AUG
Faculty of Computer and Information Sciences
Ain Shams University

Session 7

K-mers

-> Table of Contents <-

◄Extract K-mers of a seq

◆What is a k-mer

- **A *k-mer* is just a sequence of *k* characters in a string (or nucleotides in a DNA sequence). Now, it is important to remember that to get *all k-mers* from a sequence you need to get the first *k* characters, then move just a single character for the start of the next *k-mer* and so on. Effectively, this will create sequences that overlap in `k-1` positions.**

◆Extract a K-mer

- **by way of example the next sequence**
  the Seq("`ATCGATCAC`")
  One with 3-mer & the other with 4-mer

  - **(*k-mer* of size 3) => `ATCGATCAC`**

```
Sequence: ATCGATCAC
3-mer #0: ATC
3-mer #1:  TCG
3-mer #2:   CGA
3-mer #3:    GAT
3-mer #4:     ATC
3-mer #5:      TCA
3-mer #6:       CAC
```

- (*k-mer* of size 4) => `ATCGATCAC`

```
Sequence: ATCGATCAC
4-mer #0: ATCG
4-mer #1:  TCGA
4-mer #2:   CGAT
4-mer #3:    GATC
4-mer #4:     ATCA
4-mer #5:      TCAC
```

◆Why So Popular in Bioinformatics

- **Decomposing a sequence into its *k-mers* for analysis allows this set of fixed-size chunks to be analysed rather than the sequence, and this can be more efficient.**
- ***K-mers* are very useful in sequence matching (string matching with n-grams has a rich history), and set operations are faster, easier, and there are a lot of readily-available algorithms and techniques to work with them.**
- **A simple example: to check if a sequence *S* comes from organism *A* or from organism *B*, assuming the genomes of *A* and *B* are known and sufficiently different, we can check if S contains more *k-mers* present in *A* or in *B*. Yes, there are many tools that do just that.**
- **Basically, using *k-mers* simplifies bioinformatics to counting and comparing whether things are there or not.**

◆Applications of k-mer Counting

- **Genome assembly, Sequence alignment, Sequence clustering, Error correction of sequencing reads, Genome size estimation, Repeat identification.**

◄Find & Count a given K-mer

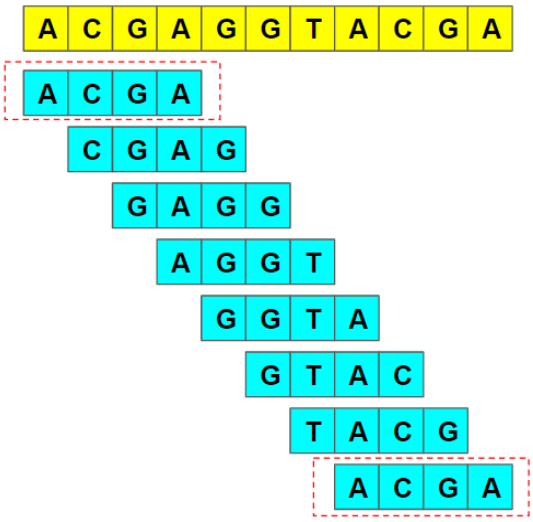
◆Finding

- We Can Find the K-mers in the sequence as a movable imaginary box consisting of a constant number that the search is based on.
- For Ex. suppose we have a seq("ATTCGAACT") and (k-mer) of size (4). Then the K-mers will be: (ATTC), (TTCG), (TCGA), (CGAA), (GAAC), (AACT). Then there is a 6 k-mers of the sequence with the size 4.

◆Counting

- The *Total Count* is simply how many times each k-mer has appeared in the given sequence. Except for ACGA, which has appeared twice, the rest of the 4-mers have appeared only once.
- (*k-mer* of size 4) => `ACGAGGTACGA`

	Total	Distinct	Unique
ACGA	2	1	0
CGAG	1	1	1
GAGG	1	1	1
AGGT	1	1	1
GGTA	1	1	1
GTAC	1	1	1
TACG	1	1	1

