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# 1. Team

## # Roles in the team

- |   |  |
|---|--|
| 1 | Gabriel Yanchev – Scrum Master         |
| 2 | Zlatin Lazarov – Back-End developer    |
| 3 | Cvetomir Stoilov – Front-End developer |

# 2. Introduction

## # Introduction

- |   |   |
|---|---|
| 1 | <i>What is the product?</i><br>CodeNova is a cutting-edge project designed to create and sort genetic sequences based on user-defined traits. It allows users to specify desired characteristics, and the tool intelligently generates plausible DNA/RNA sequences corresponding to those traits.                                     |
| 2 | <i>Main stages in the realization?</i><br>First Week – Create the idea and discuss how to go about it<br>Second Week – Study our field<br>Third Week – Start programming<br>Fourth Week – Make final touches  |
| 3 | <i>Communication?</i><br>Communication was realized through Microsoft Teams. Thanks to all the features and the provided visualization – on-screen communication and feedback were sufficiently completed.  |
| 4 | <i>What technologies were used?</i><br>We used Visual Studio 2022 as IDE, C++ as a programming language, Microsoft Word for documentation, Microsoft Teams as a communication tool, Adobe Photoshop and Adobe Illustrator for the logo, Microsoft PowerPoint as a presentation tool, and Git and GitHub as a collaborative workplace. |

### 3. Method and manner of implementation

#### # Method and manner of implementation

- 1 *Productive work.*  
The tasks are presented in a way that everyone is aware of what's done and what isn't so that teamwork is more efficient and productive.
- 2 *Distribution of tasks*  
Each task is assigned to the team member who's most familiar with the field and would be able to complete it in the best and most efficient way possible.
- 3 *Communication*  
The progress was constantly observed by the Scrum Master. Weekly meetings were held so that everyone had up-to-date information about the state of the project and tasks could be distributed evenly and efficiently.

### 4. Summary

The program helps comprehend genetic sequences in a fun and accessible way. It has generating and sorting features and can also display the traits related to a sequence next to it for even better user experience.

### 5. Libraries

#### # Which Libraries did we use?

- 1 `<Windows.h>`  
It contains declarations for all of the functions in the Windows API.
- 2 `<conio.h>`  
It includes inbuilt functions like `getch()` and `clrscr()`.
- 3 `<vector>`  
It includes vectors and functions related to them.
- 4 `<map>`  
It includes maps and functions related to them.
- 5 `<string>`  
Provides support for such objects with an interface similar to that of a standard container of bytes, but adding features specifically designed to operate with strings of single-byte characters.

## 6. Block scheme

