

InSilicoVaccine – Influenza A

Design from Scratch an Influenza Vaccine

15 October 2022 | In Silico Vaccine, Immunoinformatics, Modeling and Simulation

Background: Influenza A is a viral infection responsible for seasonal flu outbreaks. The content focuses on leveraging immunoinformatics and agent-based modeling to design and assess Influenza A vaccines more efficiently, aiming to combat the challenges posed by this infectious disease, including rapid viral mutations

Question of Interest: How can we optimize Influenza A vaccine design by specifically targeting the protein sequences of HA, NA, and M2, critical components of the virus?

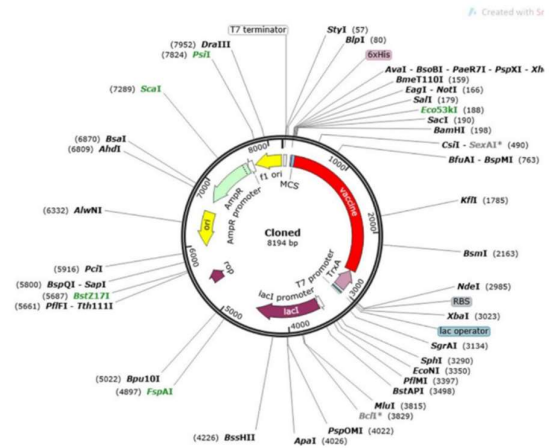
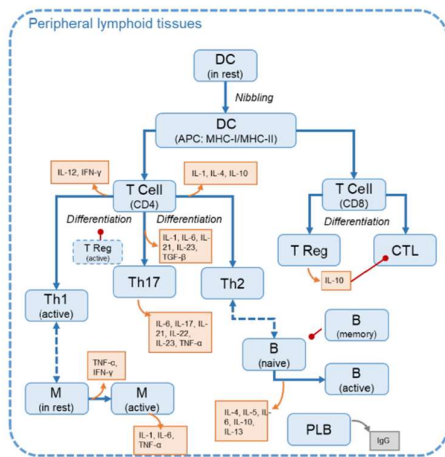
Methods:

IMMUNOINFORMATICS: Recombinant Vector Design

Epitope selection and vaccine design - Workflow of bioinformatics tools to optimize epitopes

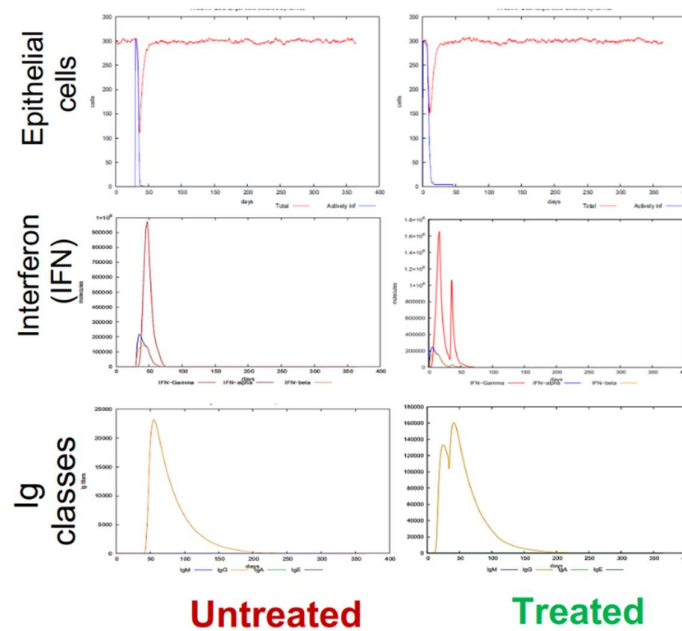
AGENT-BASED MODEL: Dynamic simulations

Immune and influenza disease stimulation - Virtual patient simulations, predicting vaccine efficacy



Results:

Personalized virtual patient prediction of response to infection - Response to vaccine administration and virus infection



Impact:

- In silico methods can help speed up the vaccine development process by using computational models to predict the efficacy and safety of potential vaccine candidates.
- In silico methods can also be used to optimize vaccine design by predicting the most effective antigen sequences or adjuvants to elicit a robust immune response. This could help improve the efficacy of vaccines and reduce the risk of viral mutations.