Neuron Selection for Decoding Dexterous Finger Movements

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Abstract—**Many brain machine interfaces (BMI) seek to use the activity from hundreds of simultaneously recorded neurons to reconstruct an individual's kinematics. However, many of these neurons are not task related since there is no way to surgically target those neurons. This causes model based decoding to suffer easily from over-fitting on noisy unrelated neurons. Previous methods, such as correlation analysis and sensitivity analysis, seek to select neurons based on which reduced order model best matches the ensemble model and thus does not worry about over fitting. To address this issue, this paper presents a new method, cross model validation, that ranks neuron importance on the neuron model's ability to generalize well to data from correct movements and poorly to data from incorrect movements. This method attempts to highlight the neurons that are able to distinguish between movements the best and decode accurately. Selecting neurons using cross model validation scores as opposed to randomly selecting them can increase decoding accuracy up to 2.5 times or by 44%. These results showcase the importance of neuron selection in decoding and the ability of cross model validation in discerning each neuron's utility in decoding.**

I. INTRODUCTION

THE goal of brain machine interfaces (BMI) is to translate neural signals into commands for a prosthetic. It is well known that single unit recordings and local field potentials from primary motor cortex encode information such as limb position, limb velocity, and muscle activity [1-7]. It is also the final cortical output available before commands are sent to the spinal cord. It therefore makes sense to base decoded motor commands from moor cortex.

The field has recently moved towards decoding with single unit and population recordings of cortical neurons from implanted microelectrode arrays [8]. These electrode arrays are surgically placed over a large population of motor related cortical regions to guarantee inclusion of task related neurons, however many neurons that are not significantly modulated during movement are also included. These unrelated neurons make it difficult to get a generalized model of how neurons encode movement due to fitting on unrelated parameters. Therefore, it is important to be able to specifically select task related neurons for both decoding accuracy as well as computational efficiency.

Traditionally, neurons were selected purely based on changes in firing rate during related tasks [9]. However, this

assumes that the speed at which a neuron fires conveys most of the information a neuron has to encode. More advanced techniques such as correlation analysis and sensitivity analysis have been developed. The former uses variance in the model's output [10] while the latter looks at the Jacobian of input-output mappings [11]. Both of these methods will have problems with generalization as they depend on the training data for neuron selection.

We developed a new method using cross model validation to account for this problem. We select neurons based on both how well they generalize to new data and on their ability to discriminate between different movements to be decoded. Selection is accomplished by comparing a neuron model's ability to distinguish movements using novel data.

We evaluate this method by decoding monkey finger and wrist movements using single unit spikes and kinematic data provided by Dr. Marc Schieber from University of Rochester. One successful model for neuron spiking is the point process model (PPM) using a generalized linear model (GLM) class. It easily includes covariates such as kinematics [12]. PPMs have been applied to neuronal spike data obtained from a variety of brain regions [12-15] and capture intrinsic and extrinsic effects on spiking activity. The GLM provides an efficient computational scheme for model parameter estimation and a likelihood framework for conducting statistical inferences [16]. This cross model validation is thus simple to implement with this framework.

II. METHODS

A. Experimental Task and Recordings

The monkey data was collected by Dr. Marc Schieber at University of Rochester Medical Center. A male rhesus monkey (*Macaca mulatta*) was trained to perform visually-cued hand movement tasks. 115 well-isolated single units with task-related activity were recorded sequentially in the M1 hand area contralateral to the trained hand. Kinematics were recorded through finger position measured by strain gauges on both sides of the wrist and digits on the manipulandum. Simultaneously recorded data was simulated by aligning the activity of each unit with its time at switch closure. More details of the experiment can be found in [17]. The trials were split into 3 mutually exclusive and completely exhaustive sets: one each for model fitting, cross model evaluation (neuron selection), and decoding.

