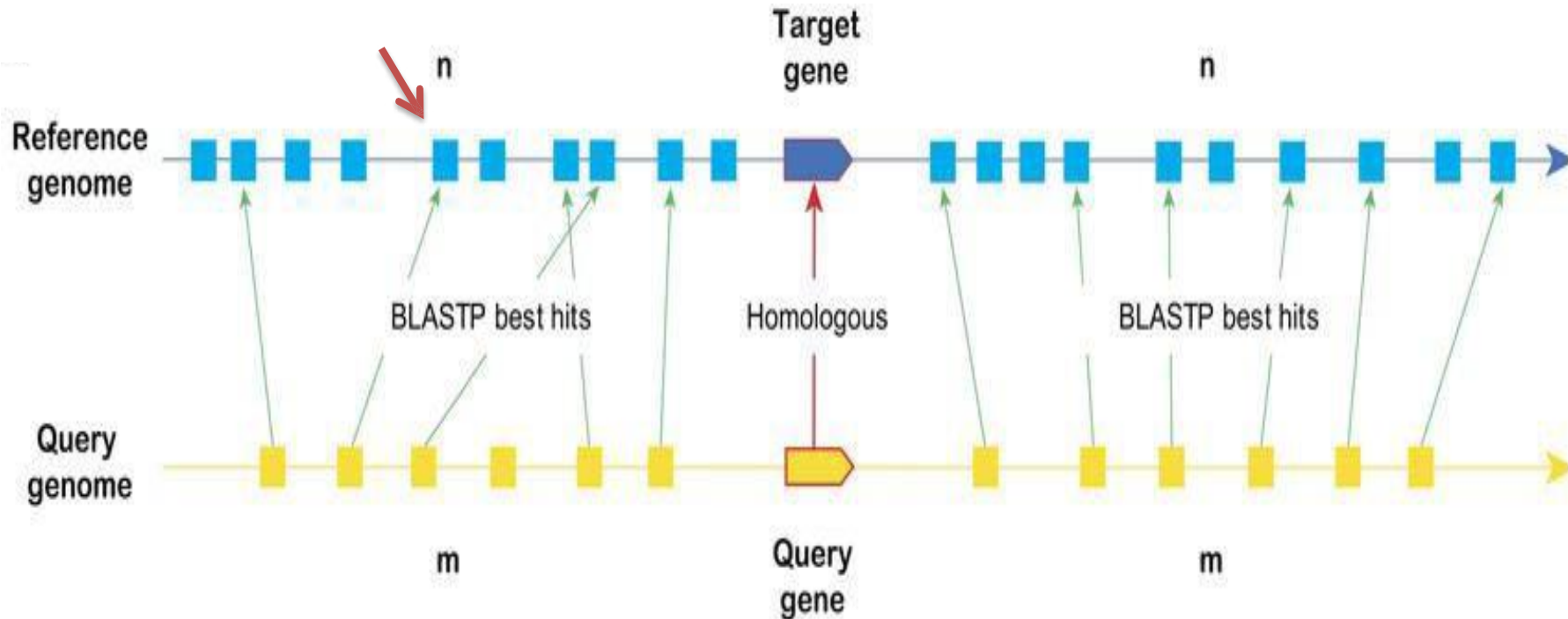
Sequence Alignment :Uses (1)

- **Sequence Assembly** : Genome sequence are assembled by using the sequence alignment methods to find the overlap between many short pieces of DNA .



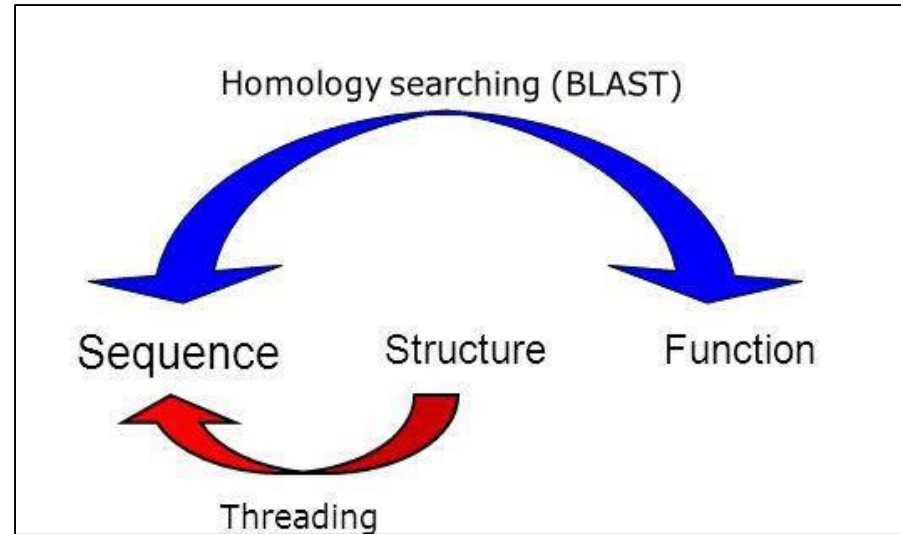
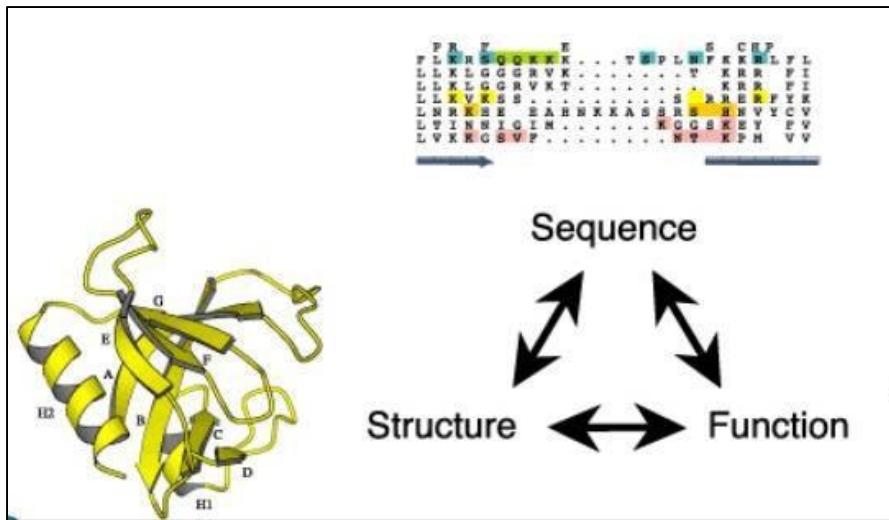
Sequence Alignment :Uses (2)

- **Gene Finding** : Sequence similarity could help us to find the gene prediction just by doing comparison against the other set of sequences.



