**Mansoura University**



**Faculty of Computers and Information**

**Department of Computer Science**

**Project Proposal**

# Arabic Title

# 

### 

##### English Title

### 

C-Tree

### **Submitted by:**

#### 

|  |  |  |
| --- | --- | --- |
| Student Name | Student Email | Section |
| Shereen Magdy | shereenmagdy@std.mans.edu.eg | 2 |
| Manar Magdy | manar\_magdy\_elbasosy@std.mans.edu.eg | 3 |
| Merna Ashraf | mernashrif@std.mans.edu.eg | 2 |
| Nehal Reda | nehalreda\_15@std.mans.edu.eg | 2 |

Project Abstract:

Website contains phylogenetic network of SARS-CoV-2 genomes sampled from across the world. These genomes are closely related and under evolutionary selection in their human hosts

The problem is that the usual sites that shows or talks about that topic are complicated for the people who have not studied this kind of materials related to genomics or computer science

We will take the topic and show the diagram of the tree and families of covid in a simple way that everyone interested in the topic will understand it

Project Objectives:

* A **phylogenetic tree** contains the family of SARS and each with its spread location and time
* Search algorithm to know the percentage of each type in all countries
* Symptoms of covid, prevention, spread timeline in present and any related information

Who are the project **competitive**? and how will your project be **different**?

<https://www.pnas.org/doi/10.1073/pnas.2004999117>

<https://www.nature.com/articles/s41598-020-79484-8>

<https://www.ncbi.nlm.nih.gov/pmc/articles/PMC8292857/>

the usual sites that show or talk about that topic are complicated for the people who have not studied this kind of materials related to genomics or computer science

We will take the topic and show the diagram of the tree and families of covid in a simple way that everyone interested in the topic will understand it

Tools, Hardware and Software Resources:

**Tools :- Phylot, SMS, FastTree, trimAl, BOOSTER**

**Software:- Linux, VS code, Pycharm**

**Hardware:-**

SCHEDULING PHASES:

|  |  |  |
| --- | --- | --- |
| **From** | **To** | **Activity** |
|  |  |  |
|  |  |  |
|  |  |  |
|  |  |  |
|  |  |  |
|  |  |  |

References:

[**https://www.khanacademy.org/science/ap-biology/natural-selection/phylogeny/a/phylogenetic-trees#:~:text=A%20phylogenetic%20tree%20is%20a,a%20series%20of%20common%20ancestors**](https://www.khanacademy.org/science/ap-biology/natural-selection/phylogeny/a/phylogenetic-trees#:~:text=A%20phylogenetic%20tree%20is%20a,a%20series%20of%20common%20ancestors)**.**

<https://www.pnas.org/doi/10.1073/pnas.2004999117>

<https://covid19.who.int/>

<https://onlinelibrary.wiley.com/doi/full/10.1002/jmv.25762>

<https://molbiol-tools.ca/Phylogeny.htm#:~:text=PhyML%2C%20SMS%2C%20FastTree%2C%20trimAl,%2C%20maximum%20likelihood%20and%20Bayesian>).

[COVID19\_phylogenetic tree | Kaggle](https://www.kaggle.com/yoshifumimiya/covid19-phylogenetic-tree)