Title: A common neural architecture for encoding finger movements

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Author Contributions: TM designed the study; TM and FA analyzed data; GW administered and supervised the project; TM, FA, FT-M and GW wrote the paper.

Competing Interest Statement: The authors declare no competing interest.

Classification:

Keywords: finger-tapping; hyperalignment; motor representations; fmri; brain decoding;

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Main Text

Figure 1

Figure 2

Abstract

Finger tapping is widely used to investigate sensorimotor brain responses, yet it remains unclear whether shared neural codes for complex finger movements exist across individuals, given the highly individual-specific topography of the sensorimotor cortex. We combined spherical searchlight Procrustes hyperalignment on 7-Tesla fMRI data with between-subject classification to investigate the existence of a shared latent neural architecture encoding sequential finger movements in the human sensorimotor cortex. Our model afforded above-chance level accuracy in both the contralateral and ipsilateral areas, suggesting that such a high-dimensional neural information space exists, is traceable, and spreads over the bilateral sensorimotor cortex. Critically, these high-dimensional neural codes were identified without task-specific training and cannot be attributed to error-related activity. These findings establish universal organizational principles of motor sequence encoding and pave the way for personalized neurotechnologies, scalable brain-computer interfaces, and optimized cross-subject models for motor learning and rehabilitation.

Main Text

Introduction

Hand movements can be described as a combination of multiple parameters, including temporal patterns, spatial trajectories, force dynamics, and sequential organization[1]. At the neural level, the sensorimotor cortex reliably encodes this multidimensional motor information within high-dimensional neural representational spaces[2–4]. These neural codes capture the rich complexity of motor behavior through population-level activity patterns, and revealing their fundamental principles is crucial for theoretical frameworks of neural computation and advancing clinical applications such as brain-computer interfaces and rehabilitation strategies[5,6].

However, revealing the shared neural representations across participants is challenging due to substantial individual differences in brain anatomy and cortical topography. At least in the visual domain, linear transformations of individual neural representations have been employed to identify common high-dimensional representational spaces despite individual-specific topographic idiosyncrasies[7,8]. The sensorimotor cortex shares analogous organizational principles, such as columnar architecture[9], somatotopic mapping with individual variability[10], and distributed population coding of multidimensional features[2], raising the possibility that a shared representational space for motor control exists across individual brains.

We hypothesize that the sensorimotor cortex shares an innate high-dimensional neural architecture for encoding sequential finger movements across individuals, and that this architecture can be revealed using transformation-based methodologies akin to those successfully applied in the visual domain. To test this, we applied spherical searchlight Procrustean transformations to 7-Tesla BOLD responses from visually guided nine-digit finger-tapping sequences in twelve right-handed participants. This approach resulted in a common neural space that preserved individual information and enabled above-chance between-subject decoding of sequence identity, revealing a common high-dimensional representational architecture for encoding finger movements in the sensorimotor cortex.

Results

We used high-field MRI data to predict the motor sequence identity (1-12) based on the BOLD signal from the sensorimotor cortex[11]. For eight runs, 12 right-handed subjects performed 12 different finger-tapping sequences[12], which were matched by their difficulty level and consisted of nine digits long that were performed at the same pace with the five fingers of the right hand. We excluded the trials containing execution errors to avoid bias. The common model was built using spherical searchlights[7] by first setting aside the data from the test subject. The train data consisted of all runs of the remaining subjects, which were used to create the common space and to train the decoder. Then, the test subject data was aligned to the common space and used to test the decoder accuracy[7,13]. We repeated this procedure so that each subject was used as a test subject once (*SI Appendix, Supporting Methods*). Importantly, we avoided overfitting and prevented circularity[14] by keeping apart the training and test data to build the common space and train the decoder. With this approach, we decoded the identity of each of the 12 finger-tapping sequences in a given subject using a model trained on brain responses to the same sequences in other subjects.

