# *IONIC CHANNELS IN BIOLOGICAL MEMBRANES: NATURAL NANOTUBES DESCRIBED BY THE DRIFT-DIFFUSION EQUATIONS*

Protein channels conduct ions ($Na^+$, $K^+$, $Ca^{++}$, and $Cl^-$) through a narrow tunnel of fixed charge ('doping') thereby acting as gatekeepers for cells and cell compartments. Hundreds of types of channels are studied everyday in thousands of laboratories because of their biological and medical importance: a substantial fraction of all drugs used by physicians act directly or indirectly on channels. Ionic channels are studied with the powerful techniques of molecular biology. Atoms can be modified one at a time and the location of every atom can be determined within 0.01 nm.

The function of open channels can be described if the electric field and current flow are computed by the Poisson-Drift-Diffusion (*PNP*) equations and the channel protein is described as an invariant arrangement of fixed charges—***not*** as an invariant potential of mean force or set of rate constants, as is done in the chemical and biological tradition. The *PNP* equations describe the flux of individual ions (each moving randomly in the Langevin trajectories of Brownian motion) in the mean electric field specified in traditional (nonlinear) Gouy-Chapman/Debye-Hückel/Poisson-Boltzmann theories of electrolyte solutions and proteins. They are nearly identical to the drift diffusion equations of semiconductor physics.

*PNP* fits a wide range of current voltage (*I-V* ) relations—whether sublinear, linear or superlinear—from 6 types of channels, over ±180 mV of membrane potential, in symmetrical and asymmetrical solutions of 20 mM to 2 M salt. Porins with known structure have been studied, and parameter estimates (in mutations of known structure) are surprisingly close to those predicted. Complex selectivity properties of calcium channels are easily explained as the result of crowding of finite size ions in narrow channels at enormous concentrations (~$10^{22}$ $cm^{-3}$) using the known properties of crowded charge in bulk ionic solutions.

Ionic channels form a biological system of great biological significance and potential

technological importance that can be immediately studied by the techniques of computational electronics. Many of those techniques have not yet been used to analyze proteins, or ionic solutions. Perhaps they should be: the application of the even the lowest resolution techniques involving the drift diffusion equation has revolutionized the study of channels and it is likely that application of higher resolution methods, like self-consistent Monte Carlo analysis, would have an even larger effect on physical chemistry and computational biology. The enormous efforts in those fields (symbolized by the billions of dollars spent on computing protein dynamics) can only benefit from the insights of computational electronics.