1	Cortical areas for planning sequences before and during movement		
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9			
10	Abbreviated title. Planning sequences before and during movement		
11			
12	Number of pages: 24		
13	Number of figures: 4		
14	Number of tables: 1		
15	Number of words for abstract: 201 / 250		
16	Number of words for introduction: 573 / 650		
17	Number of words for discussion: 965 / 1500		
18			
19	Author contributions. G.A. and J.D. designed research; G.A. performed research; M.S. and G.A. analyzed data;		
20	All authors drafted and edited the manuscript.		
21			
22	Acknowledgments. This work was supported by a Discovery Grant from the Natural Sciences and Engineering		
23	Research Council of Canada (NSERC, RGPIN-2016-04890) and a project grant from the Canadian Institutes of		
24	Health Research (CIHR, PJT-175010) to J.D., and the Canada First Research Excellence Fund (BrainsCAN).		
25			
26	Disclosures. The authors declare no conflicts of interest.		

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28 Abstract

29 Production of rapid movement sequences relies on preparation before (pre-planning) and during (online planning) 30 movement. Here, we asked how different cortical sensorimotor areas contribute to these processes. Human participants performed three single-finger and three multi-finger sequences in a delayed movement paradigm. 31 32 During preparation, 7T functional MRI revealed that primary motor (M1) and somatosensory (S1) areas showed pre-activation of the first movement, even though the overall activation level did not change from baseline. During 33 production, the activity in M1 and S1 could be explained by temporal summation of activity patterns 34 35 corresponding to constituent fingers. In contrast, dorsal premotor (PMd) and anterior superior parietal lobule 36 (aSPL) showed substantial activation during preparation of multi-finger as compared to single-finger sequences. 37 The same regions were also more activated during production of multi-finger sequences, suggesting that the same areas are involved in both pre- and online planning. Nonetheless, we observed small but robust differences 38 between the two contrasts, suggesting preferential involvements of these areas in pre- and online planning. 39 Multivariate analysis revealed sequence-specific representations in both PMd and aSPL, which remained stable 40 across both preparation and production phases. This suggests that these areas maintain a sequence-specific 41 representation before and during sequence production, likely guiding the execution-related areas. 42

43 Keywords

44 Sequential movements; Motor planning; Hand control; fMRI; MVPA.

45 Significance Statement (120 max)

Understanding how the brain orchestrates complex behavior remains a core challenge in human neuroscience. 46 Here, we combine high-resolution neuroimaging and a carefully crafted design to study the neural control of rapid 47 sequential finger movements, like typing or playing the piano. Advancing prior research, we show that the brain 48 areas involved in planning these movements maintain those representations throughout the execution of the 49 50 sequence. This representational stability across planning and execution suggests an intricate connection between these processes. Our results shed light on the nuanced contributions of different cortical areas to different aspects 51 of coordinating skilled movement. This work is well placed to inform future research in animal models and the 52 53 development of targeted interventions against movement disorders.

54 Introduction (650 max)

From buttoning a shirt to texting with a smartphone, many everyday actions depend on the brain's ability to coordinate rapid sequences of finger movements. Behavioral studies have demonstrated that, when tasked to produce a sequence of multiple finger presses, participants pre-plan the first two or three elements before sequence production starts (Ariani & Diedrichsen, 2019; Ariani et al., 2021). Once the sequence starts, planning the upcoming movements continues throughout sequence production, a process called online planning. Most

behavioral improvements during motor sequence learning can be explained by participants becoming faster at
 pre- and online planning (Ariani & Diedrichsen, 2019). Which, and how, different cortical motor areas contribute
 to these different aspects of motor sequence planning, however, is poorly understood.

Previous neuroimaging studies of motor sequences have used multivariate analysis of fMRI data to reveal 63 64 a hierarchy of sequence representations across cortical motor areas (Berlot et al., 2020; Yokoi et al., 2018; Yokoi 65 & Diedrichsen, 2019). The dorsal premotor cortex (PMd) and the superior parietal lobule (SPL) exhibit sequencespecific representations, i.e., activity patterns that encode the specific sequence of actions, not just the individual 66 67 movements themselves. Sequence-specific representations in association cortex have also been shown using 68 electrophysiology in non-human primates (Russo et al., 2020; Shima et al., 2006; Tanji & Shima, 1994). In 69 contrast, activity patterns in the primary motor (M1) and somatosensory cortex (S1) could be explained by a summation of the patterns related to the individual finger presses (Berlot et al., 2021; Yokoi et al., 2018). Due to 70 71 difficulties related to fMRI temporal resolution, however, this work did not distinguish between activity arising 72 from sequence planning or execution. Although Gallivan et al. (2016) showed that sequences of two upper-limb actions (e.g., reaching to grasp and place vs. hold a cup) could be distinguished from preparatory fMRI activity 73 74 patterns, but the nature of these representations remains unknown.

Here, we used high-field (7T) fMRI while human participants planned and executed both multi- and single-finger sequences on a keyboard device (matched number of keypresses across sequences). A delayedmovement paradigm with no-go trials (Ariani et al., 2018) allowed us to isolate brain activity related to planning and execution and address the following three questions about the role of cortical areas in sequence planning.

First, we investigated brain responses in primary sensorimotor cortex (M1 and S1) during the preparation of a sequence. For single-finger actions, we have previously shown that movement planning pre-activates the relevant finger-specific activity pattern in both M1 and S1 (Ariani et al., 2022). But what is the preparatory state in M1 for multi-finger movements?

83 Second, recent behavioral studies suggest that online planning of movement sequences shares important 84 behavioral features with sequence pre-planning—both exhibit a similar planning horizon and both contribute to 85 performance improvements with sequence learning (Ariani & Diedrichsen, 2019; Ariani et al., 2021). We 86 therefore tested to what degree pre- and online planning engage the same cortical areas by contrasting multi- and 87 single-finger movements during preparation and production phases.

