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Experience-dependent changes in functional connectome fingerprinting

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Noga Yair[1,2,3] ✉, Asaf Madar[1,2], Niv Tik[1,2], Tom Zalmenson[3], Omer Azriel[3], Dana Shamai-Leshem[4], Yaron Alon[3], Lucian Tatsa-Laur[5], Ariel Ben-Yehuda[5,6,7], Daniel S. Pine[8], Paul D. Bliese[9], Michal Bernstein-Eliav[1,2], Emily S. Finn[10], Yair Bar-Haim[1,3] & Ido Tavor[1,2]

The human functional connectome, derived from functional magnetic resonance imaging, is sufficiently unique and stable to serve as an individual "fingerprint", leading some to view it as a neural proxy of the self. However, it remains unclear whether this fingerprinting property persists following exposure to extreme or highly uniform environments. In a longitudinal study, male infantry soldiers and a comparison group of male university students each underwent four resting-state scans across key life milestones. We tracked changes in within-individual versus between-individual similarity in functional connectomes over time. Early military service was associated with a marked reduction in connectome fingerprinting accuracy among soldiers, driven by a temporary reduction in connectome distinctiveness relative to the group rather than by reduced similarity to the self. In contrast, fingerprinting remained stable in university students across the same developmental period. Reduced fingerprinting in soldiers was specifically linked to connectivity within the default mode network. These findings demonstrate that the uniqueness of the human functional connectome is not fixed, but can be substantially shaped by powerful, shared environmental contexts, highlighting the sensitivity of neural self-organization to social and institutional structure.

We often perceive our character, preferences, and personality as enduring features, shaped during childhood and adolescence[1]. But how stable are we really? How prominently can our life circumstances impact our inner workings and perceived stable self? Major shifts in life circumstances can alter one's self-concept, cognitions, emotions, and patterns of behavior[2–4]. Such changes should be reflected in brain function, and specifically in the brain's functional connectivity. Derived from functional magnetic resonance imaging (fMRI), the functional connectome has been used to predict personality traits[5,6], psychopathology[7–10], and cognitive abilities[11–15]. As such, the connectome may serve as a viable tool for representing one's internal processes collectively thought to represent one's neural self.

Finn and colleagues[16] explored the possibility of using the functional connectome as a neural "fingerprint", identifying an individual based on their connectivity patterns alone. Two important observations emerged: (a) the connectome is highly stable within individuals over a two-week period, and (b) the connectome is sufficiently unique to identify individuals with high accuracy.

[1]Sagol School of Neuroscience, Tel-Aviv University, Tel-Aviv, Israel. [2]Gray School of Medical Sciences, Gray Faculty of Medical & Health Sciences, Tel Aviv University, Tel Aviv, Israel. [3]School of Psychological Sciences, Tel-Aviv University, Tel-Aviv, Israel. [4]School of Psychological Sciences, Haifa University, Haifa, Israel. [5]Center for Mental Health Services and Mental Resilience, Israel Defense Forces Medical Corps, Ramat Gan, Israel. [6]The Adelson School of Medicine, Ariel University, Ariel, Israel. [7]Shalvata Mental Health Center, Clalit Health Services, Hod-Hasharon, Israel. [8]National Institute of Mental Health Intramural Research Program (NIMH-IRP), Bethesda, MD, USA. [9]Darla Moore School of Business, University of South Carolina, Columbia, SC, USA. [10]Department of Psychological and Brain Sciences, Dartmouth College, Hanover, NH, USA. ✉e-mail: nogayair@mail.tau.ac.il

Table 1 | The number of participants and time passed between assessments

Group	Time-point 1	Time-point 2	Time-point 3	Time-point 4
Soldiers	$N = 50$	$N = 45$	$N = 43$	$N = 41$
		$M_{months} = 15.2\ (2.25)$	$M_{months} = 11.5\ (2.16)$	$M_{months} = 11.6\ (1.79)$
Students	$N = 50$	$N = 37$	$N = 35$	$N = 14$
		$M_{months} = 11.4\ (1.09)$	$M_{months} = 12.1\ (1.35)$	$M_{months} = 12\ (1.27)$

For each group, the top row presents the number of participants in each time-point, and the bottom row presents the mean (and standard deviation) of months passed since the last time-point.

Subsequent studies tested the stability and uniqueness of the connectome over longer time periods[17], combining structural and functional data in a multimodal approach[18,19], and dissecting the effects of MRI scan parameters on fingerprinting accuracy[20]. Another work related the stability and uniqueness of the individual connectome to the stability of other personal facets, such as cognitive abilities.[21].

However, it remains unclear whether certain environmental circumstances can degrade this neural stability and uniqueness, and whether such environments relate to variations in the connectome in ways that disrupt its fingerprinting capacity. For example, family members or close friends have more similar functional connectomes than individuals who are less closely connected[22,23]. It may therefore be the case that an environment promoting homogeneity, or close-knit relationships, may lead to reduced uniqueness of the functional connectome.

Results

Fingerprinting calculation and success rates

We investigated this hypothesis using a unique longitudinal dataset of male infantry soldiers (the extreme environmental changes group) with four repeated measurements of resting-state fMRI (rsfMRI) scans, spanning from enlistment through multiple deployments, until after their honorable discharge. Life circumstances for these participants transitioned markedly from highly rigid, structured environments that limit personal autonomy and promote behavioral similarity[24,25] to environments that gradually allow for autonomy reemergence. A control group of age-matched male university freshmen (the stable environment group) was scanned at parallel intervals. See Table 1 for the number of participants assessed at each time-point and the intervals between MRI scans.

