

Computational model of layer 2/3 in mouse primary visual cortex explains observed visuomotor mismatch response

Supplementary Information

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Abstract

This supplementary information shows the results of the mismatch responses when recording from neurons from three different population codes, each encoding a 2-dimensional velocity vector projected onto a basis vector that points into a different direction. The results were similar to the results in the main article.

We modified our computational model to have three instead of one population code. Each code encodes the velocity of the visual flow along a given direction. Here, we represent the velocity by a 2-dimensional vector,

$$\vec{v} = \begin{pmatrix} 0.05m \\ 0 \end{pmatrix}, \quad (1)$$

where m was an integer chosen from the interval 1 to 10, depending on the speed trial.

We used three basis vectors, as in Fig. S1, one for each population code. That is, we have an over-complete basis. We speculate that such encoding would be more likely because the redundancy increases robustness. To compute the value represented by each population code, we projected the velocity \vec{v} onto the corresponding basis vector,

$$v_i = \vec{v} \cdot \vec{b}_i. \quad (2)$$

Then, we defined dMM and hMM neurons as in the main article and computed their mismatch response.

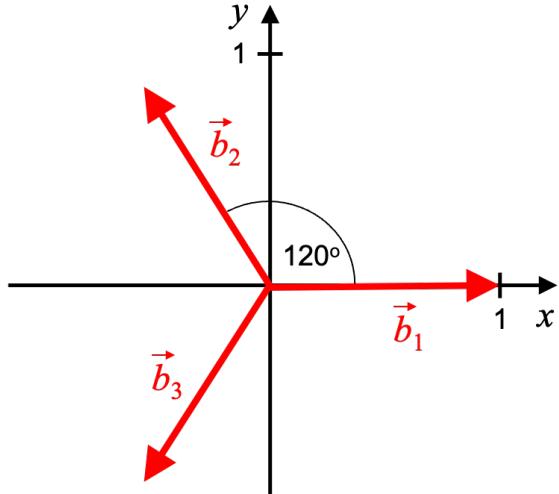


Fig. S1: Basis vectors for projecting the velocity vector onto 1-dimensional subspaces, one for each population code.

Figure S2 shows the results, which were similar to the ones presented in the main article. Different, here, we have three mismatch responses mixed together and each mismatch response had a different slope. The slope varied because the size of the projected speed values depended on the direction of the basis vector. Negative projected values did not change the slope because the mismatch responses are invariant to a change of sign of the encoded velocity.

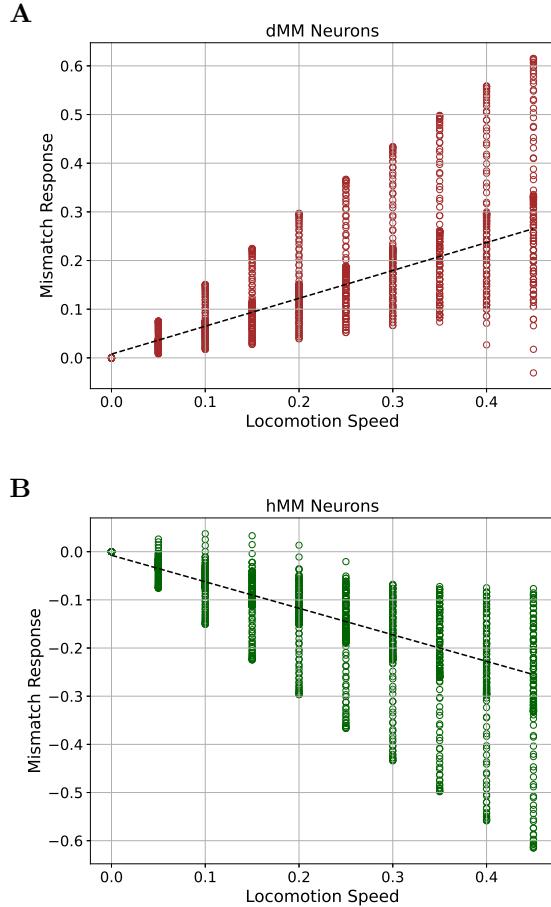


Fig. S2: Predicted scatterplot between locomotion speed and mismatch response for dMM (A) and hMM (B) neurons originating from three different population codes, each encoding the visual flow along a given direction. Each data point represents a single neuron in one trial. Dashed lines are linear fits with bisquare weighting of residuals