



PROJECT PROPOSAL

Arabic Title

English Title

C-Tree

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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/>

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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.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\).](https://molbiol-tools.ca/Phylogeny.htm#:~:text=PhyML%2C%20SMS%2C%20FastTree%2C%20trimAl,%2C%20maximum%20likelihood%20and%20Bayesian).)
[COVID19_phylogenetic tree | Kaggle](#)