

Evolving Field Models for Inhibition Effects in Early Vision

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Abstract

We present a nonlinear field model based on linear couplings for inhibition effects in early vision. The model is fitted to data from single unit recordings in the primary visual cortex of the cat. We focus on the prominent effect that responses to second stimuli are amplified, reduced, or unaffected depending on the temporal and spatial distance of the stimuli. The model is adjusted using an elaborated self-adaptive evolution strategy resulting in an accurate, easy to interpret, and well generalizing model.

Key words: neural fields; evolutionary optimization; population representation; early vision, Wiener system

1 Introduction

We propose evolutionary “analysis by synthesis” guided by neurobiological knowledge as a powerful tool in computational neuroscience. The challenge is to force artificial evolution to generate solutions that are plausible from the biological point of view. Such solutions are only likely to evolve if as much neurobiological knowledge as possible is incorporated into the design process. This can be achieved by providing sufficient experimental data to evaluate the evolved systems and by a considerate choice of the basic structure. Additional

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background information can be coded in the fitness function and in constraints that ensure biological plausibility.

In this study, we design a simple homogeneous field model for inhibition effects in early vision. The model relies on linear feed-forward couplings followed by a static sigmoidal transfer function (i.e., the model can be regarded as a Wiener system, cf. [5]), recalling the explanatory power of linear spatio-temporal filtering in computational neuroscience. The parameters of the model are adjusted by means of an elaborated self-adaptive evolution strategy to fit experimental data.

2 Neurobiological data

We performed single unit recordings in the primary visual cortex of the cat. Neural population representations for the horizontal position in visual space were constructed by means of an optimal linear estimator [8], see [2,7] for details. The calculations were based on the spike activity of 178 neurons in response to two flashed small spots of light in the central visual field (“jumping flashes” paradigm [9]).

In this investigation, we focus on the prominent effect that the amplitude of the response to the second stimulus depends on the *temporal* and *spatial* distance of the stimuli. The two stimuli do not affect each other in cases of large temporal and spatial distances. If the temporal as well as the spatial distance is small, then the responses merge and the activity is higher compared to the situation when only a single stimulus is presented, but lower compared to the superposition of the responses to each of the stimuli presented in isolation. For scenarios lying in between, a specific inhibition of the second response is observed.

3 Basic model structure

We choose a homogeneous field model with linear spatio-temporal couplings [10,11]. These feed-forward inhibitory and excitatory couplings model mainly computations by graded signals in the retina and additionally incorporate first-order approximations of the subsequent processing, see [3] for a discussion of linear interactions in early vision. The membrane potential $u(x, t)$ of a cortical model neuron representing location x in the visual field at time t is calculated as

$$u(x, t) = \int_0^t \int_{\mathbb{R}} w(x - x', t - t') s(x', t') dx' dt' + h ,$$

where h denotes the resting level and $s(x, t)$ the external input at location x and time t . The coupling function is given by

$$w(x, t) = m_1 \cdot \exp\left(-\tau_{11}t - (\tau_{12}t)^2\right) \cdot \exp\left(-(B_{11}x)^2 - (B_{12}x)^4\right) \\ - m_2 \cdot \exp\left(-\tau_{21}t - (\tau_{22}t)^2\right) \cdot \exp\left(-(B_{21}x)^2 - (B_{22}x)^4\right) .$$

Maximum excitation and inhibition are controlled by m_1 and m_2 , respectively. The temporal behavior—crucial for the observed inhibition effects—is approximated by low-pass characteristics with different time constants for excitation and inhibition, τ_{11} , τ_{12} and τ_{21} , τ_{22} , respectively. Similarly, spatial coupling is parameterized by B_{11} , B_{12} , B_{21} , and B_{22} . As steeper filter characteristics are needed in the spatial than in the temporal domain, polynomials of different order are used in the exponents. The average firing rate at location x and time t is given by the nonlinear, nondifferentiable mapping $f[u(x, t)]$, where f is a truncated sigmoidal function with three parameters:

$$f[u(x, t)] = \left[\frac{\alpha}{1 + \exp(-\beta u(x, t))} - f_{\text{shift}} \right]_+ . \quad (1)$$

Herein, $[u]_+ = \max(0, u)$ is a rectification operation, α determines the saturation, β controls the slope, and f_{shift} is an offset influencing the lower truncation.

4 Evolutionary algorithm

Natural evolution has created complex nervous systems, so it appears promising to employ evolutionary algorithms (EAs) for modeling in computational neuroscience. EAs are a class of direct, stochastic optimization methods that mimic principles of the neo-Darwinian theory of evolution [1].