Finally, employed multi-variate analysis to study two of the identified brain regions, PMd and SPL, in more depth. Previous results (Berlot et al., 2021; Yokoi & Diedrichsen, 2019) have revealed sequence-specific representations in both. Our paradigm now allowed us to ask whether these representations are present only during preparation or whether they persist during movement production. Furthermore, we investigated to what degree the sequence-specific representations underlying pre- and online planning are the same, or whether they dynamically change from preparation to production.

94 Materials and Methods

95 Participants

Twenty-three right-handed neurologically healthy participants volunteered to take part in the experiment (13 F, 96 97 10 M; age 20-31 years, mean 23.43 years, SD 4.08 years). Criteria for inclusion were right-handedness and no prior history of psychiatric or neurological disorders. Handedness was assessed with the Edinburgh Handedness 98 99 Inventory (mean 82.83, SD 9.75). All experimental procedures were approved by the Research Ethics Committee at Western University. Participants provided written informed consent to procedures and data usage and received 100 monetary compensation for their participation. One participant withdrew before study completion and was 101 excluded from data analysis (final N = 22). A part of the data used in the current paper was previously published 102 103 (Ariani et al., 2022).

104 Apparatus

Sequences of right-hand finger presses were performed on a custom-made MRI-compatible keyboard device (Fig. 1A). Participants used their fingers to press the keys. The keys of the device did not move, but force transducers underneath each key measured isometric force production at an update rate of 2 ms (Honeywell FS series; dynamic range 0-25 N). A keypress/release was detected when the force crossed a threshold of 1 N. The forces measured from the keyboard were low pass filtered to reduce noise induced by the MRI environment, amplified, and sent to the PC for online task control and data recording.

111 Task

We used a task in which participants produced sequences of keypresses with their right-hand fingers in response to numerical cues (Fig. 1B) presented on a computer screen that was visible to the participants lying in the scanner through an angled mirror. On each trial, a string of 6 numbers (instructing cue) instructed which sequence to plan (Fig. 1C, white outline).



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Figure 1. Sequence conditions and task timing. (A) Response keyboard with mapping between numbers and fingers. Numbers were not visible on the keys. (B) Digits presented on the screen for single-finger (red) and multifinger sequences (blue). (C) Temporal structure of a trial. During the preparation phase, a sequence of 6 numbers was displayed within a box at the top of the screen. With a probability of 0.6, the box frame then changed to a blue color, instructing participants (N=22) to produce the memorized sequence as fast as possible (go trials). Each correct press caused an asterisk to turn green. With 0.4 probability, the box frame turned orange, signaling participants to withhold the response (no-go trials). ITI = inter-trial interval.

The length of the preparation phase was randomly sampled to be 4 s (56% of trials), 6 s (30%), or 8 s (14%). To control for involuntary overt movements during the preparation phase, we required participants to maintain a steady force of around 0.25 N on all the keys during the delay, which was closely monitored online. As a visual aid, we displayed a red area (between 0 and 0.5 N) and asked participants to remain in the middle of that range with all the fingers (touching either boundary of the red area would count as unwanted movement, thus incurring an error).

130 At the onset of the production phase, participants received a color cue (go/no-go cue) indicating whether to perform the planned finger presses (blue outline = go, p = 0.6) or not (orange outline = no-go, p = 0.4). The 131 132 role of no-go trials was to dissociate the hemodynamic response to the successive preparation and production events, which would otherwise always overlap in fast fMRI designs due to the sluggishness of the fMRI response. 133 To encourage planning during the delay period, at the go cue, the digits were masked with asterisks at go-cue 134 onset, and participants had to perform the presses from memory. Participants had 2.5 s to complete the sequence 135 136 of 6 presses, and a vanishing white bar under the asterisks indicated how much time was left. Participants received online feedback on the correctness of each press with asterisks turning either green, for a correct press or red, for 137

incorrect presses. As long as the participants remained within task constraints (i.e., 6 keypresses in less than 2.5
s), an exact movement speed was not enforced. In no-go trials, participants were instructed to remain as still as
possible, maintaining the finger pre-activation until the end of the production phase (i.e., releasing any of the keys
would incur an error).

During the reward phase (0.5 s), points were awarded based on performance and according to the following scheme: -1 point in case of no-go error or go cue anticipation (timing errors); 0 points for pressing any wrong key (press error); 1 point in case of a correct no-go trial; and 2 points in case of a correct go trial.

145 Inter-trial-intervals (ITI, gray background) were randomly drawn from $\{1, 2, 4, 8, 16 s\}$ with the respective 146 proportion of trials $\{52\%, 26\%, 13\%, 6\%, 3\%\}$.

147 Experimental design and structure

Our chosen distribution of preparation times, inter-trial intervals, and no-go trials were determined by minimizing 148 the variance inflation factor (VIF). VIF is the ratio of the mean estimation variance of all regression weights 149 (preparation- and production-related regressors for each sequence) to the mean estimation variance had these 150 regressors been estimated in isolation. Therefore, VIF quantifies the severity of multicollinearity between model 151 regressors by providing an index of how much the variance of an estimated regression coefficient is increased 152 because of collinearity. Large values for VIF mean that model regressors are not independent of each other, 153 whereas a VIF of 1 means no inflation of variance. After optimizing the design, VIF was on average 1.15, 154 indicating that we could separate planning and execution-related activity without a large loss of experimental 155 156 power.

