

Trimmomatic command line Tool to a **Desktop Application**

Problem Statement:

- **Trimming Adapters** in selected gene using Command prompt to any bioinformation is difficult since not all know the specific commands, weather to a bioinformation or CS student who's trying to see real life examples to look at.

Solution Statement:

- Making a **Desktop Application** to improve the experience to the targeted people.

Tools:

- Using **Trimmomatic Tool**.
- Using **Java** programing language.

Methodology:

- User will have 3 options to **input**
 1. Trimmomatic Folder
 2. Reference Genome file
 3. Adapter sequence text/file

User may upload in the input filed Trimmomatic Folder. If he wanted to add a new Adapter within the folder, he can input the wanted adapter to trim it.

Or he can input the Reference Genome file along with the Adapter file to trim them.

- Data goes to Java Desktop application, **process** them by trying to trim Adapters.
 - Print **output** to the user
-

Team members:

- مريم محمد محمد زايد، سكشن 3 فصل 6، جروب أ
- عبدالرحمن محمد عبدالقادر نعينع, فصل 7 جروب أ
- روان نشأت ابراهيم الزهيري, سكشن 7 فصل 13, جروب ب
- ندى عابد عبد النبى, سكشن 3 فصل 6
- اميرة حسن محمد فلفل, سكشن 3 فصل 6