

Bibliography

Ahuja, A. S., Reddy, V. P., & Marques, O. (2020). Artificial Intelligence and covid-19: A multidisciplinary approach. *Integrative Medicine Research*, 9(3), 100434.

The COVID-19 pandemic caused enormous misery and loss of life. Due to the pandemic's rapid spread, a large amount of new scientific research and data sharing is occurring. The authors used artificial intelligence (AI) and a rising number of coronavirus-related datasets and published articles to combat the pandemic by pushing innovative approaches to drug discovery, vaccine development, and public awareness. By cross-referencing papers and searching for patterns, AI algorithms may be used to mine this avalanche of new data and publications to extract new insights. AI algorithms could help uncover new possible treatments or aid in vaccine development. Drug development is a difficult undertaking, and AI technologies such as deep learning can assist speed up the process by predicting which existing medications or drug-like compounds could be used to treat specific conditions of COVID-19.

This paper was important as it explained how AI could be beneficial for making a COVID-19 drug discovery or vaccine development.

Ong, E., Cooke, M. F., Huffman, A., Xiang, Z., Wong, M. U., Wang, H., Seetharaman, M., Valdez, N., & He, Y. (2021). Vaxign2: The second generation of the first web-based vaccine design program using Reverse Vaccinology and machine learning. *Nucleic Acids Research*, 49(W1).

Reverse vaccinology (RV) is a cutting-edge technique for predicting vaccine candidates from a pathogen's DNA, according to the paper. The authors modified Vaxign2, the first web-based vaccine design application employing reverse vaccinology and machine learning, to encourage vaccine development. Vaxign2 is a web server that includes predictive and computational workflow components for rational vaccine creation. The old Vaxign filtering-based method plus a new machine learning-based method, Vaxign-ML, make up the predictive part. The results of the benchmarking using a validation dataset revealed that Vaxign-ML outperformed other RV tools in terms of prediction performance. Aside from the prediction component, Vaxign2 added a number of post-prediction analyses to improve users' capacity to refine prediction results based on multiple vaccine design rationales and reduce user time spent analyzing Vaxign/Vaxign-ML prediction results. Users input proteome sequences, choose candidates based on Vaxign outputs and Vaxign-ML scores, and do post-prediction analysis. Vaxign2 also offers pre-calculated findings from over a million proteins in 398 proteomes from 36 infections. Vaxign2 was used to analyze SARS-CoV-2, the coronavirus that causes COVID-19, as a demonstration. Vaxign2's comprehensive architecture can aid in the development of better and more logical vaccines.

This paper used machine learning techniques on the proteins of SARS-CoV-2 coronavirus , Since machine learning is a subset of artificial Intelligence(AI) that provides systems the ability to automatically learn and improve from experience with being explicitly programmed. This is the second generation of author's 1st vaccine design program.

Ong, E., Wong, M. U., Huffman, A., & He, Y. (2020). Covid-19 coronavirus vaccine design using reverse vaccinology and machine learning.

The entire virus, as well as the spike (S) protein, nucleocapsid (N) protein, and membrane protein, have all been studied for vaccine development against SARS and MERS, according to the author's literature and clinical trial review. To anticipate COVID-19 vaccine candidates, the authors employed the Vaxign reverse vaccinology tool and the newly built Vaxign-ML machine learning technology. The authors found that the N protein was found to be conserved in the more pathogenic strains (SARS/MERS/COVID-19), but not in the milder human coronaviruses. Six proteins, including the S protein and five non-structural proteins (nsp3, 3CL-pro, and nsp8–10), were anticipated to be adhesins, which are important for viral adhesion and host invasion, according to the authors. Vaxign-ML projected that the S, nsp3, and nsp8 proteins would generate high protective antigenicity. Aside from the regularly utilized S protein, the nsp3 protein has never been tested in a coronavirus vaccination study and was chosen for future research. The nsp3 gene was discovered to be more conserved in SARS-CoV-2, SARS-CoV, and MERS-CoV than in 15 coronaviruses that infect humans and other animals. Promiscuous MHC-I and MHC-II T-cell epitopes, as well as linear B-cell epitopes, were expected to be found in certain locations and functional domains of the protein. Our projected vaccine targets offer fresh approaches to developing a COVID-19 vaccine that is both effective and safe.

This is the author's 1st generation vaccine design code using machine learning and reverse vaccinology . This paper was very helpful for my topic since machine learning is a subset of AI .

Keshavarzi Arshadi, A., Webb, J., Salem, M., Cruz, E., Calad-Thomson, S., Ghadirian, N., Collins, J., Diez-Cecilia, E., Kelly, B., Goodarzi, H., & Yuan, J. S. (2020). Artificial Intelligence for covid-19 drug discovery and vaccine development. *Frontiers in Artificial Intelligence*, 3.

There were no new antiviral medicines or licensed vaccinations available for deployment as a frontline defence at the time this research was produced by the authors. By clarifying hitherto undiscovered viral pathways, scientists may be able to contribute in the identification of effective antivirals. Using computational approaches to find novel candidate medications and vaccines in silico is one way to accomplish this. Machine learning-based models trained on specific proteins have provided low-cost and quick-to-implement ways for finding successful viral treatments in the previous decade. These models can forecast inhibitor candidates in a structural-based manner given a target biomolecule. If a model is given enough data, it can help with the search for a medication or vaccine candidate by identifying trends in the data. The authors of this paper focus on current breakthroughs in COVID-19 drug and vaccine research employing artificial intelligence, as well as the possibility of intelligent training for COVID-19 therapeutic discovery.

