

Predictive Analytics to Combat with Covid-19 using Genome Sequencing

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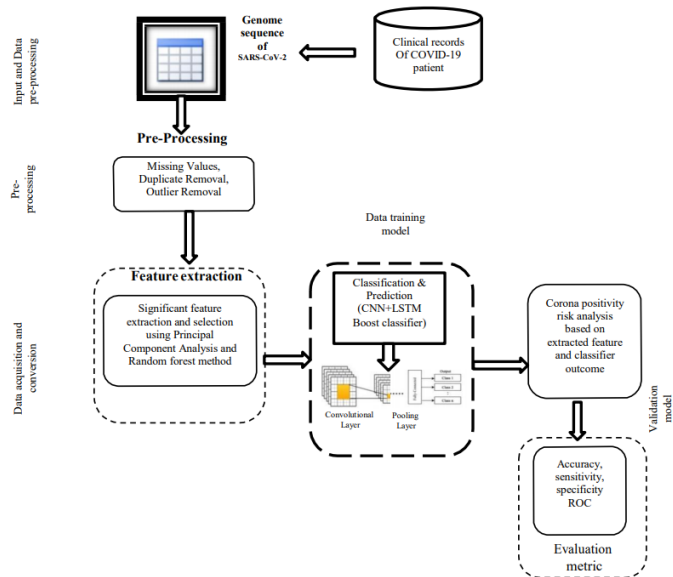
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Abstract: The coronavirus outbreak (nCoV) has created an alarming situation at international level. COVID-19 pandemic is now continuing to develop and researchers across the world are working to combat with COVID-19 & to reduce and prevent its spread. Traditional pathological

tests are used but they are time consuming & also number of test kits & centers are limited. Surprising thing is 60% patients may not have any symptoms but still they are SAR-CoV-2 positive & may work as silent carrier causing outbreak of this disease. And a reason to worry is that there is no vaccine & exact drug for this disease. Machine learning techniques can be used to analyze clinical data but again symptoms vary from person-to-person & accuracy of clinical outcomes is questionable. To tackle this problem, this paper proposes a technique to detect presence of SAR-CoV-2 in a person using genome sequencing.

This will accurately help to detect presence of virus, to develop targeted therapies & vaccines and also to learn how patient will respond to drugs. This paper summarizes primary survey of existing work & proposes a technique using predictive analytics to detect presence of SAR-CoV-2 using genome sequencing to combat with COVID-19. This system will be able to differentiate SAR-CoV2 from its other subtypes, such as MERS-CoV, HCoV-NL63, HCoV-OC43, HCoV-229E, HCoVHKU1, and SARS-CoV regardless of some missing information and noise in dataset [1]. Proposed methodology can be used by doctors & practitioners as a tool for making ease in decision making.

Figure 6 shows architecture of proposed system:



Full paper can be downloaded: <https://ssrn.com/abstract=3580692>