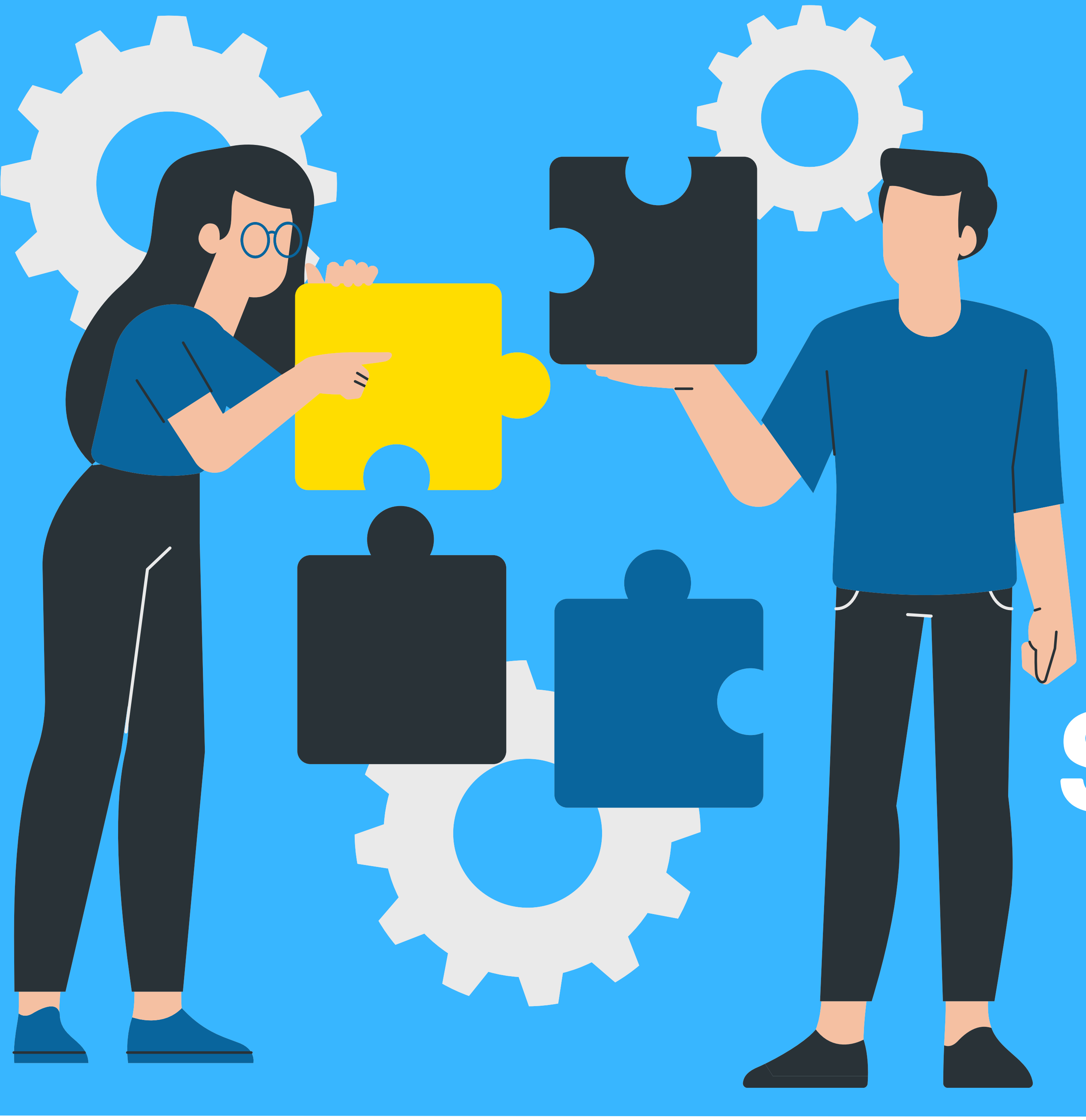