In this study we use an elaborated evolution strategy, namely the CMA-ES [4], which we have successfully applied for parameter adaptation of dynamic neural field models [6]. Each individual represents a real-valued vector composed of the 14 parameters of the field model (h , m_1 , m_2 , τ_{11} , τ_{12} , τ_{21} , τ_{22} , B_{11} , B_{12} , B_{21} , B_{22} , α , β , f_{shift}). These variables are altered by recombination and mutation. The latter is realized by adding a normally distributed random vector with zero mean, where the complete covariance matrix is adapted to improve the search process. The so-called strategy parameters that determine the covariance matrix are updated online using the covariance matrix adaptation (CMA) method. The CMA implements important concepts for strategy parameter adjustment, e.g., the notion of *derandomization*: the mutation distribution is altered in a deterministic way such that the probability to reproduce steps in the search space that have led to the actual population is increased. Another important concept is *cumulation*: in order to use the information from previous generations more efficiently, the search path of the population over a number of past generations is taken into account.

The fitness guiding the selection process in the EA is determined by an error function E , which compares the evolved model with the neural population representation (i.e., the experimental data processed as sketched in Sec. 2).

The patterns resulting from $P = 12$ different stimulus configurations are used in the error calculation. The error consists of several, additively combined parts:

$$E = \frac{1}{P} \sum_{p=1}^P \left(E_{\text{MSE}}^{(p)} + \lambda_a E_a^{(p)} + \lambda_b E_b^{(p)} \right) . \quad (2)$$

The first term $E_{\text{MSE}}^{(p)}$ is the mean-squared error between the population representation and the corresponding activation of the evolved model for stimulus configuration p . The other parts of the error function stress important aspects of the data, i.e., characteristics of the spatio-temporal pattern that are not side-effects of the processing of the measured spike data. In particular, the relative heights of the peaks are more important than the absolute heights as their scaling has been arbitrarily chosen in the construction process of the population representation. The absolute width of the peaks also depends on a manually selected parameter, which is based on average receptive field properties [2,7]. Let $f_{\text{1stPeak}}^{(p)}$ and $f_{\text{2ndPeak}}^{(p)}$ be the heights of the first and second peak generated by the model and let $d_{\text{1stPeak}}^{(p)}$ and $d_{\text{2ndPeak}}^{(p)}$ be the corresponding heights in the population representation. The error term $E_a^{(p)}$ compares the relative heights of the first and second peak within one experiment. It is given by

$$E_a^{(p)} = \left[\left| \frac{f_{\text{1stPeak}}^{(p)}}{f_{\text{2ndPeak}}^{(p)}} - \frac{d_{\text{1stPeak}}^{(p)}}{d_{\text{2ndPeak}}^{(p)}} \right| - \Theta_a \right]_+^2 \quad (3)$$

if the inter-stimulus interval between the two flashes of light in experiment p is not zero, else we set $E_a^{(p)} = 0$. The error term

$$E_b^{(p)} = \left[\left| \frac{f_{\text{1stPeak}}^{(1)}}{f_{\text{1stPeak}}^{(p)}} - \frac{d_{\text{1stPeak}}^{(1)}}{d_{\text{1stPeak}}^{(p)}} \right| - \Theta_b \right]_+^2 \quad (4)$$

compares the relative heights of the first peak in experiment p and the peak in a reference stimulus configuration. In our experiments, we select $\lambda_a = \lambda_b = 1$ and $\Theta_a = \Theta_b = 1.5$.

5 Results

Evolutionary optimization leads to qualitatively and quantitatively accurate models for the considered effects in early visual information processing. The models exhibit good generalization behavior and are easy to interpret. An example of an evolved kernel is shown in Fig. 1: The spatial couplings are of Mexican-hat shape; inhibition decays slower than excitation, resulting in the desired temporal effects. Figure 2 shows examples of the data and the corresponding behavior of an evolved model.

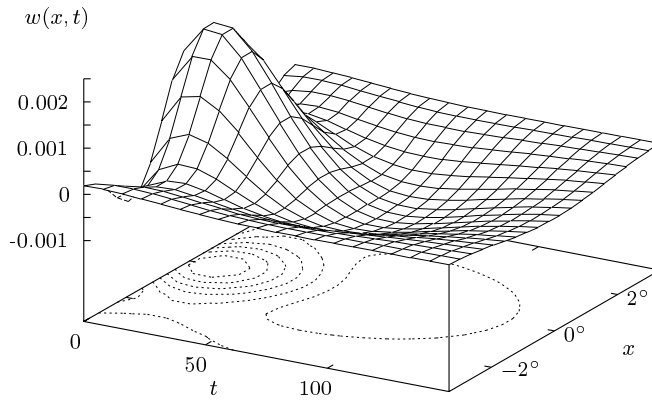


Fig. 1. Evolved kernel.

