

Bioinformatics Algorithms

Lecture Notes

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1 Definitions

1.1 Alphabet

Let Σ be a finite set of symbols (alternatively called characters), called the alphabet. No assumption is made about the nature of the symbols.

1.2 String (or word)

A string over Σ is any finite sequence of symbols from Σ . For example if $\Sigma = \{0, 1\}$ then 01011 is a string over Σ .

The **length of a string S is the number of symbols in s** (the length of the sequence) and can be any non-negative integer. It is often denoted as $|S|$.

The **empty string** is the unique string over Σ of length 0, and is denoted as ϵ .

The **set of all strings over Σ of length n** is denoted Σ^n . For example, if $\Sigma = 0, 1$, then $\Sigma^2 = \{00, 01, 10, 11\}$. Note that $\Sigma^0 = \{\epsilon\}$ for any alphabet Σ .

The **set of all strings of any length over Σ** is the *Kleene closure* of Σ and is denoted as Σ^* . Also:

$$\Sigma^* = \bigcup_{n \in \mathbb{N} \cup \{0\}} \Sigma^n$$

The **set of all non-empty strings over Σ** is denoted by Σ^+

1.3 Substrings, prefixes and suffixes

A string s is said to be a **substring** (or *factor*) of t if there exist (possibly empty) strings u and v such that $t = usv$.

Given a string t , **suffixes** and **prefixes** are special substrings of t .

A string s is said to be a **prefix** of t if there exists a string u such that $t = su$. If u is nonempty, s is said to be a *proper* prefix of t .

Simmetrically, a string s is said to be a **suffix** of t if there exists a string u such that $t = us$. If u is nonempty, s is said to be a *proper* suffix of t .

1.4 Reverse, palindrome and rotations

The **reverse** of a string is a string with the same symbols but in reverse order. For example, if $s = abc$ (where a , b , and c are symbols of the alphabet), then the reverse of s is cba .

A string that is the reverse of itself is called a **palindrome**, which also includes the empty string and all strings of length 1.

A string $s = uv$ is said to be a **rotation** of t if $t = vu$. For example, if $\Sigma = \{0, 1\}$ the string 0011001 is a rotation of 0100110, where $u = 00110$ and $v = 01$.

2 Comparing strings

2.1 Hamming distance

The **Hamming distance** between **two strings of equal length** is the **number of positions at which the corresponding symbols are different**.

- “karolin” and “kathrin” $\rightarrow 3$
- 1011101 and 1001001 $\rightarrow 2$

With Hamming distance we can formalize *substitutions* in biological sequences - or simply sequencing errors in which the wrong base pair is identified.

2.2 Edit distance

The **edit distance** is a way of quantifying how dissimilar two strings (e.g., words) are to one another by counting the **minimum number of operations required to transform one string into the other**. In the *Levenshtein distance* (the most common), edit operations are: **removal**, **insertion**, and **substitution**.

The edit distance between “kitten” and “sitting” is 3. A minimal edit script that transforms the former into the latter is:

- kitten \rightarrow sitten (substitute *s* for *k*)
- sitten \rightarrow sittin (substitute *i* for *e*)
- sittin \rightarrow sitting (insert *g* at the end)

The number of solutions (sequences of operations) is infinite.