Supplemental Figure 1. Discharge statistics of SC neurons. a. The spike count variance against spike count mean is plotted on a log-log scale for each of the 120 SC neurons in our data set. The interval of 28 to 8 ms before the onset of the saccade was used. Each blue circle (n=120×3) is a single neuron whose discharge was measured when a distractor was in its RF. The intercept of the linear regression function in the log-log plot is 1.03. Each red circle (n=120×1) is a single neuron whose discharge was measured when a target was in the RF. The intercept of the linear regression function in the log-log plot is 1.44. b. Frequency of observations is plotted against the Pearson r value. We paired two neurons out of four neurons in an individual data set and calculated the correlation between two neurons' discharge rates during the interval of 28ms to 8 ms before the onset of the saccade. Because we have four neurons in one data set, there are six possible combinations. Also we have a total of 30 data sets with four different target conditions. Thus, we have 720 possible combinations ($6_{combination} \times 4_{target\ condtion} \times 30_{data\ set} = 720$). Pearson r was calculated for the pairs and *t*-tests were used to assess significance (Matlab R2007b; corrcoef). The unfilled bars show the non-significant correlations (n = 649, $p>0.05$) and filled bars show significant correlations (n = 71, $p\leq0.05$). Only 9.86% of the pairs (71/720) had statistically significant noise correlations.

Supplemental Figure 2. Shuffled trials remove noise correlation structure. This figure shows how the data were shuffled and read-out by the model in schematic form. The column marked 'trial' shows the trial number and the four columns labeled 'neuron A, B, C and D' represent one set of four neurons recorded simultaneously. To break the correlation structure between neuronal responses, we performed a random permutation across the trials within a neuron as shown in the lower panel labeled "after shuffling". After the data set was shuffled we fed the

resulting data on a trial by trial basis into the model. The adequacy of the model prediction was compared to that from the unshuffled data. With the unshuffled data the MAP predicted 81.88% of all trials (using the uniform prior as shown in Figure 3d). When the data were shuffled, the MAP predicted 81.36% of all trials. Since there was only a 0.52% difference in the percentage of trials predicted correctly with the shuffled and unshuffled data set, we concluded that the structure of the noise correlation either was accounted for in our model or did not contribute much to the result of the model.

Supplemental Figure 3. Correlation matrices in the OLE model. a. The correlation matrix between the four neuronal responses was calculated from the neuronal discharge in the 28 to 8ms epoch before the onset of the saccade. For each data set, we measured the discharge of individual neurons during performance of each of the four different saccade choices. In the array, $r_{i1\text{-}i4}$ represents the discharge of a single neuron during performance of each different saccade choice as indicated by the small task diagram. We transposed the rows of the array to generate the column array (transposed array: left column array) and then multiplied these two arrays. The multiplication of the column array ($r_{i1\text{-}i4}$, 1×4) and the row array ($r_{i1\text{-}i4}$, 4×1) results in a new matrix (C_{r_i}, 4×4). We had four neurons in each data set. Thus, we generated four matrices for each data set and averaged those four matrices ($\frac{1}{4}\sum_{i=1}^{4}$) to create the correlation matrix. In this figure, the grand averaged correlation matrix from 120 neurons is presented. The amount of correlation is indicated by the temperature plot. Hotter colors indicating higher correlations. b. The correlation matrix between the saccade vectors and neuronal discharge rates from the same time epoch in panel a. The four neuron's discharge rates for one of the four saccade vectors are presented in the left column array ($r_{1j\text{-}4j}$, 1x4). The row column array (

$\vec{S}_j$, 2x1) contains the horizontal and vertical components of one of the four saccade vectors. The multiplication of these two arrays results in a new matrix (2x4). Since we have four saccade vectors in each data set, we repeated this calculation for four saccade vectors and obtained four matrices. We averaged these four matrices ($\frac{1}{4}\sum_{i=1}^{4}$) to get the optimized saccade vectors ($\vec{D}_j$). Each row in the final matrix contains the horizontal and vertical component of each optimized saccade vector ($\vec{D}_{1-4}$).

Supplemental Figure 4. The calculation of the population (PVA and OLE) vector from four neuronal vectors (one target and three distractors). The target neuronal vector as determined from the position of the target stimulus is the dashed, black line. The distractor neuronal vectors are black. The population vector was determined by equation (13 and 14) and is presented in red. The angular differences between the population vector and the target and three distractor vectors were measured as ∠a, b, c and d. If the angular difference between the population vector and the target vector was smaller than all others, we considered the model to correctly predict the saccade choice.