Participants underwent one fMRI session consisting of 10 functional runs and 1 anatomical scan. In an 157 event-related design, we randomly interleaved 3 types of repeated single-finger presses involving the thumb (1), 158 the middle (3), and the little (5) fingers (e.g., 111111 for thumb presses, Fig. 1B) and 3 types of multi-finger 159 sequences (e.g., 135315). The day before the fMRI scan, participants familiarized themselves with the 160 experimental apparatus and the go/no-go paradigm in a short behavioral session of practice outside the scanner 161 (5 blocks, about 15-30 minutes in total). For the behavioral practice, inter-trial intervals were kept to a fixed 1 s 162 to speed up the task, and participants were presented with different sequences from what they would see while in 163 the scanner. These 6-item sequences were randomly selected from a pool of all possible permutations of the 164 numbers 1, 3, and 5, with the exclusion of sequences that contained consecutive repetitions of the same number. 165 Each sequence trial type (e.g., 111111) was repeated 5 times (2 no-go and 3 go trials), totaling 30 trials per 166 functional run. Two periods of 10 seconds rest were added at the beginning and at the end of each functional run 167 to allow for signal relaxation and provide a better estimate of baseline activation. Each functional run took about 168 5.5 minutes, and the entire scanning session (including the anatomical scan and setup time) lasted for about 75 169 minutes. 170

171 Imaging data acquisition

High-field functional magnetic resonance imaging (fMRI) data were acquired on a 7T Siemens Magnetom 172 scanner with a 32-channel head coil at Western University (London, Ontario, Canada). The anatomical T1-173 weighted scan of each participant was acquired halfway through the scanning session (after the first 5 functional 174 175 runs) using a Magnetization-Prepared Rapid Gradient Echo sequence (MPRAGE) with a voxel size of $0.75 \times 0.75 \times 0.75$ mm isotropic (field of view = 208 x 157 x 110 mm, encoding direction coronal). To measure the 176 blood-oxygen-level dependent (BOLD) responses in human participants, each functional scan (330 volumes) used 177 the following sequence parameters: GRAPPA 3, multi-band acceleration factor 2, repetition time [TR] = 1.0 s, 178 echo time [TE] = 20 ms, flip angle [FA] = 30 deg, slice number: 44, voxel size: 2x2x2 mm isotropic. To estimate 179 and correct for magnetic field inhomogeneities, we also acquired a gradient echo field map with the following 180 parameters: transversal orientation, a field of view: 210 x 210 x 160 mm, 64 slices, 2.5 mm thickness, TR = 475 181 ms, TE = 4.08 ms, FA = 35 deg. 182

183 Preprocessing and univariate analysis

Preprocessing of the functional data was performed using SPM12 (fil.ion.ucl.ac.uk/spm) and custom MATLAB 184 code. This included correction for geometric distortions using the gradient echo field map (Hutton et al., 2002), 185 and motion realignment to the first scan in the first run (3 translations: x, y, z; 3 rotations: pitch, roll yaw). Due 186 to the short TR, no slice timing corrections were applied. The functional data were co-registered to the anatomical 187 scan, but no normalization to a standard template or smoothing was applied during preprocessing. To allow 188 magnetization to reach equilibrium, the first four volumes of each functional run were discarded. The pre-189 processed images were analyzed with a general linear model (GLM). We defined separate regressors for each 190 combination of the 6 finger-actions (single, multi) x 3 phases (preparation go, preparation no-go, production), 191 resulting in a total of 18 regressors (12 go + 6 no-go), plus the intercept, for each run. We also conducted an 192 analysis where the same preparation regressor was used in go and no-go, which resulted in qualitatively similar 193 as reported here. For the main text, however, we decided to be conservative and not use the regressors for the 194 preparation of go trials, thereby controlling for a residual bias from the execution-related activity onto the 195 196 preceding planning-related activity. Each regressor consisted of boxcar functions of length 2s convolved with a two-gamma canonical hemodynamic response function with a peak onset at 5 s and a post-stimulus undershoot 197 minimum at 10 s. Given the relatively low error rates (i.e., number of error trials over the total number of trials, 198 timing errors: 7.58 ± 0.62 %; press errors: 1.18 ± 0.26 %; see Task above), all trials were included to estimate 199 the regression coefficients, regardless of whether the execution was correct or erroneous. Ultimately, the first-200 level analysis resulted in activation images (beta maps) for each of the 18 conditions per run, for each of the 201 participants. 202

203 Surface reconstruction

Based on the 0.75mm anatomical scan, we reconstructed each individual cortical surface. Individual participants' 204 cortical surfaces were reconstructed using Freesurfer (Dale et al., 1999). First, we extracted the white-gray matter 205 and pial surfaces from each participant's anatomical image. Next, we inflated each surface into a sphere and 206 207 aligned it using sulcal depth and curvature information to the Freesurfer average atlas (Fischl et al., 1999). Subsequently, surfaces were resampled to a left-right symmetric template (fs LR.164k.spec; Van Essen et al., 2082012) included in the connectome workbench distribution (Marcus et al., 2011). The functional imaging data 209 (2mm resolution) was then mapped onto this surface. In this analysis we excluded voxels that lay within the sulci 210 and touch both banks (with more than 25% of the voxel volume in the grey matter on both sides sulcus). The 211 individual surface maps were brought into alignment by morphing the surfaces based on the depth and curvature 212 (van Essen et al., 2012). This approach is currently the state-of-the-art in imaging analysis to achieve the best 213 regional specificity of group analysis despite the considerable inter-subject variability in cortical folding. 214

215 Regions of interest (ROI)

We focused our imaging analysis on the dorsolateral aspect of the contralateral (left) hemisphere (purple area of Fig. 2A), including the motor regions of the medial wall.

