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Numerical study of Receptor-Toxin-Antibody Interaction Problem

The successful bio-medical application of antibodies is well-documented and there is increasing interest in the use of antibodies for mitigation of the effect of toxins associated with the various biological threats. Such toxins are an important potential target for designing therapies against these threats and a brood range of approaches has been taken to develop inhibitors that may be of prophylactic or therapeutic use. With the progress in bio-engineering many antibodies have been generated for this purpose with different affinity parameters and, as a result, different properties. However affinity, by itself, is a poor predictor of protective or therapeutic potential which is determined by a new consolidated kinetic parameter Receptor-Toxin-Antibody (RTA) kinetics and relative concentration of species. Generation of any new antibody necessitates development of a high fidelity model for RTA interaction.

One of the important step in improvement of this model is incorporation of the reaction-diffusion fluxes of species. Incorporation of diffusion fluxes of toxin, antibody, and associated complex into the RTA model leads to a PDEs model.

Numerical study of the protective efficiency of antibody against a given toxin in the model of cells placed into a toxin-antibody solution will be discussed.

References

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