Supplemental Figure 1
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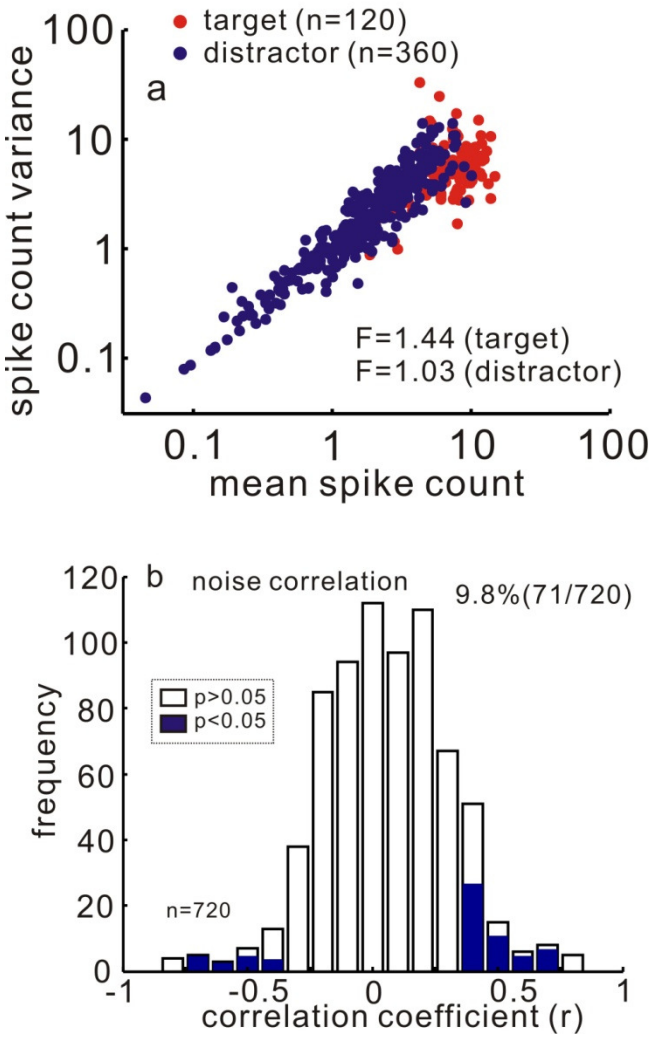
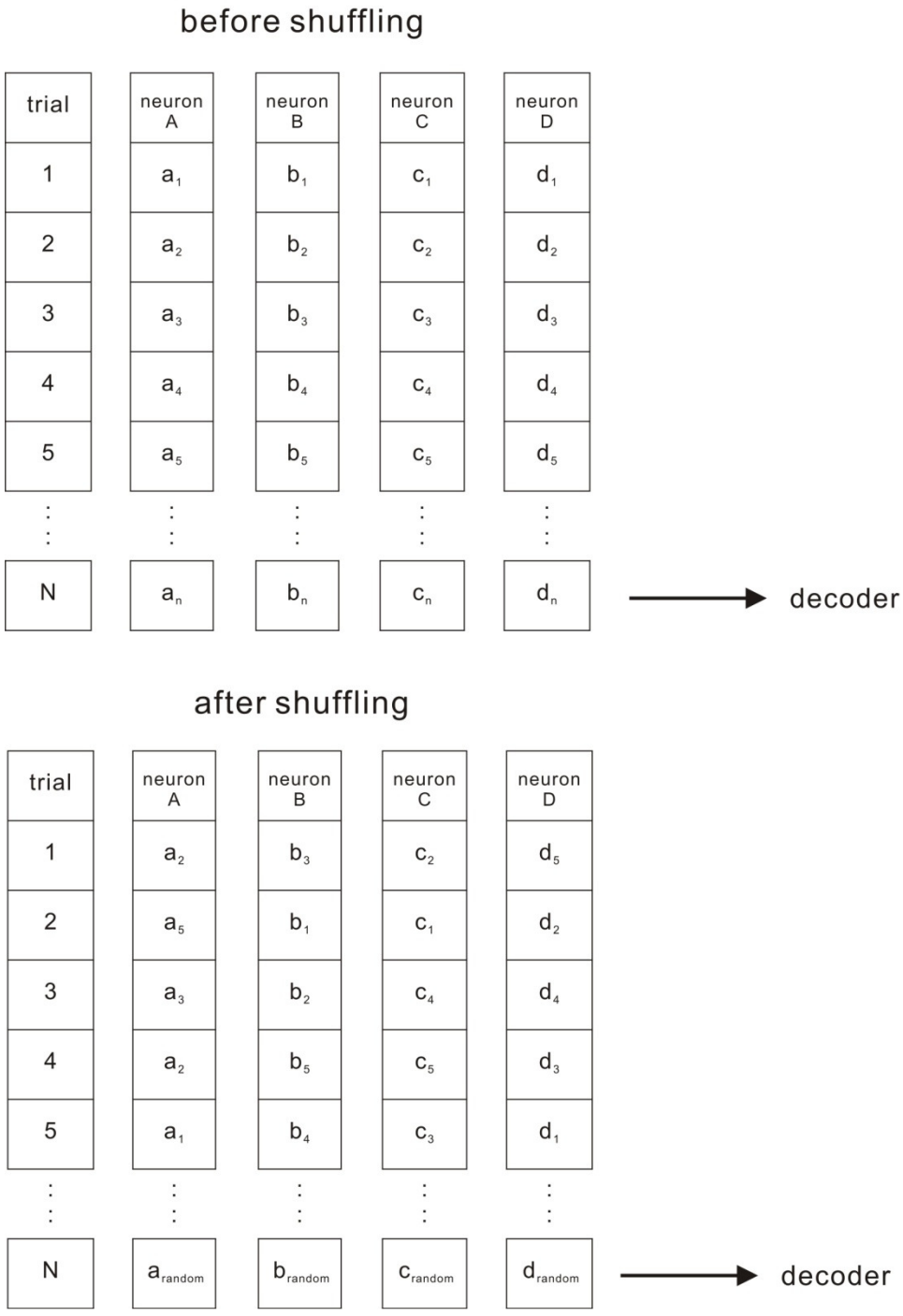
