Title: A common neural architecture for encoding finger movements

Authors: Theo Marins[1], Frederico Augusto Casarsa de Azevedo[2], and Guilherme Wood[1,3]

Affiliation:

1. Institute of Psychology, University of Graz, Graz, Austria
2. McGovern Institute for Brain Research at MIT, Cambridge, United States
3. BioTechMed-Graz, Graz, Austria

Corresponding author: Theo Marins.

Email: theo.marins@uni-graz.at

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Main Text

Figure 1

Table 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 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 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 at the population level.

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 similar transformation-based methodologies. 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 constructed 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 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 labels 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 labels). 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, Table 1). Specifically, a repeated-measures ANOVA (within-subjects factors: cortical label and hemisphere) revealed a main effect of cortical label ($F(5,55) = 9.81$, $p < .001$, $\eta^2p = 0.47$), indicating that decoding accuracy varied systematically across sensorimotor brain areas (Table 2). 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 (Table 1).

We also analyzed the sequence encoding using anatomical alignment for reference. This analysis followed the same procedure as its counterpart on hyperaligned data, except that participants' functional data remained in the template surface fsaverage. The anatomical alignment-based decoding model showed limited decoding accuracy, close to chance level: average accuracies of 8.91% and 8.43% in the left and right hemispheres, respectively. A comparison of both models (Figure 2) revealed improved decoding accuracy for all vertices in both hemispheres

with the hyperalignment model, yielding absolute gains of 11.95% and 11.57% in the left and right hemispheres, respectively, more than doubling the accuracy relative to anatomically aligned data.

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 showed that similar information content is instantiated in a variable surface structure across subjects by aligning their multivoxel activation patterns into a shared representational space using hyperalignment techniques. 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, rostral sensorimotor areas (sup. and inf. parts of the precentral sulcus, precentral gyrus) did not show hemispheric dominance, in contrast to caudal areas (central sulcus, postcentral gyrus, and postcentral sulcus), which were strongly left-lateralized.

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. Consistent with previous studies[7,8], we showed that hyperalignment improved accuracy for 100% of vertices in the sensorimotor cortex.

These 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.