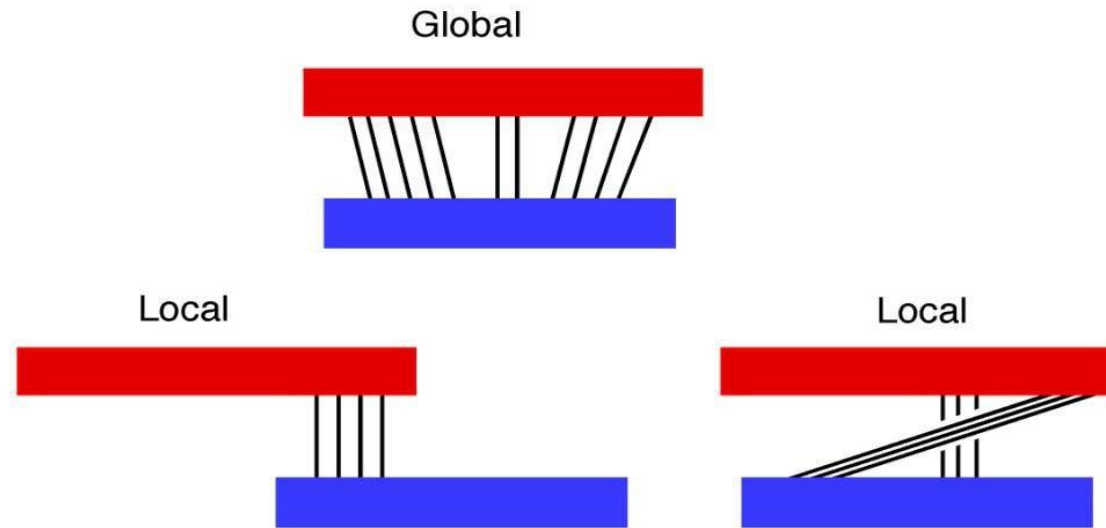
Sequence Alignment :Uses (3)

- **Function prediction** : Function of any unknown sequence could be predicted by comparing with other known sequence .



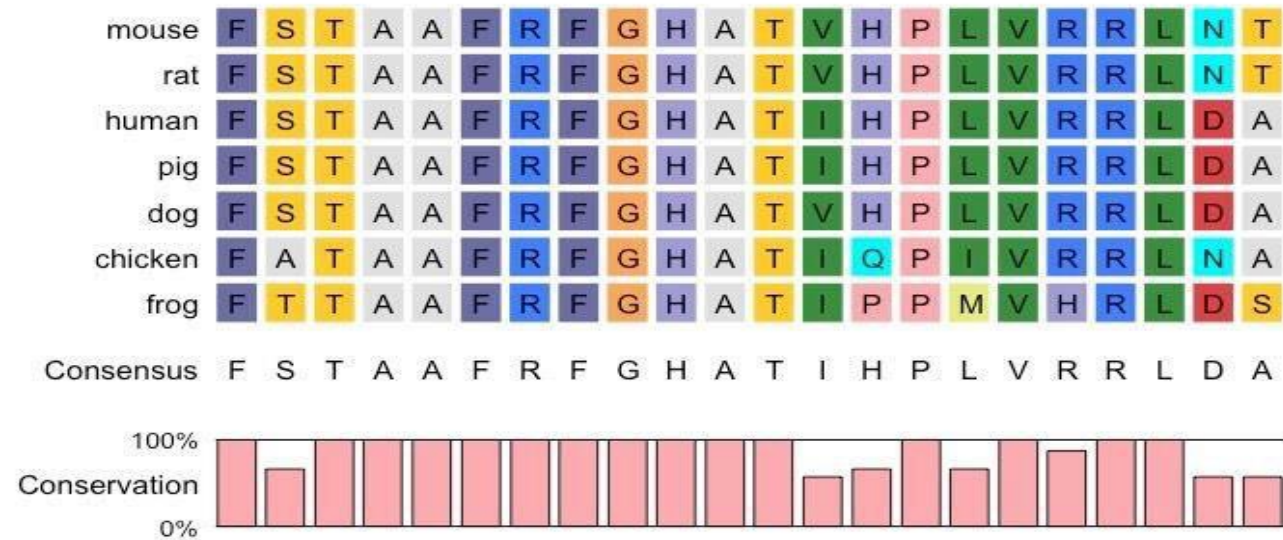
Types of Alignments

- **Global** : This attempt to align every residue in every sequence.
- **Local**: It is more useful for dissimilar sequences that are suspected to contain regions of similarity or similar sequence motifs within their larger sequence context.



Types of Alignments: Based on number of sequences

- **Pair wise Sequence Alignment** : This alignments can only be used between two sequences at a time.
- **Multiple Sequence Alignment** : This alignments can only be used between more than two sequences at a time.



