



Hamilton Institute

Analysis of Dynamical Systems with Steep
Sigmoidal Response Functions

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In models for gene regulation, the activity of a gene is regulated by the concentration of certain transcription factors. Frequently one assumes that the effect of the transcription factor (the response function) rises sharply from a low level to a saturation level around a threshold: i.e. its response function is sigmoidal or perhaps binary (a step function). Both cases are seen in experiments. If a gene is regulated by several transcription factors, Boolean-like functions determine their combined effect on the gene.

Gene regulatory models with step functions can be dealt with by means of a method devised by Filippov. After briefly sketching the idea behind this method, I will turn to models with steep sigmoidal response functions. The major problem is to analyse the behaviour when one or several variables are near a threshold. There the model becomes discontinuous in the limit when the sigmoids approach step functions.

I derive an equivalent set of equations which behave smoothly in these parts of phase space and which are much easier to analyse than the original equations. By investigating the limit when the sigmoids approach step functions, I will show how singular perturbation theory can be employed to analyse the behaviour of the model and compute solutions valid in the step function limit. These solutions are uniform approximations to the solutions for steep sigmoids. The limit solution could also be seen as an alternative to the Filippov definition of the solution to the same model with step functions instead of sigmoids.

Venue: Seminar Room, Hamilton Institute, Rye Hall, NUI Maynooth

Time: 2.00 - 3.00pm (followed by tea/coffee)

Travel directions are available at www.hamilton.ie

