A Pipeline based on Differential Evolution for Tuning Parameters of Synaptic Dynamics Models

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Abstract. Integrating the modulatory properties of Synaptic Dynamics (SD) into Spiking Neural Networks (SNNs) can enhance their computational capabilities. For improving this integration process, this paper presents a pipeline based on Differential Evolution to tune parameters of SD models. Using reference signals from *in vitro* experiments, parameters of two models are tuned as study cases: the Tsodyks-Markram and the Modified Stochastic Synaptic Model. The pipeline has an average success rate of 75% and 80% respectively. The outcome is a distribution of parameters for each model, which can be considered as prior knowledge to facilitate the integration of SD models into SNNs.

1 Introduction

Spiking Neural Networks (SNNs) are a type of Artificial Neural Networks highly inspired by neuroscientific findings. One of their most fundamental aspects is the transmission and processing of information in terms of spikes [1]. In neuroscience, synaptic plasticity refers to the spiking activity-dependent change of synapses [2]. In SNNs, the synapse is represented as a weight (i.e. absolute synaptic efficacy) that changes according to learning rules, reflecting the long-term component of plasticity (e.g. Spike-Timing Dependent Plasticity or Back Propagation for SNNs). However, the short-term component is usually modeled in a static way and its properties are not well integrated into SNNs.

Synaptic Dynamics (SD) reflects the dynamic of release and capture of neurotransmitters between the pre- and postsynaptic neuron, including the synaptic cleft. Rather than static transmission of spikes, information transmission is modulated by the mechanisms of facilitation and depression, which enhance and depress synaptic efficacy, respectively [2]. These modulatory effects are studied from computational neuroscience and are associated with computational properties of synapses [3], [4]. The integration of such properties in SNNs requires models that capture, to some extent, the mechanisms of facilitation and depression. Phenomenological and biophysical models have been proposed for this

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task, e.g. the Modified Stochastic Synaptic Model (MSSM) [5] or the Tsodyks-Markram model (TM) [6].

Both models can be tuned to simulate the mechanisms of SD. For the TM model, some methods have been proposed to tune its parameters using Generalized Linear Models [7], Least-Square methods [8], or multi-objective genetic algorithms [9]. However, there is a lack of implementations to tune the parameters of other biophysical models like the MSSM, mainly because of the more complex definitions of such models in comparison to the phenomenological ones. However, these models have the advantage of having a better physiological description of the synaptic processes, facilitating their interpretability. Therefore, finding sets of parameters for the simulation of facilitation and depression can help to integrate these more complex but more biophysical models into SNNs. In this sense, the aim of this paper is to propose a pipeline, based on the optimization technique Differential Evolution (DE) [10], to tune the parameters of SD models using reference signals from *in vitro* experiments. We demonstrate this method with two SD models (the TM model, as benchmark, and the MSSM) to simulate one example of facilitation and depression.

2 Methodology

A pipeline based on DE is designed for tuning the parameters of SD models (See figure 1). It consists of the following components: *i)* The input of the SD model and the reference signal, the latter is the desired output to be simulated by the model. *ii)* The SD model. Here the TM model and the MSSM are used, but the pipeline supports the implementation of other models as well. *iii)* The optimization technique DE, which uses the reference signals to evolve a population of individuals (each one is a set of parameters of the SD model). *iv)* The success criteria, which define if the final population of DE can simulate the reference signal within a tolerance range. The outcome of the pipeline is a distribution of parameters, that can constitute the prior knowledge of the SD model to simulate the reference signals. This pipeline can be run multiple times to increase the number of solutions that composes the distribution of parameters. The pipeline is implemented in Python and is available in this Repository[1].

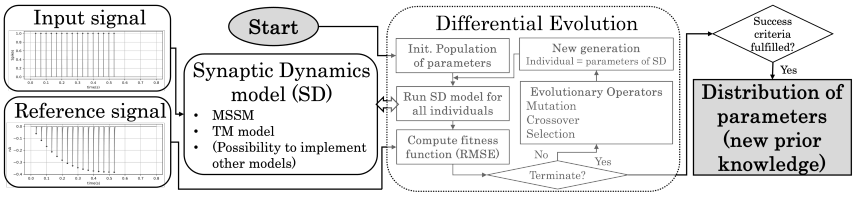

Fig. 1: Pipeline for tuning parameters of Synaptic Dynamics (SD) models. The input and reference signals are used for the SD model and Differential Evolution to find a distribution of parameters, which can simulate the reference signal.

