

# Supporting pandemic response using genomics and bioinformatics: A case study on the emergent SARS-COV-2 outbreak

## Abstract:

That paper is all about a case study on the emergent SARS-COV2 outbreak and how to solve it using genomics and bioinformatics.

Pre-clinical diagnosis were used on isolated animal models and noticing symptoms that would appear on it when using bioinformatics tools ( which offers more of fluid view) .

Phylogenetic tree: is a diagram that represents evolutionary relationships among organisms, it reflects how species or other groups evolved from series of common ancestors.

phylogenetic tree: 1- will provide of mutation in every strain in the isolated animals. 2- will provide a full study of the development in every strain.

## introduction:

there are increasing instances of emerging and re-emerging diseases caused by viruses such as: the SARS outbreak of 2002-2004, the MERS outbreak since 2012 and the current COVID since 2019 and it is a global pandemic it appeared first in bats then in human (new host) which evolved rapidly causing a change or an error in RNA sequence which leads to a mutation and creation of another strain pf the virus.

By bioinformatics tools we will be able to study epidemiology and responses to trans boundary viruses such as 1- genomic sequence technology ex: (oxford nanopore, illumine)

2-sequenced information in the public domain ex: (gen bank, GISAID)

3-comparitive analysis: of the emerging genomic diversity

4-silico approach: can provide answers to many questions about mutations

So, using bioinformatics analysis to identify emerging trends among the SARS-COV-2 isolates and identify the most representative strains for animal models and pre-clinical research.