B. Computational Model

The spiking of each neuron over time is modeled as a point process, a series of 0s and 1s generated by random events that occur over time. To help define a point process of neural spiking, we consider an observation interval $(0, T]$

and let $N(k)$ be the number of spikes counted in the interval $(k\Delta, (k+1)\Delta]$ for $k \in \left[0, \frac{T}{\Delta}\right]$ where Δ indicates bin size. Within each of these bins, we assume that a spike is determined by a Poisson process. Given a small enough bin size, it is safe to assume at most one spike per bin. A point process model can then be completely characterized by its conditional intensity function (CIF), defined as $\lambda[k|H_k, X_k] = \frac{Pr(N[k]=1|H_k, X_k)}{\Delta}$, where H_k and X_k denote spiking history and history of digit/wrist velocity respectively up until time $k\Delta$. The CIF thus generalizes the rate function for the Poisson process as temporally varying based on spike history and kinematics.

For our analyses, we use the GLM framework to estimate the CIF. Since $\log(\lambda)$ is the link function to the Poisson distribution under which the GLM is defined, we estimate the log of the CIF for every neuron/movement pair as a linear combination of the covariates as $log(\lambda[k|H_k, X_k]) = \alpha + \sum_{i=1}^{n_H} \beta_i H_k(i) + \sum_{i=1}^{n_X} \gamma_i X_k(d, i)$ [16].

The indices for the history and kinematic covariates relate to the ith window and the dth digit (d=6 for the wrist) from which either the number of spikes or average digit velocity is pulled from. The windows cover information from 1ms in the past to either 20ms, 40ms, or 60ms in the past. For the spiking history, a smaller window size is used for short term history to better resolve the refractory period.

C. Model Evaluation

Once the models were computed, we use the Kolmogorov-Smirnov (KS) plots to evaluate model performance [16]. Specifically, we use the time rescaling theorem [18] on the CIF generated by a test data for KS plots. This transforms the spike times using the CIF into a unit rate Poisson process by $\Lambda(k_i) = \sum_{k=k_{i-1}}^{k_i} \lambda[k|H_k, X_k]\Delta$. The unit rate Poisson random variables can then be transformed into a uniform distribution between 0 and 1 by $z_i = 1 - exp(\Lambda(k_i))$ [18].

The KS plot is then created by plotting the empirical cumulative distribution function (cdf) of z_i's against the cdf of a uniform distribution. An ideal model will give a KS plot of $y = x$. The performance (S) of the model for neuron n on movement j on encoding data from movement k is thus quantified by the KS plot's average deviation from $y = x$:

$$S_n(j,k) = \frac{\sum_{i=1}^{m} \left| z_i^* - \frac{i - 0.5}{m} \right|}{m} \qquad (1)$$

where z_i^* is the ith element of the z_i's sorted and m represents the number of spikes (and thus elements in z). Traditionally, the movement for the model and the data are the same. Thus, $S_n(j,j)$ is the encoding performance of the model for movement j.

D. Neuron Selection for Decoding

As stated before, neurons are selected based on their ability to encode matching/unmatching movements. For each neuron/movement pair, the associated model uses data from all 12 movements to create 12 KS plots. The data from cross validation trials is used here. Ideally, neurons would perform well for the movement it was fit for and poorly for the others.

For every neuron, a 12x12 matrix, A, of model performances is created where each row represents model fit scores of a single model created for a specific movement on the cross validation trials from each of the 12 movements (each movement corresponds to a column). Next, each row was normalized based on the score of the model on the matching data. Specifically,

$$A_n(j,k) = \frac{S_n(j,k)}{S_n(j,k)}. \qquad (2)$$

Thus, a normalized score $A_n(j,k) > 1$ implies that the model trained on data for movement j does not predict spikes from movement k as well as it does for the movement it is intended to encode. Therefore, a high score is desirable for neuron selection. The overall score for each neuron n is

$$B_n = \sum_{j \neq k}^{12} A_n(j, k). \qquad (3)$$

Neurons are then ranked from best to worst according to this score.

E. Movement Decoding

A group of neurons of size N is selected for decoding using the previously stated method. In particular, the first N ranked neurons are used. Data from one movement type is chosen among the decoding trials. The likelihood for each neuron/model pair is calculated as:

$$L = exp\left(-\sum_{k=0}^{\frac{T}{\Delta}} \lambda[k|H_k, X_k]\Delta\right)\prod_{i=1}^{n} \lambda[k_i|H_{k_i}, X_{k_i}]. \qquad (4)$$

The log likelihood for each movement type is then calculated by summing $\log(L)$'s for each neuron.

