Thesis title: Analysis of Oscillatory Behaviour in Coupled Dynamical Systems

Abstract:

Oscillatory dynamics explains various physical and biological phenomena in systems spanning different length scales, ranging from the microscopic scale of molecules to the macroscopic scale of biological and ecological systems. The mechanisms that drive these dynamics can be different in different systems. A useful approach to understand these mechanisms is to mathematically analyse the properties of a model representing the dynamics.

In this thesis, we use averaging methods to study oscillatory dynamics in three problems. The first is to analyse the collective dynamics of a periodically driven collisionless non-neutral plasma, which is usually modelled using ponderomotive theory, which in turn is generally derived using heuristic methods. By applying Hamiltonian averaging theory on the Vlasov equation, we have rigorously derived the time-averaged distribution function predicted by ponderomotive theory and clearly showed that the ponderomotive solution is only one among the infinitely many different solutions possible. We have also analysed various initial conditions which can lead to periodic solutions of the Vlasov equation for such plasmas and conjectured that the irreducible polynomial corresponding to the initial plasma distribution function must only have squares of the spatial and momentum coordinates. The time-dependent plasma distribution function for all other initial conditions is likely to be aperiodic and can lead to complex relaxation processes within the plasma. The second is in the context of understanding the conformational change of a DNA molecule. The phenomenon is important to various biological processes and is often modelled using a chain of linearly coupled oscillators subjected to a weak non-linear perturbation. Several reduced-order

models derived using averaging techniques have been used to investigate the full model's conformational dynamics; however, the influence of chain length on this dynamics is relatively less clear. These reduced-order models are based on an important approximation, i.e., the full system's nonzero modes follow the unperturbed dynamics. We examined this approximation by calculating the perturbed modal frequency of a nonzero mode both using a modified Lindstedt-Poincare method and numerical computations. We found that the approximation on which the previous reduced-order models are based may fail to hold when the chain length is large. The third is in the context of understanding the robustness of a biomolecular oscillator to transient perturbations. Biomolecular oscillators are known to operate robustly in the presence of environmental perturbations. Although the influence of circuit parameters and the mechanisms underlying the oscillator's robustness to steady perturbations have been investigated, the scenario for dynamic perturbations is relatively less clear. To address it, we first investigated the use of an averaging technique to predict the short term response of a stable limit cycle model of a biomolecular oscillator subjected to an initial condition perturbation. The application of Floquet theory was tested and was found to provide a valid prediction because of a good correlation between the time scale of the short term response obtained using the full model simulation and the time scale predicted by Floquet theory. Further, a metric derived from the Floquet time scale was used to identify the oscillator's intrinsic and structural features, which can improve the oscillator's short-term response.

These studies would help to understand better the use of averaging methods in studying oscillatory dynamics.