Between-subject classification maps were obtained with permutation testing, in which the classification was performed 100 times with randomly shuffled sequence identities for each fold. For each hemisphere and vertex, we aggregated individual-level decoding accuracies from cross-validation folds across all test subjects. The empirical null distribution was obtained by sampling decoding accuracies from permutation-based analyses (i.e., models trained on data with randomized sequence identities). For each vertex, we drew bootstrap samples randomly with replacements from the pool of permutation scores. We repeated this procedure 10,000 times, each time computing the mean of the sampled values to create a distribution of group-level means under the null hypothesis. Observed group-level decoding performance at each vertex was then compared against its corresponding null distribution. Specifically, empirical *p-values* were computed as the proportion of null distribution values greater than or equal to the observed decoding accuracy, with one added to both the numerator and denominator to avoid zero probabilities and reduce bias. This constitutes a one-sided non-parametric test for above-chance performance. The Benjamini–Hochberg procedure was subsequently applied to correct *p-values* for multiple comparisons.

We observed above-chance level (chance: 8.33%) accuracy in the sensorimotor cortical areas of both hemispheres (Figure 1). Specifically, a repeated-measures ANOVA (within-subjects factors: cortical label and hemisphere) revealed a main effect of cortical label ($F(5,55) = 9.81$, $p < .001$, $\eta^2p = 0.47$), with the precentral and postcentral gyri showing the highest decoder accuracy (FDR-corrected $p < 0.05$). Moreover, a significant main effect of hemisphere ($F(1,11) = 35.34$, $p < .001$, $\eta^2p = 0.76$) indicated a strong left-lateralization (FDR-corrected $p = 0.0005$, Cohen's $d = 0.69$), contralateral to the moving fingers. Finally, we observed a significant interaction between factors ($F(5,55) = 4.99$, $p = .001$, $\eta^2p = 0.31$), revealing greater decoder accuracy in the left side of the postcentral sulcus, postcentral gyrus, and central sulcus (FDR-corrected $p < 0.05$).

We also analyzed sequence encoding using anatomical alignment for reference, following the same procedure as for hyperaligned data, except that participants' functional data remained in the template surface fsaverage. Under anatomical alignment, decoding accuracy was close to chance, averaging only 8.91% and 8.43% in the left and right hemispheres, respectively. Comparatively, hyperalignment substantially boosted performance across all vertices in both hemispheres, yielding mean accuracies of 20.86% (left) and 19.99% (right). This corresponds to a relative

improvement of approximately 134% in the left hemisphere and 137% in the right hemisphere compared with anatomical alignment (Figure 2).

Discussion

Finger tapping movements are one of the most used paradigms to investigate sensorimotor representations in the human brain. Interestingly, these movements are executed in a combination of multiple movement parameters, such as velocity, joint angles, and spatial position. In addition to the high variability of topographic surface structure, the brain activity in response to such a complex movement is difficult to compare across brains. Here, we aligned the multivoxel activation patterns of sequential finger movements into a shared representational space using hyperalignment and showed that similar information content is instantiated in a variable surface structure across subjects. In this common space, sequence encoding was revealed with above-chance level accuracy in the sensorimotor cortex. Thus, our findings suggest that despite idiosyncratic fine-grained cortical functional topographies, the human brain follows a common encoding architecture for motor control.

Importantly, we sought to describe the innate representation structure of the sequence encoding, which does not depend on previous training or experience. This implies scanning the participant's brain before any previous training session, and providing visual support indicating the sequence order to prevent high memory load and error rates[12]. Notably, studies have shown that even brief training protocols (from 30 minutes to two hours) induce learning, functional, and structural plasticity[15–17], so caution is critical when using such protocols for familiarization purposes[18,19]. Our analysis was conducted on perfectly executed trials only to avoid the effects of error monitoring and post-error behavioral adjustments. These strategies contrast with most of the previous studies and make it difficult to directly compare them with the present findings. Still, complex finger movements are known to elicit highly contralateral activity, even before motor training[12,20], yet the role of the ipsilateral sensorimotor cortex remains poorly explored. Here, caudal sensorimotor areas (central sulcus, postcentral gyrus, and postcentral sulcus) showed a clear hemispheric dominance, in contrast to the rostral areas (superior and inferior parts of the precentral sulcus, precentral gyrus).