[1]Code available at https://github.com/kilmfer91/pipeline_DE_for_Synaptic_Dynamics

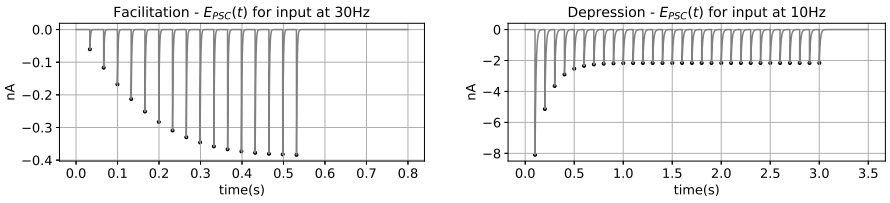

Fig. 2: Reference signals, as excitatory postsynaptic current $E_{psc}(t)$ in nA, used to simulate the mechanisms of SD of facilitation (left) and depression (right).

2.1 Reference Data

This is composed by signals coming from *in vitro* experiments, where single synapses are stimulated with regular or irregular spike trains. In this paper, the input and reference signals are obtained from [11]: the pyramidal to interneuron (for facilitation [3]) and the Calyx of Held synapses in rats (for depression [12]). The stimuli are regular spike trains at 30Hz and 10Hz, respectively (Figure 2).

2.2 Synaptic Dynamics Models

2.2.1 Tsodyks-Markram Model

The TM model is the most popular phenomenological model of SD. It simplifies the complex dynamics of synapses using three equations: $U(t)$ describes the facilitation mechanism, which increases with every input spike in proportion to U_0 and recovers with a time constant τ_f; $R(t)$ describes the depression mechanism, that decreases per input spike and recovers with the time constant τ_d; $E_{psc}(t)$ describes the postsynaptic current, considering the absolute synaptic efficacy A_{SE} that is shaped by the interaction between $U(t)$ and $R(t)$ (sometimes also with another time constant τ_{syn}). Among the variations of the TM model, the one described in [13] is used in this paper as benchmark to test the optimization pipeline. The parameters of the model are: U_0, A_{SE}, τ_f, τ_d, and τ_{syn}.

2.2.2 Modified Stochastic Synaptic Model

The MSSM extends the Maass-Zador model of short-term plasticity [14]. It describes the dynamics of the presynaptic terminal, the synaptic cleft and the postsynaptic site in way that is closer to the physiological behaviour of synapses than the TM model [5]. The MSSM is composed by four state variables: Calcium concentration $C(t)$, Vesicle release $V(t)$, Neurotransmitters buffering $N(t)$, and Postsynaptic contribution $E_{psc}(t)$ (originally as potential $E_{psp}(t)$), and one equation for the probability of release $P(t)$. The state variables are shaped by parameters proportional to the input signals (e.g. α to input spikes, k_{epsc} or $k_{N_t,V}$ to other state variables), different time constants (e.g. τ_C or τ_V), and resting states (e.g. C_o or N_{to}). For being a biophysical model, the dynamics of the state variables and the probability function describe the mechanisms of

facilitation and depression in a more physiological way [5]. Equations 1 present the MSSM used in this paper. The highlighted parameters are tuned by the pipeline (plus the initial probability P_0).

$$\frac{dC(t)}{dt} = \frac{C_o - C(t)}{\tau_C} + \alpha \cdot \sum_{i=1;t>t_i}^{N} \delta(t - t_i) \tag{1a}$$

$$\frac{dV(t)}{dt} = \frac{V_o - V(t)}{\tau_V} - P(t) \cdot \sum_{i=1;t>t_i}^{N} \delta(t - t_i) \tag{1b}$$

$$P(t) = 1 - e^{-C(t)\cdot V(t)} \tag{1c}$$

$$\frac{dN_t(t)}{dt} = \frac{-k_{N_t} \cdot N_t(t)}{\tau_{N_t}} + k_{N_t,V} \cdot \max\left\{0, -\frac{dV(t)}{dt}\right\} \tag{1d}$$

$$\tau_{epsc} \cdot \frac{dEpsc(t)}{dt} = -Epsc(t) + k_{epsc} \cdot N_t(t) \tag{1e}$$

