Effective and Stable Neuron Model Optimization Based on Aggregated CMA-ES

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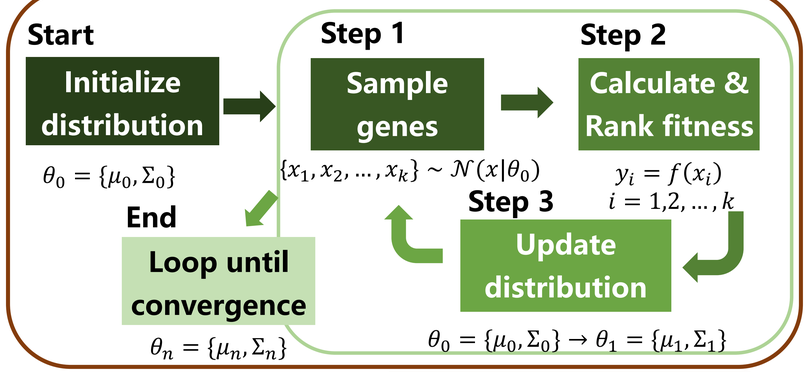
Introduction

- Neuron models can help us to understand the behavior of the brain and the effect of some medical treatment (e.g. deep brain stimulation[1]) to brain
- We apply Covariance Matrix Adaptation Evolution Strategy (CMA-ES) to Multi-timescale Adaptive Threshold (MAT) neuron model optimization for higher spike-predicting accuracy
- We improve robustness to initial conditions by aggregation strategy

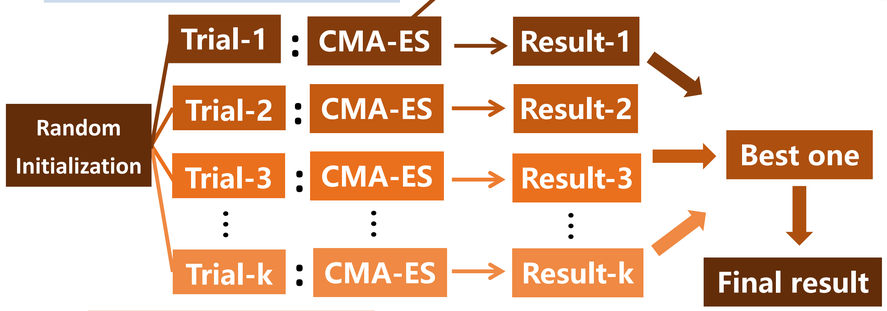
Method

CMA-ES Optimization

- An evolution strategy which uses a multivariate Gaussian distribution to represent a gene distribution



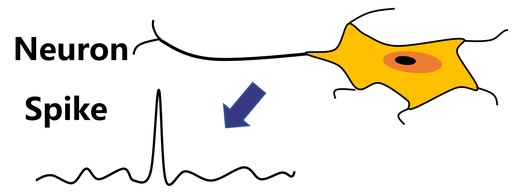
Aggregated CMA-ES



k : aggregation size

- Run CMA-ES for multiple trials with different initialization
- Find the best individual among all the trials

MAT Neuron Model[2]



How it Works

- Generate spikes when $\boldsymbol{u}$ > threshold $\boldsymbol{\theta}$

$$C_m \frac{du}{dt} = -g_L (u - E_L) + I_{ex}(t),$$

$$\theta(t) = \omega + \sum_{k:t_k<t} \alpha_1 e^{-\frac{t-t_k}{\tau_1}} + \alpha_2 e^{-\frac{t-t_k}{\tau_2}}$$

C = 160(pF) membrane capacitance

E_L = -71.5(mV) leak potential

g_L =16(nS) leak conductance

I_{ex} injected current

CMA-ES is more efficient than GA

Optimized Parameters

- Threshold Parameters {ω, α_1, α_2, τ_1, τ_2}

Performance Evalution

- Γ : The accuracy of coincidence of a model spike train with a real spike train

$$\Gamma = \frac{N_c - 2f_m N_d \Delta}{N_d + N_m} \times \frac{2}{1 - 2f_m \Delta}$$

