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RESEARCH ARTICLE

REVISED Parametrizing analog multi-compartment neurons with genetic algorithms

[version 2; peer review: 4 approved, 1 approved with reservations]

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Abstract

Background

Finding appropriate model parameters for multi-compartmental neuron models can be challenging. Parameters such as the leak and axial conductance are not always directly derivable from neuron observations but are crucial for replicating desired observations. The objective of this study is to replicate the attenuation behavior of an excitatory postsynaptic potential (EPSP) traveling along a linear chain of compartments on the analog BrainScaleS-2 neuromorphic hardware platform.

Methods

In the present publication we use genetic algorithms to find suitable model parameters. They promise parameterization without domain knowledge of the neuromorphic substrate or underlying neuron model. To validate the results of the genetic algorithms, a comprehensive grid search was conducted. Furthermore, trial-to-trial variations in the analog system are counteracted utilizing spike-triggered averaging.

Results and conclusions

The algorithm successfully replicated the desired EPSP attenuation behavior in both single and multi-objective searches illustrating the applicability of genetic algorithms to parameterize analog

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REVISED **Amendments from Version 1**

This updated version incorporates references to recent literature on genetic algorithms applied to multi-compartment neurons. Additionally, we have introduced a new experiment, *High-Dimensional Parameter Space*, in the *Results* section. In this experiment, the parameters for all leak conductances and inter-compartment conductances are individually adjusted, increasing the dimensionality of the search problem compared to the previous experiment. The results are presented in two new figures, illustrating the fitness evolution and the final optimized parameters.

Any further responses from the reviewers can be found at the end of the article

Introduction

Neuromorphic hardware describes beyond-von-Neumann computational systems, which try to implement computations in a way similar to the human brain. Often, these systems are capable of simulating neuron models, where the neurons communicate with each other in an event-based fashion using spikes. This makes neuromorphic hardware consume less energy compared to other systems[1]. Many neuromorphic systems are also inherently scalable to larger systems[2]. Whereby, neuromorphic computers differ in their physical realization ranging from purely digital[3,4] over partially analog[5] up to complete analog systems[6]. Digital realizations like SpiNNaker or Loihi focus on simulating spiking neural networks (SNNs) efficiently, for example by exploiting a network-on-a-chip architecture or by processing neural dynamics in an event-driven fashion. On the other hand, mixed-signal systems like BrainScaleS-2 (BSS-2) physically implement the neuron model, resulting in a continuous operation of the neuron in time.

In the case of BSS-2, neural time constants are usually a factor of 1000 smaller in comparison to their biological archetypes, resulting in a significant speed gain.

The hardware components which govern a neuron's dynamics are configurable. Various conductances can be altered using bias currents in order to reach a desired operation point. Identically designed circuits deviate from each other in their real-world implementation because of mismatch during fabrication. This mismatch can be compensated by configuring the bias currents appropriately. Multiple chip components must be tuned to replicate high-level observations from biological neurons. However, these chip components can all influence observations in a highly nonlinear fashion.

In this paper, we demonstrate how genetic algorithms can be utilized to parameterize multi-compartmental neuron models on analog neuromorphic hardware. As an emulation platform BSS-2 will be used. The goal is to map high-level observations motivated by measurements of real neurons to the hardware. As a methodology, we chose genetic algorithms since they are frequently used to parameterize multi-compartmental neuron models[7,8] and showed good performance in comparison with other optimization methods for multi-compartmental neuron models[9,10]. Furthermore, genetic algorithms proved their applicability in conjunction with various other neuromorphic hardware systems on many different problems. Elias and Chang[11] used a custom genetic algorithm on artificial dendritic trees, which are nonlinear analog circuits, to determine the connectivity between neurons and sensory devices and the connectivity of the neurons themselves in order to classify a set of handwritten digits. Vandesompele *et al.*[12] used a genetic algorithm to find a network topology of an SNN on SpiNNaker such that the SNN could solve the exclusive or (XOR) problem. Furthermore, the authors used this algorithm to generate a functional SNN capable of playing the arcade game Pac-Man. Dalgaty *et al.*[13] proposed a concept, which they also verified in simulation, of a neuromorphic system for motion detection, where the underlying SNN was parameterized using genetic algorithms.

While computational neuroscience often focuses on point neuron models, we will investigate multi-compartmental neuron models in this paper. Real neurons in nature possess complex structure, which point neurons disregard. However, this structure is thought to play an essential role for signal processing[14].

For example, the signal-receiving part of a nerve cell, called the dendritic tree, is thought to play an essential role in the signal-processing capabilities of a neuron[15–18]. Moreover, benefits when using dendrites are not limited to the level of single neurons but also the whole system can profit since dendrites could help to solve the credit assignment problem in biological brains[19,20].

Morphological characteristics of neurons like dendrites can be realized on BSS-2 using multi-compartmental neuron models. Multiple properties of the multi-compartment emulation on BSS-2, like passive attenuation properties but also active characteristics like back-propagating action potential activated calcium spike firing (BAC), were demonstrated in Kaiser *et al.*[21].

The following subsection will briefly introduce the hardware platform alongside the used multi-compartmental neuron model. In the "experiment" section, we present the task which the genetic algorithm will be applied to. After that, in the "methods" section, the genetic algorithms will be outlined. Subsequently, the results of the experiments are presented in the "results" section. Finally, in the "conclusions" section, the paper is concluded.

BrainScaleS-2

BrainScaleS-2 is a mixed-signal neuromorphic chip that implements analog neurons and synapses. In total, there are 512 neurons implementing the adaptive exponential integrate-and-fire (AdEx) neuron model[22,23]. Those neurons are arranged in two rows with 256 neurons each. Above the upper neuron row there is a synapse matrix which can establish up to 256 synaptic connections per neuron circuit within that row. Similarly, there is a synapse matrix below the bottom neuron row. The AdEx model can be reduced to the simpler leaky integrate-and-fire (LIF) neuron model by disabling parts of the analog circuit[22]. Through direct switches and

adjustable conductances, single neuron circuits can be interconnected to form larger structured neurons (cf. Figure 1), resulting in a multi-compartmental model. Two possible types of connections exist. First, direct switches, which can be used to shorten a neuron's membrane to its horizontal (S_{mh}) or vertical (S_{mv}) neighbors. Those switches can be used to increase the synaptic fan-in of a neuron. The second type of connection between neurons uses a shared line. Each neuron circuit can connect either *via* a switch (S_{ms}) or an adjustable conductance (g_{ic}) to that shared line. Furthermore, this shared line can be interrupted between neuron circuits using switches (S_s). A neuron can be separated into different compartments, by using the conductances g_{ic}.

Besides the adjustable inter-compartment conductance, other properties of a neuron can be adjusted using various bias currents. The membrane voltage of a neuron can be recorded using the fast on-chip analog-to-digital converter (ADC) with a sampling frequency of 29MHz and a resolution of 10 bit[24]. For a more in-depth description of the neuron circuit, refer to Schemmel *et al.*[5] or to Kaiser *et al.*[21] for more information about the multi-compartment features.

Experiments are formulated in the high-level neural network description language `PyNN`[25], which is supported by the software stack of BSS-2[26].

Multi-compartmental neuron model

The cable equation can be used to model passive charge transport in structured neurons. Segments of a neuron are represented as cylinders of fixed radii with constant electrical properties. Multiple cylinders can be concatenated to replicate a desired morphology[27]. The one-dimensional cable equation is given by:

$$\tau_m \frac{\partial U_m(x,t)}{\partial t} - \lambda_m^2 \frac{\partial^2 U_m(x,t)}{\partial x^2} + U_m(x,t) = \frac{I^{ext}}{g_l}. \quad (1)$$

Here $U_m(x, t)$ describes the membrane potential at position x at the time t, τ_m is the membrane time constant, λ_m is the electronic length scale, g_l is the leak conductance and I^{ext} accounts for any external current onto the cable[28].