Four "candidate" movements are chosen from these log likelihoods purely by maximum likelihood. We allow each neuron to then have one vote for each of these four candidates and the movement with the most votes was the decoded movement. We use this two-step voting process in order to reduce the effect of single neurons with relatively small likelihoods (i.e. very largely negative log likelihoods) drastically impacting maximum likelihood estimates. Table I shows a truncated example of this two-step decoding process where the original movement is *e2*. N16 skews total log likelihood heavily away from *e2* despite all other neurons having a very high likelihood.

We perform this decoding for each movement using 10 different sets of randomly selected test trials. Thus, we attempt to decode 120 times in total, 10 for each individual movement. Decoding accuracy is judged based on percentage of times that the movement was correctly classified. This is then repeated over a range of neuron group sizes (n) and different lengths of history to ascertain its effects on decoding.

TABLE I
DECODING EXAMPLE: LOG LIKELIHOODS OF NEURON/MOVEMENT PAIRS

|	e1	e2	e3	e4	e5
N12	-29.8	-7.4	**-4.1**	-1.8	-6.5
N16	-169.7	-345.7	**-155.0**	-531.6	-254.0
N33	-51.3	**-10.6**	-51.7	-4.4	-132.7
N48	-64.6	**-50.9**	-84.0	-6.7	-69.1
N66	-3.4	**-1.2**	-15.2	-17.0	-49.5
Total	-318.8	-415.8	-310.0	-561.5	-511.8

Table I. Truncated example of two-step decoding procedure. Top three movement candidates (italicized) selected from the five based on total log likelihood. Each neuron is forced to vote (bold) amongst those three and the winner is selected based on most votes. Ties broken based on total likelihood.

III. RESULTS

A. Point Process Model Evaluation

We first examined the feasibility of using this modeling technique of point processes with the GLM framework. Specifically, we constructed models of the form (2) and then 95% confidence bounds for KS plots were generated for each neuron/model pair for varying history lengths. About half of the models created stayed within these bounds (20ms history: 47.7%, 40ms history: 46.0%, 60ms history: 43.8%). Some models strayed for a couple points while some also strayed for most of the plot. Thus, this method for modeling neuronal spikes works well on roughly half of the neuron/movement pairs given.

In addition, we looked at the parameters estimated to verify modulation of a single neuron's spiking patterns between different movements. Figure 1 shows an example of this for the same neuron between two different movements. Movements *e3* and *e4* have roughly the same average firing rate as shown by   . However, this neuron is more dependent on shorter term history (10-20ms) during movement *e3* and longer term history during movement *e4* (20-35ms).
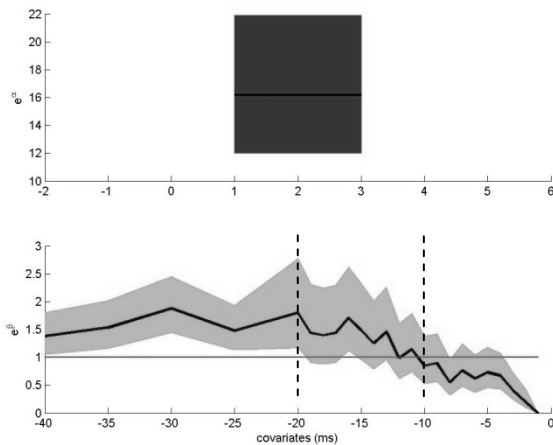
Though average firing rate is important, this modulation in history dependency shows that there are other possible distinguishing factors that can be gleaned through this model type. For example, despite the average firing rate during both movements being the same, oscillations in the upper half of the gamma band are more likely during movement *e3* while oscillations in the lower half are more likely during movement *e4*.

Given these sanity checks that the modeling works well and captures movement to movement changes, we continue on with decoding.

B. Decoding Evaluation

As a control for comparison, decoding was first performed on a random selection of neurons. Decoding accuracies with both random and optimally selected neurons are shown in Figure 2 for 3 different model structures. In particular, the history lengths in the models ranged from 20, 40 and 60 msec.