2.3 Optimization Process based on Differential Evolution

DE is a population optimization technique part of evolutionary algorithms [10], designed to work on real-domain search spaces. It is implemented to tune the parameters of the models TM and MSSM. The search space is defined based on proof-of-concept experiments. Its boundaries can be modified in the pipeline according to the reference signals and the model to be tuned. The population of DE consists of solution candidates -individuals- (a set of parameters of a SD model), whose postsynaptic response is computed by running the SD model using the input reference data. The fitness function guiding the search of DE is the Root-Mean-Square Error (RMSE) between the reference signal and the time-response of each individual. Following the principles of Evolutionary Algorithms, DE creates an initial population, selecting individuals based on evolution-inspired rules (mutation, crossover, selection) and evaluating them according to the fitness function [10] (see figure 1). Once the algorithm of DE converges, the individuals of the final population compose sets of parameters. Given that DE uses only the dynamic of $Epsc(t)$ to fit each model, it can find multiple successful solutions in the search space. These multiple solutions create the outcome of the pipeline: the distribution of parameters for the SD models, where each solution is able to simulate its corresponding reference signal. The most important parameters of DE for one experiment are: 1000 generations, population size of 15, 0.7 as cross-probability, mutation rate $[0.5, 1)$, and a *best1bin* strategy.

3 Results

40 experiments of the pipeline are run to tune the parameters of the SD models and to simulate facilitation and depression. The success criteria consists of two components: first the time-response of an individual must reproduce the dynamic of facilitation or depression. Second the RMSE between the time-response and the reference data must be lower than 10^{-6} order of magnitude. In the case of the MSSM, 72.5% and 87.5% of experiments fulfil the success criteria for facilitation

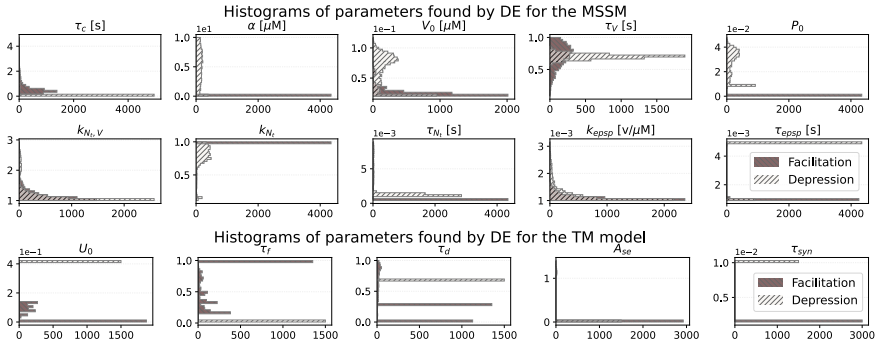

Fig. 3: Parameter distributions of models MSSM (top two rows) and TM (bottom row) found after running 40 experiments of the pipeline. Each plot shows the histograms for the mechanisms of depression (magenta) and facilitation (blue).

and depression (80% on average), and 100% and 50% in the case of the TM model (75% on average). Figure 3 shows the distributions of parameters found for both models. In the case of the TM model, all solutions for depression converge to one value per parameter, while for facilitation there are multiple solutions. The ranges found by our pipeline for U_0, τ_f, and τ_d ($[4.9e^{-8}, 0.143]$, $[173, 970]ms$, and $[0.41, 999]ms$) contain or are intersected with the empirical ranges provided by the authors of the model ($[0.012, 0.08]$, $[550, 3044]ms$, and $[104, 694]ms$ [3], [4]). This finding can be considered as evidence of the effectiveness of the pipeline. In the case of the MSSM there is no prior knowledge to compare the results of the pipeline. However, the values of parameters correspond to the expected behavior of facilitation and depression: high values of τ_C, low values of α, low values of P_0, and high values of k_{N_t} contribute to the expression of facilitation, while the opposite contributes for the expression of depression. These distributions can be used as the prior knowledge of the MSSM for the integration into SNNs.

4 Discussion and Future Work

In this paper a pipeline based on the population optimization technique DE is presented, with the aim of tuning the parameters of SD models and simulating the mechanisms of facilitation and depression. A distribution of parameters for one phenomenological model (the TM model) and one biophysical (the MSSM) are found, which allows the models to have multiple dynamics to simulate the reference signals. Understanding the meaning of these multiple dynamics will be explored in future studies, as well as studying which parameters are more influential to distinguish between facilitation and depression. The pipeline is effective in finding parameters of the models MSSM and TM with an average success rate of 80% and 75%, respectively. Other SD models can be implemented in the pipeline, and the reference signals can also be multiple irregular time-responses with a variety of frequencies, covering different types of signals recorded *in vitro*

experiments. More details are found in the repository of the pipeline [1]. The parameters found for the TM model are in similar ranges described by the authors of the model, which is evidence of the effectiveness of the pipeline. In the case of the MSSM, the ranges of values found by the pipeline are consistent with the expected expression of facilitation and depression. This is considered the main contribution of this paper: the distribution of parameters found by the pipeline can be used first to simulate the reference signals and second as prior knowledge of how to integrate SD models (like the MSSM) in simulations of SNNs.

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