The authors highlight various molecular targets of COVID-19, suppression of which may increase patient survival, to make deep learning applications for SARS-COV-2 easier. Furthermore, the researchers published CoronaDB-AI, a library of chemicals, peptides, and epitopes found in silico or in vitro that may be used to train models to extract COVID-19 treatment. This review's data and information can be utilized to train deep learning-based models and speed up the development of successful viral medicines. This was a important paper relating to my research .

Keshavarzi Arshadi, A., Webb, J., Salem, M., Cruz, E., Calad-Thomson, S., Ghadirian, N., Collins, J., Diez-Cecilia, E., Kelly, B., Goodarzi, H., & Yuan, J. S. (2020). Artificial Intelligence for covid-19 drug discovery and vaccine development. *Frontiers in Artificial Intelligence*, 3.

The authors of this review study emphasized the importance of artificial intelligence (AI) and machine learning (ML) techniques in finding a possible therapy for COVID-19. They also looked at how viromics and AI interact, in the hopes of finding a solution to the epidemic. For recent studies on the usage of AI, a review of different articles was conducted using the following databases: MEDLINE/PubMed, SCOPUS, Web of Science, ScienceDirect, and Google Scholar, looking for the spread of different infectious diseases using relevant MeSH subheadings. 30 papers were chosen after a careful review of various articles, and key information was extracted from them. Finally, in order to gather more data, the authors widened their focus. Their findings suggested that AI/ML could be a promising drug development strategy.

The topic of artificial intelligence (AI) holds immense potential for forecasting environmental changes. Breakthroughs could pave the path for novel vaccinations and antiviral medications if this technology is employed in pandemic conditions like COVID-19.

McGowan, E., Rosenthal, R., Fiore-Gartland, A., Macharia, G., Balinda, S., Kapaata, A., Umvilighozo, G., Muok, E., Dalel, J., Streatfield, C., Coutinho, H., Monaco, D. C., Morrison, D., Yue, L., Hunter, E., Nielsen, M., Gilmour, J., & Hare, J. (2020). Utilizing computational machine learning tools to understand immunogenic breadth in the context of a CD8 T-cell mediated HIV response.

The authors of this paper used the concept of assessing the HIV proteome for defined regions of immunogenicity using two key parameters: a diversity metric of individuals' HLA profiles within a population and consideration of sequence diversity in the context of an individual's CD8 T-cell immune repertoire. The discovery of areas within the proteome that offer high conservation, HLA recognition within a population, low prevalence of HLA adaptation, and shown immunogenicity using this method was made possible by analysing HLA adaptation and functional immunogenicity data. As a supplement to vitro functional assays, the authors

felt that this unique and original approach to vaccine design offered a tailored pipeline for accelerated and rational CD8 T-cell vaccine creation for HIV and potentially other infections, with the potential for both global and local coverage.

This paper utilized the use of conceptual machine learning tools, this helped to understand how a subset of AI could be useful in understand the T-cell mediated HIV response

Gawriljuk, V. O., Foil, D. H., Puhl, A. C., Zorn, K. M., Lane, T. R., Riabova, O., Makarov, V., Godoy, A. S., Oliva, G., & Ekins, S. (2021). Development of machine learning models and the discovery of a new antiviral compound against yellow fever virus. *Journal of Chemical Information and Modeling*, 61(8), 3804–3813.

This paper mentions about Yellow fever, which is a haemorrhagic viral disease spread by infected mosquitoes. When the virus is brought into densely inhabited areas with high mosquito density and insufficient immunization coverage, large outbreaks of YF develop. The lack of a unique small molecule medicinal treatment for YF, as well as analogous illnesses like Zika and dengue fever, emphasizes the flaviviruses importance as a public health threat. New techniques based on machine learning approaches have been introduced into drug discovery as a means to use the rising high throughput screening (HTS) data collected to cut costs and speed up drug development, thanks to advancements in computer hardware and bioactivity data availability. In this research, predictive machine learning models were utilized to enable the identification of compounds with optimal bioactivity and absorption, distribution, metabolism, and excretion profiles utilizing previously published data from HTS campaigns or data available in public sources. In this research, predictive machine learning models were utilized to enable the identification of compounds with optimal bioactivity and absorption, distribution, metabolism, and excretion profiles utilizing previously published data from HTS campaigns or data available in public sources.

The authors gathered data on yellow fever virus cell-based assays from the literature and public databases. The information was used to create predictive models using a variety of machine learning techniques to help prioritize drugs for in vitro testing.

Russo, G., Reche, P., Pennisi, M., & Pappalardo, F. (2020). The combination of artificial intelligence and Systems Biology for Intelligent Vaccine Design. *Expert Opinion on Drug Discovery*, 15(11), 1267–1281.

According to the author, a new body of evidence demonstrates the use of artificial intelligence and systems biology in vaccine research and design. Both ideas will transform healthcare by speeding up clinical trial processes and decreasing the expenses and time spent on medication research and development. The principles of artificial intelligence and systems biology techniques in the vaccine development pipeline are explored in this paper. A full

discussion of epitope prediction tools for creating epitope-based vaccinations and agent-based models for immune system response prediction, as well as their potential to speed up clinical trial phases, are among the subjects covered. Artificial intelligence in silico trials approaches fed by systems biology data in the vaccine development pipeline are currently being approached by regulatory bodies for qualification/approval.

The collection of specific data from a combined strategy like this could help us better understand and monitor viral propagation and immune responses in the wake of the 2019-Novel Coronavirus (2019-nCoVrecent)'s debut and rapid spread, as well as the sickness it causes (COVID-19). Furthermore, a combined methodology like this can allow health experts and biologists to focus their time and energy on how to respond to infectious disease risks and quickly identify potential targets for immune responses to 2019-nCoV, allowing for the development of new vaccine interventions to be sped up.