

This project was a result of my continuous association with former colleagues at the Centre of Membrane Proteins and Receptors over at Nottingham, UK. They were looking at running simulations on pharmacokinetic systems defined using a variety of differential equations. Such simulations are key for understanding biological interactions between drugs and their target proteins. I was tasked with the following:

- Reading up on the literature and finding the right mathematical model for an interaction
- Solving the corresponding differential equations using R
- Running a simulation taking arrange of input parameters
- Packaging all of this into an easy to use Shiny App.

I developed 3 different Shiny Apps in this project, links for which can be found below.

The study involving the shiny apps has been submitted to another journal for peer-review.

Links for Shiny Apps:

- https://palashisback.shinyapps.io/Receptor_Occupancy_Model/
- <https://palashisback.shinyapps.io/Kinetic>
- https://palashisback.shinyapps.io/Max_response_model