Genetic Algorithms for Fitting Hodgkin-Huxley Type Ion Channel Models

July 13, 2018

Here are some basic observations about the techniques in Gurkiewicz and Korngreen [1]. The specific are spelled out in the Methods section of their paper, but it took me some trial and error to fully understand the details, so I will try to make them explicit here. The model optimized in the scripts in this repo is for the EGL-19 voltage gated calcium channel:

Model Name	EGL-19
Channel Type:	Voltage-gated calcium channel
Model:	$I(V) = \underbrace{\left[G_{max} / 1 + e^{\frac{(V_{0.5} - V)}{k}} \right]}_{G_0} \cdot (V - V_{rev})$ $\frac{dG}{dt} = \frac{G_0 - G}{\tau}$
Parameters to Fit:	G_{max}, $V_{0.5}$, k, V_{rev}

Some clarifications that helped in implementing their techniques:

- Each organism is characterized by a 4-tuple $(G_{max}, V_{0.5}, k, V_{rev})$.
- The initial population is created by randomly sampling from the parameters space. Heuristically, a population size of 20 times greater than the number of parameters is sufficient. I used a population size of 100 in the scripts here.
- The sample space does not need to be discretized.
- The tournament and subsequent generations are created as follows:
  - Two sets of organisms are selected. The best fit organism is selected from each pair.
  - A crossover operator is applied to the resulting pair where an index is randomly selected and the corresponding values are swapped.
  - **Adaptive sampling:** after a certain number of generations (1000 in this repo), future generations are selected in a more targeted manner. After picking the highest scoring solution from *all previous generations*, a new population is generated by randomly sampling from Gaussian distributions centered around the values of the highest scoring solution with a variance of 5%.
  - There is no rigorous definition for the termination criterion. I used that the variance of the past 1000 or so generations was less than a fairly small threshold (for example 10^{-5}.)
- **Mutation operators:**
  - Random Mutation: randomly sample from the entire parameter space.

- Random Gaussian drift: sample from a Gaussian distribution centered at the given parameter value with 5% variance (the same function is used in the adaptive sampling method described above).
- Random Crossover: randomly select an index from two organisms and swap their entries.

References

[1] M. Gurkiewicz and A. Korngreen, "A numerical approach to ion channel modelling using whole-cell voltage-clamp recordings and a genetic algorithm," *PLOS Computational Biology*, vol. 3, no. 8, p. e169, 2007.