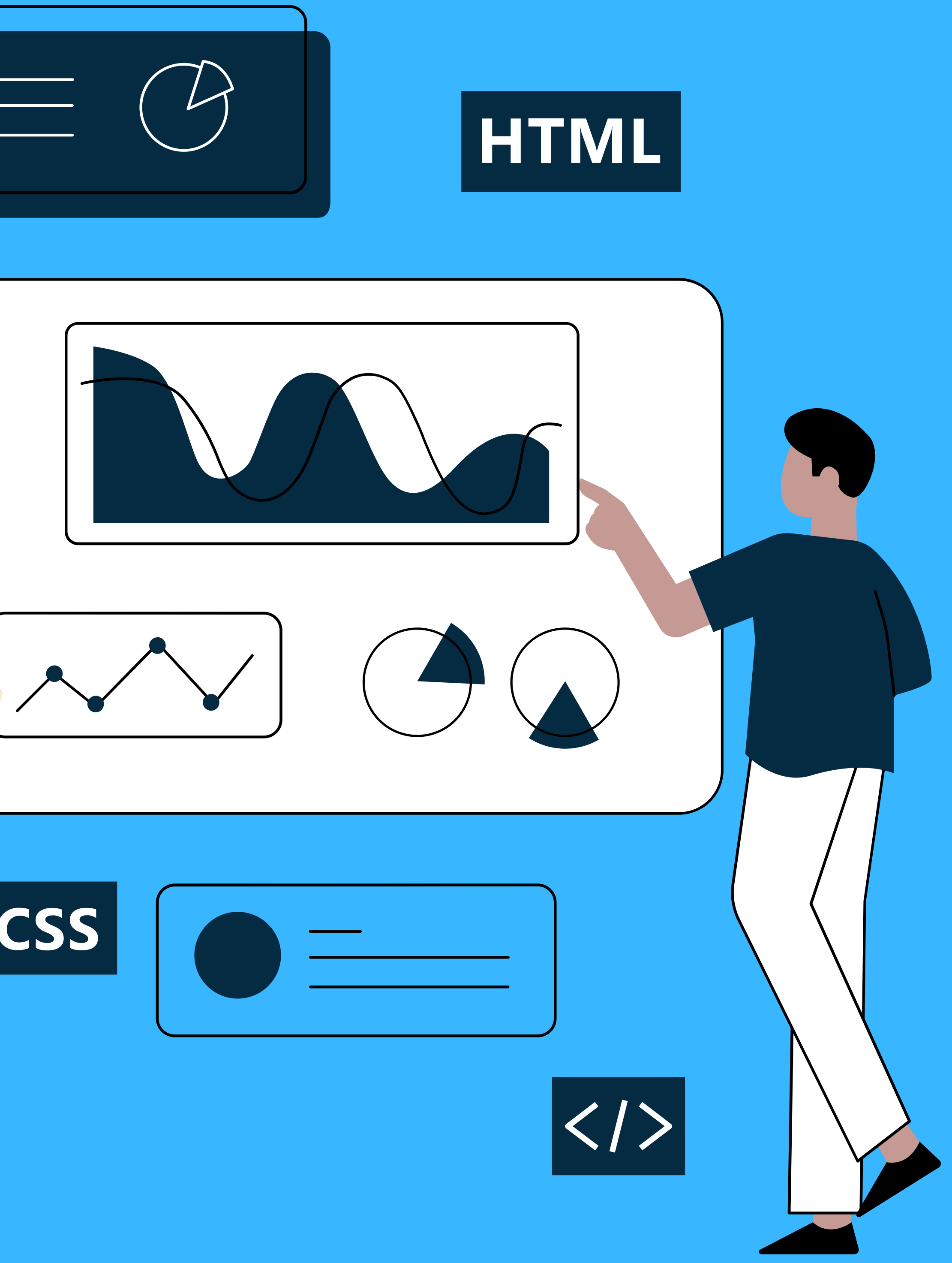