Tools for Sequence Alignments



There are many tools for sequence Alignment. In this session, we will discuss about

- **BLAST**

- **CLUSTALW**

Sequence Alignment : BLAST

- **BLAST** stands for **B**asic **L**ocal **A**lignment **S**earch **T**ool



Journal of Molecular Biology
Volume 215, Issue 3, 5 October 1990, Pages 403-410

Basic local alignment search tool

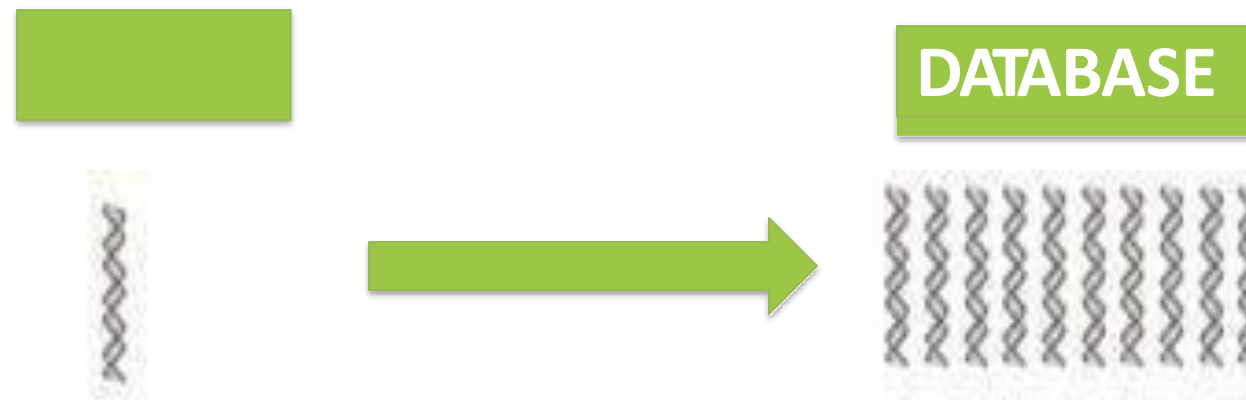
Stephen F. Altschul ¹, Warren Gish ¹, Webb Miller ², Eugene W. Myers ³, David J. Lipman ¹

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[https://doi.org/10.1016/S0022-2836\(05\)80360-2](https://doi.org/10.1016/S0022-2836(05)80360-2) [Get rights and content](#)

A new approach to rapid sequence comparison, basic local alignment search tool (BLAST), directly approximates alignments that optimize a measure of local similarity, the maximal segment pair (MSP) score. Recent mathematical results on the stochastic properties of MSP scores allow an analysis of the performance of this method as well as the statistical significance of alignments it generates. The basic algorithm is simple and robust; it can be implemented in a number of ways and applied in a variety of contexts including straight-forward DNA and protein sequence database searches, motif searches, gene

- A BLAST search enables a researcher to compare a query sequence with a library or databases of sequences, and identify library sequences that resemble the query sequence above a certain threshold.



Types of BLAST (1)

- **BLASTN**

nucleotide query : search nucleotide databases using a

(A)Query : ATGCATCGATC

(B) Database : ATCGATGATCGACATCGATCAGCTACG

- **BLASTP** : search protein databases using a protein query

(A)Query : VIVALASVEGAS

(B) DATABASE : TARDEFGGAVIVADAVISASTILHGGQWLC

- **BLASTX** : search protein databases using a translated nucleotide query

(A)Query : ATGCATCGATC

(B)DATABASE : TARDEFGGAVIVADAVISASTILHGGQWLC

Types of BLAST (2)

▪ **TBLASTN** : search translated nucleotide databases using a protein query

(A)Query : TARDEFGGAVI

(B)DATABASE : ATCGATGATCGACATCGATCAGCTACG

▪ **TBLASTX** : search translated nucleotide databases using a translated nucleotide query

(A)Query : CGATGATCG

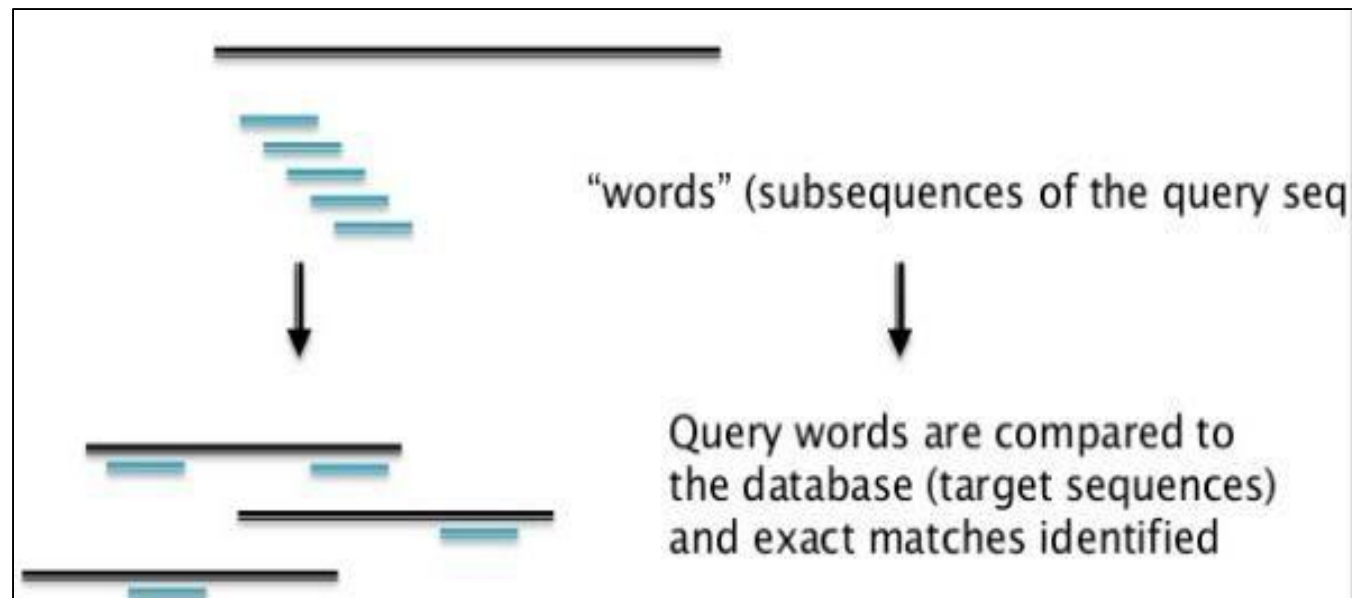
(B)DATABASE : ATCGATGATCGACATCGATCAGCTACG

Types of BLAST : ALL

Program	Database	Query
BLASTN	Nucleotide	Nucleotide
BLASTP	Protein	Protein
BLASTX	Protein	Nt. → Protein
TBLASTN	Nt. → Protein	Protein
TBLASTX	Nt. → Protein	Nt. → Protein

How does BLAST Works?