The soldiers' baseline scan (time-point 1) was conducted shortly after enlistment. The 15-month period between this baseline and the 2nd scan (time-point 2) was devoted to combat training and an initial deployment cycle. During this time, participants lived in the same barracks, ate the same food, wore identical uniforms, followed the same highly structured training schedule, were assigned the same tasks, and followed the same sleep routines. This regime allows very little personal time and space, creating strong comradery among the soldiers and introducing high homogeneity in environmental circumstances[24,25]. Prior studies have shown that interpersonal closeness is associated with greater neural similarity[22,23]. Hence, we hypothesized that this highly homogeneous environment and schedule would relate to low fingerprinting accuracy.

The next 12 months before the 3rd MRI scan (time-point 3) mark a considerable change in circumstances for the soldiers. They were scattered between different battalions and companies in different military bases with different missions and experiences. At this point, these participants worked in smaller teams, comprised of more experienced soldiers from difference recruitment cohorts, and split their time between active combat deployments and downtime. Thus, each soldier was in a more unique environment. In line with an environmental impact hypothesis, these changed circumstances were expected to lead to an increase in fingerprinting accuracy.

Finally, the 4th MRI scan (time-point 4) was conducted when the participants were already honorably discharged from the military for approximately six months, fully regaining their personal autonomy as civilians and starting their separate adult life trajectories. In contrast to the soldiers, the control students were immersed in the rather stable environment of the university, mostly still living with their parents and subjected to minimal changes in their personal environments. We therefore expected stable, high fingerprinting success as shown in previous studies[16]. The extreme difference in circumstances in the soldiers' group relative to the undergraduate controls allowed for an examination of the influence of distinct environments on the stability and uniqueness of the connectome.

For each participant and MRI scan, we computed the pairwise Pearson correlations between the averaged blood-oxygenation-level-dependent (BOLD) signal timeseries of each brain region[26] (Fig. 1A). This yielded functional connectivity matrices for each participant at each time-point. The connectomes at time-point 1 served as the baseline against which all subsequent time points were compared (Fig. 1B), resulting in similarity matrices containing each participant's self-correlation (in the diagonal) and cross-time-point correlation with every other participant (in the off-diagonal; Fig. 1C). These similarity matrices, for soldiers and for students, are shown in Fig. 2A. See Methods for fMRI preprocessing and fingerprinting procedure. Results from the final student time-point (time-point 4) are marked to highlight a reduced sample size at this time-point in this group.

We tested whether each participant's connectome at time-points 2, 3, and 4 is more strongly correlated with their own at baseline (i.e., fingerprinting success), or with their fellow group members (i.e., fingerprinting failure). For example, if a participant's connectome at time-point 2 was the most strongly correlated with their own connectome at time-point 1 relative to the correlation magnitudes with each of the other members of their group at time-point 1, a fingerprinting success was recorded. Conversely, if the strongest correlation was with another group member's connectome at time point 1, it was considered a fingerprinting failure (Fig. 1D). Following Finn et al.[16], fingerprinting success was defined as the percentage of successful fingerprints across participants. Missing data were addressed with multiple imputations (see Methods).

A generalized estimating equations (GEE) model indicated a significant group-by-time interaction effect in fingerprinting success rates ($z = 2.13$, $p = 0.03$; see Methods for GEE calculation and significance permutation tests). As in past work, high and stable fingerprinting success rates (≥90%) were noted for the students (stable environment group) at all time-points. In contrast, the soldiers displayed lower fingerprinting success following their initial phase of military service, with a steady improvement in success rates over time, peaking following their honorable discharge (Fig. 2B): At the second time-point, after 15-months of extremely close-knit, rigid living environment[24,25], only 80% of soldiers' functional connectomes were most strongly correlated with their own functional connectomes at enlistment. The connectomes of the remaining soldiers failed to function as fingerprints. This success rate is significantly lower than that of the students, who at time-point 2 had a 97% success rate ($p = 0.005$). At the third

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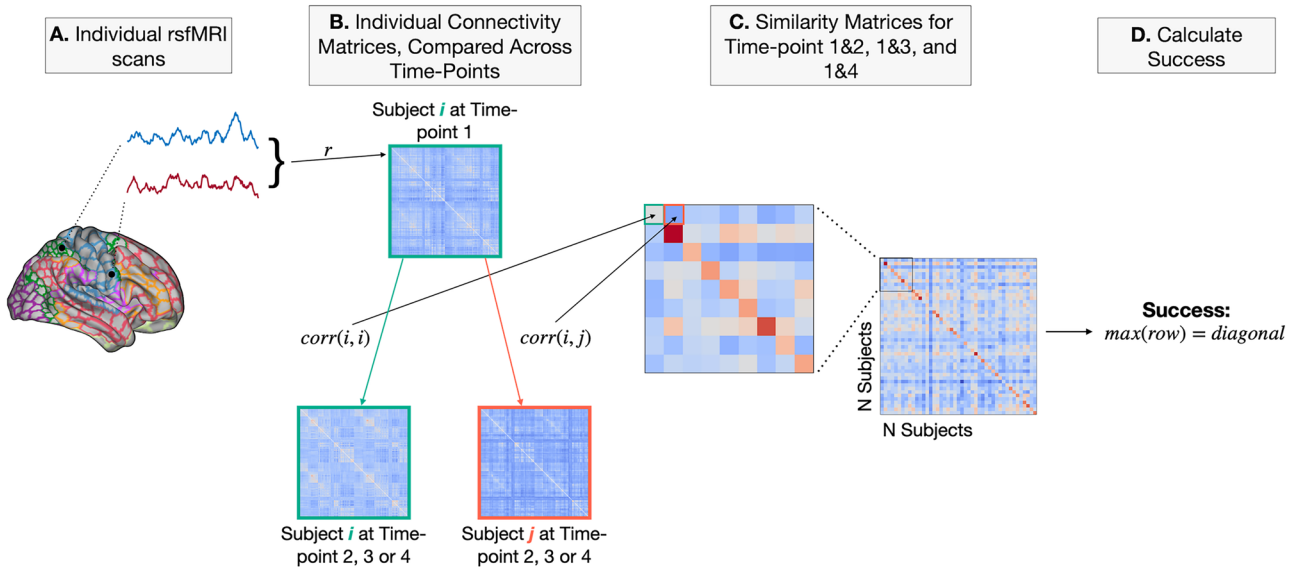