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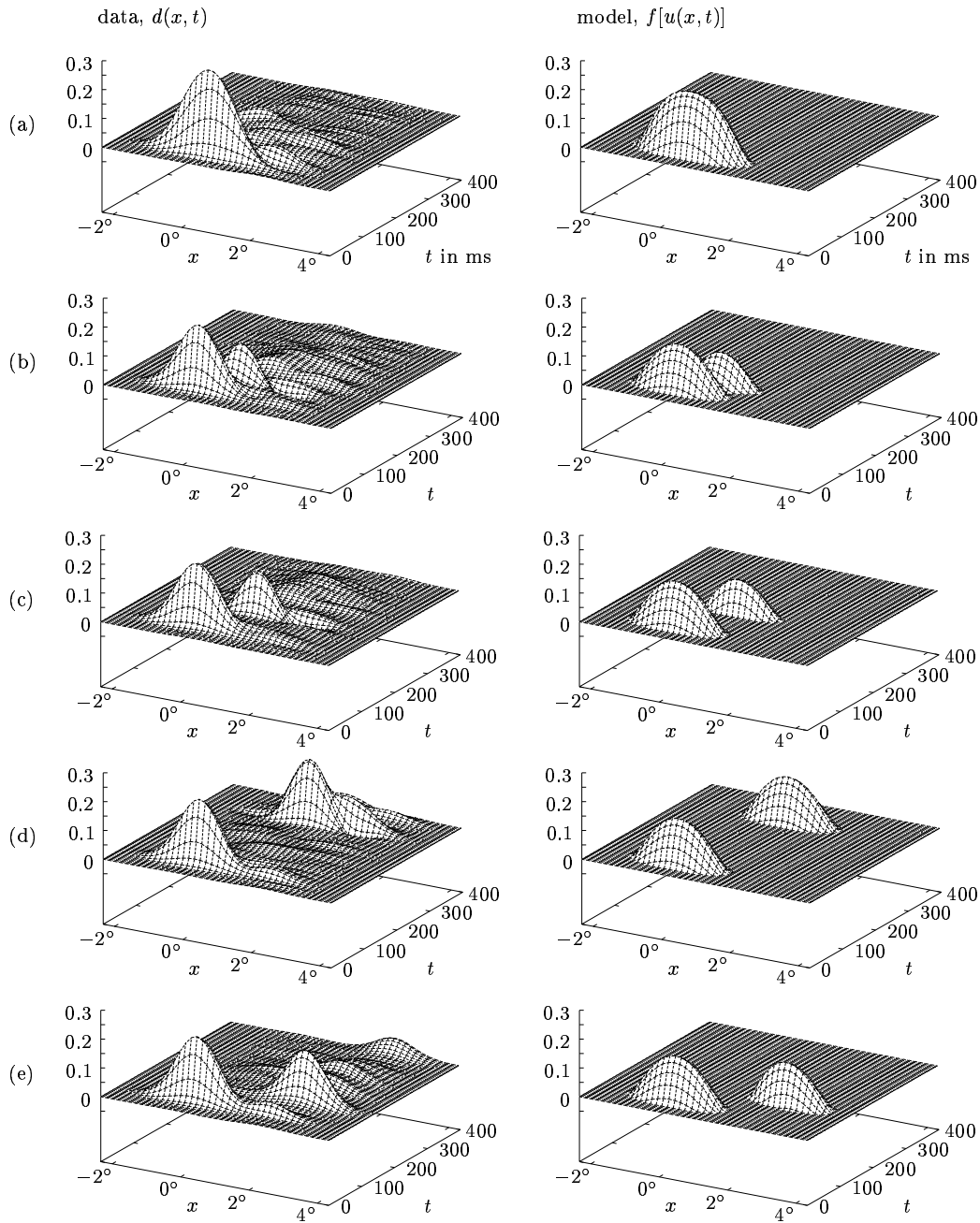


Fig. 2. Neural population representations (left) and the corresponding behavior of an evolved model (right). In (a)–(d), the two stimuli are horizontally separated by 0.8° , the inter-stimulus intervals are 0, 50, 100, and 250 ms, respectively. In (a), the responses merge and are amplified; (b) and (c) are examples of inhibition. In (d), the stimuli do not affect each other because of large temporal distance. In (e) the stimuli are horizontally separated by 2.4° and 75 ms resulting in less inhibition compared to (c).