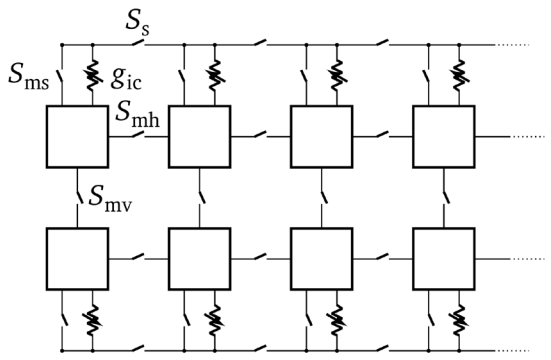


Figure 1. Overview of the connections available for implementing multi-compartmental neuron models on BrainScaleS-2. The squares illustrate neuron circuits which are physical implementations of the adaptive exponential integrate-and-fire neuron model. For more details refer to Schemmel *et al.*[5], Kaiser *et al.*[21].

While the temporal part of the cable equation is emulated continuously on BSS-2, due to the physical implementation of the neurons, the space can not be modeled continuously. However, the spatial component of the cable equation can be discretized by using a second-order central difference on the second derivative with respect to space. This will lead to a multi-compartmental neuron model, which can be implemented on BSS-2, since single point neurons can be connected using conductances between them (compare Figure 1). We can extend the LIF neuron model to a multi-compartmental model, whose dynamics are given by:

$$C_{m,i} \frac{dU_{m,i}(t)}{dt} = -g_{l,i} \cdot (U_{m,i}(t) - E_{l,i}) + \sum_j g_{ic,i\leftrightarrow j} \cdot (U_{m,j}(t) - U_{m,i}(t)) + I_i^{ext}. \quad (2)$$

Here the second term on the right-hand side accounts for connections between neighboring compartments. In Equation 2, $C_{m,i}$ describes the membrane capacitance of compartment i. The summation is performed over all neighboring compartments j of compartment i. $U_{m,i}$ is the membrane potential of compartment i, $E_{l,i}$ is the leak potential, $g_{l,i}$ the leak conductance, while $g_{ic,i\leftrightarrow j}$ is the conductance connecting compartment i with a neighboring compartment j. I_i^{ext} accounts for any external input current onto compartment i[29].

Genetic algorithms

Genetic algorithms are used for search problems as well as optimization and belong to the class of evolutionary algorithms. As the name suggests, genetic algorithms are inspired by natural evolution[30,31].

The first step of a genetic algorithm is to initialize random solutions to a problem. Each solution is called an individual. Individuals are constructed out of genes, which describe how the individuals solve the problem. Often genes are represented as arrays of numerical values. The collection of all individuals is referred to as population. In a sequential process, the population's individuals are mutated, recombined and selected in order to create the next generation's population. Usually, the selection is governed by the individual's fitness, which is a score of how well the individual solves the problem. This process is repeated until an individual satisfyingly solves the problem or a predefined maximal number of generations is reached.

Experiment

In this section, we explain the purpose and the experiment setup that will be used to investigate the genetic algorithm in the "results and discussion" section.

Our task is to tune a chain of compartments to match an observation. The observations are based on experiments that measured the decay of excitatory postsynaptic potentials (EPSPs) along a dendrite, see Berger *et al.*[32].

To replicate an attenuation experiment on BSS-2, first, we need to model the neuron's morphology. Rather than modeling exact replicas of real neurons, we will only consider a linear chain of five compartments. This approach is sufficient for our purpose, as the focus of this paper is on the methodology of parametrizing the compartments.

A schematic of the considered compartment chain is given in Figure 2A alongside a possible implementation on BSS-2 in Figure 2B. By connecting the first compartment with a pre-synaptic partner, that elicits a spike, we can observe an EPSP. This EPSP travels along the chain of compartments, as shown in Figure 2C. The amplitude $U_{\mathrm{m,max}}$ of the EPSP within each compartment is shown in Figure 2D. Empirically we determined that the attenuation of the maximal EPSP height approximately obeys an exponential law with a length constant λ_{emp}. A similar behavior was found in 32.

Since we work with an analog substrate, trial-to-trial variations are inevitable. In Figure 3, the histograms illustrate the deviations between 1000 experiment runs using the same parameterization of the chip. Both the variation of the empirical length constant λ_{emp} and of the EPSP amplitude inside the first compartment are shown.

To counteract the trial-to-trial variations, we use the spike-triggered average (STA) over several measurements[33]. The STA describes the average membrane potential of a compartment in response to an input spike. Accordingly, we can modify the experiment by injecting N_{spikes} spikes with a time delay into the first compartment resulting in N_{spikes} EPSPs. The time delay between the spikes is set such that the membrane potential has enough time to return to its resting state. This way, multiple EPSPs can be recorded in one hardware run. For all results in this paper that use the STA, we will average the membrane potential over $N_{\mathrm{spikes}} = 10$ input spikes, as this reduces the standard deviation of the trial-to-trial variations below the measurement resolution of the ADC. In Figure 4, the STA is calculated from ten experiment runs. The resulting traces are less noisy compared to the gray traces illustrating single experiment runs.

Ultimately, we can extract the amplitudes of the EPSPs from the STA and fit an exponential function to those amplitudes to obtain λ_{emp}. This method decreases the standard deviation of the observables, which becomes apparent by the orange histograms in Figure 3. As a result, both observables exhibit a three times smaller standard deviation. Consequently, if not otherwise mentioned, all following results use the STA

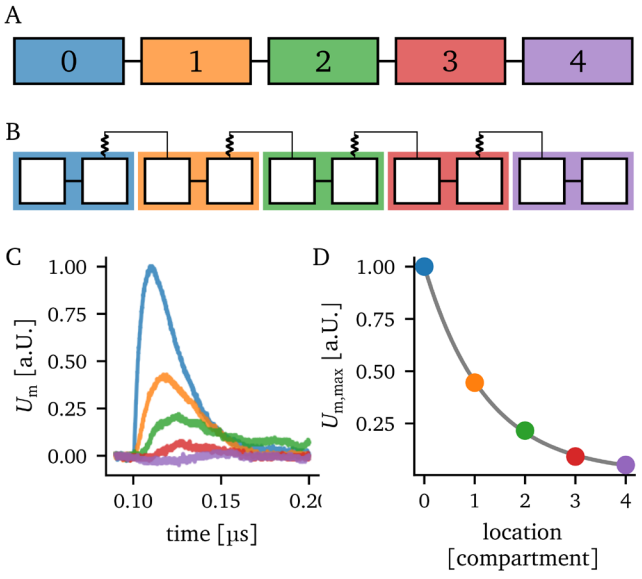


Figure 2. Experiment overview. A) Schematic of a linear compartment chain of length five. **B**) Possible realization of the compartment chain on BrainScaleS-2 using the same schematic as in Figure 1. **C**) Recordings of the excitatory postsynaptic potential (EPSP) in each compartment. The input is injected into compartment 0. Furthermore, the color of the EPSP traces indicate the compartment they belong to. **D**) Attenuation of the EPSP amplitudes along the chain of compartments. Additionally, an exponential of the form $U_{\mathrm{m,max}} = a \cdot \exp(-x/\lambda_{\mathrm{emp}}) + c$ is fitted to the data.

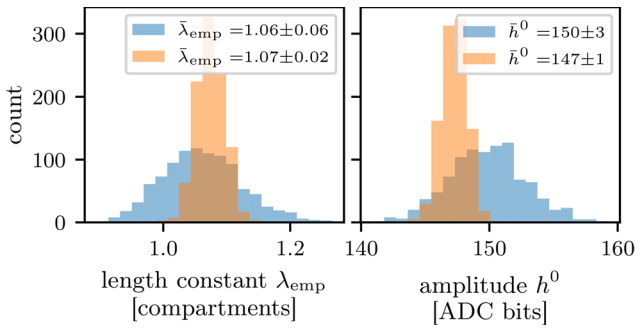


Figure 3. Trial-to-trial variations. A) Trial-to-trial variation of the length constant measurement and **B**) excitatory postsynaptic potential amplitude within the first compartment. The blue histograms show the single measurement scheme and the orange histograms show the results using the spike-triggered average over $N_{\mathrm{spikes}} = 10$ spikes. Both evaluation methods were executed 1000 times with the same parameterization of the chip.