Fig. 1 | Fingerprinting procedure. A Individual functional connectomes were created by applying a 1000-region parcellation[26] to all rsfMRI scans. We calculated the Pearson correlation between every pair of regions' average BOLD signal resulting in a symmetrical 1000 × 1000 connectivity matrix (one for each participant at each time-point). **B** Time-point 1 was defined as the baseline for both groups, to which all future time-points were compared. **C** Similarity matrices were created by correlating every pair of participants across timepoints. The diagonal values in these matrices contain each participant's self-correlation across time-points, while the off-diagonal contains the correlations of each participant at baseline with all other participants at the selected time-point (lower triangle) or the correlations between all participants at the selected time-point and every other participant at baseline (upper triangle). **D** Fingerprinting was considered successful if the diagonal value was the highest in the row, i.e., if a participant at time-point *t* was most strongly correlated with themselves at baseline.

time-point, after a year of combat deployments and downtimes, no longer living or functioning together, an improvement in fingerprinting success was observed for the soldiers (90%), while the students maintained a stable high success rate (96%; $p = 0.29$ compared to soldiers fingerprinting). Finally, at the fourth time-point, six months after the soldiers were honorably discharged and integrated into civilian life, their fingerprinting success rate (93%) slightly surpassed that of the control students (90%; $p = 0.89$), who remained stable and high.

These results suggest that living in markedly changing environments can alter the properties of the functional connectome. Stable academic life was expressed in a stable brain connectome with high capacity for participant identity detection, extending extant findings on the stability of neural fingerprinting[17] to even longer time intervals. In contrast, the marked environmental changes associated with military service appear to have had a destabilizing effect on the neural connectome and fingerprinting capacity. Split-half reliability within each time-point has ruled out the possibility that the reduction in fingerprinting accuracy was driven by data quality at either time-point (Supplementary Fig. S1; See Methods).

Stability and uniqueness

Two distinct properties may affect connectome fingerprinting capacity: a) its stability (i.e., ***intra***-subject similarity) and b) uniqueness (i.e., ***inter***-subject similarity). If the observed decrease in fingerprinting accuracy in the soldiers group was driven by stability, it could suggest that the individual functional connectivity patterns of the soldiers are changing more drastically between time-points. If, however, the decrease in accuracy is driven by uniqueness, it might reflect increased levels of neural convergence among the soldiers as a group. We therefore examined which of these factors led to the observed altered fingerprinting (Fig. 3). Connectome *stability* at each time-point was defined as the correlation between every participant's connectome at baseline and their own connectome at each following measurement. This measure is also used to calculate fingerprinting success as defined above. *Uniqueness* was defined as the average cross-time-point correlation between each participant's connectome and all other connectomes, both at baseline and the subsequent time-point. A third measure, *typicality*, represents how similar one's connectome is to the "typical", or average connectome. Typicality is a complementary value for uniqueness and was only used to estimate the third and final measure of interest, *discriminability* - defined as the ratio between stability and typicality. A high discriminability score represents an individual whose connectome is more easily discerned from the group[21,27]. Missing values were again addressed with multiple imputation (see Methods for further details). Results from the final student time-point (time-point 4) are highlighted to caution the reader of the reduced sample size in this time-point for the students.

GEE analysis indicated a significant group-by-time interaction for uniqueness ($\beta = -0.02$, $\%95CI = -0.03$ to -0.01, $z = -3.84$, $p = 0.0001$), but not for stability or discriminability ($\beta = 0.02$, $\%95CI = -0.01$ to 0.05, $z = 1.06$, $p = 0.290$ and $\beta = -0.05$, $\%95CI = -0.12$ to 0.03, $z = -1.22$, $p = 0.211$, respectively). As shown in Fig. 3 (middle), soldiers and students differed in the uniqueness of their connectomes when comparing time-points 1 and 2: while students maintained a relatively high level of uniqueness, the soldiers' connectomes were initially less unique and became more unique over time. These results indicate that the reduced fingerprinting success of the soldiers relative to the students at time-point 2 was driven by a decrease in connectome uniqueness, i.e., an increase in the neural similarity between the soldiers, which diminished over time.

To determine whether reduced fingerprinting reflected increased similarity among individuals at the same time-point, we analyzed within-time-point inter-subject similarity (ISS), calculated from the off-diagonal elements of the similarity matrix at each time-point. ISS did not increase among soldiers from baseline to the second time-point, indicating that reduced fingerprinting was not driven by greater overall between-individual similarity (see Methods). The aim of this study was to examine the preservation of individual connectomes over time. Consistent with prior work[21,27–29], we operationalized uniqueness relative to baseline, testing whether a participant's connectome at later