As we predicted, the decoding model based on anatomical alignment yielded poor between-subject classification accuracies, as vertices in the same anatomical locations do not share tuning functions across individuals. Here, the hyperalignment improved accuracy for 100% of the vertices in the sensorimotor cortex, reinforcing its ability to align and reveal latent high-dimensional information across individual brains[7,8].

Our findings provide compelling evidence that, despite individual variability in cortical anatomy, the human brain expresses a shared, high-dimensional encoding architecture for complex motor sequences. This common neural code lays the groundwork for future work in personalized neurotechnologies, scalable brain-computer interfaces, and cross-subject models of motor learning and rehabilitation.

Materials and Methods

The high-field fMRI data used in this study are a publicly available dataset previously published by Berlot and colleagues[12]. Data has been acquired on a 7-Tesla Siemens Magnetom scanner with a 32-receive channel head coil

(8-channel parallel transmit). For the present study, we used fMRI data from 12 participants (8 females, mean age of 22.4, sd=2.84, sample details in SI). Data has been preprocessed using fmriprep workflow, version 23.2.1, which included realignment, temporal denoising, and coregistration.

Human subjects: Informed consent and data usage agreement have been obtained from participants before the onset of the study. It was emphasized that participants could withdraw from the study at any timepoint. The experimental procedures have been approved by the local ethics committee at Western University[12], where the data have been collected.

Acknowledgments

This work was supported by the Austrian Science Fund FWF (ESP 397-BBL), the Foundation for Research Support in the State of Rio de Janeiro (FAPERJ), and intramural grants of the D'Or Institute for Research and Education (IDOR).

References

1. Yan, Y., Goodman, J. M., Moore, D. D., Solla, S. A. & Bensmaia, S. J. Unexpected complexity of everyday manual behaviors. *Nat. Commun.* **11**, 3564 (2020).
2. Georgopoulos, A. P., Schwartz, A. B. & Kettner, R. E. Neuronal Population Coding of Movement Direction. *Science* **233**, 1416–1419 (1986).
3. Gallego, J. A., Perich, M. G., Chowdhury, R. H., Solla, S. A. & Miller, L. E. Long-term stability of cortical population dynamics underlying consistent behavior. *Nat. Neurosci*. **23**, 260–270 (2020).
4. Chehade, N. G. & Gharbawie, O. A. Motor actions are spatially organized in motor and dorsal premotor cortex. *eLife* **12**, e83196 (2023).
5. Mathis, M. W., Perez Rotondo, A., Chang, E. F., Tolias, A. S. & Mathis, A. Decoding the brain: From neural representations to mechanistic models. *Cell* **187**, 5814–5832 (2024).
6. Gallego, J. A., Makin, T. R. & McDougle, S. D. Going beyond primary motor cortex to improve brain–computer interfaces. *Trends Neurosci*. **45**, 176–183 (2022).
7. Haxby, J. V. *et al*. A Common, High-Dimensional Model of the Representational Space in Human Ventral Temporal Cortex. *Neuron* **72**, 404–416 (2011).

