

Bio Lite

Project supervised by : Dr . Sara El-Metwally

Developed By :



Omar Essam



Hany Mohamed



Mazen Moataz

- **Problem :**

Bioinformatics files from different types (fasta – fastq – sametc) might come too big to be processed in some programming's operations .. so that may disable the bioinformaticians' work !

- **Solution :**

Using this application we can compress and resize the Bioinformatics files from different types so it can be suitable and easy to use in more processes . also we can read files in zipped format from large datasets .

- **Previous Techniques**

Spring for NGSS fastq . And we will try to make it for many types of file formats with fastq (fasta – sam - ..etc) .

- **Technologies uses :**

- ✓ Python
- ✓ Python tkinter
- ✓ Python gzip