To summarize the results and for statistical analysis, we have used a set of motor-related ROIs on the 218 cortical surface that we have used consistently in previous papers (Ariani et al., 2022; Berlot et al., 2020, 2019; 219 Jörn Diedrichsen et al., 2013; Yokoi et al., 2018). The definition relies on a post-mortem cytoarchitectonic 220 analysis of 10 human brains (Fischl et al., 2008) that were normalized into a spherical (surface-based) group atlas. 221 In comparison to a volume-based normalization of the same maps (Eickhoff et al., 2007), this approach leads to 222 a cleaner separation of cortical areas. One of the limitations of such ROI-based approaches is potentially 223 224 combining functional heterogeneous regions into a single ROI. For the current paper, we therefore chose a more refined approach that allows us to study differences in function within these ROIs in a more continuous manner, 225 while still summarizing the data better than the map-wise approach. 226

For visualization of the functional profiles along the cortical surface, we defined an anterior-posterior line 227 through the anatomically defined hand-knob (Yousry et al., 1997) that ran approximately orthogonal to the 228 boundaries between different Brodmann areas (BA; Fischl et al., 2008). By extending the line ±20 mm above and 229 below the line, we defined a strip of surface area in each hemisphere that mainly captures the hand area of M1 230 and S1 (white area in Fig. 2B). We subdivided this area into 50 vertical sections running from anterior to posterior. 231 allowing us to summarize the result on a one-dimensional profile-view (e.g., Fig 2G,H; Fig. 3E,F). For statistical 232 analysis only, we combined results by major region (grouping vertical sections together) according to the 233 cytoarchitectonic probabilistic atlas. We defined the region of interest for the primary motor cortex (M1; BA4), 234 primary somatosensory cortex (S1; BA 1, 2, and 3), dorsal premotor cortex (PMd; BA 6), and the anterior parietal 235

lobules (aSPL; BA 5) by selecting the strips that had the highest probability (averaged over all vertices within the
strip) as determined by a probabilistic cytoarchitectonic atlas (Fischl et al., 2008) of belonging to their respective
BA. The supplementary motor areas (SMA) lay outside of the defined strip of surface area. We therefore defined
the SMA ROI by choosing the part of BA6 that was situated in the medial wall.

ROI-based analyses were conducted in the space of the individual data acquisition for each individual participant by determining the voxel that would be projected onto the set of surface nodes associated with each ROI. In this analysis (as well as for surface-based mapping), we excluded voxels with more than 25% of their volume in the grey matter on the opposite side of a sulcus. This avoided cross-contamination of activity measured in M1 and S1, as well as across the pre-central and post-central sulcus. No smoothing of functional activity in the volume was applied. This approach has allowed us in one previous paper to carefully analyze the specialization of subregions of human S1 and M1 (Arbuckle et al., 2022).

247 Analysis of activation

We calculated the percent signal change for each condition relative to the baseline activation for each voxel for each functional run and averaged it across runs. For ROI analysis, these values were averaged across all voxels in the native volume space of each participant selected for the respective ROI. For surface-based group maps, individual data were projected onto the group map via the individual surfaces, using all voxels touching the line that connected corresponding nodes on the pial and white-matter surfaces.

Statistical analyses to assess the cortical activity of each sequence type during each phase of preparation or production included a two-sided one-sample t-test vs. zero. For statistical tests on the surface, we used an uncorrected threshold of p=0.001 and controlled the family-wise error by calculating the size of the largest suprathreshold cluster across the entire cortical surface (estimated smoothness of FWHM 7.9 mm) that would be expected by chance (p=0.05) using Gaussian field theory as implemented in the fmristat package (Worsley et al., 1996).

259 Multivariate distance analysis

To evaluate which brain areas displayed sequence-specific representations, we used the representational similarity 260 analysis (Kriegeskorte & Diedrichsen, 2019). We calculated the cross-validated Mahalanobis distances (Walther 261 et al., 2016) between evoked regional patterns (beta estimates from first-level GLM) of different pairs of 262 conditions, 6 sequences (3 single, 3 multi) x 2 phases (preparation no-go, production). Prior to calculating the 263 distances, beta weights for each condition were spatially pre-whitened (i.e., weighted by the matrix square root 264 he noise covariance matrix, as estimated from the residuals of the GLM). The noise covariance matrix was of t 265 slightly regularized towards a diagonal matrix (Ledoit & Wolf, 2003). Multivariate pre-whitening has been shown 266 267 to increase the reliability of dissimilarity estimates (Walther et al., 2016).

Cross-validation ensures the distance estimates are unbiased, such that if two patterns differ only by measurement noise, the mean of the estimated value would be zero (Diedrichsen et al., 2020). This also means that estimates can sometimes become negative. Therefore, dissimilarities significantly larger than zero indicate that the two patterns are reliably distinct, akin to an above-chance performance in a cross-validated pattern classification analysis.

Multivariate analysis was conducted for ROI and surface analysis. For surface-based maps, we also conducted a searchlight analysis (e.g., Fig 3A). For each surface node, we selected a circular region of 100 voxels (with a maximal radius of 12 mm) and assigned the result to the central node of the searchlight.

276 **Dispersion metric**

To determine whether there were significant differences in the dispersion of the representations for multi- and single-finger sequences during preparation, we first set all negative dissimilarity values to 0. We then normalized the dissimilarities for each sequence type such that all vertices' dissimilarities in the white strip (Fig. 2A) summed up to 1. This defined the weight of each surface vertex. The center-of-gravity (COG) per participant was then the weighted average of the x and y coordinates of these vertices on the flat map. Then, we calculated the dispersion (*d*) around this COG by calculating the squared distance between each vertex and COG and averaging them weighted by w_i .

$$d = \sum_{i \in vertices} w_i \left[(x - COG_x)^2 + (y - COG_y)^2 \right]$$

The difference in dispersion between multi- and single-finger sequences was assessed using a two-sided paired ttest.

287 Correlation analysis

To assess the relationship between planning and execution-related activity, we estimated the correlation between 288 them. For estimation, we employed two different approaches. First, we used simple Pearson's correlation. When 289 estimating the correlation between sequence-specific activity patterns, we first removed the mean pattern for the 290 preparation and production phase. We then stacked the three activity patterns into a single vector. The average 291 (across runs) activity patterns for preparation and production were correlated directly. When estimating the 292 correlation between multi vs. single contrasts across preparation and production, we first calculated the difference 293 between activity patterns of 3 multi-finger sequences and the corresponding single-finger movements (i.e., 294 sequence 135351 with 111111, etc.) and then averaged the three maps. The average (across runs) difference maps 295 for preparation and production were then correlated directly. Correlations were calculated separately within each 296 297 participant. To test for a positive correlation, we performed a two-sided paired t-test against zero.