8. Visconti di Oleggio Castello, M., Haxby, J. V. & Gobbini, M. I. Shared neural codes for visual and semantic information about familiar faces in a common representational space. *Proc. Natl. Acad. Sci.* **118**, e2110474118 (2021).
9. Amunts, K. & Zilles, K. Architectonic Mapping of the Human Brain beyond Brodmann. *Neuron* **88**, 1086–1107 (2015).
10. Kolasinski, J. *et al.* Investigating the Stability of Fine-Grain Digit Somatotopy in Individual Human Participants. *J. Neurosci.* **36**, 1113–1127 (2016).
11. Destrieux, C., Fischl, B., Dale, A. & Halgren, E. Automatic parcellation of human cortical gyri and sulci using standard anatomical nomenclature. *NeuroImage* **53**, 1–15 (2010).
12. Berlot, E., Popp, N. J. & Diedrichsen, J. A critical re-evaluation of fMRI signatures of motor sequence learning. *eLife* **9**, 1–24 (2020).
13. Taschereau-Dumouchel, V. *et al.* Towards an unconscious neural reinforcement intervention for common fears. *Proc. Natl. Acad. Sci. U. S. A.* **115**, 3470–3475 (2018).
14. Kriegeskorte, N., Simmons, W. K., Bellgowan, P. S. F. & Baker, C. I. Circular analysis in systems neuroscience: the dangers of double dipping. *Nat. Neurosci.* **12**, 535–540 (2009).
15. Marins, T. *et al.* Structural and functional connectivity changes in response to short-term neurofeedback training with motor imagery. *NeuroImage* **194**, 283–290 (2019).
16. Tavor, I., Hofstetter, S. & Assaf, Y. Micro-structural assessment of short term plasticity dynamics. *NeuroImage* **81**, 1–7 (2013).
17. Hofstetter, S., Tavor, I., Moryosef, S. T. & Assaf, Y. Short-term learning induces white matter plasticity in the fornix. *J. Neurosci.* **33**, 12844–12850 (2013).
18. Ariani, G., Pruszynski, J. A. & Diedrichsen, J. Motor planning brings human primary somatosensory cortex into action-specific preparatory states. *eLife* **11**, (2022).
19. Nambu, I. *et al.* Decoding sequential finger movements from preparatory activity in higher-order motor regions: a functional magnetic resonance imaging multi-voxel pattern analysis. *Eur. J. Neurosci.* **42**, 2851–2859 (2015).
20. Ariani, G., Shahbazi, M. & Diedrichsen, J. Cortical Areas for Planning Sequences before and during Movement. *J. Neurosci.* **45**, e1300242024 (2025).