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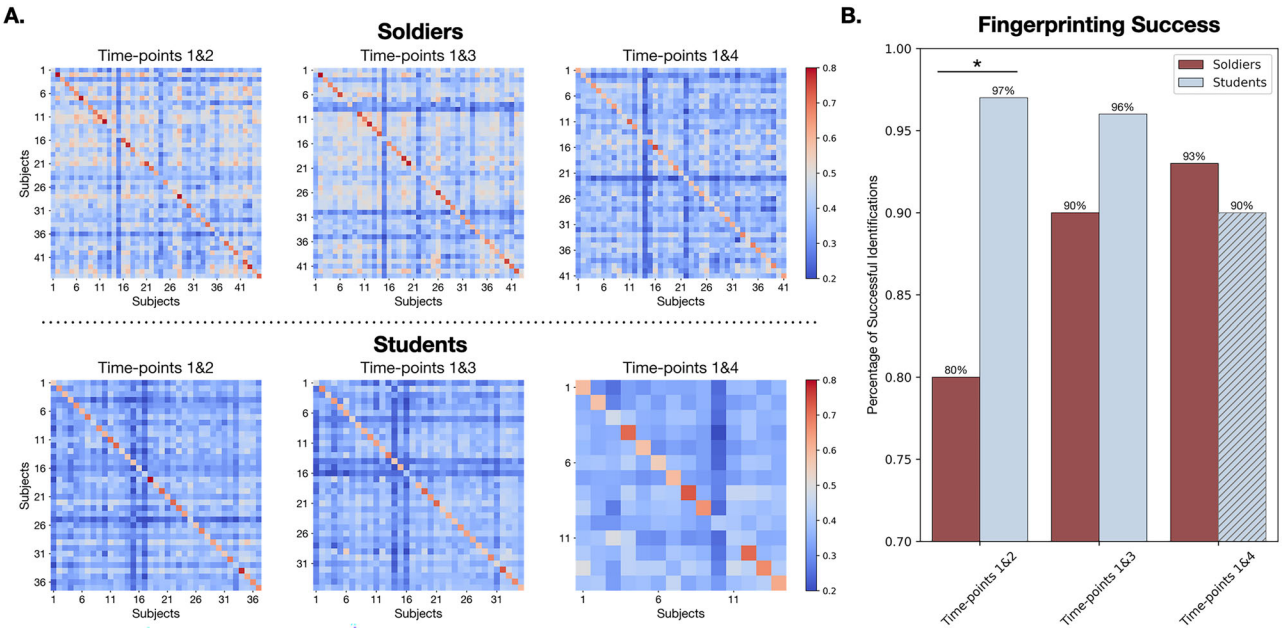

Fig. 2 | Similarity matrices and fingerprinting success rates as a function of group and time. A Similarity matrices between soldiers (top) and students (bottom) connectomes at baseline and subsequent time-points. In these similarity matrices, the diagonal values reflect participants' self-correlations while the off-diagonal values are the correlations between all pairs of baseline- and non-baseline connectomes across participants. Students' time-point 4 results should be interpreted with caution due to the low number of returning participants (see Table 1). Color bars mark the Fisher z-transformed Pearson correlation between every pair of connectomes. **B** Fingerprinting success rates of soldiers (red) and students (gray) over time. A successful fingerprint was counted if a participant at time-point 2, 3 or 4 was most correlated with themselves at time-point 1 than with any other participant. A two-sided generalized estimating equations (GEE) model revealed a significant group-by-time interaction ($\beta = 1.45$, 95%$CI = 0.11 - 2.79$, $z = 2.13$, $p = 0.03$). Follow-up two-sided permutation tests showed that fingerprinting success was significantly lower in soldiers than in students at time-point 2 ($p = 0.005$), but not at time-points 3 or 4. Source data are provided as a Source Data file.

time-points remained more similar to their own baseline connectome than to those of others. Within this framework, fingerprinting failure does not necessarily imply increased within-time-point similarity. Instead, it reflects reduced cross-time discriminability between the connectomes of self and others. Within-time-point ISS addresses a distinct question: whether participants become more similar to one another at a given time-point. In contrast, baseline-referenced uniqueness assesses whether individuals preserve their distinctive functional connectome over time.

Functional network contribution

Finally, we examined the distinct roles of different functional connectivity networks in fingerprinting success (Fig. 4). Specifically, we investigated which networks positively contributed to fingerprinting accuracy, as such networks may demonstrate unique activation patterns across participants. We also investigated which networks had a negative impact on fingerprinting accuracy. Such networks may share similar functional profiles across individuals. We used a predefined parcellation that groups regions of the brain into seven cortical networks[26,30]. We repeated the fingerprinting procedure with every possible combination of these seven networks to generate 126 distinct combinations (e.g., the first iteration included only edges from network 1, the second iteration included edges from network 2, the eighth iteration included edges from networks 1 + 2, the ninth iteration included edges from networks 1 + 3, etc.). Each network's contribution to fingerprinting was defined as the difference between the average success rate of every combination including the network, and the average success rate of every combination excluding the network. For example, a network contribution of 5% indicates an improvement of 5% in fingerprinting accuracy whenever edges from the network were included in the combination (See Methods for further details). Empirical null distributions were generated by repeating the same combinatorial procedure on pseudo-networks constructed by randomly sampling parcels from across the cortex. The observed contribution of each real network was then compared against its corresponding null distribution to test whether it exceeded chance expectations. Only networks whose contribution values survived this permutation procedure were considered statistically significant and are reported in Fig. 4.

The networks that showed the strongest positive contribution for fingerprinting in both groups and across all time-points were the dorsal attention network (DAN) and the executive control network (CON). This is in line with Finn et al.'s original work[16], where fronto-parietal regions had the strongest positive contribution to fingerprinting accuracy. Notably, prior work has shown that the default mode network (DMN) contains highly individual-specific information and positively contributes to connectome fingerprinting[16,18]. In the current study, the DMN negatively affected fingerprinting success in soldiers at time-point 2. At the group level, this time-point was also characterized by a reduction in overall connectome uniqueness in soldiers, reflecting increased similarity between individuals. To clarify the source of this effect, we conducted a targeted post-hoc analysis examining the DMN's contribution to uniqueness, stability and discriminability (see Methods further details). This analysis revealed that the DMN's negative contribution to fingerprinting success was accompanied by a significant negative contribution to stability (FDR-corrected permutation $p = 0.020$), alongside significant positive contributions to uniqueness ($p = 0.015$) and discriminability ($p = 0.015$; see Supplementary Fig. S4). This pattern was not observed in the student group (all p's >0.05), indicating that the DMN effect was context dependent. Thus, while previous studies have linked the DMN to increased neural similarity among socially connected individuals[22,31], the present findings suggest a separate mechanism in which group-level reductions in connectome uniqueness and network-specific reductions in DMN stability jointly contribute to reduced fingerprinting success. Future work could shed

