Artificial Neural Network Model for fMRI timeseries and a Framework for Comparison of Convolution Models

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Introduction

The fMRI signal is often modeled from a system identification point of view as a linear response to the activation reference function. A number of different impulse response functions have been suggested: Poisson density kernel [1], gamma density kernel (e.g. [2]), FIR kernel (e.g. [3]), Gaussian kernel [4]. It has been noted that the response is not necessarily linear, e.g., the fMRI-signal transition time at the onset of the stimulus is shorter than the decay time in the end of the stimulus, in linear models these rise and decay times are coupled by symmetry to be identical. Nonlinear modelling of the hemodynamic response was proposed in [5]. Here *we propose an artificial neural network (ANN) model of the hemodynamic response.*

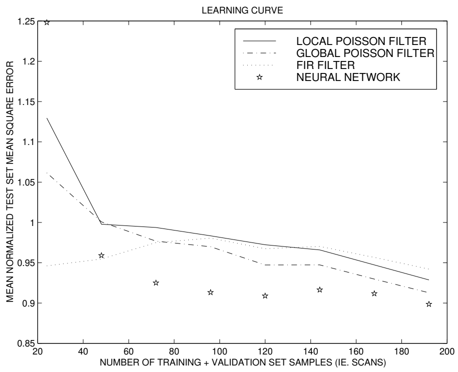
When invoking parametrized models, and in particular hyper-flexible models like power series or ANN's it is of great importance that we control the generalization performance to avoid overfitting. Generalization defined as the average performance of the fitted model on an independent *test datum* can be estimated empirically on a hold out test set or analytically using asymptotic theory.

Method

The specific neural network we will use is a two-layer feed-forward type. Parameters are optimized by least square minimization on a "training set" and selection of pruned nets is done via a "validation set". As input we will use a vector containing the stimulus function from time t and back to time $t - L$ where L is a lag, equivalent to a representation using linear response models. The output of the neural network should predict the corresponding fMRI-signal af time t. We will use different sizes of the combined training and validation set, and use the second half of the full data set as the unbiased "test set" to monitor generalization of all procedures. The specific fMRI data we will use is a sequential finger opposition study previously described in [3]. We restrict our investigation to a set of 16 voxels comprising both activated and non-activated voxels. For each voxel we will train an independent neural network as well as adapt a number of the above mentioned linear response models and similarly measure their generalization.

Result

The figure shows a so-called "learning-curve": The test set error as a function of the training set (including the validation set used for model optimization). The performance of the neural network is shown against that of a FIR filter, a Poisson filter with local Poisson parameter and one with a global Poisson parameter (as in [1]). We also found that the neural network signal showed an asymmetry between the rise and decay transitions.



Conclusion

A non-linear hemodynamic response model has been suggested allowing for a more flexible response than is possible with a linear system. In particular, the non-linear model can avoid the typical symmetry constraints that are associated with linear models. We have suggested a simple method for comparing convolution models providing an unbiased quality measure for both non-linear and linear models. We have shown that the network can be optimized to perform well on data sets comparable to those necessary to determine parameters in simple linear models.

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