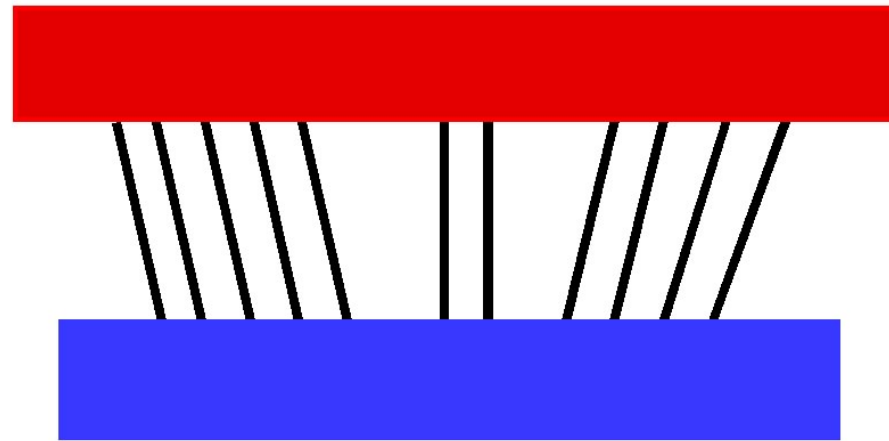
- **Construct a dictionary of all words in the query**
- **Initiate a local alignment for each word match between query and DB**



BLAST: Global Alignment

- It compares the whole sequence with another sequence.
- So, output of Global is one to one comparison of two sequences.
- This method is useful if you have small group of sequences.

Global alignment



Global alignment (NW -Needleman–Wunsch)

- Sequences are aligned end-to-end along their entire length
- Many possible alignments are produced
 - The alignment with the highest score is chosen
- Naïve algorithm is very inefficient (O^{exp})
 - Impractical for sequences of length >20 nt
- Used to analyze homology/similarity of
 - genes and proteins
 - between species

Methodology of global alignment (1 of 4)

- Define scoring scheme for each event
 - mismatch between a_i and b_j
 - $s(a_i, b_j) = -1$ if $a_i \neq b_j$
 - gap (insertion or deletion)
 - $s(a_i, -) = s(-, b_j) = -2$
 - match between a_i and b_j
 - $s(a_i, b_j) = +2$ if $a_i = b_j$
- Provide no restrictions on minimal score
- Start completing the alignment MxN matrix

s1: ..AA**T**A..

s2: ..AA**C**A..

s1: ..AAT-A..

s2: ..AA**C**A..

s1: ..AA**T**A..

s2: ..AA**T**A..

Methodology of global alignment (2 of 4)

- The matrix should have **extra** column and row
 - **M+1** columns , where M is the length sequence M
 - **N+1** rows, where N is the length of sequence N

1. Initialize the matrix

- introduce **gap penalty** at every **initial** position along rows and columns
- Scores at each cell are **cumulative**

		W	H	A	T	
		0	-2	-4	-6	-8
W	-2					
H	-4					
Y	-6					

Methodology of global alignment (3 of 4)

2. Alignment possibilities

Gap (horiz/vert)

		W	H
	0	-2	-4
W	-2	-4	

Diagram illustrating a gap in the alignment. A red arrow points from the cell (row 2, col 3) containing -2 to the cell (row 3, col 3) containing -4, indicating a vertical gap. Another red arrow points from the cell (row 3, col 2) containing -2 to the cell (row 3, col 3) containing -4, indicating a horizontal gap.

-OR-

Match (W-W diag.)

		W	H
	0	-2	-4
W	-2	+2	

Diagram illustrating a match in the alignment. A red arrow points from the cell (row 2, col 3) containing -2 to the cell (row 3, col 2) containing -2, indicating a match. A purple arrow points from the cell (row 3, col 2) containing -2 to the cell (row 3, col 3) containing +2, indicating a match.

3. Select the maximum score

- Best alignment

		W	H	A	T
	0	-2	-4	-6	-8
W	-2	2	0	-2	-4
H	-4	0	4	2	0
Y	-6	-2	2	3	1

Methodology of global alignment (4 of 4)

4. Select the most **very bottom right** cell
5. Consider different path(s) going to **very top left cell**
 - How the next cell value was generated? From where?

		W	H	A	T
	0	-2	-4	-6	-8
W	-2	2	0	-2	-4
H	-4	0	4	2	0
Y	-6	-2	2	3	1

WHAT
WHY-

		W	H	A	T
	0	-2	-4	-6	-8
W	-2	2	0	-2	-4
H	-4	0	4	2	0
Y	-6	-2	2	3	1

WHAT
WH-Y

Exercise

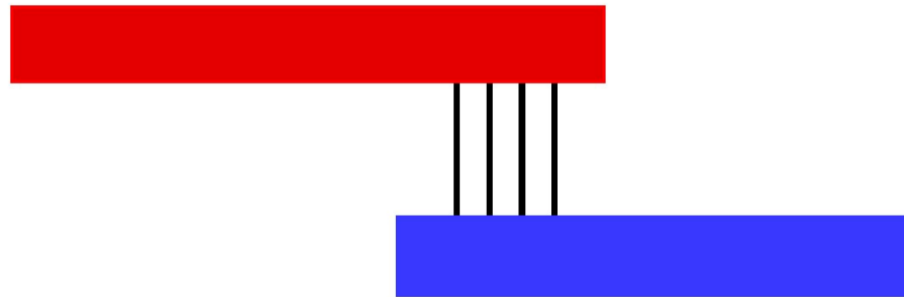
1. Create scoring matrix of CTTCA and CTACA
where mismatch -1,
gap -2 and
Match +5
2. Give the track back arrow
3. Write alignment