# APPLICATIONS OF BIOINFORMATICS SOFTWARES AND TOOLS

# Bioinformatics Tools



## BLAST

BLAST (Basic Local Alignment Search Tool) comes under the category of homology and similarity tools. It is a set of search programs designed for the Windows platform and is used to.

perform fast similarity searches regardless of whether the query is for protein or DNA. Comparison of nucleotide sequences in a database can be performed. Also, a protein database can be searched to find a match against the queried protein sequence.

# DEPENDING ON THE TYPE OF SEQUENCES TO COMPARE, THERE ARE DIFFERENT PROGRAMS:

## BLASTn

compares a nucleotide query sequence against a nucleotide sequence database.

## BLASTx

compares a nucleotide query sequence translated in all reading frames against a protein sequence database.

## BLASTp

compares an amino acid query sequence against a protein sequence database.

## tBLASTn

compares a protein query sequence against a nucleotide sequence database dynamically translated in all reading frames.

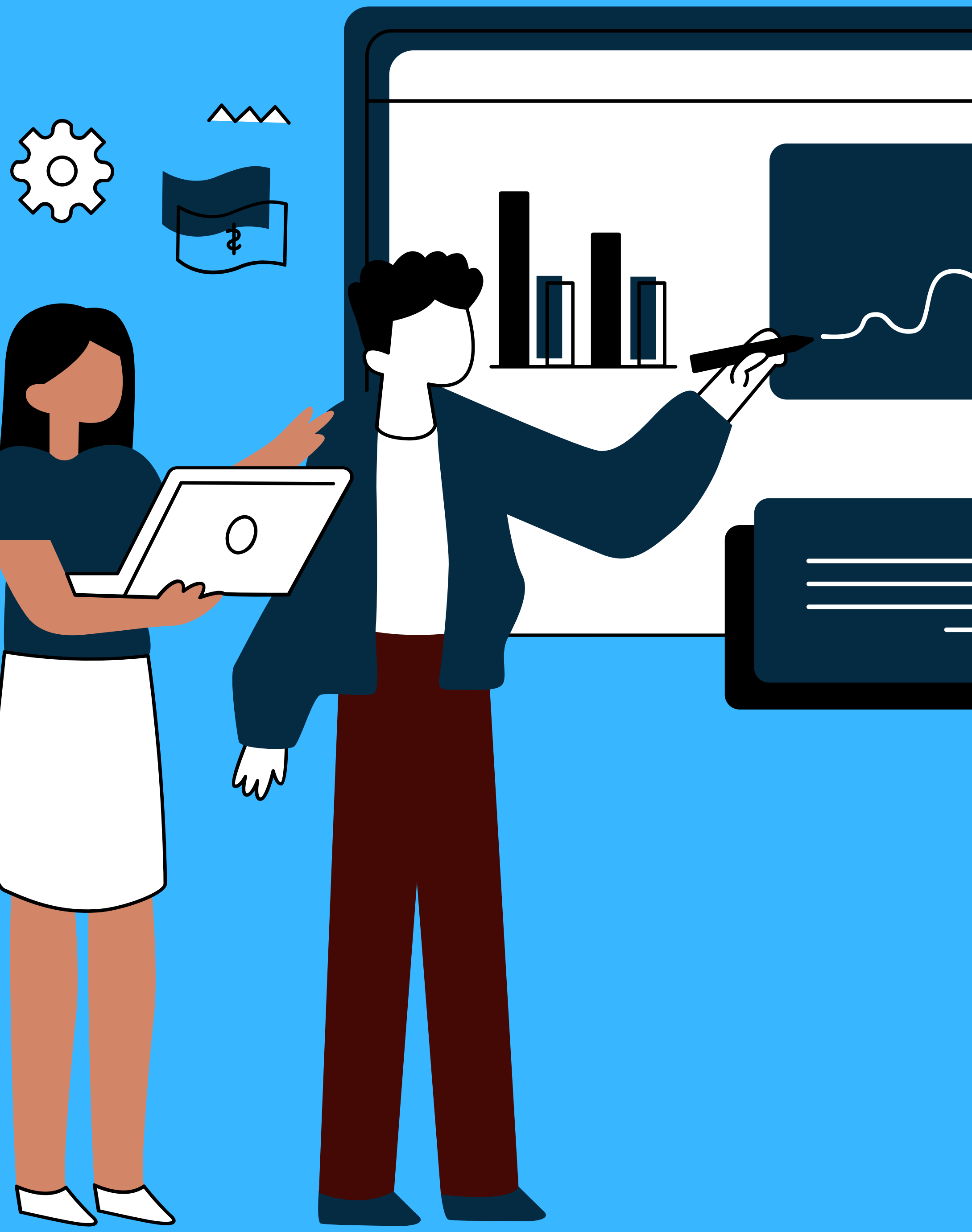
## tBLASTx

compares the six-frame translations of a nucleotide query sequence against the six-frame translations of a nucleotide sequence database.