Figures

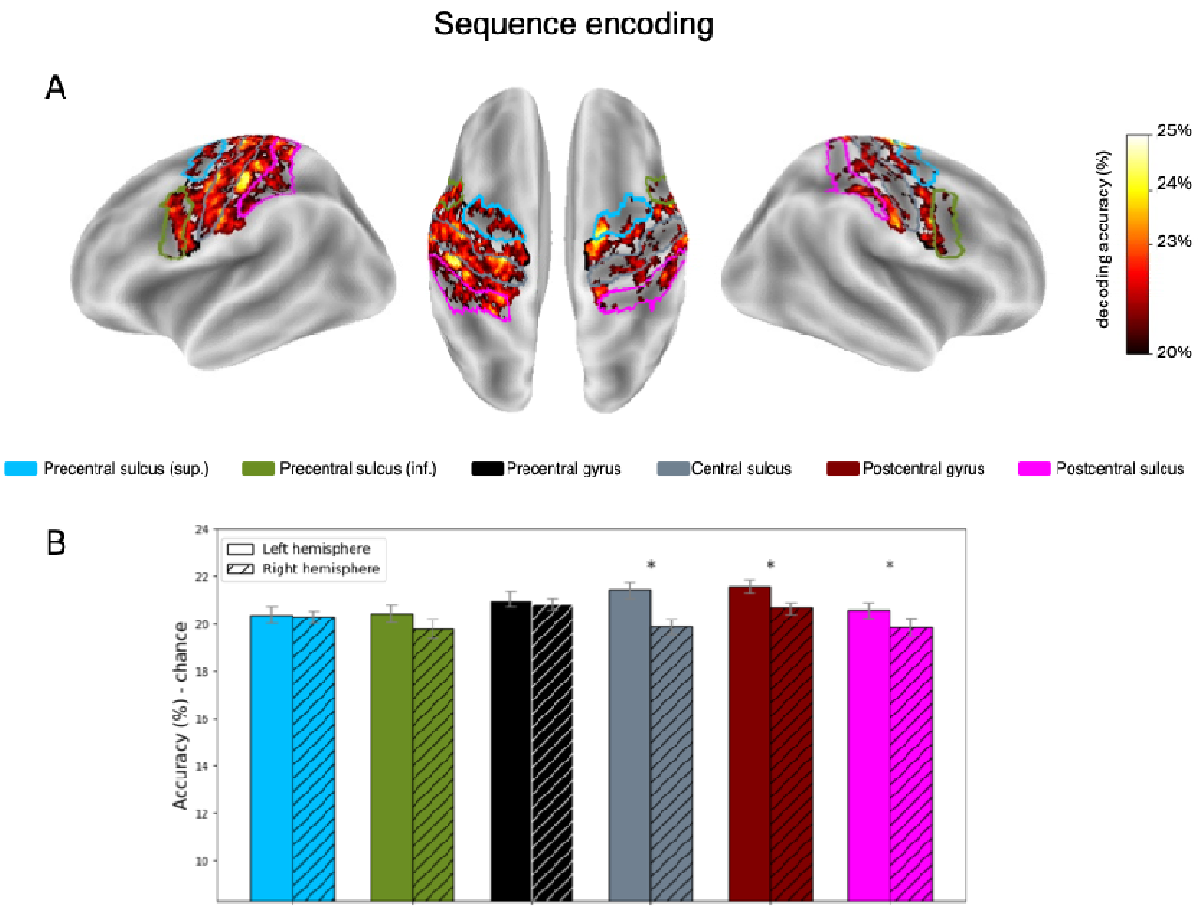

Figure 1. Results. Group-level map of between-subject classification of sequence identity (1-12). (A) The heatmap shows vertex-wise classification accuracy obtained with permutation testing and FDR correction. The chance level is 8.3%. (B) Average accuracy above chance level in each cortical label in the left and right (dashed) hemispheres. Error bars indicate standard error, stars highlight $p < 0.05$ in the *cortical label x side* comparison. All cortical labels showed above chance-level accuracy. The sensorimotor cortical areas were obtained from the Destrieux atlas[11].

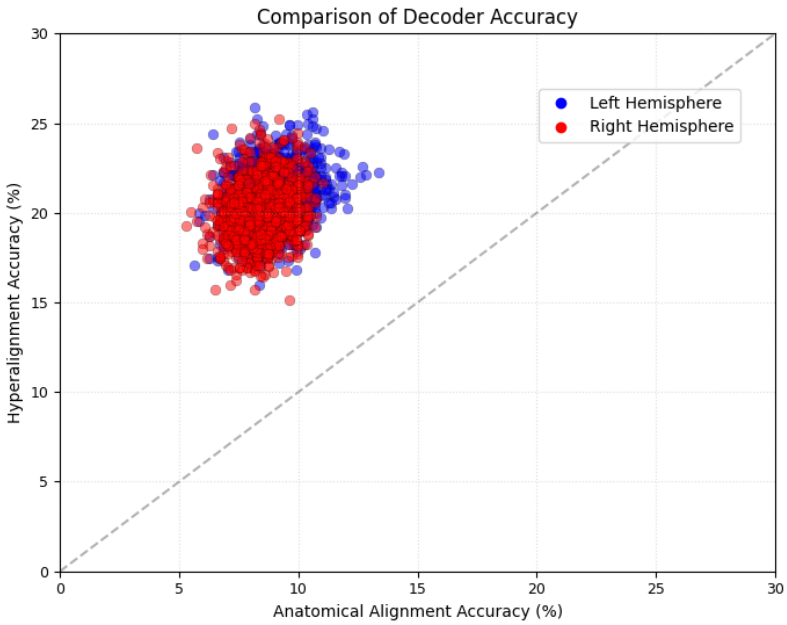

Figure 2. Comparison of decoder accuracy obtained with hyperaligned or anatomically-aligned data. All the vertices of both the left (blue) and right (red) hemispheres showed improved decoder accuracy when using hyperaligned data. The average accuracy improvement was 130% and 137% for the left and right hemispheres, respectively.