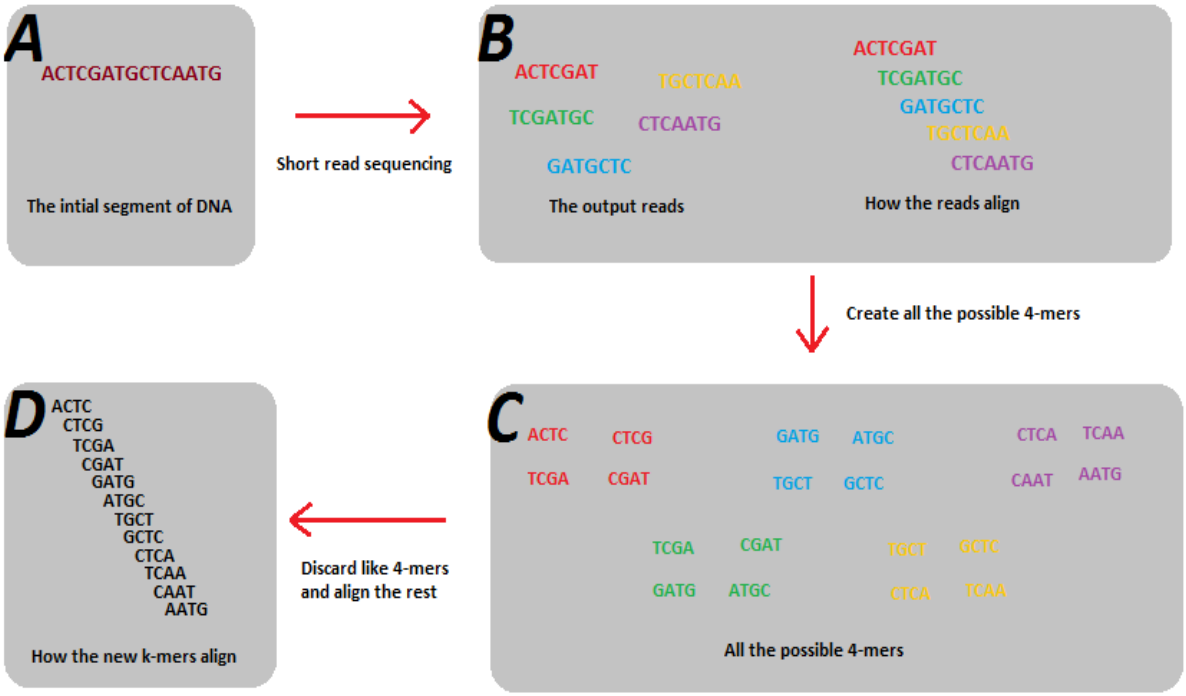


- The distinct k-mers are counted only once regardless of how many times they appear. For example, even though ACGA has appeared twice, we count it only once. The *Distinct Count* provides us the information of if a k-mer has appeared or not (not how many times it has appeared).

- **The unique k-mers are those which appear only once. In the above example, since ACGA has appeared twice, its unique count is zero.**

  The *Unique Count* reveals which k-mers have appeared only once.

- **The next Ex. shows all the possible (6 & 4 K-mers) in a Sequence:**

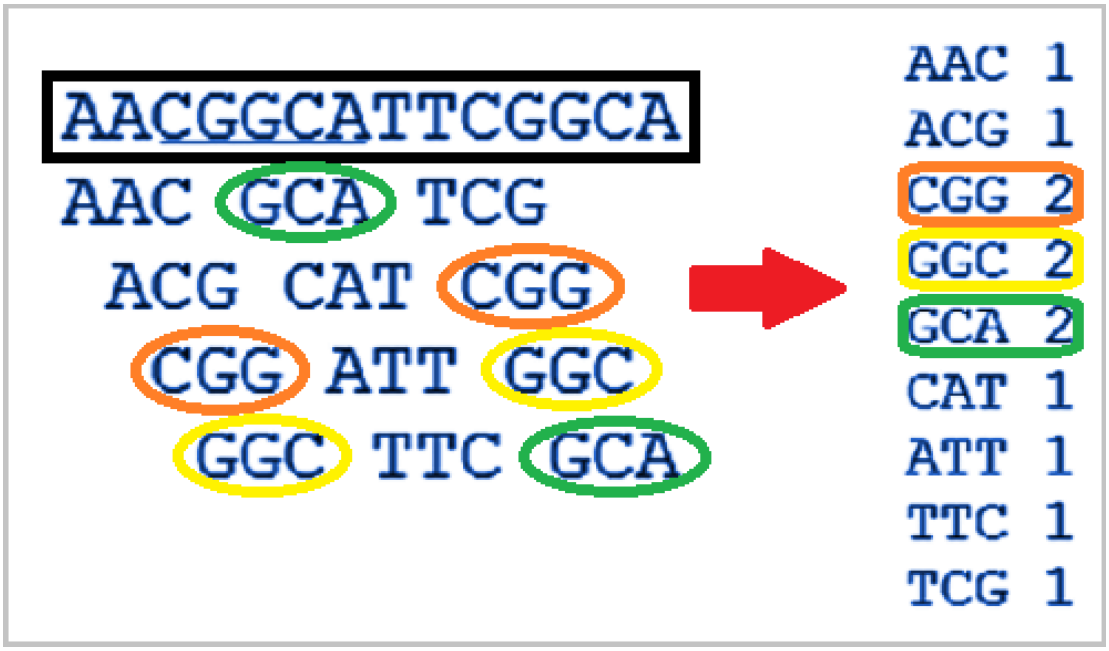


◆Forces Affecting K-mer Freq

- **The frequency of *k*-mer usage is affected by numerous forces, working at multiple levels, which are often in conflict.**
- **It is important to note that *k*-mers for higher values of *k* are affected by the forces affecting lower values of *k* as well.**
- **For example, if the 1-mer A does not occur in a sequence, none of the 2-mers containing A (AA, AT, AG, and AC) will occur either, thereby linking the effects of the different forces.**

◆Most Popular K-mers

- We say that k-mer is popular or not depending on how often it is repeated in the Sequence.



Here we see that there are Popular K-mers: (CGG), (GGC), (GCA)
Each of them repeated 2 times in the Sequence so they are the most Popular in the Sequence.

◆Most Popular K-mers with (X) Mismatches

- Here Our Sequence is: "ATGTCGATCATTATG" and we have already a popular K-mer but with num of (x) Mismatches.
- That means if we Suppose there is a popular K-mer which is: "ATG" and we want to find if there is (1) Mismatches of this popular K-mer,
  It could be:

  (TTG), (CTG), (GTG),
  (AAG), (ACG), (AGG),
  (ATA), (ATT), (ATC)

  These are all the Possible tries to get all the ((1) Mismatches) of "ATG"
- Then we return to the Sequence and Compare all its K-mers with these Probabilities of mismatches.
- When we Compare Both of Them, we will find that the ((1) Mismatches) of "ATG" which is popular is: (ATC), (ATT). so we have 2 Mismatches.