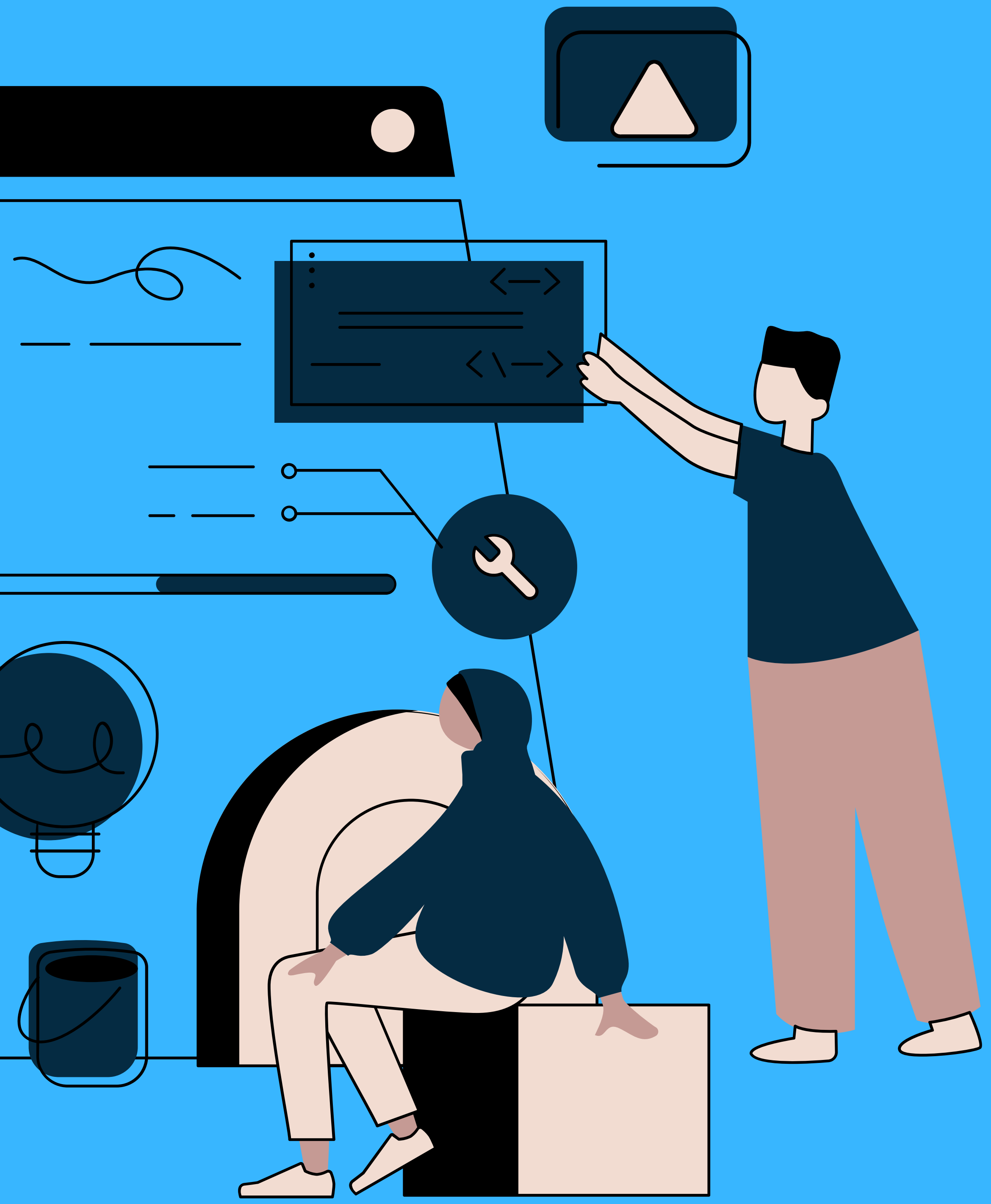
# Bioinformatics Tools

## EMBOSS

(European Molecular Biology Open Software Suite) is a software-analysis package. It can work with data in a range of formats and retrieve sequence data transparently from the Web. Extensive libraries are also provided with this package, allowing other scientists to release their software as open source. It provides a set of sequence-analysis programs, and also supports all UNIX platforms.