To obtain an estimate of the correlation, corrected for the level of measurement noise, we used pattern component modelling (PCM, Diedrichsen et al., 2018). The problem with Pearson's correlations estimated on the

noisy data is that they are always smaller than 1, even if the underlying patterns are identical. PCM solves this 300 issue by modelling the noise and true pattern separately and estimating the likelihood of the data given any value 301 of correlation (Diedrichsen et al., 2023). We created 100 correlation models with correlations in the range [0–1] 302 in equal step sizes and assessed the likelihood of the observed data from each participant under each correlation 303 model (Fig. 4C). First, we used the winning model as an estimate of the noise-corrected correlation (maximum-304 likelihood estimate). To test whether two sets of activity patterns are identical, we compared the likelihood of the 305 best-fitting model within each participant to the likelihood of a competing correlation model (r=1), using a two-306 sided paired Wilcoxon signed-rank test. The choice of the best-fitting model was acquired using a cross-validated 307 308 approach, estimating the group-winning model from n-1 participants, and determining the log-likelihood of this 309 model for the left-out participant (for whom this model may not be the best one).

310 Analysis of principal components

To test if the activity patterns for the difference between multi- and single-finger sequences across preparation 311 production are systematically different in some brain regions, we employed principle competent analysis 312 (PCA). The simple contrast between the two difference maps could not answer this question because they have 313 different scales. We obtained the multi vs. single contrast during preparation and production averaged across 314 sequences for all voxels within the region of interest (Fig. 2A, purple area). For each individual, we then 315 conducted a singular value decomposition on the 2xP matrix, in which the two rows represented the preparation 316 and production contrasts. The first PC captured the common neural activity shared by processes happening during 317 preparation and production while accounting for the differing degrees of activation in specific voxels. The second 318 PC represented the tendency of each voxel to be relatively more engaged during one process than the other. We 319 ensured that for each participant the positive value on the second PC represented relatively more engagement 320 during the production phase. Lastly, we projected the value for each voxel to the nearest vertex and created a 321 preference map. These maps were then submitted to a surface-based group analysis (see above). 322

323 Results

324 Pre-planning of multi-finger sequences activates the first finger in M1 and S1

First, we asked what processes occur during sequence preparation in the core sensorimotor areas S1 and M1. For single-finger movements (Fig. 2C), BOLD activity in these regions was suppressed relative to rest (Fig. 2G; M1: $t_{21}=-6.939$, p=7.4e-07; S1: $t_{21}=-5.508$, p=1.8e-05). For multi-finger movements (Fig. 2E), we also observed some suppression deep in the central sulcus, however, averaged across the ROI, the activation was not different from the resting baseline (M1: $t_{21}=-0.692$, p=0.496; S1: $t_{21}=-0.523$, p=0.606).

We then used multi-voxel pattern analysis to examine whether the fine-grained pattern of activity in these areas differed between the planned sequences. To this end, we calculated cross-validated Mahalanobis distances

(Diedrichsen et al., 2020; Walther et al., 2016) between the activity patterns associated with the 3 sequences. Systematically positive values of this measure indicate reliable multivariate pattern differences. As previously reported (Ariani et al., 2022), we found that during the preparation of single-finger movements (Fig. 3A), the core hand areas of M1 and S1 exhibited finger-specific activity patterns (M1: $t_{21}=2.343$, p=0.029; S1: $t_{21}=3.137$, p=0.005). Analysis of multi-finger sequences revealed a similar result: although M1 and S1 were not activated overall, there were significant differences between activity patterns for three sequences (Fig. 3E; M1: $t_{21}=2.991$, p=0.007; S1: $t_{21}=2.829$, p=0.010).





Figure 2. Premotor and superior parietal lobule are activated during sequence preparation. (A) inflated cortical surface of the contralateral (left) hemisphere, highlighting the displayed areas (B-F, purple). **(B)** Flat

representation of the neocortex with major sulci indicated by white dotted lines, and the boundaries of different 342 regions indicated by black dashed lines. The strip highlighted in white was used for the profiles (G, H) and region-343 of-interest definition. (C) Group-averaged percent signal change during preparation and (D) production of 344 single-finger sequences. (E.F) Same as (C.D) but for multi-finger sequences. (G) Profile ROI analysis (see 345 Materials and methods) of the mean percent signal change (\pm standard error of the mean [SEM]) during the 346 preparation and (H) production of single-finger (red) and multi-finger sequences (blue). The x-axis corresponds 347 to Brodmann areas (BA) shown in (B). **p < 0.01, ***p < 0.001 in a two-sided one-sample t-test vs. zero for 348 selected ROIs. Vertical black lines mark the approximate boundaries between the BAs (see Methods). Black 349 triangles point to the approximate location of the main anatomical landmark. Sulci: superior frontal sulcus (SFS). 350 inferior frontal sulcus (IFS), precentral sulcus (Pre-CS), central sulcus (CS), post central sulcus (Post-CS), intra-351 parietal sulcus (IPS), lateral occipital sulcus (LOS), superior temporal sulcus (STS), ROIs: anterior superior-352 parietal lobule (aSPL, BA 5), primary somatosensory cortex (S1, BA 3, 1, 2), primary motor cortex (M1), dorsal 353 premotor cortex (PMd, BA 6), secondary motor area (pre-SMA and SMA, BA 6). 354

