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eLife's transparent reporting form

We encourage authors to provide detailed information *within their submission* to facilitate the interpretation and replication of experiments. Authors can upload supporting documentation to indicate the use of appropriate reporting guidelines for health-related research (see EQUATOR Network), life science research (see the BioSharing Information Resource), or the ARRIVE guidelines for reporting work involving animal research. Where applicable, authors should refer to any relevant reporting standards documents in this form.

If you have any questions, please consult our Journal Policies and/or contact us: editorial@elifesciences.org.

Sample-size estimation

- You should state whether an appropriate sample size was computed when the study was being designed
- You should state the statistical method of sample size computation and any required assumptions
- If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

Although we did not perform a formal power analysis, the sample size used here (N=23) was comparable to that in previous fMRI studies on movement planning (N=20-25). In fact, given that the BOLD-fMRI signal during planning is much weaker than during movement, we chose a sample size that was substantially larger than typical studies that involved just movement (N=10-15). Information about the used sample can be found under 'Participants' in the Methods section.

Replicates

- You should report how often each experiment was performed
- You should include a definition of biological versus technical replication
- The data obtained should be provided and sufficient information should be provided to indicate the number of independent biological and/or technical replicates
- If you encountered any outliers, you should describe how these were handled
- Criteria for exclusion/inclusion of data should be clearly stated
- High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

Details about the experimental paradigm can be found in the Methods section under 'Task' and 'Experiment design and structure'. The experiment was performed once and did not constitute a replication. The distinction between biological and technical replicate does not apply to this submission. The only criterion for data inclusion was to complete the experiment (a full dataset), which was the case for 22 out of 23 participants, as one participant dropped out mid-session (see 'Participants' in the Methods section).

Statistical reporting

- Statistical analysis methods should be described and justified
- Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
- For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
- Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

Detailed information about statistical reporting can be found in the Results and Methods section of the submission and in the figure captions. Each performed statistical test is reported with the exact *t* / *p* value throughout the Results section.

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

Group allocation

- Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
- Indicate if masking was used during group allocation, data collection and/or data analysis

Please outline where this information can be found within the submission (e.g., sections or figure legends), or explain why this information doesn't apply to your submission:

This study consisted of only one experimental group and the within-subject design included trial-by-trial randomization within functional runs as described in the Methods section ('Experiment design and structure'). No blinding or masking was used.

Additional data files ("source data")

- We encourage you to upload relevant additional data files, such as numerical data that are represented as a graph in a figure, or as a summary table
- Where provided, these should be in the most useful format, and they can be uploaded as "Source data" files linked to a main figure or table
- Include model definition files including the full list of parameters used
- Include code used for data analysis (e.g., R, MATLAB)
- Avoid stating that data files are "available upon request"

Please indicate the figures or tables for which source data files have been provided:

Source data files, MATLAB code, and toolboxes used for data analysis can be found on GitHub: https://github.com/g14r/single-finger-planning, https://github.com/jdiedrichsen/pcm_toolbox, https://github.com/rsagroup/rsatoolbox, https://github.com/jdiedrichsen/dataframe, https://github.com/nejaz1/plotlib. The raw fMRI dataset can be found on OpenNeuro https://openneuro.org/datasets/ds003684 (Dataset DOI: 10.18112/openneuro.ds003684.v1.0.0).The Pattern Component Modeling (PCM) toolbox is described in detail in the following paper https://doi.org/10.1016/j.neuroimage.2017.08.051 and we provide a Jupyter notebook with examples of PCM usage https://pcm-toolbox-python.readthedocs.io/en/latest/index.html, https://pcm-toolbox-python.readthedocs.io/en/latest/demos/demo_correlation.html