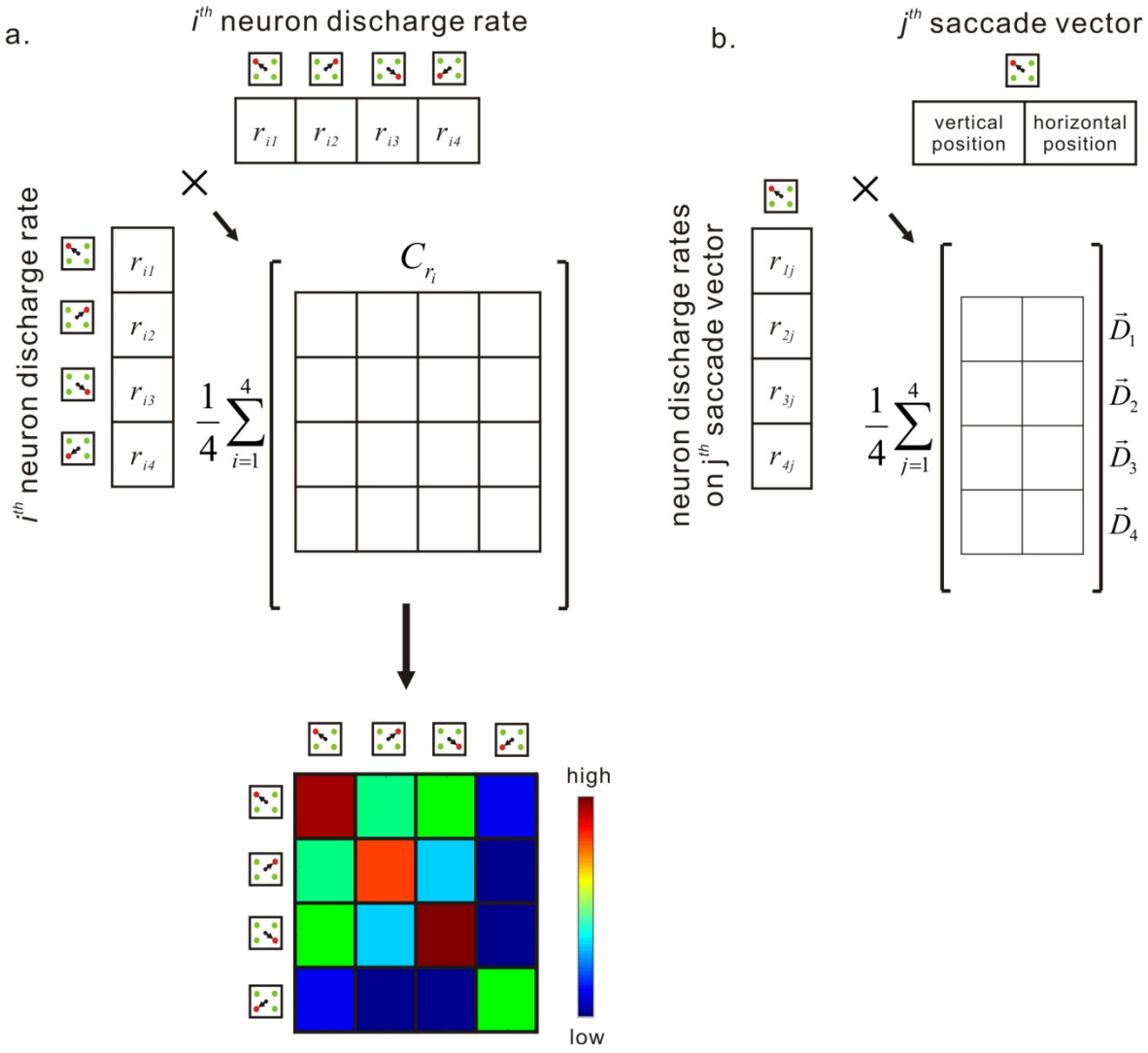


Supplemental Figure 2
Kim and Basso



Supplemental Figure 3
Kim and Basso



Supplemental Figure 4
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