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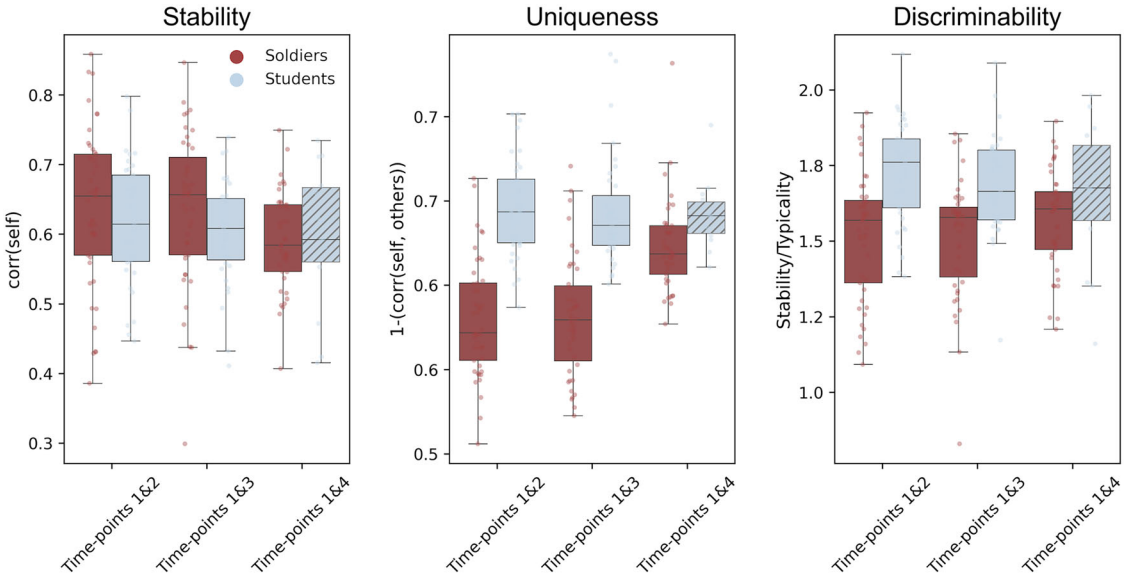

Fig. 3 | Connectome stability, uniqueness and discriminability for soldiers (red) and students (gray). Stability (left) was calculated as the Pearson's correlation between each participant's connectome, at time-points 2, 3 and 4, and themselves at baseline. Uniqueness (middle) was calculated as 1 minus the average Pearson correlation between each participant and every other participant, both within time-point and at baseline (lower correlations between self and others reflect high uniqueness). Discriminability (right) was calculated as the ratio between stability (self-correlation) and typicality (average Pearson correlation between each participant and every other participant, or the complementary value of uniqueness). Students' time-point 4 should be interpreted with caution due to the low number of returning participants (see Table 1). Box plots show the median (center line), 25th and 75th percentiles (box bounds), and whiskers extending to the most extreme observations within 1.5 times the interquartile range. Individual participant values are shown as overlaid points; boxplot outliers are not displayed separately. See Methods for additional details. Source data are provided as a Source Data file.

light on the nature of the relations, or lack thereof, between these two mechanisms.

Discussion

We examined the effects of an extremely cohesive and homogenous environment on the uniqueness and stability of the functional connectome. Soldiers during the initial training and deployment cycle who experience a highly structured environment exhibited a marked reduction in connectome fingerprinting accuracy. This effect was most pronounced during the period of most intense social and physical cohesion. This disruption was driven not by reduced within-individual stability, but by increased neural similarity between individuals.

These findings underscore the differential sensitivity of the fingerprinting metrics employed. Fingerprinting success rate was particularly sensitive to increased neural similarity among soldiers. As a rank-based measure that determines whether an individual's connectome is more similar to their own than to others', even moderate increases in between-subjects similarity can lower identification accuracy. By contrast, discriminability indexes the ratio between within-individual stability (self-correlation across time) and average similarity to others in the cohort (typicality; see Methods). Because it integrates both components, moderate increases in between-subject similarity may have only limited impact when within-individual stability remains high. Together, these results demonstrate that fingerprinting metrics differ in their sensitivity to environmental influences on neural similarity.

Prior work suggests that individuals living in close-knit groups express more similar neural activations than individuals who are less close[22,23]. This neural similarity was especially pronounced among individuals who were close neighbors or living together[22]. Beyond social proximity, the military environment experienced by the soldiers was tightly regulated. During early service, the soldiers were exposed to strict standardization of daily behavior and markedly reduced personal autonomy, including identical schedules of physical exertion, regimented sleep–wake cycles, synchronized dietary timing, and highly constrained daily routines[24,25]. Any or all of these features may have contributed to the observed reductions in connectome uniqueness. The unique contribution of these separate elements could be explored in future studies. It is also conceivable that the observed fingerprinting disruption reflects the cumulative impact of a highly standardized environment, in which multiple dimensions of experience are aligned across individuals. Under such conditions, preserved similarity to one's own prior connectome may no longer be sufficient to maintain neural identifiability relative to others. The current results speak to the plasticity of the connectome in response to changing environments. When later in service the soldiers were dispersed between military bases and missions, and were no longer physically close, they exhibited increased uniqueness, which eventually peaked in the months after their honorary discharge from service.

The current results raise questions about core facets of the neural self. While there is a decrease in neural uniqueness for the soldiers as a group, self-correlation values reveal that most soldiers still displayed remarkable neural stability even under extreme conditions such as early military training and combat deployment. These findings highlight several broad areas for future inquiry. What other extreme conditions might connectome fingerprinting endure? What would it take to disrupt the connectome enough so that it no longer functions as a neural fingerprint? How such disruptions in the connectome might manifest in behavior and cognition? Answers to these questions can carry important implications to the study of psychological resilience and psychopathology. It would also be important to study what distinguishes soldiers whose functional connectome became more similar to someone else, rather than their own. What might make these individuals more prone to changing their functional connectivity patterns in extreme environmental circumstances?