What do these activity differences for multi-finger sequences reflect? One possibility is that during 355 sequence preparation, the first element of the sequences is pre-activated in M1. Because each sequence started 356 357 with a different finger, this would cause large differences between the activity patterns without constituting a sequence representation. This idea predicts that the activity pattern during preparation should correlate with the 358 activity pattern observed when only the first finger movement is pressed. To test this, we correlated the 359 preparation activity of 3 multi-finger sequences with the production activity of the corresponding single-finger 360 sequences (i.e., sequence 135351 with 111111, etc.) after subtracting the mean activity pattern. This analysis 361 revealed a significant correlation in both M1 (average r=0.043, $t_{21}=2.366$, p=0.027) and S1 (r=0.047, $t_{21}=2.285$, 362 p=0.032) but not in PMd ($t_{21}=-1.227$, p=0.233) and aSPL ($t_{21}=-0.242$, p=0.811) with the values of correlation 363 being significantly larger in M1/S1 than PMd/aSPL (t_{21} =3.068, p=0.005). While these correlations are very small, 364 correlation estimated on noisy data consistently underestimate the true correlation (Diedrichsen et al., 2023). To 365 account for measurement noise in a principled way, we used Pattern Component Modeling (PCM, see Methods) 366 to build potential models of the correlation between activity patterns for the preparation of multi-finger sequences 367 and production of single-finger sequences and evaluate the likelihood of the data given each model. We removed 368 the average activity pattern common to all sequences from the patterns (separately for multi- and single-finger 369 sequences), and then correlated the patterns across the two conditions. The group maximum-likelihood estimates 370 of correlation indicated substantial correspondence with r=0.40 for S1 and r=0.34 for M1. Thus, there is 371 372 substantial overlap between the patterns during pre-planning of multi-finger sequences and the patterns during the execution of the first finger in the sequence. 373

In previous studies, we have found that the activity patterns in M1 and S1 (averaged over preparation and production phases) can be explained by a temporal summation of the patterns related to the individual finger

presses, with an especially high weight from the first finger in the sequence (Berlot et al., 2021; Yokoi et al., 2018). If this weighting is due to the pre-activation of the first finger during movement preparation, we would predict that the pattern differences between sequences should disappear during the execution phase, as all three involved the same three fingers (albeit in a different order). Indeed, the pattern differences were significantly attenuated during the production phase (Fig. 3D, planning vs. execution in M1: $t_{21}=2.123$, p=0.0458, and S1: $t_{21}=2.305$, p=0.0345), with a small pattern difference remaining only in M1 ($t_{21}=2.814$, p=0.0104).

In sum, these results are consistent with the idea that the first finger in a sequence is pre-activated during the preparation phase and that after production starts, the activity pattern in M1 and S1 are determined by a temporal summation of the patterns related to the individual finger presses (Yokoi et al., 2018).

385 *Pre- and online planning engage a highly overlapping set of cortical areas*

If the activity patterns in the M1 and S1 are related to the individual finger presses, then continuous input from 386 higher-level regions that retain a representation of the entire sequence is required to move reliably from finger to 387 finger. We refer to this process as planning, whether it occurs before (pre-planning) or after movement onset 388 (online planning; Ariani & Diedrichsen, 2019; Ariani et al., 2021). Here investigate whether pre- and online 389 planning engage exactly the same, or different sets of cortical areas. Given that the number, speed, and force of 390 the finger presses were closely matched across single and multi-finger movements (Table 1), we assumed that 391 both conditions involve similar execution-related processes. Therefore, the difference between the production of 392 single-finger and multi-finger sequences should mostly reflect activity related to online planning. If pre-planning 393 and online planning involve the exact same cortical areas, then this difference should be similar to the difference 394 between single-finger and multi-finger movement during preparation (reflecting the need for increased pre-395 396 planning).

	Single-finger	Multi-finger	Difference
ET [ms]	1450 ± 58	1370 ± 70	t ₂₁ =1.815, p=0.083
Force [N]	1.7 ± 0.1	1.8 ± 0.1	t ₂₁ =1.423, p=0.169

Table 1. Average execution time (ET, i.e., time needed to complete a sequence) and average peak force for singlefinger and multi-finger sequences across participants. A two-sided paired t-test for a difference between conditions is reported in the last column.

In contrast to single-finger movements (Fig. 2C), preparation of multi-finger sequences (Fig. 2E) strongly activated the dorsal premotor cortex (Fig. 2G; PMd, $t_{21}=5.125$, p=4.4e-05), the supplementary motor areas (SMA/pre-SMA, $t_{21}=4.016$, p=2.3e-04) and the anterior part of the superior parietal lobule (aSPL, $t_{21}=7.482$, p=2.3e-07). Thus, the demands of planning multiple different finger movements evoked significant brain activation in premotor and parietal areas.

During the production, we found widespread activity in both primary sensorimotor, parietal, and premotor areas for both sequence types (Fig. 2D, F). The contrast between these two conditions revealed higher activity for multi-finger over single-finger sequences in PMd (Fig. 2H, 4B; t_{21} =6.022, p=5.6e-6) and aSPL (t_{21} =8.264, p=4.8e-08). In contrast, in caudal M1 and rostral S1 the same two conditions elicited very similar activity levels, consistent with the idea that the basic motor requirements were well matched between single- and multi-finger sequences.

Importantly, the spatial distribution of multi vs. single contrast during production was very similar to multi vs. single contrast during preparation (Fig. 4A, B). When we correlated the unsmoothed voxel-wise activity maps within each participant, we found a highly significant correlation between the brain activity patterns under these two conditions (r=0.12, t_{21} =10.796, p=4.9e-10). Thus, pre- and online planning activated overlapping cortical areas.



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Figure 3. Sequence representations during preparation and production phases. (A) Group-averaged multivariate searchlight map of the crossnobis distance between the preparation and (B) production of the three single-finger. (C) Same as A but for mean crossnobis distance between the preparation and (D) production of three multi-finger sequences. (E) Profile ROI analysis of the mean crossnobis distance (±SEM) during the preparation of single-finger (light red line) and multi-finger (light blue) sequences. (F) Same as E but for the production of single-finger (dark blue) and multi-finger (dark red) sequences. *p < 0.05, **p<0.01, ***p<0.001 in a two-sided one-sample t-test vs. zero for selected ROIs.

