analysis of including distributed population ideas and parallelism into the basic genetic algorithm are carried out to solve the problem more accurately and efficiently than with ordinary sequential techniques, and we present two versions of the algorithm: one centralized (panmictic), GAseq, and one distributed, GAdis, with the aim of evaluating the effect of separating one single population into several subpopulations in terms of numerical cost (visited points in the problem landscape), and the resulting trim loss of the best solution found. Moreover, the second version has been run in a single processor system and in a cluster of workstations, in order to measure the speedup of the parallel GAdis.
Experimental evidence in this work show that the proposed parallelized distributed algorithm outperform its sequential counterpart in time (high speedup) and outperform the centralized algorithm numerically (lower number of visited points during the search to find the solutions, and best solution found). Also we address an interesting issue analyzing the algorithm performance on instances of larger dimensions, to definitely show how promissory the parallelism line is for this kind of applications (high speedup of the parallel algorithm proposed), since we firmly believe that time is very important in the works of this area that are actually aimed at a practical utilization.

Limit Cycles and Bifurcations in a Biological Clock Model

B. Nagy

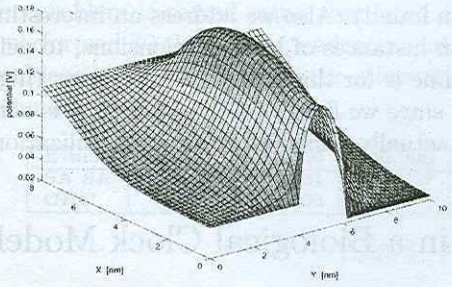
A three-variable dynamical system describing the circadian oscillation of two proteins (PER and TIM) in cells is investigated. We studied the saddle-node and Hopf bifurcation curves and distinguished four cases according to their mutual position in a former article. Other bifurcation curves were determined in a simplified, two-variable model by Simon and Volford. Here we show a system of bifurcation curves that divide the parameter plane into regions according to topological equivalence of global phase portraits, namely the global bifurcation diagram, for the three-variable system. We determine the Bautin-bifurcation point, the homoclinic bifurcation curves and fold bifurcation of cycles numerically. We also investigate instable limit cycles and the case when two stable limit cycles exist.

WIgner ENSemble Monte Carlo: Challenges of 2D Nano-Device Simulation

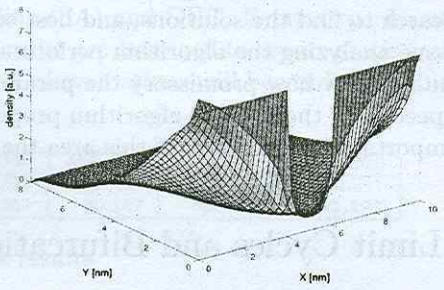
M. Nedjalkov, H. Kosina, D. Vasileska

The Wigner formulation of the quantum statistical mechanics provides a convenient kinetic description of carrier transport processes on the nanometer scale, characteristic of novel nanoelectronic devices. The approach is based on the concept of phase

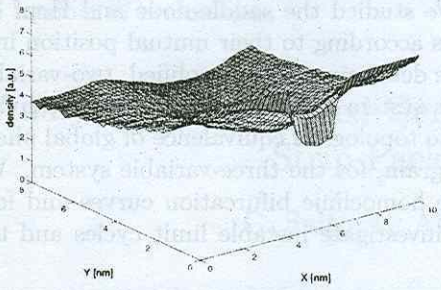
space and has been utilized in 1D device simulators. With deterministic mehtods an increase of the number of dimensions is infeasible due to prohibitive memory requirements. Recently a stochastic model has been developed, where the quantum character of carrier transport is taken into account by generation and recombination of positive and negative particles. This model is now utilized for the development of a 2D WIgner ENSemble (WIENS) device simulation approach. Here we discuss the first application of the approach, with an emphasis on the variety of raised computational challenges. The latter are large scale problems, introduced by the temporal and momentum variables involved in the task.



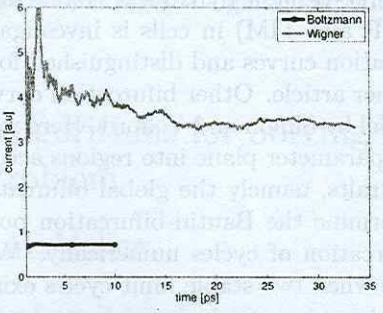
(a) Electrostatic potential profile



(b) Classical electron density



(c) QM electron density



(d) Current versus evolution time

(a) shows the potential of a MOSFET structure of a model semiconductor used in the simulations. A comparison of the classical (Boltzmann) and quantum mechanical (Wigner) carrier densities in (b) and (c) illustrates the feasibility of the approach. (d) compares the currents as obtained from Boltzmann and Wigner simulations and demonstrates the much slower convergence of the quantum transport task.