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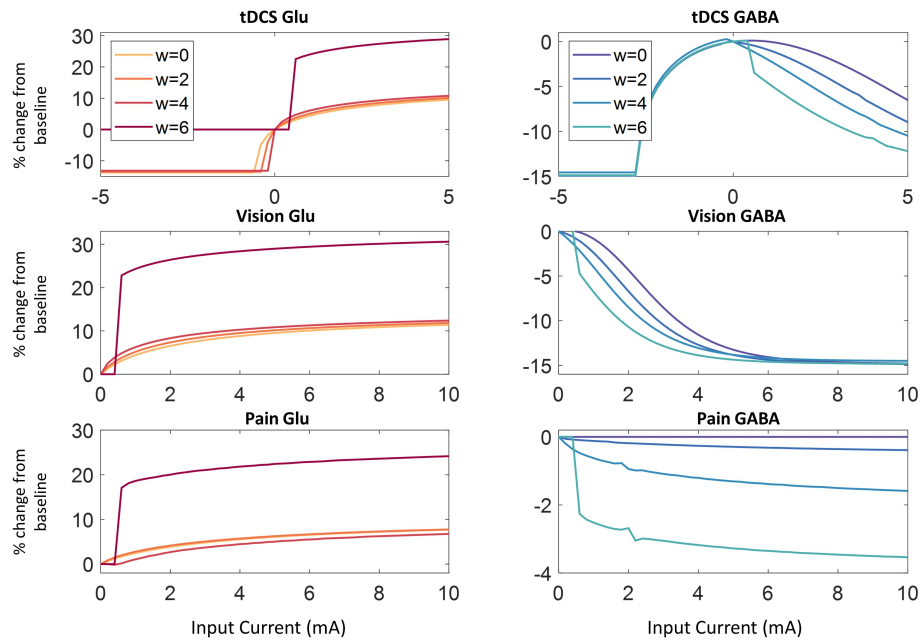
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## S1 Supplementary Information

Values in the model that are arbitrary include the connection strengths used in all simulations, and the TE values used in simulation 6 and we present the results for a variety of these parameter values and describe the effect each has on model output below.

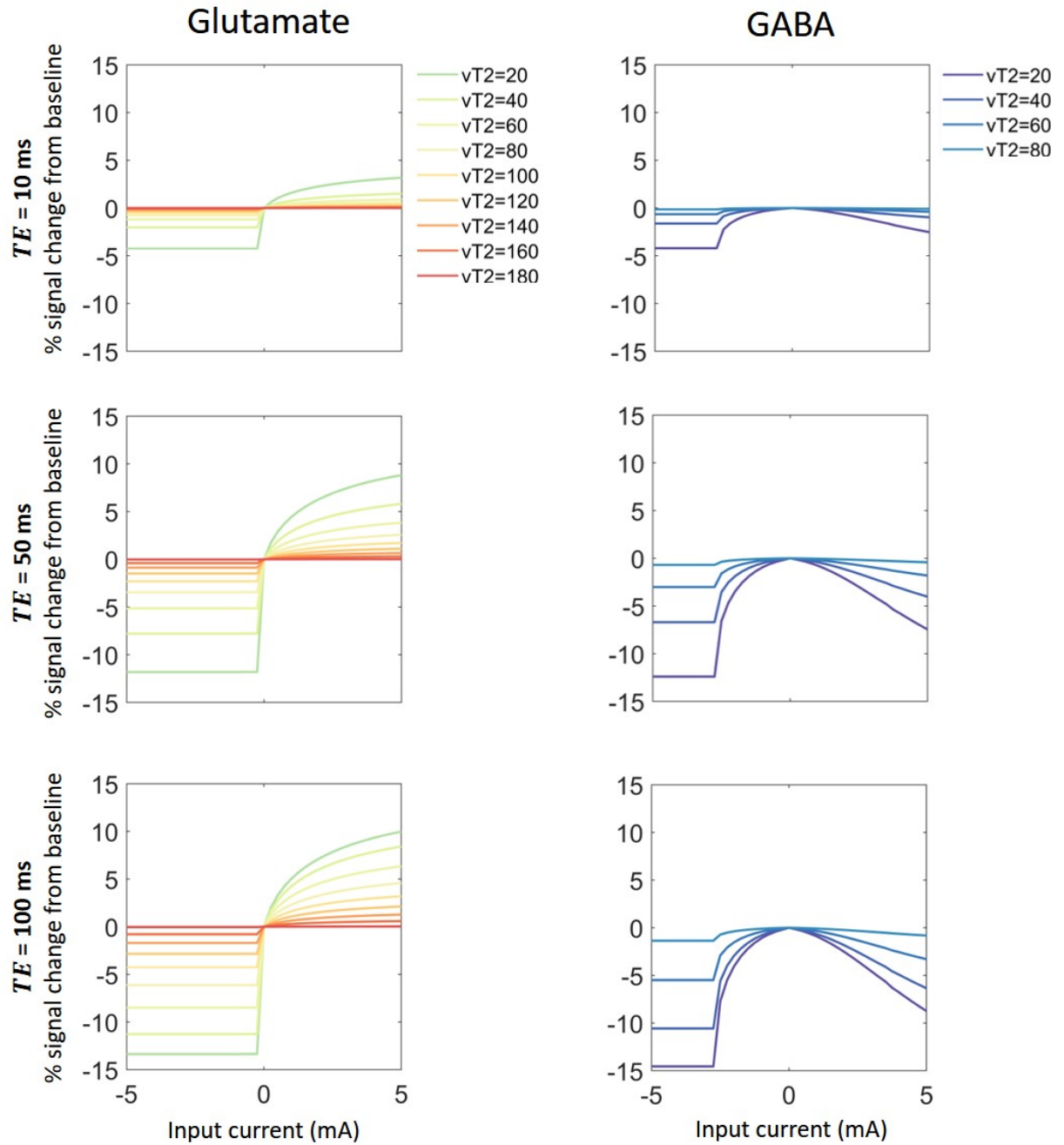
### S1.1 Connectivity Weights



**Figure S1: Effect of connectivity strengths**

We recreate Fig. 7 (lower panel) in the manuscript with different values for the weights ( $w = w_{EE}, w_{IE}, w_{EI}$ ) varied between 0 and 6 (apart from  $w_{II}$  which is always set to 0). Top panel shows the response to tDCS, middle panel to vision, and lower panel to pain stimuli with Glu (left) and GABA (right) presented as a change from baseline values. The precise values that the model predicts changes slightly for each input value as the 2 populations exert different levels of influence on each other, however the overall pattern of activity remains the same. Results are shown in the same plot so that they can be compared easily. For example, changing the weights from 0 to 4 results in an approximately 4 % change in GABA signal for an input of 2 mA using 'tDCS' stimulation, whereas a 'step-change' in behaviour is seen when the weights are set to equal 6 causing differences of up to 20 % in the predicted signal.

## S1.2 Effect of vesicular T2 and TE over an extended range



**Figure S2: Effect of vesicular T2 and TE over an extended range**

We recreate Fig. 7 (lower panel) for the tDCS input over an extended range of vesicular T2. For Glu, we vary vesicular T2 between 20 and 180 ms, for GABA we use 20 to 80 ms (so as to always be lower than cytosolic T2). Echo times used are 10 ms (top row), 50 ms (middle row), and 100 ms (bottom row). The effect of compartmental redistribution of the metabolites on the predicted MRS signal change is reduced at the shortest TE and also as vesicular T2 approaches cytosolic T2 for each metabolite.