Using Deep Hybrid Modeling to Determine Treatment Strategies for COVID-19 Patients

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COVID-19 has had a devastating impact on the world in terms of high infection rates and mortality. Though social distancing, PPE, and vaccination has helped reduce the transmission rate, more effective therapeutic solutions are still needed. Goyal et al. developed a differential equations model for the immune system response to SARS-CoV-2 based on data derived from 25 patients from different parts of the world. They then used their mathematical model to determine the best time to administer therapeutics, including two small molecular agents (remdesivir and selinexor), along with broadly neutralizing antibodies (bNAbs) and cellular immuno-therapies. Our goal is to explore the role of each parameter in this model using the Deep Hybrid Modeling (DeepHM) software package provided by IBM Research [1]. DeepHM uses conditional Generative Adversarial Networks (cGANs) as an inverse surrogate model to distinguish the parameter regions corresponding to the distributions of various features (peak viral load, time of peak viral load, and time to clear the virus) extracted from the original data. Then we can provide the feature values of the 25 patients to check how the cGAN maps these feature values to parameter space. We hypothesize that by taking into account the distributions of parameters that produce these features, we can get a more accurate picture of how patient heterogeneity affects response to therapy.

1. Parikh J, Kozloski J, and Gurev V (2020). Integration of AI and mechanistic modeling in generative adversarial networks for stochastic inverse problems. *arXiv*, arXiv:2009.08267v2 [stat.ML].