BLAST: Local Alignment

- Local method uses the subset of sequence and attempts to align against the subset of another sequence.
- So, output of local alignment gives the subset of regions which are highly similar.
- Example : Compare two sequence A and B

```
(A) GCATTACTAATATATTAGTAAATCAGAGTAGTA
      |||||
(B) AAGCGAATAATATATTATACTCAGATTATTGCGCG
```

Local alignment



Local alignment (Smith–Waterman)

- Sequences are aligned to find regions where the best alignment occurs (i.e. highest score)
- Assumes a local context (aligning parts of seq.)
- Ideal for finding short motifs, DNA binding sites
 - helix-loop-helix (bHLH) - motif
 - TATAAT box (a famous promoter region) – DNA binding site
- Works well on highly divergent sequences

Methodology of local alignment (1 of 4)

- The scoring system is similar with one exception
 - The minimum possible score in the matrix is zero
 - **There are no negative scores in the matrix**
- Let's define the scoring system as in global

mismatch between seq. a_i and b_j

$$s(a_i, b_j) = -1 \text{ if } a_i \neq b_j$$

gap (insertion or deletion)

$$s(a_i, -) = s(-, b_j) = -2$$

match between a_i and b_j

$$s(a_i, b_j) = +2 \text{ if } a_i = b_j$$

Methodology of local alignment (2 of 4)

- Construct the $M \times N$ alignment matrix with $M+1$ columns and $N+1$ rows
- Initialize the matrix by introducing gap penalty at 1st row and 1st column

		W	H	A	T
		0	0	0	0
W		0			
H		0			
Y		0			

← $s(a,b) \geq 0$
(min value is zero)

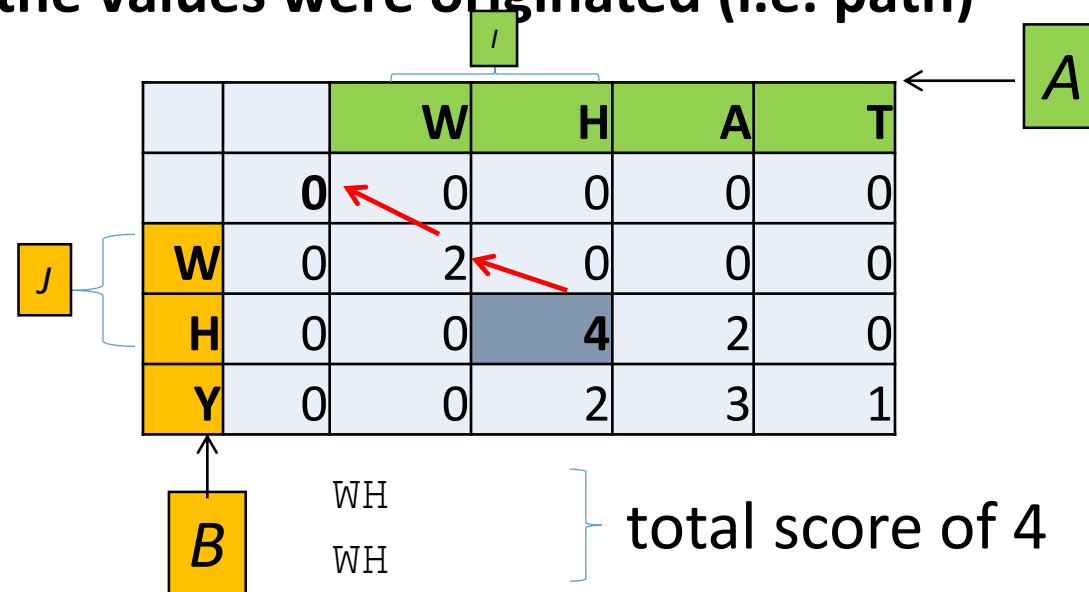
Methodology of local alignment (3 of 4)

- For each subsequent cell consider alignments
 - Vertical $s(l, -)$
 - Horizontal $s(-, J)$
 - Diagonal $s(l, J)$
- For each cell select the highest score
 - If score is negative → assign zero

		W	H	A	T
		0	0	0	0
W		0	2	0	0
H		0	0	4	2
Y		0	0	2	3

Methodology of local alignment (4 of 4)

- Select the initial cell with the **highest score(s)**
- Consider different path(s) leading to score of **zero**
 - Trace-back the cell values
 - Look how the values were originated (i.e. path)



- Mathematically
$$M(A, B) = \max\{S(I, J) : I \subset A, J \subset B\}$$
 - where $S(I, J)$ is the score for **sub-sequences** I and J

Local alignment illustration (1 of 2)

- Determine the best **local** alignment and the maximum alignment score for
- **Sequence A:** ACCTAAGG
- **Sequence B:** GGCTCAATCA
- Scoring conditions:
 - $s(a_i, b_j) = +2$ if $a_i = b_j$,
 - $s(a_i, b_j) = -1$ if $a_i \neq b_j$ and
 - $s(a_i, -) = s(-, b_j) = -2$

Local alignment illustration (2 of 2)

		G	G	C	T	C	A	A	T	C	A
	0	0	0	0	0	0	0	0	0	0	0
A	0	0	0	0	0	0	2	2	0	0	2
C	0	0	0	2	0	2	0	1	1	2	0
C	0	0	0	2	1	2	1	0	0	3	1
T	0	0	0	0	4	2	1	0	2	1	2
A	0	0	0	0	2	3	4	3	1	1	3
A	0	0	0	0	0	1	5	6	4	2	3
G	0	2	2	0	0	0	3	4	5	3	1
G	0	2	4	2	0	0	1	2	3	4	2

Local alignment illustration (3 of 3)

		G	G	C	T	C	A	A	T	C	A
	0	0	0	0	0	0	0	0	0	0	0
A	0	0	0	0	0	0	2	2	0	0	2
C	0	0	0	2	0	2	0	1	1	2	0
C	0	0	0	2	1	2	1	0	0	3	1
T	0	0	0	0	4	2	1	0	2	1	1
A	0	0	0	0	2	3	4	3	1	1	3
A	0	0	0	0	0	1	5	6	4	2	3
G	0	2	2	0	0	0	3	4	5	3	1
G	0	2	4	2	0	0	1	2	3	4	2

