# Spiking network inference using a modular gradient-based optimisation framework

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Inferring biologically meaningful spiking neural network models (SNNs) using only spike train data presents several significant challenges, including traversing a high-dimensional parameter state space, as well as using spike trains as the only signal. We address these issues by implementing a modular SNN inference framework in Pytorch using gradient-based optimisation, inspired by René et al. (2020)[1]. We generate target data spike trains by hand-engineering a biologically plausible spiking sleep regulation model, and show that we may recover the model's parameters, even under strong Poisson input noise, starting from different parameter configurations. Further, inferred models have neuronal ensembles that are similar to the original model's, and also similar firing rates, as well as spike patterns.

This work addresses the issue of scarcity of computational models in the field by providing a basis for a general modular spiking model inference framework using only spike trains as the target signal.
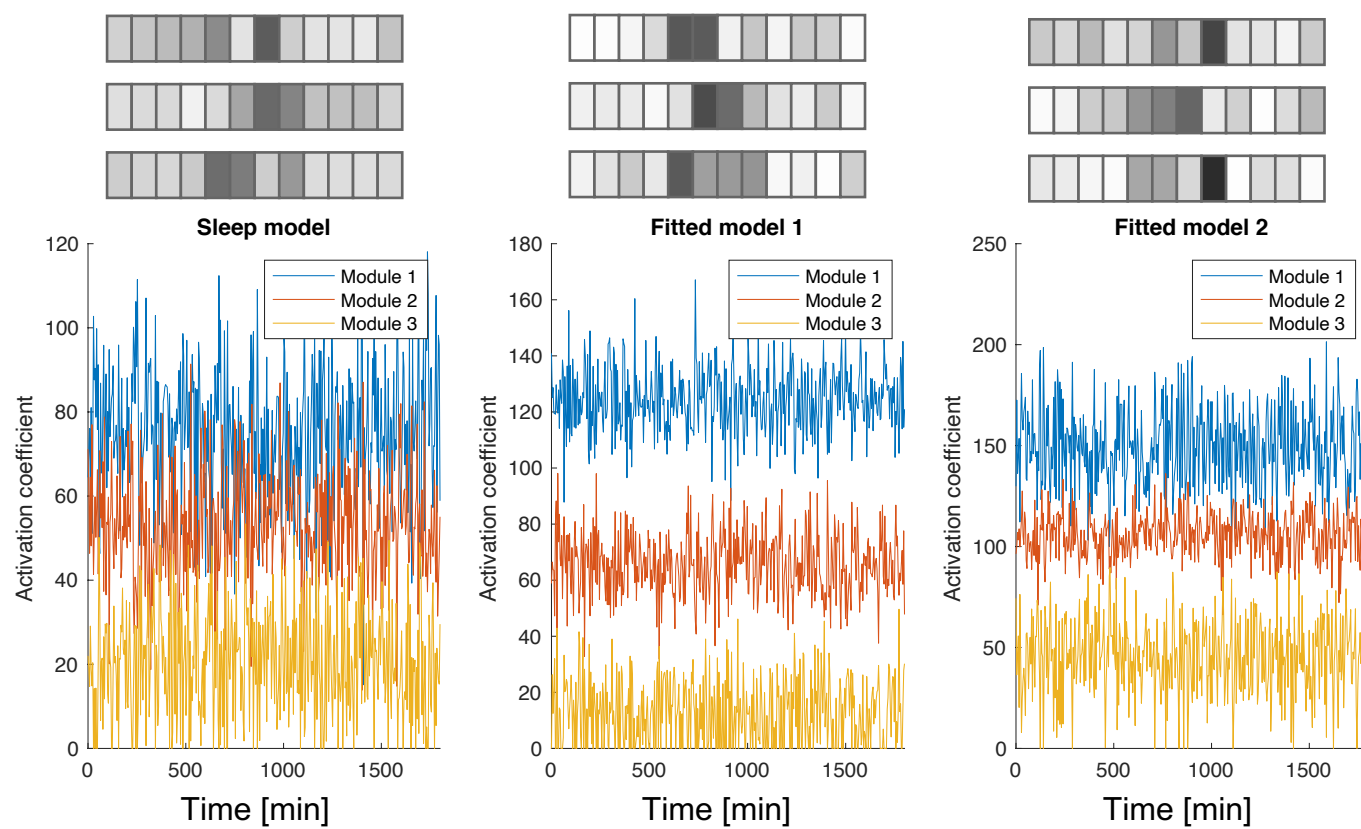
**Figure 1:** (Top) factorised spike train modules, and (bottom) their corresponding activation coefficients.

