

Description of Codes for Chapter 8: Cellular Electrophysiology

Section 8.2: The Hodgkin-Huxley model of the squid giant axon

The kinetic model for the potassium channel kinetics, Equations (8.7) and (8.8), is captured by the ODE script 'dXdT_n.m'. This script computes the time derivative of the n gate, which determines the conductivity of the potassium channel. The script 'HH_potassium_current.m' simulates the voltage-clamp experiments illustrated in Figure 8.4 of the text, and generates the figure. In brief, Equation (8.7) is integrated for each experiment, to generate plots of conductivity versus time for each different voltage clamp value. Two items are worth noting:

1. The ordinates in Figures 8.4 and 8.7 in the text are mislabeled. These plots are of the potassium and sodium conductivities (g_K and g_{Na}) versus time, not the currents.
2. Second, the assumed values of \bar{g}_K are adjusted to obtain the fits in the text. Hodgkin and Huxley report $\bar{g}_K = 24 \text{ mS cm}^{-2}$. This is necessary to obtain fits that agree with the data given the assumed form of Equation (8.10) for α_n and β_n . For example, the computed values of α_n and β_n at $v = 6 \text{ mV}$ are 0.813 and 0.116 ms^{-1} , which yield a value of $n_\infty = 0.4122$, which would result in an asymptotic values of $g_{K\infty} = 0.69 \text{ mS cm}^{-2}$, considerably smaller than the observed value of approximately $g_{K\infty} = 1 \text{ mS cm}^{-2}$. Therefore, at $v = 6 \text{ mV}$, \bar{g}_K is set to 40 mS cm^{-2} to obtain a value of $g_{K\infty} = 1.15 \text{ mS cm}^{-2}$, consistent with the fits to the data. (The values for \bar{g}_K at all voltage clamps are found in the script.)

The kinetic model for the sodium channel kinetics, Equation (8.11), is captured by the ODE script 'dXdT_mh.m'. This script compute the time derivative of the m and h gates, which determine the conductivity of the potassium channel. The script 'HH_sodium_current.m' simulates the voltage-clamp experiments illustrated in Figure 8.7 of the text, and generates the figure. Here, rather than using Equations (8.14) to compute α_m , β_m , α_h , and β_h , we directly use the estimated values from Table 2 of Hodgkin and Huxley (J. Physiol, 116:500-544, 1952). As a result, in this case, we can hold the value of \bar{g}_{Na} fixed at 70 mS cm^{-2} , the value estimated by Hodgkin and Huxley. As an additional exercise, one could modify the code to use Equation (8.14), in which case it is likely that the \bar{g}_{Na} value will have to be adjusted for each individual experiment to obtain good fits to the data. (Similarly, one could use the α_n and β_n values from Table 1 of Hodgkin and Huxley in the potassium channel kinetic simulation and hold the \bar{g}_K value fixed.)

The full Hodgkin-Huxley model is captured by the script 'dXdT_HH.m'. (This is the code that appears in Box 8.1 in the text, with the addition that additional output arguments are added to output the computed values of the conductivities.) The script 'HodHux.m' simulates the model and generates the plots in Figure 8.12.

The refractory period simulation can be repeated by running the script 'HodHux_refractory.m'. (This script is set up to generate the simulations in Figure 8.14. As an exercise, one can easily modify the script to obtain Figure 8.13.)

Section 8.4: Stochastic simulations

The script 'StochSim1.m' applies the stochastic simulation algorithm of Section 8.4 to simulate the 8-state model of the sodium channel. Note that each time this script is called, a different result will be obtained, with the same general trends as the trajectory shown in Figure 8.18.

The script 'StochSim2.m' applies the same algorithm to compute 100 trajectories for the depolarization experiment of Figure 8.19. As above, each time this script is called, a different result will be obtained, with the same general trends as the trajectory shown in Figure 8.19.