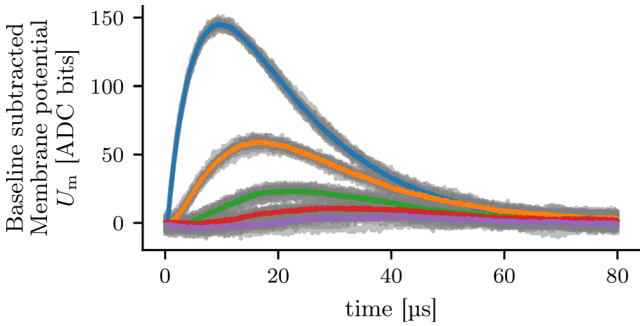


Figure 4. Spike-triggered average calculated from ten experiment runs. The color indicates the compartment where the excitatory postsynaptic potential was recorded (compare Figure 2). The traces of the single experiments are illustrated by the gray lines. For each run and compartment, the baseline is subtracted so that the resting potential is at zero.

with N_{spikes} = 10. In Figure 3, we can see a small shift of approximately three bits towards smaller EPSP amplitudes. The STA helps to remove noise from the signal by smoothing it, which reduces the occurrence of slightly higher amplitudes caused by the noise of the membrane. Both recording methods agree within one standard deviation for the estimated length constant λ_{emp}.

Recalling Equation 2, we can see that the dynamics of the membrane potential within each compartment depend on the membrane capacitance $C_{m,i}$, the leak conductance $g_{l,i}$ and the inter-compartment conductance $g_{ic,i\leftrightarrow j}$. Therefore, we can change the attenuation behavior of the chain by changing these properties. Both the inter-compartment conductance and the leak conductance are adjustable using bias currents. Those bias currents are set by a digital-to-analog converter (DAC) with 10-bit resolution[34].

In order to get an overview of how these parameters influence the empirically found length constant λ_{emp}, we sweep both the leak conductance and the inter-compartment conductance.

We extract the EPSP amplitude in each compartment for each parameter setting and fit an exponential function to the attenuation of the EPSP amplitudes (compare Figure 2D). This way, the empirical length constant λ_{emp} can be determined.

Figure 5 shows that larger leak conductances will lead to smaller length constants, while larger inter-compartment conductances will increase the length constant. Additionally, the grid search indicates that there are multiple possible configurations of the pair of conductances resulting in the same length constant. Points in the solution space with the same length constant can be distinguished from one another by taking an additional observable into account, namely the amplitude of the resulting EPSPs. Since the strength of the synaptic event is constant, increasing the leak conductance will lead to a smaller EPSP. Likewise, increasing the inter-compartment conductance will lead to a smaller EPSP as well, as charge can more easily propagate to neighboring compartments. Consequently, increasing either the leak conductance or the inter-compartment conductance, will result in smaller amplitudes of the EPSP in the first compartment. This relationship is visualized in Figure 5B.

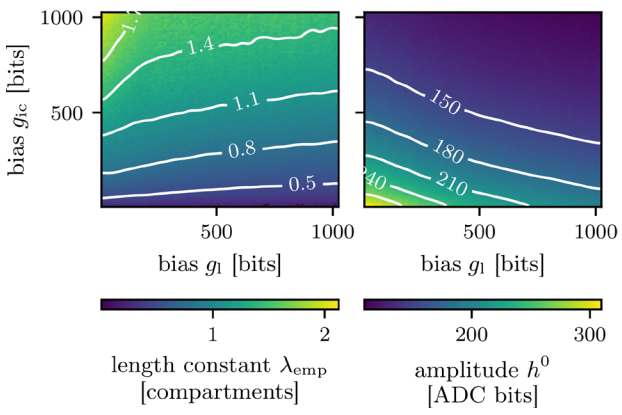


Figure 5. Grid search result over the whole parameter space. **A**) Empirically found length constant λ_{emp}. **B**) Amplitude of the excitatory postsynaptic potential in the first compartment h^0.

For our following investigations of the genetic algorithm, we pick one point in this parameter space, record it and extract a target observation for our algorithmic investigations. Then, the algorithm must find appropriate values for the inter-compartment and leak conductance that reproduce that observation. We pick the middle of the parameter space at a DAC value of 511 for both the leak conductance and the inter-compartment conductance to obtain our target observation, which will be the length constant with a value of $\hat{\lambda}_{emp}$ = (1.07 ± 0.02) compartments.

This value was determined by taking the mean of 1000 measurments at the described fixed DAC values (compare Figure 3). For all other parameters the chip's default calibration was used. The presented error describes the trial-to-trial variation calculated from the standard deviation of the different runs.

Furthermore, considering the amplitude of the EPSP, the problem can be extended to a multi-objective search problem.

In the next section, the used genetic algorithm will be introduced.

Methods

In this paper, the `Python` (RRID:SCR_008394) library `DEAP`[1] is used as backbone, which was developed for genetic algorithms with a high level of customizability[35]. Figure 6

[1]version 1.3.0 https://github.com/DEAP/deap

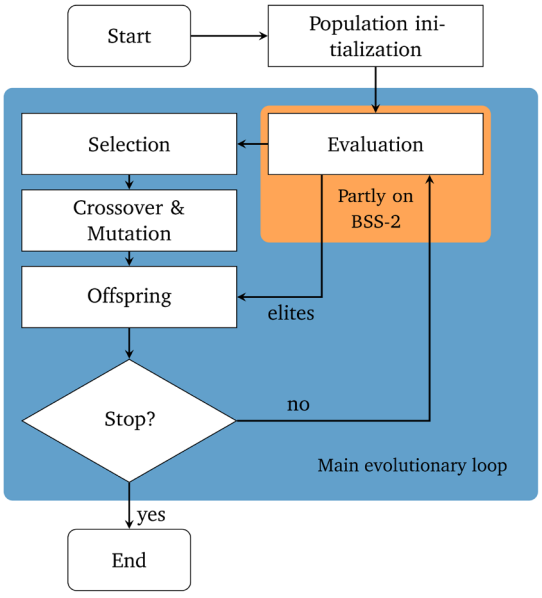


Figure 6. Flowchart of the used genetic algorithm with elitism. Only the evaluation step uses the neuromorphic hardware.

illustrates the procedural flow of our customized genetic algorithm.

The algorithm is based on `DEAPs eaSimple`[36] and extended to use an elitism mechanism[37]. First, the algorithm randomly instantiates a set of $n_{\text{individuals}}$ initial solutions. In our case, an individual will consist of two integer values, each describing a DAC setting. The first gene will describe the setting of the DAC responsible for the leak conductance and the second gene will describe the setting for the inter-compartment conductance. Because of that, the genes are bound to the value ranges of the respective DAC, which in our case is [0,1022] for both DACs.

Each individual's fitness is determined in the evaluation step using the experiment described in the previous "experiment" section from which we obtain the corresponding length scale λ_{emp}. By taking the difference between the measured length scale λ_{emp} and the desired target length scale $\hat{\lambda}_{\text{emp}}$ the fitness f can be calculated:

$$f = \left|\lambda_{\text{emp}} - \hat{\lambda}_{\text{emp}}\right|. \tag{3}$$

As we are interested in individuals that produce observations that deviate as little from the target as possible we want to minimize this fitness f. The evaluation step is the only component of the genetic algorithm that executes instructions on the neuromorphic hardware.

Since we employ an elitism mechanism the n_{elites} fittest individuals are directly passed on to the next generation. The elitism mechanism ensures that the minimum fitness of each generation is not increasing.

Subsequently, the selection process begins, where we use tournament selection. Tournament selection randomly draws k individuals from the population, including the elites, and the individual with the best fitness score, *i.e.* the individual with the smallest fitness, will be selected. Since we use an elitism mechanism, we repeat the selection $n_{\text{selection}} = n_{\text{individuals}} - n_{\text{elites}}$ times, where $n_{\text{selection}}$ describes the number of selected individuals and n_{elites} is the number of elites.