We hand-engineer two spiking models inspired by the rate based sleep model of Héricé et al. (2020)[2], attaining models with spike features that are qualitatively similar to biological spike trains. To evaluate and compare the inferred models with the sleep models, we use **non-negative matrix factorisation** (NMF) on the spike trains. This is an external statistical analysis, which yields a parts-based representation naturally due to its non-negativity constraint, leading to neuronal ensemble identification, which may be seen in figure 1.

Formally, NMF may be outlined as

$$X = WH$$

where $X$ is an $n{\times}m$ spike train matrix, $W$ is an $n{\times}k$ activation coefficient matrix, and $H$ a $k{\times}m$ matrix of the modules.

This work mainly focussed on fitting **leaky integrate-and-fire** (LIF) models, which may be outlined as follows,

$$\frac{dv}{dt} = \frac{v_{rest} - v + I}{\tau_m}$$

where $v$ is the membrane potential, $v_{rest}$ is the rest potential, $I$ is the synaptic current, and $\tau_m$ is a membrane time constant. Additionally, we also implement and test Izhikevich neurons. In both cases, we used an exponentially decaying **conductance based synapse model**, which may be written as

$$I = Wg + I_{ext}, \qquad dg = -\frac{g}{\tau_g}$$

where $W$ is a weight matrix, $g$ is synaptic conductance $I_{ext}$ is extenal input (e.g. Poisson input), and $\tau_g$ is a conductance decay time constant.

The **Van Rossum distance** [3] $D_R$ is the Euclidean distance between two transformed spike trains convolved with an exponential kernel. This may be written as

$$D_R(\tau_R) = \sqrt{\left(\frac{1}{\tau_R}\int_0^\infty [\tilde{x}(t) - \tilde{y}(t)]^2\right)}, \qquad f(t) = e^{-\frac{t}{\tau_R}}, t > 0$$

where $\tau_R$ is a time constant, and $\tilde{x}$ and $\tilde{y}$ are the spike trains $x$ and $y$ convolved with $f$, transforming each spike to an exponentially decaying signal.