The current study should be viewed in light of some limitations. First, only young male participants in a military vs. university environments were studied. Future research could explore different age groups, sex, military entities, and non-military contexts to test the generalizability of the current findings. Second, the age of the current

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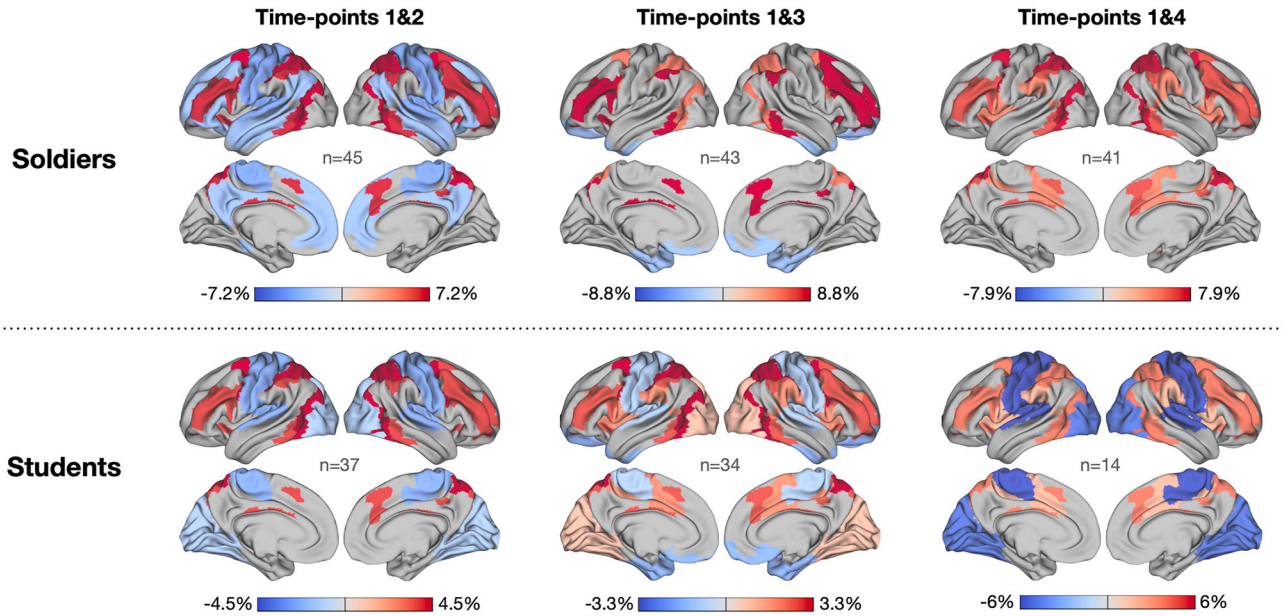

Fig. 4 | Network contribution to fingerprinting accuracy in soldiers (top) and students (bottom). The fingerprinting procedure was repeated with every possible combination of seven functional, cortical networks[30], for a total of 126 combinations. Each network's contribution was calculated as the difference between the average success rate of all combinations including that network, and the average success rate of all combinations excluding the network. Significance was evaluated with permutation testing, and only networks whose contribution was significant are presented here (see Methods). Positive contribution (red shades) indicates that fingerprinting accuracy improved when using this network's data whereas negative contribution (blue shades) indicates the inclusion of the network reduced fingerprinting accuracy. Source data are provided as a Source Data file.

participants (18–23 years) represents a period of significant neural plasticity and active brain maturation[32,33]. While the functional connectome has been shown to be highly unique and identifiable at this age[17,34], it is also a stage where similarity to the group average is typically higher than in middle adulthood[29]. It remains unclear whether the effects observed here also occur in older populations with more settled neural connectomes. Third, the student group exhibited a high attrition rate by the final time-point, and although the statistical approach taken here accommodates missing data, students' time-point 4 results should be interpreted with caution. Fourth, future studies with similar designs could benefit from the collection of measures reflecting personality traits, clinical symptoms, socioeconomic background, and social hierarchies and friendships among the participants. Examining how these factors interplay with the uniqueness and stability of the functional connectome could shed light on potential brain-behavior associations.

In conclusion, three key findings emerged from the current study: a) One year of military service in a highly structured close-knit environment considerably affected the functional connectomes of soldiers, disrupting their capacity as a neural "fingerprint"; b) this disruption in fingerprinting capacity was driven by a decrease in the uniqueness of soldiers' neural connectivity patterns, which was alleviated as their subsequent environments allowed greater autonomy; and c) The DAN, CON, and DMN played a key role in fingerprinting disruption. These results emphasize the dynamic nature of the functional connectome and its potential for plasticity under extreme life circumstances, and support the notion that the brain is highly malleable in response to environmental pressure. The environment shapes our brain long after childhood, as evident by the changes observed here during young adulthood. Ultimately, this research underscores the profound influence of our surroundings, suggesting that the environments we inhabit can reshape our neural connectome patterns in response to ever-changing life circumstances. The results also indicate that perceived stability in the neural self may reflect predominantly stable environments rather than a stable internal core. As we continue to explore the boundaries of these effects, it becomes increasingly clear that our brains are not only shaped by where we come from but are continually being molded by where we are and who is around us.

Methods

Participants

Soldiers were recent recruits in the Israeli Defense Forces (IDF) 35th Paratroopers Brigade ($N = 50$, males only, mean age = 19.5, SD = 0.8). As part of their recruitment process, all soldiers were determined to be physically and mentally healthy. Only males were included in this study because, as of writing this manuscript, only males are recruited as paratroopers in the IDF.