After the selection process, the selected individuals are subject to evolutionary operations, like crossover and mutation. Two consecutive individuals are recombined with the probability p_{cx}. The here used one-point crossover operator will recombine the genes (in our case, the single integer values of an individual) of two randomly picked individuals to create two offspring-individuals as depicted in Table 1.

Next, the mutation operator will apply point mutations on randomly chosen positions in the genome of the selected individuals with a fixed probability p_{mut}. Here we use a custom mutation procedure: the gene's new value is calculated by randomly adding or subtracting 2^x from the initial value, where $x \in [0,9]$ is as well randomly chosen from a uniform distribution. If the new value falls outside the parameter boundaries, it will be rejected and a new value will be generated until it resides within the parameter boundaries.

Now, the procedure will start from the evaluation again if the stop criterion is not yet matched. In this implementation, we set a hard limit of 30 generation for the stop criterion. Finally, the fittest individual can be picked as a solution to the problem.

Several hyperparameters need to be set to run the algorithm. Unfortunately, there is no universal set of default hyperparameters that applies to every problem. Often the right hyperparameters are objective to trial-and-error methods and user experience. In Table 2, the used hyperparameters are summarized, which lead to sufficient results on our problem as can be seen in the next section. The hyperparameters are based on the findings in Keren *et al.*[38] and Xia *et al.*[39].

Results

In this section, we apply the just-described genetic algorithm to the experiment described in the "experiment" section and present the results.

The algorithm was run ten times and the average fitness of the population and the fitness of the best individual in each generation are shown in Figure 7. The population's

Table 1. Example of one-point crossover applied to two parent individuals and the resulting offspring individuals.

gene	g_{l}	g_{ic}
parent 1	408	139
parent 2	364	975
offspring 1	364	139
offspring 2	408	975

Table 2. Hyperparameters used for the genetic algorithm to generate the presented results.

parameter	value	description
$n_{\text{individuals}}$	50	Population size of each generation.
n_{elites}	5	Number of elites directly passed to the next generation.
$n_{\text{generations}}$	30	Number of generations to run.
Crossover	One-point	Cut genome at one point.
p_{cx}	50%	Crossover probability.
Mutation	"Bit-flip"	Add/subtract 2^x to/from a gene.
p_{mut}	10%	Mutation probability.
p_{gen}	50%	Probability that a gene is mutated if individual is selected for mutation.
Selection	Tournament selection	Choose k individuals randomly and pick the fittest.
k	3	Tournament size.

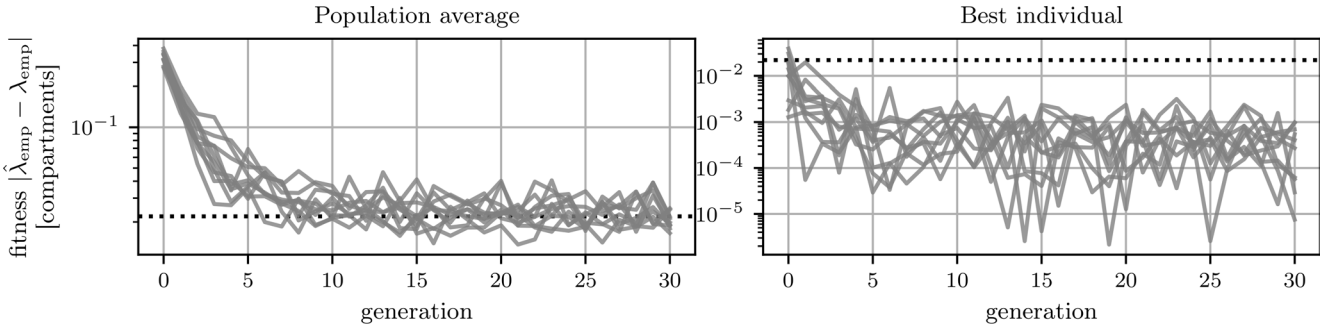


Figure 7. Fitness evolution of the genetic algorithm. The dashed black line indicates the error of the length scale measurement due to trial-to-trial variation. **A**) Average performance of the population in each generation. Each line indicates one of the ten runs. **B**) Performance of the best individual in each generation. Again each line represents one of the ten runs. Due to trail-to-trial variations, the fitness of the best individual does not decrease monotonically.

average fitness is approaching the limit given by the standard deviation of the trial-to-trial variation of the searched-for target. However, there is always the chance that an evaluation of an individual leads to a length scale λ_{emp}, which is closer than the trial-to-trial error to the target length scale $\hat{\lambda}_{emp}$. This is the case for the best-performing individuals in Figure 7B. The fitness of the best individuals in all runs plateaus already after approximately five generations. This indicates that a solution is already found. Furthermore, trial-to-trial variations are the reason for fluctuations of the fittest individual within this plateau. This can be seen in Figure 7B, even though we employ an elitism mechanism, which on digital hardware would ensure that the best fitness does not increase[2].

Next, in Figure 8, the resulting parameters of the single algorithm runs are visualized. The red cross illustrates the parameters which were used to create the target length scale $\hat{\lambda}_{emp}$. The blue crosses represent the solutions of the genetic algorithm. All ten solutions are in the vicinity of the red contour line, which marks the length scale of 1.12 compartments. Since the problem was to find the length constant, all provided solutions are valid.

By considering the amplitude h^0 of the EPSP in the first compartment of the chain for the fitness evaluation we can change the fitness landscape.

This will further reduce the space for valid solutions since a solution must now match *both* the searched-for length scale λ_{emp} and the EPSP amplitude of the first compartment h^0. An example of an adapted fitness function, considering the length constant λ_{emp} and the EPSP amplitude h^0, can be expressed as:

$$f_2 = \sqrt{\left(\frac{\hat{\lambda}_{emp} - \lambda_{emp}}{\hat{\lambda}_{emp}}\right)^2 + \left(\frac{\hat{h}^0 - h^0}{\hat{h}^0}\right)^2}. \quad (4)$$

[2]Note that we want to minimize the fitness here.

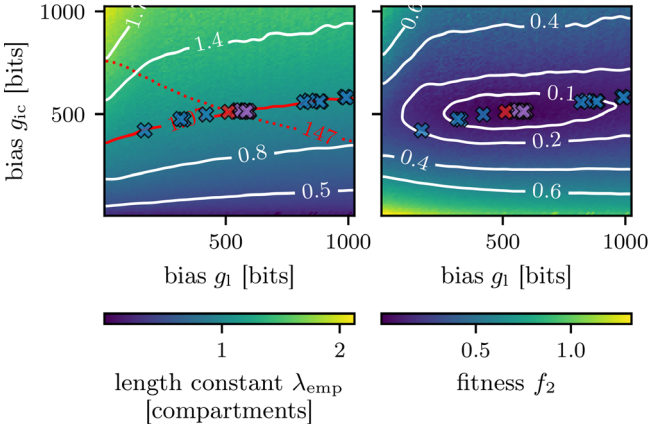


Figure 8. Solutions from ten runs using fitness function f (blue crosses) and f_2 (purple crosses). A) The color of the background indicates the empirically found length constant λ_{emp} like in Figure 5A. The red line denotes the searched for target length scale of $\hat{\lambda}_{emp}$ = 1.07 compartments, and the red cross the parameterization which resulted in the searched for target length scale. The red dotted line illustrates the corresponding target amplitude of the excitatory postsynaptic potential in the first compartment $\hat{h}^0$ of 147 bits. The blue crosses show the final solutions of the genetic algorithm with fitness function f from Equation 3, while the purple crosses exhibit the solutions of the genetic algorithm using the fitness function f_2 from Equation 4. **B**) Here the background shows the fitness landscape, which was calculated using the grid search result from Figure 5 and the fitness function from Equation 4.