N_c Number of coincident spikes

N_d / N_m Number of spikes of the real/model neuron

f_m Spike frequency of the model neuron

Δ =4(ms) Allowable time range

Experimental Setup

Dataset

- Dataset of recorded rat neocortex neuron stimulus and voltage from the International Competition on Quantitative Single-Neuron Modeling 2009[3]

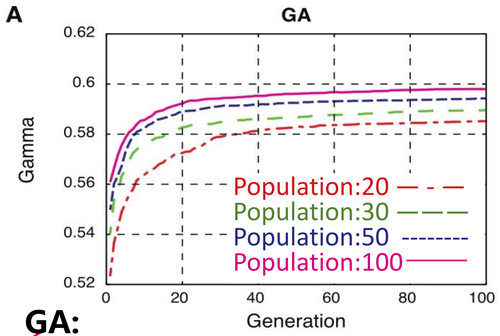
Tools & Initialization

- **GA:** DEAP[a] library / a set of random genes
- **CMA-ES:** Hansen's[b] Tookit / a random gene

Problem: Sensitive to the initial condition

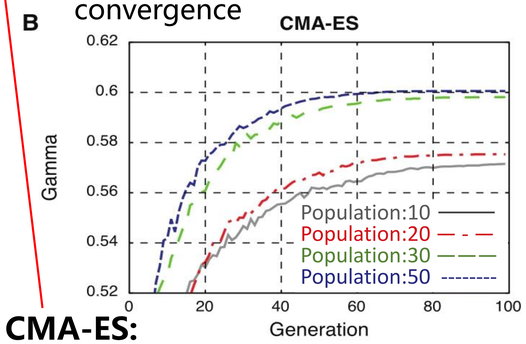
Results

Average results of GA/CMA-ES



GA:

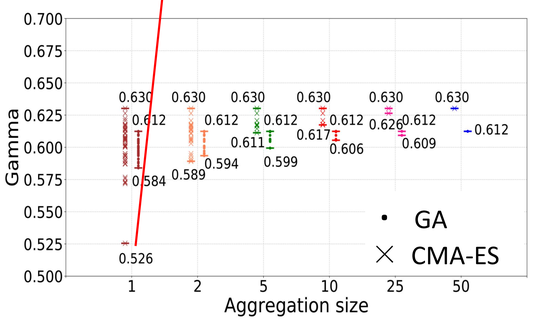
- Needs larger population size for good performance
- Needs more generations for convergence



CMA-ES:

- Converges faster (< 100th generation)
- Needs smaller population size (30 to 50)

Aggregated GA/CMA-ES



CMA-ES: Populaition size:50 generations:100
GA: Populaition size:100 generations:150

- Aggregated CMA-ES provides higher Γ than GA when aggregation size is larger than 10

Results of optimization

	A-GA	A-CMA-ES	Nelder
Γ	0.612	0.630	0.618
α_1	70.2	63.4	70.8
α_2	7.18	9.10	6.85
ω	-47.9	-49.4	-47.88
τ_1	9.62	9.71	10.54
τ_2	90.3	85.6	104.4

Conclusion

- CMA-ES's averaged performance outperforms GA and Nelder-Mead method
- Aggregated CMA-ES is robust against the initial condition

References
1. C.C Mcintyre and T.J. Foutz, "Computational modeling of deep brain stimulation," in Handbook of clinical neurology, vol. 116, pp. 55–61. Elsevier, 2013
2. Kobayashi, R., Tsubo, Y. and Shinomoto, S.: Made-to-Order Spiking Neuron Model Equipped with a Multi-Timescale Adaptive
3. W. Gerstner and R. Naud, "How good are neuron mod-els?,"Science, vol. 326, no. 5951, pp. 379–380, 2009

[a]https://github.com/deap/deap
[b]https://www.lri.fr/~hansen/cmaes_inmatlab.html