

Biomedical Signal Processing and Control

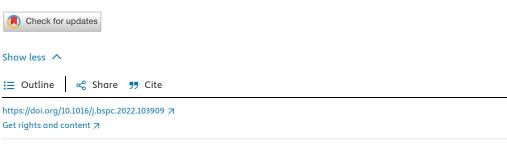
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Identification of characteristics frequency and hot-spots in protein sequence of COVID-19 disease

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Highlights

- Proposed BPN lattice IIR filter architecture for hot-spots identification in SARS CoV-2.
- Hot-spot identification is useful for vaccine development of new variants of COVID-19.
- Synthesis is done using Xilinx ISE and implemented on Zynq-series FPGA.
- Experimentation is carried out on five proteins and identified hot-spots are reported.
- Comparative analysis of proposed filter is done with MATLAB simulation.

Abstract

COVID-19 has threatened the whole world since December 2019 and has also infected millions of people around the globe. It has been transmitted through the SARS CoV-2 virus. Various proteins of the SARS CoV-2 virus have an important role in its interaction with human cells. Specifically, the interaction of S-protein with human ACE-2 protein helps in entering of SARS CoV-2 virus into a human cell. This interaction take-place at some specific amino-acid locations called as hot-spots. Understanding of this interaction is helpful for drug designing and vaccine development for new variants of COVID-19 disease. An attempt has been made in this paper for understanding this interaction by finding the characteristics frequency of SARS-related protein families using the resonance recognition model (RRM). Hardware implementation of Bandpass notch (BPN) lattice <u>IIR filter system architecture</u> is also carried out, which is used for hot-spots identification in SARS CoV-2 proteins. Various <u>signal processing techniques</u> like retiming, pipelining, etc. are explored for performance improvement. Synthesis of proposed <u>BPN filter</u> system has been done using Xilinx ISE EDA tool on Zynq-series (Zybo-board) <u>FPGA</u> family. It is found that retimed and <u>pipelined architecture</u> of hardware-implemented BPN lattice IIR filter-based hot-spots detection system improves the speed (computational time) by 14 to 31 times for different SARS CoV2 related proteins as compared to its MATLAB simulation with similar functionality.