Here $\hat{h}^0$ is the target amplitude of the EPSP in the first compartment, which is (147 ± 1) bits. This value is the average measured amplitude for the EPSP at a DAC setting of 511 for both the leak and inter-compartment conductance (compare Figure 3).

The fitness landscape of the fitness function f from Equation 3 would be minimal along the red contour line of Figure 8A and would increase on both sides of it. Using the fitness function f_2, the fitness landscape changes according to the

shape depicted in Figure 8B. Now solutions with minimal fitness can only be found around the target marked by the red cross.

Rerunning the genetic algorithm ten times with the adapted fitness function f_2 results in the solutions marked by the purple crosses in Figure 8.

Now all solutions are much closer to the red cross marking our target setting.

High-dimensional parameter space

Previously, we used a two-dimensional parameter space to easily visualize how the genetic algorithm works and validate its results with a systematic grid search. In this section, we want to demonstrate that the genetic algorithm is also capable of finding suitable solutions in a high-dimensional parameter space for which a grid search or random search would be too expensive.

Therefore, we will alter the leak conductance $g_{l,i}$ and the inter-compartment conductance $g_{ic,\ i\leftrightarrow j}$ individually for each compartment and the connections between compartments; this results in a nine-dimensional parameter space.

In order to have a more informative observation, we will connect each compartment to a pre-synaptic partner and inject a spike in one compartment after another while we record the EPSP amplitudes in all compartments.

Therefore, we have access to the EPSP amplitudes $h_{i,j}$ which was recorded in compartment i for an input to compartment j.

As for the two-dimensional case, we perform STA and repeat the experiment 1000 times to find target amplitudes $\hat{h}_{i,j}$, compare Figure 3

The fitness takes EPSP amplitudes into account,

$$f_3 = \sqrt{\sum_{i,j}^{x} \left(\hat{h}_{i,j} - h_{i,j}\right)^2}$$

As before, we applied the genetic algorithm ten times to our high-dimensional problem. For the two-dimensional case the fitness saturated after around 20 generations, Figure 7A. In the case of the high-dimensional optimization, the genetic algorithm needs more generations until the fitness starts to saturate, Figure 9.

To quantify the performance of the genetic algorithm, we extracted the best individual from the ten runs of the genetic algorithm and measured the EPSP amplitudes 100 times for each of these individuals. In Figure 10 we compare these measurements of the trial-to-trial variation when performing the experiment with the target parameters. The mean amplitudes of the solutions found with the genetic algorithm and the target parameters agree well. When the amplitude is measured near the injection site, i.e. the histograms on or near the diagonal in Figure 10, the histograms of the target parameter are narrower.

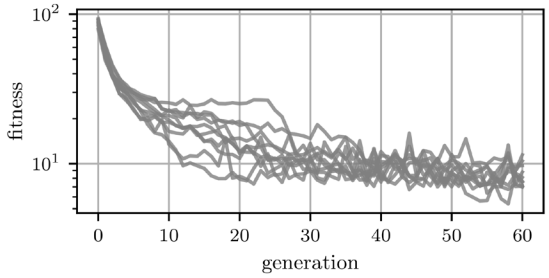


Figure 9. Evolution of the fitness for a nine-dimensional parameter space. The leak conductance gl,i and the inter-compartment conductance $g_{ic,i\leftrightarrow j}$ are optimized for each compartment and the connections between compartments individually. Each line shows the evolution of the mean fitness of the population for one of ten runs of the genetic algorithm; we used the fitness given in Equation 5.

The further away from the input site the EPSP amplitude is measured, the better the spread of the histogram agree between the solutions found by the genetic algorithm and the target parameters.

Conclusions

In this paper, we have demonstrated that genetic algorithms can be utilized to parameterize analog neurons on BSS-2 such that high-level observations can be replicated. We parameterized two neuron parameters such that the desired attenuation behavior of an EPSP along a compartment chain could be replicated.

First, the trial-to-trial variations of experimental observations due to the analog nature of the used hardware were quantified and used as an estimate for the error. Employing STA reduced the trial-to-trial variation of different experiment runs. Then, through a grid search, the solution space was visualized.

The solutions produced by the genetic algorithm replicated observations within the error boundaries defined by the observed trial-to-trial variations. Additionally, the genetic algorithm could cope with an extension to the problem, making it a multi-objective search. The optimizer was able to simultaneously minimize the distance to a target length constant $\hat{\lambda}_{\text{emp}}$ and a target EPSP amplitude within the first compartment $\hat{h}^0$. Furthermore, we extended the optimization problem to a higher-dimensional parameter space (nine parameters) and showed that the genetic algorithm was also able to find suitable parameters in this case.

Overall genetic algorithms could profit twofold from accelerated analog neuromorphic hardware, first through the speed gain and second through its intrinsic parallelization capabilities as genetic algorithms are predestined for running in parallel. Neurons on BSS-2 possess membrane time constants a thousand times smaller than their biological archetypes. Therefore, each evaluation of an individual profits from that speed-up, especially for long experiment run times.

Genetic algorithms can be parallelized since the evaluation of an individual is independent of other individuals. Therefore,

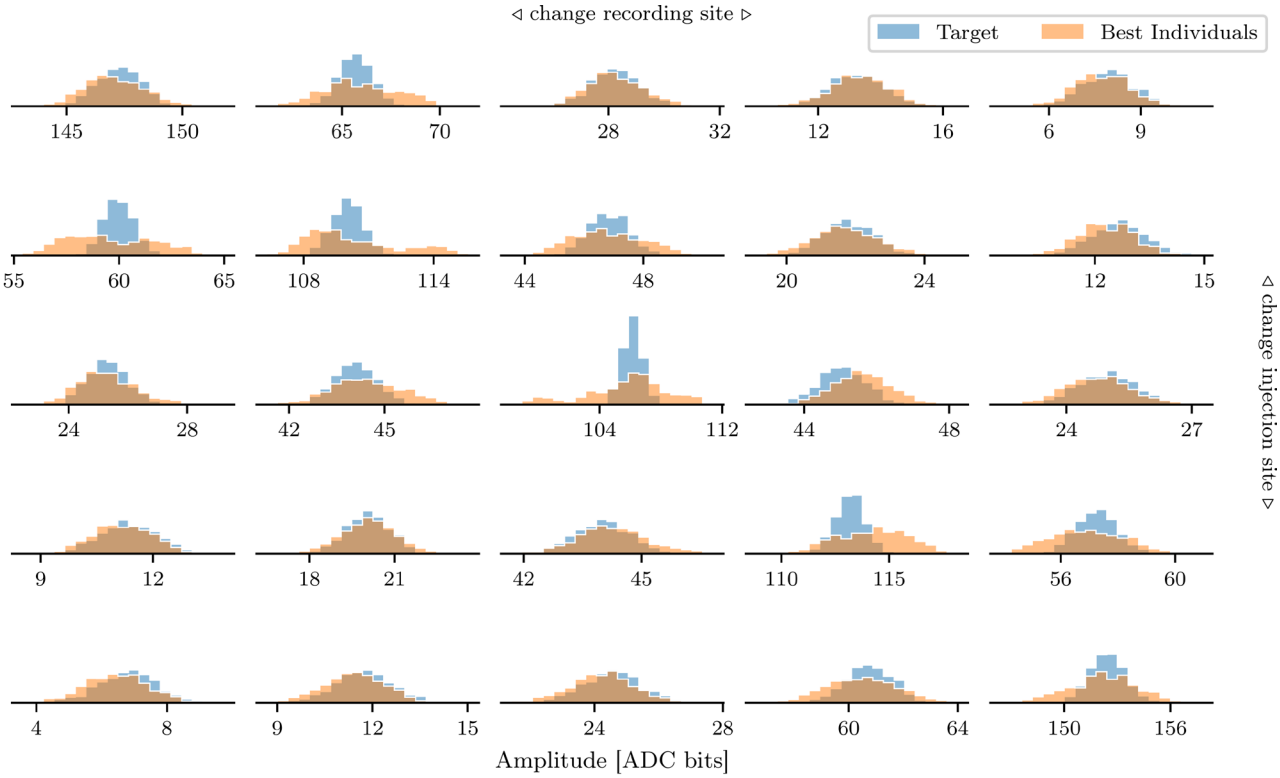


Figure 10. Comparison of measured EPSP height between the solutions found by the genetic algorithm and the target parameters. As in the two-dimensional case, we choose a DAC value of 511 for all parameters as a target. The blue histograms show the trial-to-trial variation over 1000 trials. We executed the genetic algorithm ten times, extracted the individual with the best fitness in each run and performed the experiment 100 times for each of these individuals (orange histograms).

the whole population can be evaluated at once. On BSS-2, there are 512 neuron circuits so multiple experiments can be run in parallel. However, there is fixed-pattern variation between neuron circuits. The same bias current applied to different neuron circuits can therefore lead to slightly different observations. Especially, the effectiveness of the crossover operation would suffer from that. Nevertheless, this problem can be circumvented by working on model parameters, which in turn requires a parameter transformation using chip-specific calibration data.