The control group consisted of university students ($n = 50$, males only, mean age = 18.4, SD = 0.6), all members of the Israeli Academic Reserve program, in which high school graduates delay their mandatory IDF service until the completion of their bachelor's degree. Sex was determined based on self report.

Exclusion criteria included MRI contraindications (e.g., claustrophobia, medical implants, piercings, tattoos in neck or head region, shrapnel), reading difficulties or dyslexia, or neurological diagnoses (e.g., epilepsy, migraines). All participants provided written informed consent. The study was approved by the Tel-Aviv University Institutional Review Board and the IDF Medical Corps Ethics Committee (Clinicaltrials.gov Identifier: NCT04651192).

Study timeline

All participants were scanned four times. The number of participants for each group at each time-point and the number of months elapsed between time-points are detailed in Table 1.

The soldiers were scanned first during basic training, and then again ~15 months later (time-point 2), after basic and advanced training, and their first combat deployment. The third scan (time-point 3) took place one year later, during which the soldiers were deployed multiple times. The fourth scan (time-point 4) took place again one

year later, after most soldiers were already honorably discharged from service and returned to civilian life.

The students were similarly scanned four times in parallel intervals during each year of their bachelor's degree.

MRI data acquisition and preprocessing

MRI acquisition and preprocessing routines are detailed elsewhere[35]. In short: MRI data were acquired on a 3T Siemens Magnetom Prisma MRI with a 64-channel head coil. Anatomical high-resolution (1 mm^3, Matrix 224 × 224 cm) images were acquired using a standard 3D Magnetization-Prepared Rapid Gradient-Echo (MPRAGE) T1 weighted sequence. Resting-state functional data were acquired with T2*-weighted gradient-echo echo-planar protocol (GE-EPI) with the following parameters: TR = 1000 ms, TE = 30 ms, GRAPPA acceleration factor = 2, Multiband acceleration factor = 4, matrix size 204 × 204 cm, 64 contiguous oblique axial slices covering the whole brain, Voxel size = 2 mm^3. The total number of volumes collected was 600. Image processing for the rsfMRI data followed the minimal preprocessing pipeline suggested by the Human Connectome Project[36], and included: high-pass filtering at 0.01 Hz, correction for motion artifacts, linear registration to the T1w anatomical scan, nonlinear registration to 152MNI space, and smoothing with 5 mm Gaussian kernel, all using FMRIB Software Library (FSL, www.fmrib.ox.ac.uk/fsl, FMRIB, Oxford). Residual noise was cleaned using FMRIB's ICA-based Xnoiseifier (FIX[37]), which is a semi-automatic ICA-based method to identify and remove structured noise from fMRI scans.

Fingerprinting procedure

Creation of similarity matrices. The fingerprinting procedure was conducted via MATLAB (MATLAB version: 9.13.0 (R2022b)), R (version 2025.09.2 + 418) and Python (version 3.7.4). After preprocessing, a 1000-node parcellation (Schaefer et al.,[26] Replication of the results with other parcellations is presented in Supplementary Fig. S2) was applied to each individual rsfMRI scan. Averaging the BOLD time-series of all voxels within each node resulted in a 1000 × 600 functional matrix per participant, per time-point (600 volumes by 1000 regions). Then, individual connectivity matrices (CMs) were created, again per time-point, by calculating the Pearson's correlation coefficient between every pair of nodes in the brain, resulting in symmetrical 1000 × 1000 CMs (Fig. 1A). The next step was creating similarity matrices: correlating the lower triangle of each pair of individual connectivity matrices, using time-point 1 as the baseline (Fig. 1B), created asymmetric, square matrices (Fig. 1C; see Fig. 2A for all similarity matrices). For example, correlating the soldiers' time-point 2 matrices with all time-point 1 matrices created similarity matrix A, where $A_{i,i}$ denotes the correlation between participant i's CM_{Time1} and CM_{Time2}, $A_{i,j}$ denotes the correlation between participant i's CM_{Time1} and participant j's CM_{Time2}, and $A_{j,i}$ denotes the correlation between participant i's CM_{Time2} and participant j's CM_{Time1}.

Fingerprinting reliability test. To further explore data reliability at each time-point and ensure the observed effects were not driven by sporadic differences in data quality, we repeated the fingerprinting procedure within time-point by dividing each individual 600-volume scans into two 300-volume parts and treating these two halves as repeated-measures for each participant (Supplementary Fig. S1). Within each time-point, the fingerprinting success rates were 100% for both groups, at all four time-points. Hence, we found no decreased reliability of data or any pervasive quality issues for any specific time-point which could have influenced success rates in either direction.

Success rates calculation and imputation. Fingerprinting success was defined as:

$$\mathbb{I}\{A_{i,i} = max(A_{i,1}, A_{i,2}, \ldots, A_{i,n})\}$$

for all $i = 1, 2, \ldots, n$ Where $A \in \mathbb{R}^{n \times n}$ corresponds to the similarity matrix and n corresponds to the number of participants.

In other words, if among all participants from a specific time-point, a participant was most strongly correlated with themselves at baseline (time-point 1), it was taken as a success. Group success rates were calculated per time-point as the percentage of successful identifications.

Missing data were addressed with multiple imputation using the MICE package in R (Van Buuren 2011). Specifically, a dataset of imputed success measures (a binary measure of 1 = success and 0 = failure) of all dropouts who completed at least the first two time-points was created five times (the maximal recommended number of imputations[38]). This was conducted separately for each group. For each of the imputed datasets, a nested Generalized Estimating Equations (GEE) model using the binary success measure as the dependent variable and a group by time interaction as the independent variable was executed. The robust Z-score of the interaction effect was averaged across the five datasets. Success rates for both groups, after data imputation, are shown in Fig. 2B. For the non-imputed success, see Supplementary Fig. S3.