With random selection, decoding performs quite poorly. It rises slowly with neuron pool size and caps out at about 60% accuracy regardless of history length. It is also interesting to note, that if anything, the models with larger history lengths perform worse than those models with shorter history lengths since all the covariates for the latter are included in those for the former. However, more data is required to know if this is statistically significant since the traces are quite noisy. Once optimal selection from cross model validation is introduced, the decoding performance improves across the board for all history and neuron pool sizes (with a neuron pool of at least five). Improvement is most notable with a small neuron pool of at least five. The largest absolute increase in decoding performance in this range is 44% (8 neurons, 40 ms history) and the largest relative increase is about 1.5 times (5/8 neurons, 40/60 ms history). Accuracy in general improves with neuron pool size much faster but then declines as more neurons are included for decoding.

A.

B.
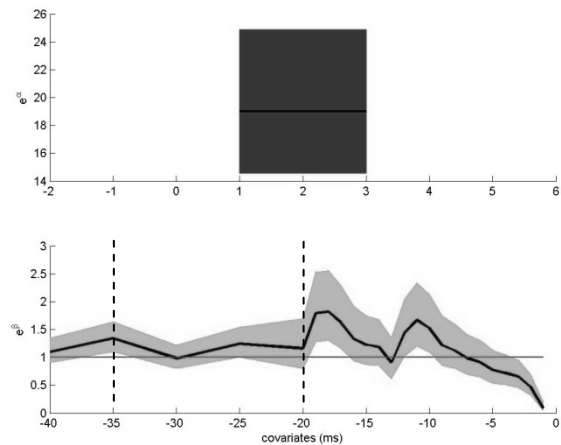
ovements. Values above 1
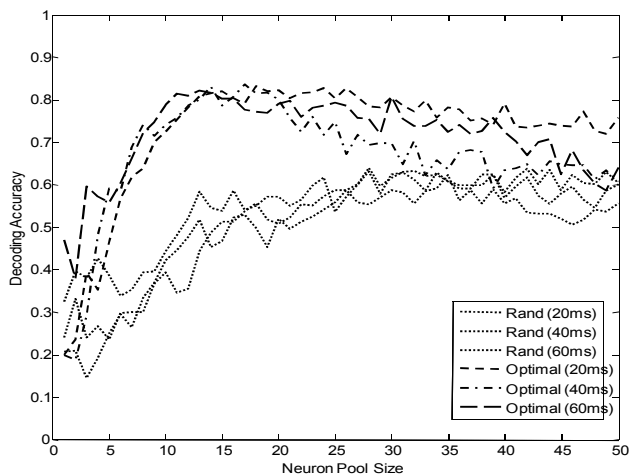ow a statistically significant
ow a statistically significant

Fig. 2. Movement decoding accuracy with varying history lengths and neuron pool sizes with or without optimal neuron selection from cross model validation using KS plots.

IV. DISCUSSION

The motivation of this study was to examine optimal neuron selection in decoding based off of performance in cross model validation on novel data. In all cases, neuron selection succeeded in terms of marked increases in decoding performance. Our method was able to highlight those neurons well tuned to the model type.

It is important to note that since this is a model based approach, that scoring poorly with this method does not necessarily mean a neuron is not task-relevant. It merely means that any relevancy cannot be resolved by the model being used. Expanding from this, we see that decoding accuracy plateaus and drops as too many neurons are added because neurons not well tuned to the model start being used for decoding. It is interesting to note that this drop happens at about 15-20 neurons or about 15% of the neurons available despite almost 50% of the neuron/movement model pairs encoding well. This disparity highlights the main motivation for the cross model validation. It is possible for a model to encode well while at the same time decode poorly since it does not discriminate well between movements.

Though we use this method specifically with KS plots and PPMs, there is no barrier in its use for other models and modes of evaluation. As long as there is a method to ascertain encoding success and the model based decoding occurs between discrete states, then this idea of cross model validation should still work. In the case of continuous state decoding, it is even possible to discretize the continuous states into bins and proceed accordingly. However, in this case weights should be applied in such a way to penalize less models that encode well for data from states that are close to the original state. It would be interesting to compare performance of this method to existing methods for continuous state decoding as a way of outlining the effect of introducing novel data in neuron selection.

In closing, this new method for neuronal selection has succeeded in both assisting decoding and highlighting neurons well tuned to a specific model structure. The method can also be easily generalized to many different models and thus shows much promise for model based decoding.

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