For example, in our experiment, the leak conductance g_l and the inter-compartment conductance g_{ic} could have functioned as universal parameters. Finally, this would allow a translation from one neuron circuit to another and therefore allow parallelization.

Ethics and consent

Ethical approval and consent were not required.

Data availability

Underlying data

The underlying data can be accessed via heiDATA: https://doi.org/10.11588/data/U2U1IB[40].

The archived folder contains all experiment results.

Data are available under the terms of the Creative Commons Attribution 4.0 International license (CC-BY 4.0).

Following the instructions in the corresponding repository, https://github.com/electronicvisions/model-paper-mc-genetic, the underlying data also contains all information to reproduce the experiment results and generate the plots presented in this publication.

The BSS-2 system can be accessed *via* EBRAINS.

Software availability

Source code available from: https://github.com/ electronicvisions/model-paper-mc-genetic.

Archived source code at the time of publication: https://doi.org/10.5281/zenodo.14046603[41].

License: LGPL-2.1 license.

Acknowledgments

The authors wish to thank A. Baumbach, S. Billaudelle, A. Grübl, J. Ilmberger, C. Mauch, C. Pehle, Y. Stradmann, P. Spilger and, J. Weis for their contributions to BSS-2; as well as all present and former members of the Electronic Vision(s) research group.

References

1. Schuman CD, Potok TE, Patton RM, *et al.*: **A survey of neuromorphic computing and neural networks in hardware.** 2017.
Reference Source
2. Schuman CD, Kulkarni SR, Parsa M, *et al.*: **Opportunities for neuromorphic computing algorithms and applications.** *Nat Comput Sci.* 2022; **2**(1): 10–19.
PubMed Abstract | Publisher Full Text
3. Furber SB, Lester DR, Plana LA, *et al.*: **Overview of the SpiNNaker system architecture.** *IEEE Transactions on Computers.* 99(PrePrints), 2013; **62**(12): 2454–2467.
Publisher Full Text
4. Davies M, Srinivasa N, Lin TH, *et al.*: **Loihi: a neuromorphic manycore processor with on-chip learning.** *IEEE Micro.* 2018; **38**(1): 82–99.
Publisher Full Text
5. Schemmel J, Billaudelle S, Dauer P, *et al.*: **Accelerated analog neuromorphic computing.** In: *Analog Circuits for Machine Learning, Current/Voltage/Temperature Sensors, and High-speed Communication: Advances in Analog Circuit Design 2021.* Springer International Publishing, 2022; 83–102.
Publisher Full Text
6. Prezioso M, Merrikh-Bayat F, Hoskins BD, *et al.*: **Training and operation of an integrated neuromorphic network based on metal-oxide memristors.** *Nature.* 2015; **521**(7550): 61–64.
PubMed Abstract | Publisher Full Text
7. Gouwens NW, Berg J, Feng D, *et al.*: **Systematic generation of biophysically detailed models for diverse cortical neuron types.** *Nat Commun.* 2018; **9**(1): 710.
PubMed Abstract | Publisher Full Text | Free Full Text
8. Druckmann S, Banitt Y, Gidon A, *et al.*: **A novel multiple objective optimization framework for constraining conductance-based neuron models by experimental data.** *Front Neurosci.* 2007; **1**(1): 7–18.
PubMed Abstract | Publisher Full Text | Free Full Text
9. Mohácsi M, Török MP, Sáray S, *et al.*: **A unified framework for the application and evaluation of different methods for neural parameter optimization**. In: *2020 International Joint Conference on Neural Networks (IJCNN).* IEEE, 2020; 1–7.
Publisher Full Text
10. Vanier MC, Bower JM: **A comparative survey of automated parameter-search methods for compartmental neural models.** *J Comput Neurosci.* 1999; **7**(2): 149–171.
PubMed Abstract | Publisher Full Text
11. Elias JG, Chang B: **A generic algorithm for training networks with artificial dendritic trees.** In: *[Proceedings 1992] IJCNN International Joint Conference on Neural Networks.* IEEE, 1992; **1**: 652–657.
Publisher Full Text
12. Vandesompele A, Walter F, Röhrbein F: **Neuro-evolution of spiking neural networks on SpiNNaker neuromorphic hardware.** In: *2016 IEEE Symposium Series on Computational Intelligence (SSCI).* 2016; 1–6.
Publisher Full Text
13. Dalgaty T, Vianello E, Ly D, *et al.*: **Insect-inspired elementary motion detection embracing resistive memory and spiking neural networks.** In: *Biomimetic and Biohybrid Systems.* Springer, Springer International Publishing, 2018; 115–128.
Publisher Full Text
14. Gidon A, Zolnik TA, Fidzinski P, *et al.*: **Dendritic action potentials and computation in human layer 2/3 cortical neurons.** *Science.* 2020; **367**(6473): 83–87.
PubMed Abstract | Publisher Full Text
15. Vetter P, Roth A, Häusser M: **Propagation of action potentials in dendrites depends on dendritic morphology.** *J Neurophysiol.* 2001; **85**(2): 926–937.
PubMed Abstract | Publisher Full Text
16. Williams SR, Stuart GJ: **Dependence of EPSP efficacy on synapse location in neocortical pyramidal neurons.** *Science.* 2002; **295**(5561): 1907–1910.
PubMed Abstract | Publisher Full Text
17. Polsky A, Mel BW, Schiller J: **Computational subunits in thin dendrites of pyramidal cells.** *Nat Neurosci.* 2004; **7**(6): 621–627.
PubMed Abstract | Publisher Full Text
18. Schaefer AT, Larkum ME, Sakmann B, *et al.*: **Coincidence detection in pyramidal neurons is tuned by their dendritic branching pattern.** *J Neurophysiol.* 2003; **89**(6): 3143–3154.
PubMed Abstract | Publisher Full Text
19. Richards BA, Lillicrap TP: **Dendritic solutions to the credit assignment problem.** *Curr Opin Neurobiol.* 2019; **54**: 28–36.
PubMed Abstract | Publisher Full Text
20. Urbanczik R, Senn W: **Learning by the dendritic prediction of somatic spiking.** *Neuron.* 2014; **81**(3): 521–528.
PubMed Abstract | Publisher Full Text
21. Kaiser J, Billaudelle S, Müller E, *et al.*: **Emulating dendritic computing paradigms on analog neuromorphic hardware.** *Neuroscience.* 2022; **489**: 290–300.
PubMed Abstract | Publisher Full Text
22. Billaudelle S, Weis J, Dauer P, *et al.*: **An accurate and flexible analog emulation of AdEx neuron dynamics in silicon.** In: *2022 29th IEEE International Conference on Electronics, Circuits and Systems (ICECS).* 2022; 1–4.
Publisher Full Text
23. Brette R, Gerstner W: **Adaptive exponential integrate-and-fire model as an effective description of neuronal activity.** *J Neurophysiol.* 2005; **94**(5): 3637–3642.
PubMed Abstract | Publisher Full Text
24. Pehle C, Billaudelle S, Cramer B, *et al.*: **The BrainScaleS-2 accelerated neuromorphic system with hybrid plasticity.** *Front Neurosci.* 2022; **16**: 795876.
PubMed Abstract | Publisher Full Text | Free Full Text
25. Davison AP, Brüderle D, Eppler J, *et al.*: **PyNN: a common interface for neuronal network simulators.** *Front Neuroinform.* 2009; **2**: 11.
PubMed Abstract | Publisher Full Text | Free Full Text
26. Müller E, Arnold E, Breitwieser O, *et al.*: **A scalable approach to modeling on accelerated neuromorphic hardware.** *Front Neurosci.* 2022; **16**: 884128.
PubMed Abstract | Publisher Full Text | Free Full Text
27. Gerstner W, Kistler W, Naud R, *et al.*: **Neuronal dynamics.** Cambridge University Press, 2014.
Reference Source
28. Zador AM, Agmon-Snir H, Segev I: **The morphoelectrotonic transform: a graphical approach to dendritic function.** *J Neurosci.* 1995; **15**(3 Pt 1): 1669–1682.
PubMed Abstract | Publisher Full Text | Free Full Text
29. Gerstner W, Kistler W: **Spiking neuron models: single neurons, populations, plasticity.** Cambridge University Press, 2002.
Reference Source
30. Goldberg DE: **Genetic algorithms in search, optimization, and machine learning.** Addison Wesley Longman Inc., 1989.
Reference Source
31. Wirsansky E: **Hands-On genetic algorithms with python.** Packt Publishing Ltd., 1st edition, 2020.
Reference Source
32. Berger T, Larkum ME, Lüscher HR: **High I_h channel density in the distal apical dendrite of layer V pyramidal cells increases bidirectional attenuation of EPSPs.** *J Neurophysiol.* 2001; **85**(2): 855–868.
PubMed Abstract | Publisher Full Text
33. Chichilnisky EJ: **A simple white noise analysis of neuronal light responses.** *Network.* 2001; **12**(2): 199–213.
PubMed Abstract
34. Hock M, Hartel A, Schemmel J, *et al.*: **An analog dynamic memory array for neuromorphic hardware.** In: *2013 European Conference on Circuit Theory and Design (ECCTD).* 2013; 1–4.
Publisher Full Text
35. Fortin F, De Rainville F, Gardner M, *et al.*: **DEAP: evolutionary algorithms made easy.** *J Mach Learn Res.* 2012; **13**(1): 2171–2175.
Reference Source
36. Baeck T, Fogel DB, Michalewicz Z: **Evolutionary computation 1: basic algorithms and operators.** CRC press, 2000; **1**.
Reference Source
37. De Jong KA: **An analysis of the behavior of a class of genetic adaptive systems.** PhD thesis, 1975.
Reference Source
38. Keren N, Peled N, Korngreen A: **Constraining compartmental models using multiple voltage recordings and genetic algorithms.** *J Neurophysiol.* 2005; **94**(6): 3730–3742.
PubMed Abstract | Publisher Full Text
39. Xia X, Jiang S, Zhou N, *et al.*: **Genetic algorithm hyper-parameter optimization using taguchi design for groundwater pollution source identification.** *Water supply.* 2019; **19**(1): 137–146.
Publisher Full Text
40. Stock R, Kaiser J, Müller E, *et al.*: **Parametrizing analog multicompartment neurons with genetic algorithms [data].** 2023.
http://www.doi.org/10.11588/data/U2U1IB
41. Electronic Vision(s): **Publication software collection: "parametrizing analog multi-compartment neurons with genetic algorithms".** 2023.
http://www.doi.org/10.5281/zenodo.8109123

