Distributed range adaptation in human parietal encoding of numbers

SUPPLEMENTARY INFORMATION

Arthur Prat-Carrabin[1,⋆], Gilles de Hollander[2,3⋆], Saurabh Bedi[2,3],
Samuel J. Gershman[1], and Christian C. Ruff[2,3]

[1]Department of Psychology and Center for Brain Science, Harvard University, Cambridge, MA, USA
[2]Zurich Center for Neuroeconomics, Department of Economics, University of Zurich, Switzerland
[3]University Research Priority Program (URPP), Adaptive Brain Circuits in Development and Learning, University of Zurich, Zurich, Switzerland

⋆equal contribution
⋆*arthurpc@fas.harvard.edu, gilles.de.hollander@gmail.com*

Figure S1 shows the proportion of voxels with cv$R^2 > 0$ with the different nPRF models that we fit. Models fit on the participants' estimates (orange line) consistently outperform the models fit on the presented number (teal line).

The precision of the neural encoding depends on the amplitude of the populations' receptive fields, in addition to their preferred numerosities and their widths. Here we test for changes in the amplitudes. Thus we fit models in which the amplitude of each voxel may vary across conditions. Specifically, first we consider a model that features efficient shifts of the preferred numerosities, fixed scaling of the widths (as in the main text), and in which for each voxel we let the amplitudes in the two conditions be free parameters, a_n and a_w. This model yields a significantly lower fit than our best-fitting model (with estimates: $t(38) = 6.12$, $P = 3.9 \times 10^{-7}$; with correct numbers: $t(38) = 6.41$, $P = 1.6 \times 10^{-7}$; Fig. S1, last-but-one model). Second, we enforce a relation of proportionality between each participant's voxels amplitudes in the Narrow condition and in the Wide condition, with a fixed ratio for each participant (i.e., $a_w = r_a a_n$). This model yields a better fit than the previous one, but a significantly worse one than our best-fitting model (with estimates: $t(38) = 2.36$, $P = 0.024$; with correct numbers: $t(38) = 2.71$, $P = 0.0099$; Fig. S1, last model). We conclude that assuming that the amplitudes change across conditions does not yield a better fit of the fMRI data.

Finally, we consider alternatives to our efficient-shift hypothesis (which posits that $\mu_w = 10 + 2(\mu_n - 10)$ if $\mu_n > 10$, otherwise $\mu_w = \mu_n$). First we consider a model in which for all voxels the preferred numerosity in the Wide condition is twice the preferred numerosity in the Narrow condition (i.e., $\mu_w = 2\mu_n$). We compare this model to the model with efficient shifts (and unchanging widths and amplitudes): it yields a lower proportion of voxels with cvR^2 positive, with a significant difference when fitting on the correct numbers ($t(38) = 2.63$, $P = 0.012$; Fig. S1, second model). Then we consider a model in which the preferred numerosity in the Wide condition is proportional to that in the Narrow condition, with a fixed parameters for each participant (i.e., $\mu_w = r_\mu \mu_n$; Fig. S1, third model). This model also fits significantly worse than the model featuring the efficient-shift hypothesis (fitting on estimates: $t(38) = 3.19$, $P = 0.003$, fitting on correct numbers: $t(38) = 3.85$, $P = 0.0004$). Thus we conclude that the efficient-shift hypothesis ($\mu_w = 10 + 2(\mu_n - 10)$ if $\mu_n > 10$) better accounts for the data than the hypothesis that μ_w is proportional to μ_n.