CTCAA
 CT-AA
 locally

BLAST: Input Format

Many program for sequence alignment expect sequences to be in FASTA format

Example 1 :

```
>L37107.1 Canis familiaris p53 mRNA, partial cds
GTTCCGTTTGGGGTTCCTGCATTCCGGGACAGCCAAGTCTGTTACTTGGACGTACTCCCCTCTCCTCAAC
AAGTTGTTTTGCCAGCTGGCGAAGACCTGCCCGTGCAGCTGTGGGTCAGCTCCCCACCCCACCCAATA
CCTGCGTCCGCGCTATGGCCATCTATAAGAAGTCGGAGTTCGTGACCGAGGTTGTGCGGCGCTGCCCCA
CCATGAACGCTGCTCTGACAGTAGTGACGGTCTTGCCCCTCCTCAGCATCTCATCCGAGTGGAAGGAAAT
TTGCGGGCCAAGTACCTGGACGACAGAAACACTTTTTCGACACAGTGTGGTGGTGCCTTATGAGCCACCCG
AGGTTGGCTCTGACTATAACCACCATCCACTACAACACTACATGTGTAACAGTTCCTGCATGGGAGGCATGAA
CCGGCGGCCCATCCTCACTATCATCACCCTGGAAGACTCCAGTGGAAACGTGCTGGGACGCAACAGCTTT
GAGGTACGCGTTTGTGCCTGTCCCGGGAGAGACCGCCGGACTGAGGAGGAGAATTTCCACAAGAAGGGGG
AGCCTTGTCTGAGCCACCCCCGGGAGTACCAAGCGAGCACTGCCTCCCAGCACCAGCTCCTCTCCCC
GCAAAGAAGAAGCCACTAGATGGAGAATATTTACCCTTCAGATCCGTGGGCGTGAACGCTATGAGATG
TTCAGGAATCTGAATGAAGCCTTGGAGCTGAAGGATGCCAGAGTGGAAAGGAGCCAGGGGGAAGCAGGG
CTCACTCCAGCCACCTGAAGGCAAAGAAGGGGCAATCTACCTCTCGCCATAAAAAACTGATGTTCAAGAGAG
AA
```

Example 2 :

```
>NM_033360.3 Homo sapiens KRAS proto-oncogene, GTPase (KRAS), transcript
variant a, mRNA
TCCTAGGCGGCGGCCGCGGGCGGCGGAGGCAGCAGCGGCGGCGGCGAGTGGCGGCGGCGAAGGTGGCGGCGG
CTCGGCCAGTACTCCCGGCCCCCGCCATTTCCGGACTGGGAGCGAGCGCGGCGCAGGCACTGAAGGCGGCG
GCGGGGCCAGAGGCTCAGCGGCTCCAGGTGCGGGAGAGAGGCCTGCTGAAAATGACTGAATATAAACTT
GTGGTAGTTGGAGCTGGTGGCGTAGGCAAGAGTGCCTTGACGATACAGCTAATTCAGAATCATTTTTGTGG
ACGAATATGATCCAACAATAGAGGATTCCTACAGGAAGCAAGTAGTAATTGATGGAGAAACCTGTCTCTT
GATATTCTCGACACAGCAGGTCAAGAGGAGTACAGTGCATGAGGGACCAGTACATGAGGACTGGGGAG
GGCTTTCTTTGTGTATTTGCCATAAATAATACTAAATTCATTTGAAGATATTCACCATTATAGAGAACAAA
```

NCBI BLAST SERVER

Open the website : <https://blast.ncbi.nlm.nih.gov/Blast.cgi>

The screenshot shows the NCBI BLAST website interface. At the top, there is a navigation bar with the NIH logo, "U.S. National Library of Medicine", "NCBI National Center for Biotechnology Information", and a "Sign in to NCBI" link. Below this is a secondary navigation bar with "BLAST" and links for "Home", "Recent Results", "Saved Strategies", and "Help".

The main content area features a "Basic Local Alignment Search Tool" section. It includes a description: "BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance." and a "Learn more" link. To the right of this section is a "NEWS" box with the headline "Magic-BLAST 1.3.0 released" and the subtext "A new version of the BLAST RNA-seq mapping tool is now available." The news box also shows the date "Thu, 28 Sep 2017 16:00:00 EST" and a link for "More BLAST news...".

Below the main text is a "Web BLAST" section with three large buttons. The first button is "Nucleotide BLAST" with the subtext "nucleotide ▶ nucleotide" and a background image of a DNA double helix. The second button is "blastx" with the subtext "translated nucleotide ▶ protein". The third button is "tblastn" with the subtext "protein ▶ translated nucleotide". To the right of these buttons is a "Protein BLAST" button with the subtext "protein ▶ protein" and a background image of a protein ribbon structure.

Window of BLASTN

NIH U.S. National Library of Medicine NCBI National Center for Biotechnology Information Sign in to NCBI

BLAST » blastn suite Home Recent Results Saved Strategies Help

Standard Nucleotide BLAST

blastn blastp blastx tblastn tblastx

Enter Query Sequence [BLASTN programs search nucleotide databases using a nucleotide query. more...](#) [Reset page](#) [Bookmark](#)

Enter accession number(s), gi(s), or FASTA sequence(s) [Clear](#) Query subrange [From](#) [To](#)

Or, upload file [Choose file](#) No file chosen [Job Title](#) [Enter a descriptive title for your BLAST search](#)

[Align two or more sequences](#)

Choose Search Set

Database Human genomic + transcript Mouse genomic + transcript Others (nr etc.) [Nucleotide collection \(nr/nt\)](#)

Organism Optional [Enter organism name or id—completions will be suggested](#) Exclude [Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown](#)

Exclude Optional Models (XM/XP) Uncultured/environmental sample sequences

Limit to Optional Sequences from type material

Entrez Query Optional [You Tube](#) [Create custom database](#) [Enter an Entrez query to limit search](#)