Open Peer Review

Current Peer Review Status: ✔ ✔ ? ✔ ✔

Version 2

Reviewer Report 17 January 2025

https://doi.org/10.21956/openreseurope.20368.r46276

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✔ **Wenhao Song**
University of Southern California, Los Angeles, California, USA

I appreciate the authors' efforts in performing extended experiments with nine parameters. The extended experiments in Figures 9 and 10 provide more solid evidence of the effectiveness of the genetic algorithm. Unsurprisingly, there will be a discrepancy between the targets and observations in Figure 10 due to the hardware device-to-device variations and the authors discussed it. The concern is whether this inaccuracy would become more and more severe as the parameter space scales up or if there is a way to control it. The second concern is about the efficiency of the genetic algorithm. Grid search is extremely inefficient, and beating grid search is not strong enough evidence to prove the practiceness of the proposed algorithm. Adding a little more discussion and comparison on the efficiency of the algorithm would be great.

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: neuromorphic computing, in-memory computing, device and circuit modeling, memristors.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Reviewer Report 09 January 2025

https://doi.org/10.21956/openreseurope.20368.r47743

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✔ **Arianna Rubino**

University of Zurich and ETH Zurich, Zurich, Switzerland

This work proposes to use genetic algorithms to parametrize configurable components on the BrainScaleS-2 hardware.

The BrainScaleS-2 chip enables the creation of complex multi-compartment neurons by interconnecting simple individual neurons. In this paper, the authors exploit this feature to design a chain of compartments to replicate observed EPSP attenuation phenomena. Genetic algorithms are employed to optimize neuron model parameters, specifically leak and inter-compartment conductances, to accurately replicate the EPSP attenuation experiment.

The effectiveness of genetic algorithms for parameterizing analog neurons on the BrainScaleS-2 chip is demonstrated across problems with both low- and high-dimensional parameter spaces.

The manuscript is clear, detailed, and well-structured. It provides sufficient background to understand the study, and the methods and results sections are comprehensive and easy to follow. Additionally, the authors present results obtained from a neuromorphic hardware and share the necessary data and source code to facilitate experiment replication.

I have only one suggestion and curiosity. The authors justify their choice of genetic algorithms by claiming (and reporting previous related work) that they are well-suited for parameterizing multi-compartment neuron models and outperform other optimization methods. However, it would strengthen the study to include a comparison of the genetic algorithm's performance with other optimization techniques for this specific experiment. Furthermore, it would be interesting to know more details on the time required for the genetic algorithm to complete the parameterization.

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and does the work have academic merit?
Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
Yes

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Neuromorphic mixed-signal circuit design, Spiking Neural Networks

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Reviewer Report 20 December 2024

https://doi.org/10.21956/openreseurope.20368.r47157

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Erika Covi
University of Groningen, Groningen, The Netherlands
Andrea Giuntoli
University of Groningen Zernike Institute for Advanced Materials (Ringgold ID: 332143), Groningen, Groningen, Netherlands Antilles
Nayan Vengallur
University of Groningen Zernike Institute for Advanced Materials (Ringgold ID: 332143), Groningen, Groningen, Netherlands Antilles

This work uses genetic algorithms to find the model parameters for multi-compartment neuron models. The model is then physically implemented and demonstrated on the BrainScaleS-2 hardware.

The manuscript is clear, well written, logically organised and well structured. The work is well motivated and the results are fully satisfactory.

The hardware implementation is very solid and well described. The motivation for using genetic algorithms for this type of problem is convincing.

There are only two details missing that should be included in the manuscript for better clarity of the impact of this work:
1) it is not very clear how an element of the population is encoded precisely, meaning how the set of impedances is uniquely codified into a string that defines a member of the population.
2) as a consequence of (1), the dimensional space explored by the genetic algorithm (i.e., the number of possible different population elements) is not easy to extract from the paper. A brief and more explicit discussion on this would be relevant, especially in the context of quantifying how big their "high-dimensional" case is, and the efficiency in convergence time of the GA compared to the estimated time needed to find the same solution via a grid search.

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and does the work have academic merit?
Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Partly

If applicable, is the statistical analysis and its interpretation appropriate?
Yes

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Analogue circuit design

We confirm that we have read this submission and believe that we have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Reviewer Report 11 December 2024

https://doi.org/10.21956/openreseurope.20368.r47745

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?

Tanguy Damart
Ecole Polytechnique Federale de Lausanne, Lausanne, Vaud, Switzerland

Constraining the parameters of a neuron model using an optimisation algorithm is a well-established method. In the present paper, the authors demonstrate that this method can be applied to a multi-compartment dendrite model implemented on a neuromorphic platform (BrainScaleS-2).

