

## Project Work 2 Option 1: Hodgkin-Huxley Model

Deadline 28.4.2019 at midnight

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In this project, you will take a look at the Hodgkin-Huxley neuron model. Use the HHsim-simulator available at [www.cs.cmu.edu/~dst/HHsim/](http://www.cs.cmu.edu/~dst/HHsim/). The simulator code is also available in Moodle with some modifications by Inkeri Vornanen to work on TUNI's computers. The website has instructions on how to use the simulator. Note that the HHsim has a graphical user interface, so no coding is needed in this project. There is no requested format for the report or minimum length, as long as you answer the questions and include the requested things. Remember to cite your references in the text!

By using literature and the provided model, answer the following questions.

- a) Describe how action potential forms. What ion currents and what kind of ion channels take part?
- b) How does the action potential travel along an unmyelinated axon? What about myelinated axon? What cons and pros are there for myelination?
- c) Describe the Hodgkin-Huxley model (the equations, currents, variables, etc.).
- d) Do you find the Hodgkin-Huxley model biologically realistic? Why or why not?
- e) Find the smallest positive stimulus to induce an action potential. Does the length of the stimulus affect this value, and if yes, how? Further, does the stimulation amplitude affect the shape of the action potential?
- f) Find the highest frequency of action potential train you are able to produce with the stimuli available in the simulator. What restricts the frequency?
- g) Is it harder or easier to induce an action potential, if the (i) sodium, (ii) potassium, or (iii) chloride concentration outside the cell is half of the default? Why?
- h) What are the effects of the three drugs available in the model on to the neurons and how this effect is seen in the simulations?

## Running the HHsim

- Download the zip in Moodle and extract it
- Open Matlab
- Browse to the location you have the HHsim code in
- When inside the HHsim code folder, run command `hhsim`