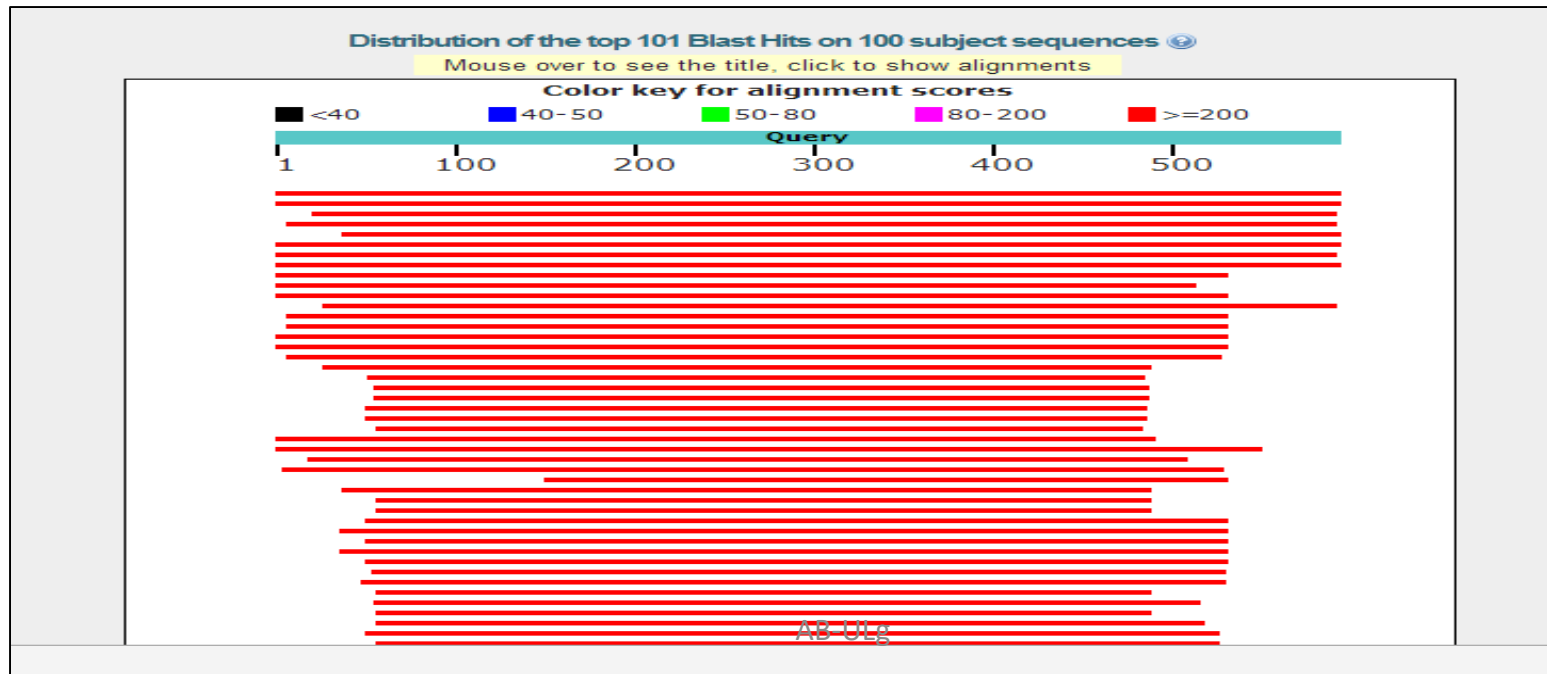
Let us work on BLASTN

- Select following sequence and give input into NCBI BLASTN query section

>Seq1

```
ACCAAGGCCAGTCTTGAGCAGGCCCAACTCCAGTGCAGCTGCCACCCCTGCCGCCATGTCTCTGACCAAG ACTGAGAGGACCATCATTTGTGTCCATGTGGGCAAGATCTCCACGCAGGCCGACACCATCGGCACCGAGA  
CTCTGGAGAGGCTCTTCCTCAGCCACCCGCAGACCAAGACCTACTTCCCGCACTTCGACCTGCACCCGGG GTCCGCGCAGTTGCGCGGCACGGCTCCAAGGTGGTGGCCCGTGGGCGACGCGGTGAAGAGCATCGAC  
GACATCGGCGGCGCCCTGTCCAAGCTGAGCGAGCTGCACGCCTACATCCTGCGCGTGGACCCGGTCAACT TCAAGCTCCTGTCCCCTGCCTGCTGGTACCCCTGGCCGCGCGCTTCCCGCCGACTTCACGGCCGAGGC  
CCACGCCGCTGGGACAAGTTTCCTATCGGTTCGTATCCTCTGTCTGACCGAGAAGTACCGCTGAGCGCCG CCTCCGGGACCCCAAGGACAGGCTGCGGCCCTCCCCGTCTGGAGGTTCCCCAGCCCCACTTACCGCG  
TAATGCGCCAATAAACCAATGAACGAAGC
```

- You will get list of Hits



- You will see statistic of alignments (Identity, E value)

Descriptions

Sequences producing significant alignments:

Select: [All](#) [None](#) Selected:0

[Alignments](#) [Download](#) [GenBank](#) [Graphics](#) [Distance tree of results](#)