**Goal:** We demonstrate retrieval of model parameters close and far from the intial setting.



**Figure 2:** Bursting, sparse and regular firing.
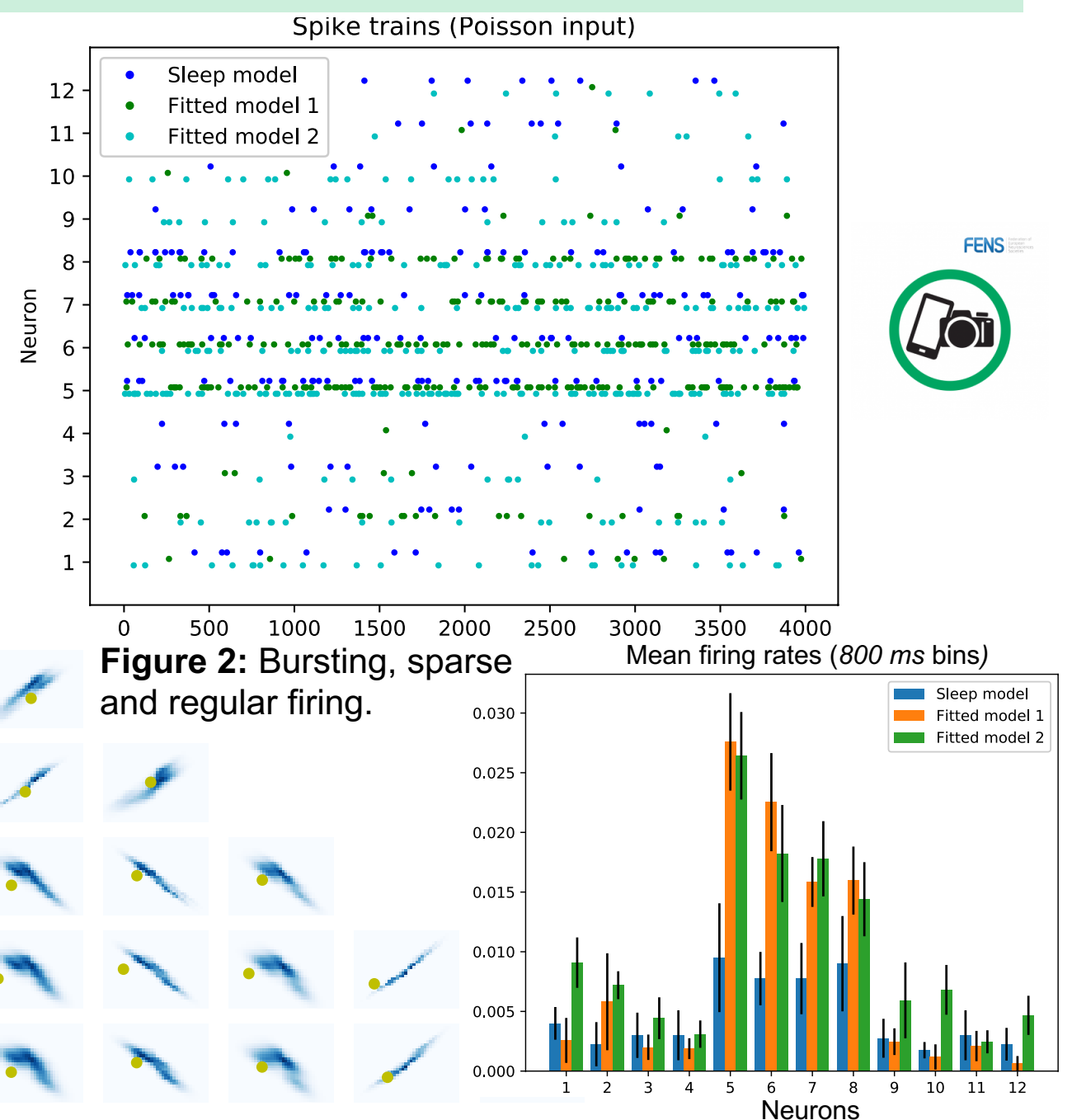


**Figure 3:** (Left) Gaussian kernel density estimates of fitted model parameters across training iteration (blue), with the true values (yellow dots).

In sum, spiking model inference using spike train data may allow inferring models capturing biologically realistc spike patterns. This provides a basis for assessing the dynamics of an area by model analysis, which when coupled with NMF allows comparable neuronal ensemble identification.

Future work includes addressing limitations of gradient-based methods in parameter space exploration. This will include looking into using adaptive optimisation methods for each parameter, which might also reduce the required overhead and framework complexity.

[1] René, et al. (2020). Inference of a Mesoscopic Population Model from Population Spike Trains. *Neural Computation*, 1–51.
[2] Héricé & Sakata. (2019). Pathway-Dependent Regulation of Sleep Dynamics in a Network Model of the Sleep–Wake Cycle. *Frontiers in Neuroscience*, 13, 1380.
[3] Van Rossum. (2001). A novel spike distance. *Neural Computation*, 13(4), 751–763.