We recapitulate the assumptions of the models shown in Figure S1:

- 'No shift': $\mu_w = \mu_n$, $\sigma_w = \sigma_n$, and $a_w = a_n$.
- '$\mu_w = 2\mu_n$': $\mu_w = 2\mu_n$, $\sigma_w = \sigma_n$, and $a_w = a_n$.
- '$\mu_w = r_\mu \mu_n$': $\mu_w = r_\mu \mu_n$, $\sigma_w = \sigma_n$, and $a_w = a_n$.
- 'Free shifts': μ_w and μ_n free parameters, $\sigma_w = \sigma_n$, and $a_w = a_n$.
- 'Efficient shifts': $\mu_w = 10 + 2(\mu_n - 10)$ if $\mu_n > 10$, else $\mu_w = \mu_n$; $\sigma_w = \sigma_n$, and $a_w = a_n$.
- 'Participant-specific slopes': $\mu_w = 10 + r_\mu(\mu_n - 10)$ if $\mu_n > 10$, else $\mu_w = \mu_n$; $\sigma_w = \sigma_n$, and $a_w = a_n$.
- 'Free widths': $\mu_w = 10 + 2(\mu_n - 10)$ if $\mu_n > 10$, else $\mu_w = \mu_n$; σ_w and σ_n free parameters, and $a_w = a_n$.
- 'Participant-specific scaling': $\mu_w = 10 + 2(\mu_n - 10)$ if $\mu_n > 10$, else $\mu_w = \mu_n$; $\sigma_w = r_\sigma \sigma_n$, and $a_w = a_n$.
- 'Free amplitudes': $\mu_w = 10 + 2(\mu_n - 10)$ if $\mu_n > 10$, else $\mu_w = \mu_n$; $\sigma_w = r_\sigma \sigma_n$, and a_w and a_n free parameters.
- 'Participant-specific amplitude ratio': $\mu_w = 10 + 2(\mu_n - 10)$ if $\mu_n > 10$, else $\mu_w = \mu_n$; $\sigma_w = r_\sigma \sigma_n$, and $a_w = r_a a_n$.

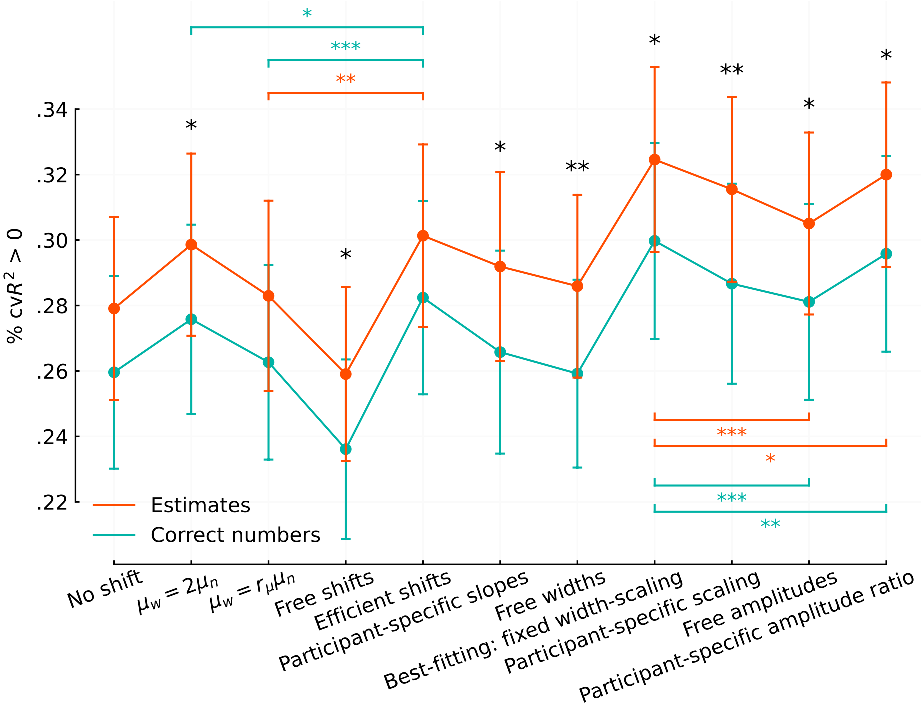

Fig. S1: Proportion of voxels with positive cross-validated variance explained (cvR^2>0) for the different models. See text for the specifications of each model. Error bars show ±1 standard error of the mean. ***: $P < 0.001$, **: $P < 0.01$, *: $P < 0.05$.