	Description	Max score	Total score	Query cover	E value	Ident	Accession
<input type="checkbox"/>	PREDICTED: Homo sapiens hemoglobin subunit zeta (HBZ), transcript variant X2, mRNA	1088	1088	100%	0.0	100%	XM_005255288.3
<input type="checkbox"/>	Homo sapiens hemoglobin subunit zeta (HBZ), mRNA	1088	1088	100%	0.0	100%	NM_005332.2
<input type="checkbox"/>	Homo sapiens hemoglobin, zeta, mRNA (cDNA clone MGC:34397 IMAGE:5224569), complete cds	1048	1048	96%	0.0	100%	BC027892.1
<input type="checkbox"/>	PREDICTED: Pan paniscus hemoglobin, zeta (HBZ), mRNA	1035	1035	98%	0.0	99%	XM_003809392.2
<input type="checkbox"/>	PREDICTED: Homo sapiens hemoglobin subunit zeta (HBZ), transcript variant X1, mRNA	1020	1020	93%	0.0	100%	XM_005255287.3
<input type="checkbox"/>	PREDICTED: Papio anubis hemoglobin subunit zeta (HBZ), mRNA	968	968	100%	0.0	96%	XM_021931587.1
<input type="checkbox"/>	PREDICTED: Macaca nemestrina hemoglobin, zeta (HBZ), transcript variant X1, mRNA	968	968	99%	0.0	97%	XM_011748565.1
<input type="checkbox"/>	PREDICTED: Cercocebus atys hemoglobin subunit zeta (LOC105574663), mRNA	966	966	100%	0.0	96%	XM_012035766.1
<input type="checkbox"/>	PREDICTED: Pan troglodytes hemoglobin subunit zeta (HBZ), mRNA	941	941	89%	0.0	99%	XM_016928972.1
<input type="checkbox"/>	PREDICTED: Gorilla gorilla gorilla hemoglobin subunit zeta (HBZ), mRNA	918	918	86%	0.0	99%	XM_004056859.2
<input type="checkbox"/>	PREDICTED: Macaca nemestrina hemoglobin, zeta (HBZ), transcript variant X2, mRNA	896	896	89%	0.0	97%	XM_011748566.1
<input type="checkbox"/>	PREDICTED: Rhinopithecus roxellana hemoglobin subunit zeta (LOC104676970), mRNA	893	893	95%	0.0	96%	XM_010381860.1
<input type="checkbox"/>	PREDICTED: Macaca fascicularis hemoglobin subunit zeta (HBZ), mRNA	891	891	88%	0.0	98%	XM_005590729.2
<input type="checkbox"/>	PREDICTED: Macaca mulatta hemoglobin subunit zeta (LOC100428886), mRNA	880	880	88%	0.0	97%	XM_015125184.1
<input type="checkbox"/>	PREDICTED: Cebus capucinus imitator hemoglobin subunit zeta (HBZ), mRNA	863	863	89%	0.0	96%	XM_017510871.1

■ How well alignment is ? : Bad, Good, Very Good?

PREDICTED: Homo sapiens hemoglobin subunit zeta (HBZ), transcript variant X2, mRNA
 Sequence ID: [XM_005255288.3](#) Length: 1342 Number of Matches: 1

Range 1: 748 to 1336 [GenBank](#) [Graphics](#) ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
1088 bits(589)	0.0	589/589(100%)	0/589(0%)	Plus/Plus
Query 1		ACCAAGGCCAGTCCTGAGCAGGCCCAACTCCAGTGCAGCTGCCACCCTGCCGCCATGTC		60
Sbjct 748		ACCAAGGCCAGTCCTGAGCAGGCCCAACTCCAGTGCAGCTGCCACCCTGCCGCCATGTC		807
Query 61		TCTGACCAAGACTGAGAGGACCATCATTGTGTCCATGTGGGCCAAGATCTCCACGCAGGC		120
Sbjct 808		TCTGACCAAGACTGAGAGGACCATCATTGTGTCCATGTGGGCCAAGATCTCCACGCAGGC		867
Query 121		CGACACCATCGGCACCGAGACTCTGGAGAGGCTCTTCTCAGCCACCCGCAGACCAAGAC		180
Sbjct 868		CGACACCATCGGCACCGAGACTCTGGAGAGGCTCTTCTCAGCCACCCGCAGACCAAGAC		927
Query 181		CTACTTCCCGCACTTCGACCTGCACCCGGGGTCCGCGCAGTIGCGCGCGCACGGCTCCAA		240
Sbjct 928		CTACTTCCCGCACTTCGACCTGCACCCGGGGTCCGCGCAGTIGCGCGCGCACGGCTCCAA		987
Query 241		GGTGGTGGCCGCCGTGGGGCAGCGCGGTGAAGAGCATCGACGACATCGGCGGCGCCCTGTC		300
Sbjct 988		GGTGGTGGCCGCCGTGGGGCAGCGCGGTGAAGAGCATCGACGACATCGGCGGCGCCCTGTC		1047
Query 301		CAAGCTGAGCGAGCTGCACGCCTACATCCTGCGCGTGGACCCGGTCAACTTCAAGCTCCT		360
Sbjct 1048		CAAGCTGAGCGAGCTGCACGCCTACATCCTGCGCGTGGACCCGGTCAACTTCAAGCTCCT		1107
Query 361		GTCCCACTGCCTGCTGGTACCCCTGGCCGCGCGCTTCCCCGCCGACTTCACGGCCGAGGC		420
Sbjct 1108		GTCCCACTGCCTGCTGGTACCCCTGGCCGCGCGCTTCCCCGCCGACTTCACGGCCGAGGC		1167
Query 421		CCACGCCGCCTGGGACAAGTTTCTATCGGTTCGTATCCTCTGTCTGACCGAGAAGTACCG		480
Sbjct 1168		CCACGCCGCCTGGGACAAGTTTCTATCGGTTCGTATCCTCTGTCTGACCGAGAAGTACCG		1227
Query 481		CTGAGCGCCGCCTCCGGGACCCCCAGGACAGGCTGCGGCCCTCCCCGTCCTGGAGGTT		540
Sbjct 1228		CTGAGCGCCGCCTCCGGGACCCCCAGGACAGGCTGCGGCCCTCCCCGTCCTGGAGGTT		1287
Query 541		CCCCAGCCCCACTTACCGCGTAATGCGCCAATAAACCAATGAACGAAGC	589	
Sbjct 1288		CCCCAGCCCCACTTACCGCGTAATGCGCCAATAAACCAATGAACGAAGC	1336	

Resources

- Online Tutorial on Sequence Alignment
 - <http://a-little-book-of-r-for-bioinformatics.readthedocs.org/en/latest/src/chapter4.html>
- Pairwise alignment of DNA and proteins using your rules:
 - http://www.bioinformatics.org/sms2/pairwise_align_dna.html
- Documentation on libraries
 - Biostings: <http://www.bioconductor.org/packages/2.10/bioc/manuals/Biostrings/man/Biostrings.pdf>
 - SeqinR: http://seqinr.forge.r-project.org/seqinr_2_0-7.pdf