# Bioinformatics Tools



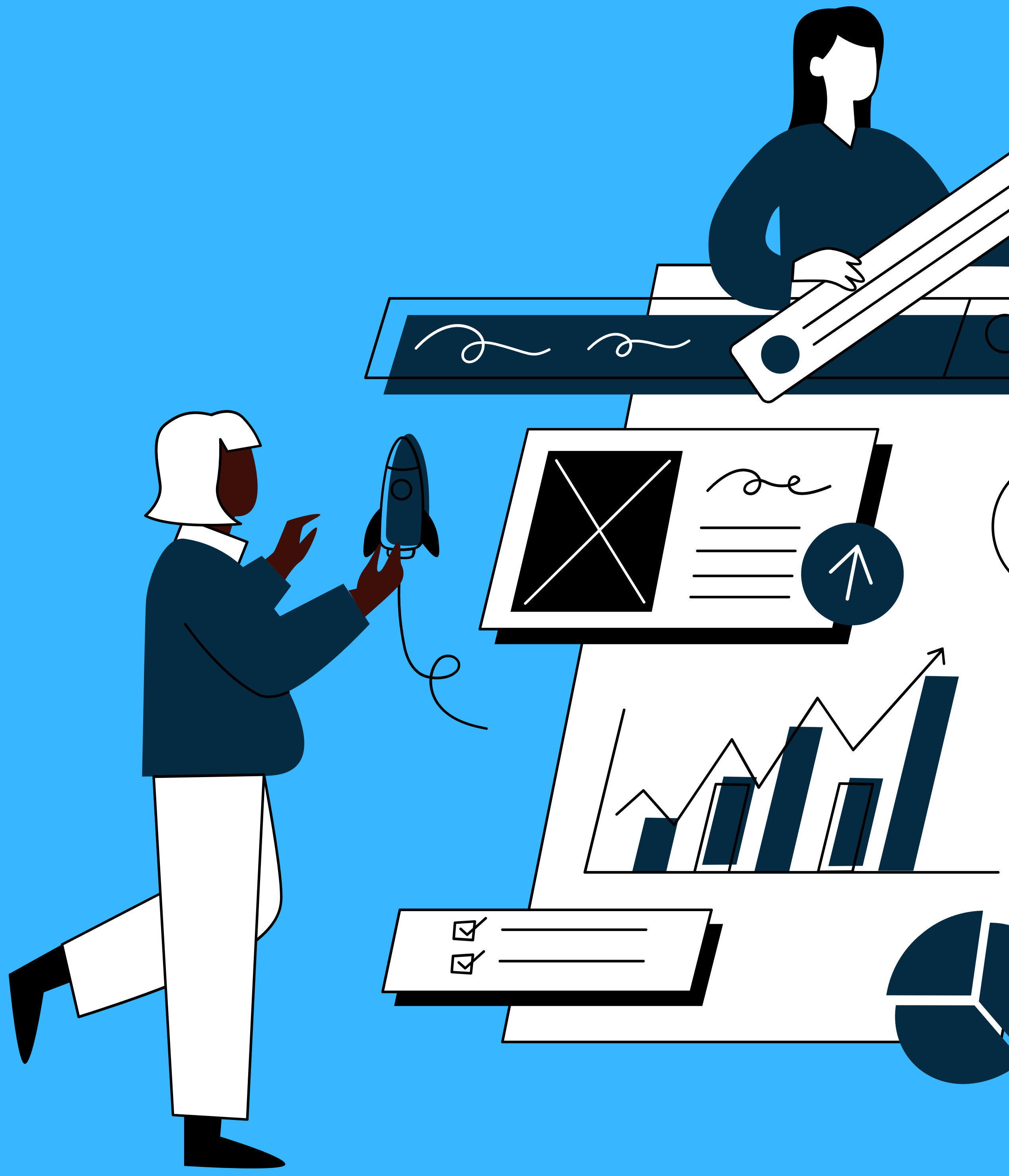
## FASTA

The program is one of the many heuristic algorithms proposed to speed up sequence comparison. The basic idea is to add a fast prescreen step to locate the highly matching segments between two sequences, and then extend these matching segments to local alignments using more rigorous algorithms such as Smith-Waterman.

# Bioinformatics Tools

## CLUSTALW

It is a fully automated sequence alignment tool for DNA and protein sequences. It returns the best match over a total length of input sequences, be it a protein or a nucleic acid.



# APPLICATION OF BIOINFORMATICS

## Drug Discovery

Computational biology, an essential element of bioinformatics help scientists to analyse the disease mechanism process and validate new and cost-effective drugs. If we consider the COVID 19 outbreak, bioinformatics can be effectively used to produce an effective drug at a low cost.

## Crop Improvement

It makes effective usage of proteomic, metabolomic, genetic, and agricultural crop production to develop strong, more drought-resistant, and insect-resistant crops. Thereby enhancing the quality of livestock and making them disease resistant.

## Gene Therapy

It is a process through which genetic materials are incorporated into unhealthy cells to treat, cure as well as prevent diseases. Analyzing protein targets, identifying cancer types, evaluating data, assessing MicroRNA.

## Waste Clean-up

Here, the primary objective is to identify and assess the DNA sequencing of bacteria and microbes in order to use them for sewage cleaning, removing radioactive waste, clearing oil spills, etc.