

Erratum to: Social Inclusion Enhances Biological Motion Processing: A Functional Near-Infrared Spectroscopy Study

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Unfortunately, Figs. 2 and 3 are incorrectly published in the original publication. The two figures are corrected with this erratum.

In our continued use of the analysis package employed in the study presented in this paper, we discovered an error in the automated detection of our protocol timing. The automated detection of protocol timing was used to generate task predictors for our general linear models (GLMs). Instead of reading marks in the data as onsets and offsets of experimental blocks lasting over 20 s each, the program read each mark as a discrete onset of an instantaneous event. We verified this error was consistent among all participants. To correct this error, we manually reprocessed all of our data with the correct timing of our GLM task predictors. This affected the results presented in the two figures, leading to the corrected figures.

Moreover, the authors continue, in our results section, we described the active regions depicted in Figs. 2 and 3. Illustrated in Fig. 2, we originally found right supramarginal gyrus as the single region showing a robust response to biological > scrambled motion collapsed across experimental conditions. In the corrected results, the sole region showing this effect is inferior temporal cortex (a

region also represented in our comparative fMRI results). Illustrated in Fig. 3, following social inclusion, the reported effect in right dorsolateral prefrontal cortex did not remain in the corrected results. All other text descriptions of Figs. 2 and 3 remain true with the correction. We also describe results of GLM analyses not illustrated in any figures. Of these results, brain responses to biological versus scrambled motion increased post-inclusion compared to baseline only in a very small region of right cerebellum. Regions of precentral gyrus and right cerebellum extending into inferior temporal cortex showed decreased activation to biological (vs. scrambled) motion post-exclusion compared to baseline. All other text descriptions of non-illustrated data remain true with the correction.

Data presented in Fig. 4 (ROI analyses) was not generated using a GLM, and thus was not affected by the error. However, in our thorough re-evaluation of the data, we noted that the degrees of freedom were misreported in our repeated measures ANOVAs. For the first three ANOVAs reported in “Results: ROI Analyses”, the degrees of freedom should be (2,22) instead of (10,2). For the second two ANOVAs, the degrees of freedom should be (1,11) instead of (11,1).

The theoretical conclusions of the study are not affected by the correction of the data.

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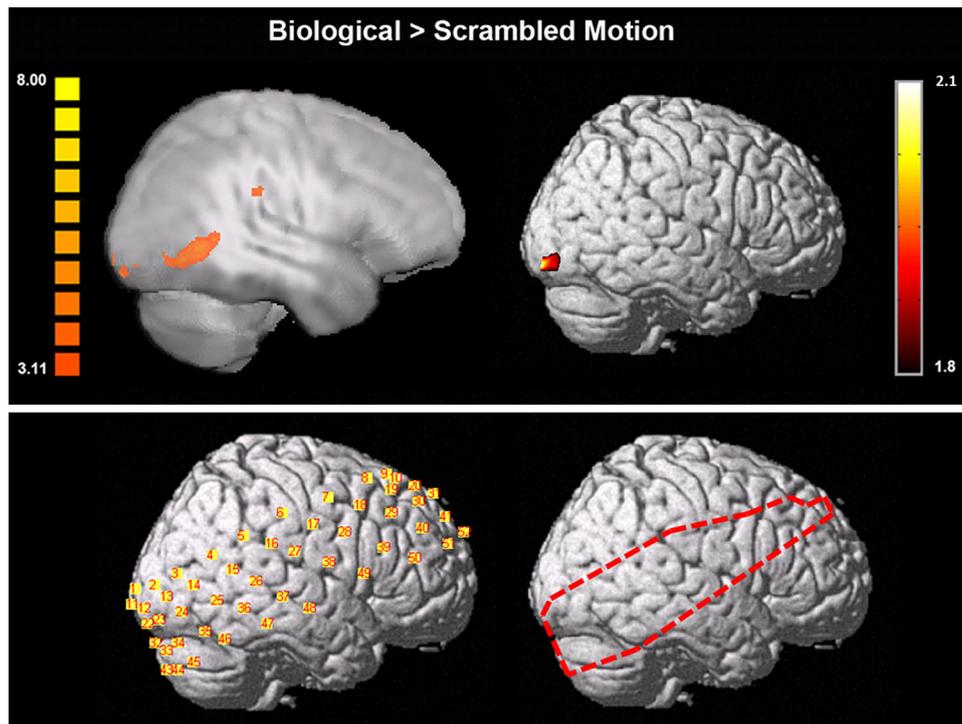


Fig. 2 Activation to biological > scrambled motion measured with functional MRI (*top left*) and functional NIRS (collapsed across conditions; *top right*) in an identical group of 12 participants. Functional MRI activation is displayed on a Talairach-transformed template brain depicting functional activation in the plane $x = 54$ projected onto a smoothed surface map. Functional NIRS activation is displayed on a template brain normalized to MNI space. Functional

MRI results were assessed at a corrected threshold of $\alpha < 0.05$. Functional NIRS results were assessed at a threshold of $p < 0.05$. An example of normalized recording channel placement in MNI space for one participant is shown on the bottom left, while the outline of pixels used in the group analysis (where 11 or more participants had functional data) is shown on the bottom right

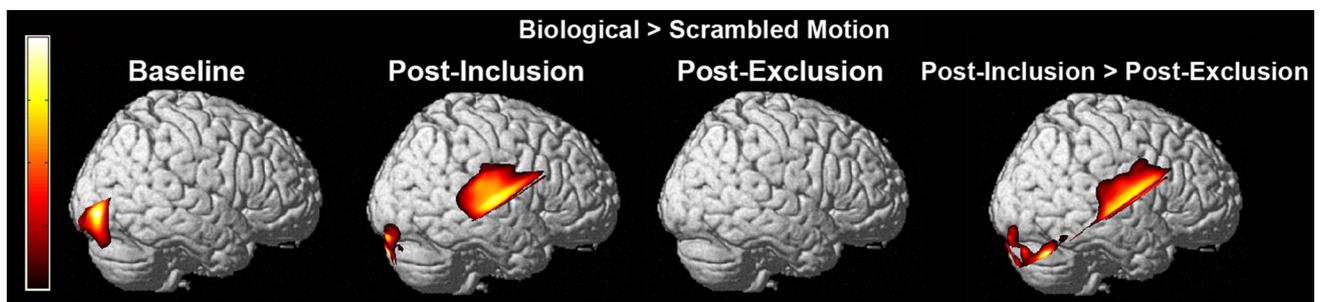


Fig. 3 Activation to biological > scrambled motion in each experimental condition and in the contrast of post-inclusion > post-exclusion, measured with functional NIRS. Activation is displayed on a template brain normalized to MNI space, and assessed at a threshold of $p < 0.05$