424 Preferential activation for planning before and during movement

The strong overlap between the activity maps for pre- and online planning, however, does not tell us whether the 425 two maps were identical (in other words, pre- and online planning activated - within each participant - exactly the 426 same voxels) or whether there were true differences between the maps. This is because measurement noise will 427 428 lead to an observed correlation smaller than 1, even if two maps are identical (Diedrichsen et al., 2023). Again, we applied PCM to model the correlation between multi-single contrast activity patterns in both preparation and 429 production, followed by an assessment of data likelihood for each model (see Fig. 4C). The group maximum-430 likelihood estimate of correlation was r=0.65 with strong evidence that the patterns were not identical (against 1-431 corr model: z = 3.815, p=0.0001). 432

Therefore, we asked whether there were systematic differences across participants, which would indicate 433 that some areas have a preference toward either pre- or online planning. Because the contrast during pre-planning 434 was generally larger than during execution, we could not simply subtract the two difference maps. Instead, we 435 plotted the multi-single difference for each voxel during preparation (Fig. 4E, x-axis) against the difference during 436 production (y-axis). We then estimated the average relationship between the two contrasts using Principal 437 Component Analysis (PCA) within each participant. The first principal component (PC1) captured the tendency 438 of voxels to be similarly responsive for pre- or online planning. The loading on the second principal component 439 captured the deviation from this lawful relationship, with positive values indicating relatively more activity during 440 online planning and negative values more activity during pre-planning. By mapping the voxel preferences back 441 to the surface, we created an average preference map across participants within our window of interest (Fig. 4F). 442 This map revealed that clusters (solid outlines in Fig. 4F) in PMd (p=5.9e-07, corrected for multiple comparisons, 443 see Methods). M1/S1 (p=8.8e-06), and aSPL (p=5.9e-07) were more active during online planning, while clusters 444 in SMA (p=3.1e-06), the ventral premotor cortex (PMv, p=7.2e-07 and p=0.0096), and the inferior parietal lobule 445 (IPL, p=0.0492) were relatively more active during pre-planning (Fig. 4F). This set of results indicates that pre-446 planning and online planning of movement sequences preferentially activated slightly different sets of cortical 447 448 areas.

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Figure 4. Activation maps for pre- and online planning are highly, but not perfectly, correlated. (A) The difference in evoked activation between multi-finger and single-finger sequences during the preparation and (B) production. (C) PCM evaluation of models assuming a correlation between the sequence-general activity patterns shown in A and B of 0 to 1. The group average (black line) and individual curves (thin gray lines) express the difference from the log-likelihood from the mean value (i.e., zero on the y-axis). Red dots indicate the best-fitting correlation model for each participant and the red solid line cross-validated best-fitting model across all participants. Yellow-shaded area indicates models that perform significantly worse than the best-fitting

correlation model (p < 0.05). (D) Similar to (C), but for the correlation between sequence-specific activity 458 patterns evoked during preparation and production of multi-finger sequences in PMd and aSPL. For each 459 participant, we averaged the curve corresponding to each of the two areas. (E) Voxel-wise values of the 460 preparation multi-single contrast, plotted against the voxel-wise values of the production multi-single contrast. 461 Two principal components (PCs) of the data are shown. Voxels in the red area (positive PC2) show a preference 462 for online planning, whereas voxels in the blue area (negative PC2) show for pre-planning. An example of a 463 single participant is shown. (F) Group t-value for the second PC projected on the flat map. Areas with black solid 464 outlines represent significant clusters. Note that for this surface-based (rather than ROI-based) analysis, there is 465 no strict correspondence between the clusters on the map and our pre-defined ROIs. The labels next to the 466 significant clusters correspond to the more closely matching ROI. 467

468 PMd and SPL maintain sequence-specific representations both during preparation and production

469 If the increased activation for multi-finger sequences in PMd and SPL (Fig. 4A-B) was related to pre-planning 470 and online planning, then these areas should exhibit sequence-specific representations during both the preparation 471 and production phases.

Indeed, for the preparation phase multivariate analysis (Fig. 3C) revealed that both areas showed 472 sequence-specific representations of multi-finger sequences. We found significant pattern differences in PMd 473 (Fig. 3E, $t_{21} = 2.266$, p=0.034) and aSPL ($t_{21}=3.491$, p=0.002). In contrast to the preparation of single-finger 474 movements (Fig. 3A), the representations of multi-finger sequences appeared to be more widespread on the 475 cortical sheet. To quantify this observation, we calculated a spatial dispersion metric, which reflects the spatial 476 variance of pattern dissimilarities (see Methods). This analysis confirmed that the planning of multi-finger 477 sequences was associated with a more widespread representation across the sensory-motor network compared 478 with single-finger sequences ($t_{21}=3.542$, p=0.002). Therefore, premotor and parietal areas were not only more 479 480 active during the preparation of multi- than single-finger sequences (Fig. 4A), but also represented the identity of the sequence. 481

Importantly, we also found that these representations were maintained during the execution phase (Fig. 482 3D, PMd: t_{21} =3.221, p=0.004; aSPL: t_{21} =2.490, p=0.021). When comparing the multivariate distances between 483 484 preparation (Fig. 3C) and execution (Fig. 3D) we found a strong reduction in M1 ($t_{21}=2.123$, p=0.045) and S1 $(t_{21}=2.305, p=0.0314)$. In contrast, the pattern differences in PMd and aSPL did not attenuate from the preparation 485 to the execution phase (PMd: $t_{21}=0.271$, p=0.7889, and aSPL: $t_{21}=1.895$, p=0.0719). Note that the multivariate 486 distances reported in Fig. 3 are measured with noise, so the small-scale differences that can be observed between 487 Fig. 3C and Fig. 3D should not be overinterpreted. When conducting a map-wise comparison, none of the subtle 488 differences are significant after controlling for multiple comparisons. We therefore chose a ROI approach to 489

490 increase our statistical power. These results are consistent with the idea that premotor and parietal areas are 491 involved in the planning of movement sequences both before and during sequence production.