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Figures

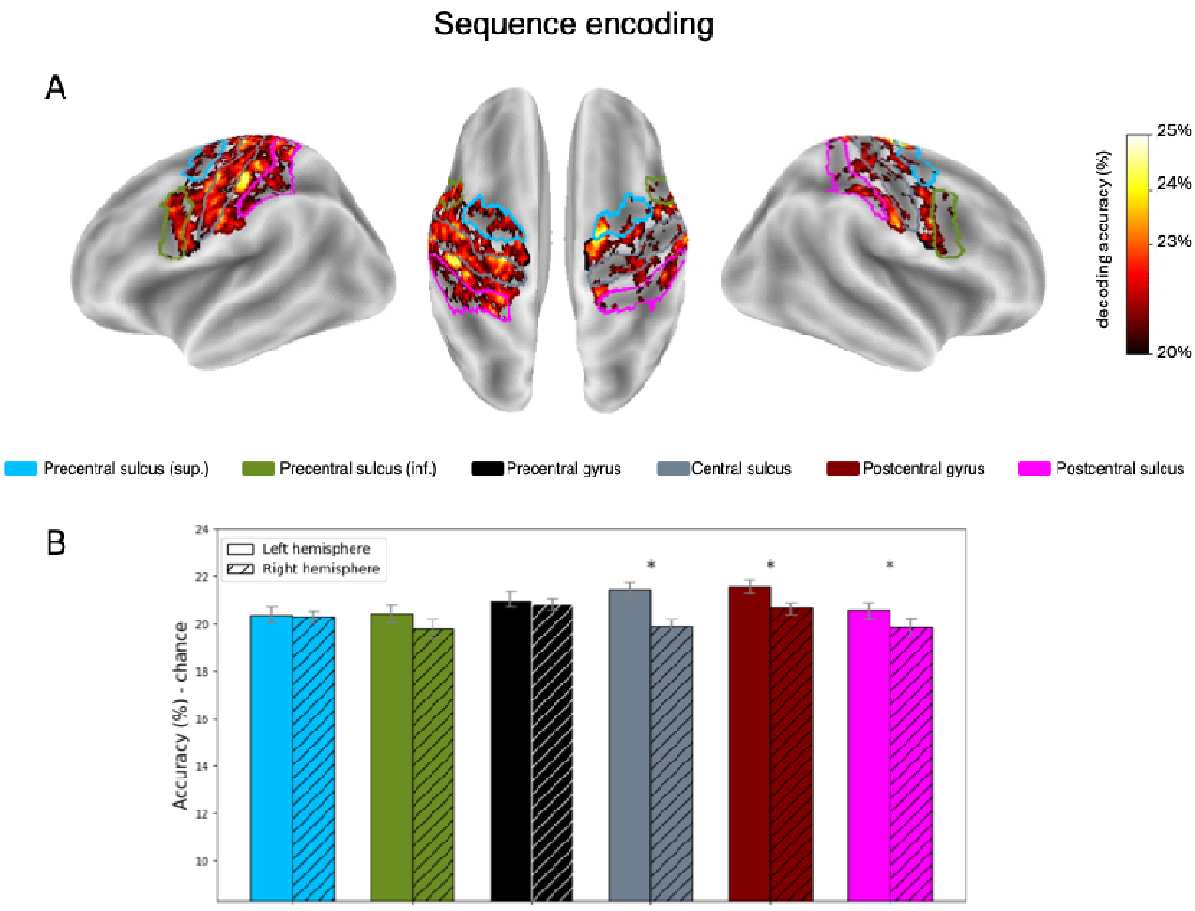

Figure 1. Results. Group-level map of between-subject classification of sequence identity (1-12). (A) The heatmap shows vertex-wise classification accuracy obtained with permutation testing and FDR correction. The chance level is 8.3%. (B) Average accuracy above chance level in each sensorimotor label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

Table 1. Descriptive decoder accuracy by cortical region and side.

Cortical label	Left		Right		Interaction Label * Side		
	Mean	**95% CI**	**Mean**	**95% CI**	**t-value**	**Cohen's *d***	**p-value**
Postcentral Sulcus*	20.57	19.89, 21.17	19.86	19.15, 20.56	2.83	0.56	0.03021
Postcentral Gyrus*	21.58	21.02, 22.14	20.66	20.11, 21.13	5.74	0.94	0.0006
Central Sulcus*	21.42	20.69, 22.03	19.9	19.37, 20.44	6.49	1.37	0.0005
Precentral Gyrus	21.03	20.43, 21.60	20.82	20.28, 21.29	1.44	0.2	0.2185

Precentral Sulcus (inf.)	20.42	19.75, 21.12	19.79	19.04, 20.52	2	0.48	0.1029
Precentral Sulcus (sup.)	20.36	19.69, 21.01	20.29	19.82, 20.78	0.23	0.07	0.819

*Cortical labels that showed a statistically significant effect of side in a *post hoc* comparison after FDR correction. Inf: inferior part; sup: superior part; CI: confidence interval; sd: standard deviation; p-value: FDR-corrected p-value.

Table 2. Post-hoc test of the main effect of cortical label

Label comparison		Cohen's d	p-value
Postcentral Gyrus	Central Sulcus	0.464509	0.004586
Postcentral Gyrus	Postcentral Sulcus	0.853103	0.000754
Postcentral Gyrus	Precentral sulcus (inf.)	0.945732	0.000532
Postcentral Gyrus	Precentral sulcus (sup.)	0.851834	0.005721
Precentral Gyrus	Postcentral Sulcus	0.65283	0.015807
Precentral Gyrus	Precentral sulcus (inf.)	0.744105	0.000532
Precentral Gyrus	Precentral sulcus (sup.)	0.621379	0.005721
Central Sulcus	Precentral sulcus (inf.)	0.496841	0.015601

P-values are FDR-corrected. Only the significant comparisons are shown.

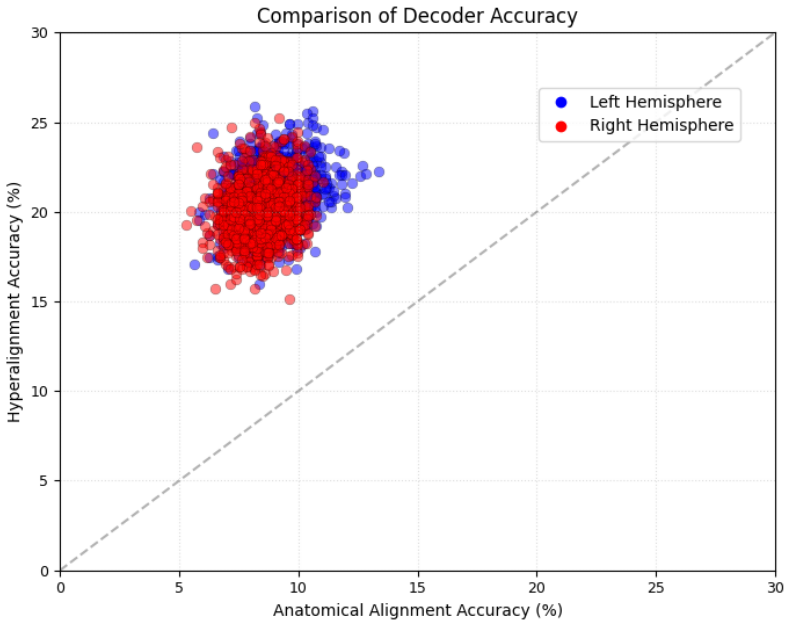

Figure 2. Comparison of decoder accuracy obtained with hyperaligned or anatomically-aligned data. All the vertices of both the left (blue) and right (red) hemispheres showed improved decoder accuracy when using hyperaligned data. The average accuracy improvement was 11.95% and 11.57% for the left and right hemispheres, respectively.