The authors created a five-compartment model of a dendrite, each including a leak and inter-compartment conductance. Performing a grid search, they showed how the amplitude and spatial attenuation of an EPSP vary as a function of these two parameters and discussed in detail the trial-to-trial variability inherent to the use of a neuromorphic platform.

In a second experiment, the authors used an evolutionary strategy to show that starting from a random set of solutions, an optimiser can converge toward a solution reproducing the EPSP properties observed for one parameter set obtained from the grid-search experiment.

Overall the work is interesting, and I recognize the effort that went into it. Constraining the parameters of neuron models is a computer-intensive task and making use of neuromorphic computing could be fruitful in that regard.

Despite that, I have reservations that need to be addressed before recommending this work for indexing.

The present manuscript has been proposed to Open Research Europe as a Research Article, as such, we expect an in-depth discussion of the scientific relevance of the work. However, the manuscript does not discuss the scientific motivation for the optimisation of dendritic parameters on neuromorphic hardware. More specifically:

1. The motivation for the use of BrainScaleS-2 for parameter optimisation seems to be the speed gain mentioned by the author in the introduction. However, in the rest of the manuscript, no discussion describing the effective speed-up brought by the use of such a platform versus traditional hardware is present. Without the characterisation of the advantages brought by neuromorphic hardware, the question of whether the use of such hardware is relevant for parameter optimisation stays unanswered.
2. The present authors made the choice of using an elitist genetic algorithm as an optimizer. However, the motivation for the choice of such an algorithm is missing. As illustrated in Fig 7, genetic algorithms present an inherent lack of convergence once a low-fitness subspace of the parameter landscape has been reached and, as such, are not necessarily a good fit for well-behaved problems. Other methods, such as Newtonian methods or covariant matrix adaptation, have to be benchmarked to evaluate their competitiveness on the present problem.

Is the work clearly and accurately presented and does it cite the current literature?
Partly

Is the study design appropriate and does the work have academic merit?
Partly

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
Not applicable

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: spiking neural networks, detailed neuron modeling, multi-objective optimisation methods

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have

significant reservations, as outlined above.

Version 1

Reviewer Report 19 April 2024

https://doi.org/10.21956/openreseurope.17040.r38498

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Charles P. Rizzo
The University of Tennessee Knoxville, Knoxville, Tennessee, USA

The authors demonstrate how genetic algorithms can be employed to parameterize multi-compartmental neurons on analog neuromorphic hardware. They provide an overview of how the BrainScaleS-2 neuromorphic chip works as it is relevant to their experiments, their neuron model, and how genetic algorithms work.

They perform an experiment, using spike-triggered averaging (STA) to counteract trial-to-trial variations, in which they derive the empirical length constant and the excitatory postsynaptic potential amplitude (EPSP) within the first compartment of their evaluated 5-compartment chain. They then employ a genetic algorithm to optimize the values for both inter-compartment and leak conductance to reproduce their observed length constant measurement.

Overall, the experiment is interesting, well-formed, and a great use of genetic algorithms. Their methods are sound, and sufficient details to reproduce the experiment are provided. Their chosen hyperparameters and experiment length are appropriately justified. All of their figures are drawn well and help the reader further understand the experiment. Their results are also displayed well, match expectations, and are thoroughly discussed in the text. Additionally, they take a step further and present a multi-objective fitness function that reduces the valid solutions space, and they highlight better results when using said fitness function.

The only small point of confusion I had was in parsing Figure 7B, and trying to work out how the best individual's fitness for each generation in each run was not consistently decreasing or constant (given that the authors employed an elitism mechanism), but had I read the rest of the paragraph preceding Figure 7B. first, I'd have noticed that the authors address this.

I have no reservations in strongly recommending this work for indexing, and I applaud the authors on a job well done.

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and does the work have academic merit?

Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
Not applicable

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: neuromorphic computing, spiking neural networks, event-based cameras, genetic algorithms

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Author Response 15 Nov 2024

Raphael Stock

We thank Charles P.Rizzo for his review and positive feedback.
In order to avoid the confusion regarding figure 7B, we added an additional sentence to the caption.
This should make the figure more self-contained.

Competing Interests: No competing interests were disclosed.

Reviewer Report 19 April 2024

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?

Wenhao Song
University of Southern California, Los Angeles, California, USA

The authors Raphael *et al.* introduced an example that using genetic algorithms to find the optimal hardware parameters on the BrainScaleS-2 neuromorphic hardware platform. More

specifically, they used multiple neurons in BrainScaleS-2 to build a multi-compartmental neuron, and tried to determine the best parameters that give the desired length constant and the EPSP amplitude. There are only two parameters in the search space, the leak conductance g_l and the inter-compartment conductance g_ic.

Overall, this manuscript is well written with adequate or even abundant details explained. The figures are of proper form and drawn with high quality. And there are many highlights in this work: BrainScaleS-2 is a novel platform with lots of potentials, and the multi-compartment neuron models can capture more important details compared with point neuron models.

The relative weakness is mainly about the method used for this optimization: the genetic algorithms. Genetic algorithm is a classic algorithm that performs well when we don't have any prior knowledge. As long as it can be proven suitable for this task, this manuscript can still be of high quality.

1. The efficiency of the genetic algorithm. "we chose genetic algorithms since they outperformed conjugate-gradient descent and stochastic search as demonstrated by Vanier and Bower7 in a task to constrain a multi-compartmental neuron model." However, this reference was in 1999 and we believe both methods have been developed further and new methods including machine learning have been developed as well. A more recent or direct comparisons on the efficiency of possible algorithms are desired to maintain this assertion's validity.

2. The necessity of using genetic algorithms, or the scale of the problem solved. With only 2 parameters (g_l ad g_ic) to be optimized and at most 2 objectives, the parameter space can be easily thoroughly search as shown in Fig 5. This cannot show the advantages of genetic algorithms, which is more suitable for more parameters. Moreover, the objectives shown in Fig 5 or 7B are quite simple with only one minimal, which may just be solved by conjugate gradient without much problem. In other words, genetic algorithm may be an overkill for a simple parameter search problem proposed in the manuscript. Therefore, a larger experiment with more parameters to be optimized would be desired to show the necessity and advantage of the genetic algorithm used. For similar reasons, the claimed "speed gain" lacks the data support from comparison.

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and does the work have academic merit?
Partly

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
Yes

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Partly

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: neuromorphic computing, in-memory computing, device and circuit modeling, memristors.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Author Response 15 Nov 2024

Raphael Stock

We thank Wenhao Song for the thorough revision and the helpful feedback.
In the following we address the comments by Wenhao Song and state what improvements we implemented in the presented manuscript. 1. We added two more recent publications which also employed genetic algorithms and compared them to different optimization methods.
Furthermore, the explicit mention of "conjugate-gradient descent" was misleading.
We rephrased the paragraph to make more clear that we chose genetic algorithms because of their competitive performance compared with other algorithms and since they are frequently used to optimize the parameters of multi-compartmental neuron models.
Furthermore, we chose genetic algorithms since they were previously used in combination with neuromorphic hardware.
This is mentioned in the next paragraph of the manuscript. 2. We agree that for a two-dimensional parameter space genetic algorithms do not show their advantages.
Therefore, we extended the experiment to optimize nine parameters in parallel.
In case of a grid search with ten points per parameter, a nine-dimensional problem would require 10^9 measurements.
The results we added to the manuscript show that the genetic algorithm is able to find suitable solutions in less then 3000 (60 generations, 50 individuals) measurements.

Since we performed additional experiments for the current revision, we updated our code and performed all experiments again.
Due to the analog nature of the BrainScaleS-2 system, the new software state and a different calibration, the exact values differ slightly form the previous results.
The main results and conclusions are the same.
We updated the figures in the manuscript and created a new version of the data set (which is shared via heiDATA and referenced in the paper).

Competing Interests: No competing interests were disclosed.