Finally, we asked whether the sequence-specific representations in these areas remained stable or whether 492 they changed dynamically from preparation to production. To address this question, we again used PCM. We 493 removed the average activity pattern common to all multi-finger sequences from the patterns (separately for 494 preparation and production phase), and then correlated these sequence-specific pattern differences between 495 sequences across the two phases. Figure 4D shows the likelihood curves for different correlation models averaged 496 across PMd and aSPL. The small signal-to-noise for relatively subtle differences between multi-finger sequences 497 resulted in small model evidence for almost all participants. The cross-validated group-winning model predicted 498 that sequence-specific activity patterns were perfectly correlated with strong evidence that patterns were not 499 uncorrelated (against 0-corr model: PMd: z = 2.646, p=0.008; aSPL: z = 2.873, p=0.004). These results suggest 500 that sequence-specific representations remain stable across pre-planning and execution. 501

502 Discussion (1500 max)

We used 7T fMRI and multivariate analyses to investigate the role of human cortical areas in the preparation of movement sequences, separating processes that occur before and during movement production. We found that primary sensorimotor cortices (M1, S1) showed activity patterns resembling the first movement in the sequence during preparation, and of a temporal summation of individual movements during production. In contrast, secondary sensorimotor areas (PMd, SMA, SPL) were more activated during both pre- and online planning of motor sequences. These regions also maintained a stable representation of the sequence across preparation and production phases.

In previous fMRI studies, we found that the activity patterns in M1 and S1 during sequence production 510 can be explained by the linear combination of the patterns associated with the individual movements (Berlot et 511 al., 2021; Yokoi & Diedrichsen, 2019). The pattern for the first finger in the sequence contributed substantially 512 513 more to the overall pattern (average over preparation and execution) than all the subsequent fingers (Yokoi et al., 2018). Our results now provide evidence that this 'first finger effect' was caused by the pre-activation of the first 514 sequence element during preparation rather than by the transition from planning to execution state space 515 (Kaufman et al., 2016; Yokoi et al., 2018): the pre-planning of a multi-finger sequence activated a pattern similar 516 to that observed during the execution of the first movement in that sequence. 517

In a study using sequences of object-directed reach-to-grasp movements, Gallivan et al. (2016) found that the activity patterns in M1 were also slightly different between two sequences that started with the same movement but differed in the second movement. This suggests that, not only the first, but possibly also the second movement may be reflected in M1 preparatory activity patterns. This observation would be consistent with the "competitive queuing" hypothesis (Averbeck et al., 2002), the idea that the first movement in a sequence being

most, the second less, and subsequent movements even less activated (Kornysheva et al., 2019). However, because the first reach-to-grasp movement was always the same across conditions, it was unclear whether these findings would generalize to longer and more complex sequences where every sequence element is different and needs to be planned anew from trial to trial.

After sequence production began, the pattern differences in M1 and S1 between the 3 multi-finger sequences were strongly attenuated. This is likely due to the fact the pattern corresponding to the single-finger movements were sequentially activated. Due to the low temporal resolution of fMRI, these patterns combined additively, such that the three multi-finger sequences (which were matched in terms of the involved fingers) elicited overall similar activity pattern when we isolated the activity during the production phase.

These results also suggest that the production of the sequence cannot be maintained autonomously by primary motor areas, but that it depends on input from secondary motor areas (Russo et al., 2020; Tanji & Shima, 1994; Yokoi & Diedrichsen, 2019). Consistent with this idea, we found that PMd, SMA, and SPL (but not caudal M1 and rostral S1) were more activated during the preparation and production of multi-finger as compared to single-finger movements. We also found sequence-specific activity patterns in these areas, which were correlated across preparation and production phases. This suggests that premotor and parietal areas maintained a stable representation of the sequence throughout, likely to drive the next movements in M1.

As shown in recent behavioral studies (Ariani & Diedrichsen, 2019; Ariani et al., 2021; Kashefi et al., 539 2023), even relatively short 5-item sequences cannot be fully pre-planned. Instead, planning of remaining items 540 needs to continue throughout sequence production. To determine if the same areas are involved in the pre- and 541 online planning, we contrasted the univariate multi-finger to single-finger activity maps. As basic execution 542 processes were matched, we interpreted these contrasts as reflecting the increased need for planning. We found 543 that the contrast maps were highly correlated across preparation and production phases (Fig. 4C), indicating that 544 pre-planning and online planning activated similar regions. Within two of these regions, the PMd and aSPL, we 545 also found that the sequence-specific activity patterns were highly correlated across these preparation and 546 production (Fig. 4D), suggesting that the sequence-specific representations remained stable. Together these two 547 findings are evidence that the processes involved in online planning are similar to those involved in pre-planning. 548

Despite considerable overlap in brain activation between pre- and online planning (Fig. 3A,B), however, further analysis revealed small but systematic differences in the involvement of different brain areas: PMd, S1, and SPL tended to be more active during online planning, and SMA and ventral premotor cortex (PMv) more during pre-planning. This indicates that the two processes are not exactly identical. One possible explanation could be the differential engagement of brain areas in memory encoding and memory retrieval processes that, as part of planning processes, happened during preparation and production, respectively. The exact nature of these differences, however, remains to be tested in future studies.

Our results offer testable predictions for future neurophysiological recordings in sensorimotor areas of 556 non-human primates. They predict that M1 shows fast dynamics related to each individual movement, with linear 557 superposition of subsequent movements (Zimnik & Churchland, 2021). Additionally, they predict the presence 558 of sequence-specific representation in premotor and superior parietal areas both during preparation and 559 production. The observed consistency of these representations during preparation and production suggests that 560 these representations have slow dynamics and change very little from preparation to production. However, it is 561 also possible that these patterns are stable at a voxel level—i.e., pre- and online planning activate the same cortical 562 columns—but show faster dynamics at the single neuron level. Studying these representations at a neuronal level 563 at high temporal resolution will provide additional insight into how the motor system solves the fundamental 564 problem of serial order in behavior (Lashley, 1951). 565

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