Significance testing. To test for the significance of the group differences in fingerprinting success, we performed a permutation test. For each pair of time-points (time-point 1 and time-point 2, time-point 2 and time-point 3, and time-point 1 and time-point 4), we shuffled the labels of soldiers and students while maintaining the ratio of soldiers to students and then repeated the fingerprinting procedure ($N = 1000$ permutations). For each permutation, the success rate of each shuffled "group" was calculated, and a distribution of the difference in success rates between the groups was created, which allowed us to calculate the significance of the actual difference in success rates between the groups for each pair of time-points.

Within-time-point inter-subject similarity (ISS). To determine whether reduced fingerprinting reflected increased similarity among individuals within a time-point, we quantified within-time-point inter-subject similarity (ISS) separately for each group and time-point. Pearson correlations between each participant's connectome and the connectomes of all other participants within the same group and time-point were calculated and averaged, generating an individual ISS value for each participant. Group-level ISS at each time-point was calculated as the mean of these participant-level ISS values. To assess whether the decreased fingerprinting accuracy observed in soldiers at time-point 2 was driven by an increase in ISS from time-point 1 to time-point 2, ISS values at the two time-points were compared in the soldier group using a paired permutation test.

Uniqueness, stability and discriminability calculations. To identify the source of the observed group differences in fingerprinting success, we calculated connectome features, in an approach similar to two previous works using the fingerprinting method[21,27]: stability, typicality, uniqueness, and discriminability. These features were calculated as follows:

Given a similarity matrix $A^t \in \mathbb{R}^{n \times n}$ at time-point t, the *stability* of participant i at time-point t is the i-th diagonal element of A, which corresponds to the Pearson correlation between their CM at baseline and their CM at that specific time-point:

$$Stability_i^t = A_{i,i}^t$$

The *typicality* of participant i at time-point t is the average of all cross-time-point correlations between their CM and every other participant ($A_{i,j}$ and $A_{j,i}$), while removing their correlation with themselves ($A_{i,i}$). For instance, for the comparison between time-points 1 and 2, a participant's typicality was calculated as the average of the correlations between their CM at time-point 1 and all other

participants' CMs at time-point 2, and their CM at time-point 2 and all other participants' CMs at time-point 1. High typicality marks high correlation between self and others (i.e., one's connectome is similar to the "typical" connectome):

$$Typicality_i^t = \sum_{j=1,\, j\neq i}^{n} A_{i,j}^t + \sum_{j=1,\, j\neq i}^{n} A_{j,i}^t$$

Likewise, to estimate participants' *uniqueness*, we subtracted the typicality from 1, such that high uniqueness translates to low correlation between self and others:

$$Uniqueness_i^t = 1 - \frac{1}{2\cdot(n-1)} \cdot Typicality_i^t$$

Finally, the *discriminability* of participant i at time-point t is the ratio between their stability and typicality:

$$Discriminability = \frac{Stability}{Typicality}$$

These measures are presented, per group and per time-point, in Fig. 3. Missing data were again addressed using multiple imputation in an identical approach to Section "Success rates calculation and imputation". All individual measures were imputed in five datasets, and a nested GEE model was executed to examine possible interactions between group and time, and their effect on the uniqueness, stability, and discriminability of the individual functional connectome.

Network contribution calculation

To examine the role of functional connectivity networks in the stability and uniqueness of the functional connectome, we conducted the following analysis. All nodes in the parcellation used in this analysis were labeled as one of seven functional cortical networks based on the original mapping suggested in the atlas[26,30]. We then repeated the fingerprinting procedure, as described in Fig. 1, with the individual CMs of all participants filtered to include only edges from a specific combination of the seven functional networks. We performed this analysis 126 times, once for every possible combination of the seven networks (e.g., the first repetition would include only edges from the visual network, second repetition would include edges from the both the visual and somatomotor networks, third repetition would include edges from the visual, somatomotor and dorsal attention networks, etc.). This was done, as before, for both groups separately, while correlating time-point one with time-points two, three, and four. The fingerprinting success of every iteration was calculated, and the relative contribution of each network was defined as the difference between the average success rate for all iterations which included the network, and the ones that excluded it. Results are shown in Fig. 4. To assess the statistical significance of these network contribution scores, we performed a permutation-based analysis. For each network, we generated empirical null distributions by constructing size-matched pseudo-networks composed of randomly selected cortical parcels. For each pseudo-network, we repeated the full combinatorial fingerprinting procedure and computed a contribution score using the same include–exclude contrast described above. This procedure was repeated 200 times to generate null distributions reflecting the range of contribution values expected by chance for networks of equivalent size. Observed network contributions were then compared against their corresponding null distributions, and statistical significance was evaluated using an FDR correction for seven network comparisons.

In addition, to clarify the mechanism underlying the negative contribution of the default mode network (DMN) to fingerprinting success observed in the main analysis for the soldiers at time-point 2, we conducted a targeted post-hoc examination of the DMN's contribution to the other identification-related measures. Using the same combinatorial framework, we quantified the DMN's contribution to within-subject stability, uniqueness, and discriminability, and assessed significance using the same permutation-based procedure, with FDR correction across the three measures. This post-hoc analysis allowed us to dissociate whether the DMN's negative contribution to fingerprinting success reflected increased between-subject similarity or reduced within-subject stability. Results of this analysis are presented in Supplementary Fig. S4.

Reporting summary

Further information on research design is available in the Nature Portfolio Reporting Summary linked to this article.

Data availability

The raw imaging data are protected medical data collected from active-duty military personnel, the sharing of which is prohibited by the study protocol approved by the institutional ethics committee and by the informed consent provided by participants. De-identified vectorized functional connectivity data supporting the findings of this study are available from the corresponding author upon request. Requests will typically be processed within 30 days. Source data are provided with this paper.

Code availability

The code used for all processing, analyses and statistics is publicly available on GitHub and has been archived on Zenodo to provide a permanent versioned record[39]: https://doi.org/10.5281/zenodo.21594215.

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Author contributions

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Correspondence and requests for materials should be addressed to Noga Yair.

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