The influence of the head model on magnetoencephalography-derived functional connectivity fingerprinting

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Abstract

Functional connectivity (FC)-based neural fingerprinting is an approach that promises to distinguish subjects within a cohort on the basis of the patterns of statistical dependencies between time series recorded mostly if not always noninvasively, with electroencephalography (EEG), magnetoencephalography (MEG), or functional magnetic resonance imaging (fMRI). The message is that brain activity is what differentiates subjects, or in other words, what makes a neural fingerprint “unique”. In EEG- and MEG-derived FC fingerprinting, the activity recorded at the sensors is projected back into cortical sources by means of an inverse model containing the shape of the head and its conductivity, and further averaged to obtain time series of regional activity, used to compute FC. In this study we investigated the role of the head model in fingerprinting. Through a set of experiments aimed to decouple recorded activity and head model for each subject, we found that the head model has a strong influence on the fingerprinting performance, according to two different sets of metrics.

Introduction

Biometrics is the science of identifying people using physiological features (Ratha et al., 2001). Automated person recognition is an important technology that allows recognition of individuals through unique behavioral or physical characteristics. The most common techniques use fingerprints, face, iris or signature (Jain et al., 2008).

Although it is not easy to see how the human brain could be used in this context in the future, there has been a great interest in the so-called brain fingerprinting in recent years. Rather than on physical/morphological characteristics of the brain, the neuroimaging community has focused on the recorded activity, also extending the focus to differentiability (how difficult it is to identify a specific individual), not without some confusion. A few years ago it was proposed that there are significant individual differences in patterns of statistical dependencies among neuroimaging time series (functional connectivity, FC), and that these can act as a “fingerprint” that can accurately identify subjects from a large group in a repeated fMRI scanning scenario (Finn et al., 2015). Similar efforts have been made in EEG (Fraschini et al., 2015; La Rocca et al., 2014) and MEG (Colenbier et al., 2023; da Silva Castanheira et al., 2021; Sareen et al., 2021).

It’s on these latter that we will focus here, our hypothesis being that both the inverse model (projecting sensor data to sources in the brain using a kernel function based on the head model), as well as the forward model (the spread of cortical activity to the sensors) will lead to an influence of the anatomy on reconstructed activity and connectivity, and hence on fingerprinting. Our hypothesis stems from the evidence that electrical field spread and source mixing are not completely eliminated by source reconstruction (Anzolin et al., 2019; Hauk et al., 2022; Hincapié et al., 2017; Mahjoory et al., 2017; Palva et al., 2018; Schoffelen & Gross, 2009).

Together with the obvious fact that the shape of the head is clearly pretty unique, it is thus reasonable to imagine that the head model could contribute to the identifiability and differentiability of source reconstructed FC, unlike previously reported (da Silva Castanheira et al., 2021).

Methods

Data

In this paper we used resting state data from a subset of the CAM-CAN MEG dataset (Shafto et al., 2014; Taylor et al., 2017), consisting of 46 young adults (18–35 years) and 74 older adults (60–85 years).
The retrieved data were already partly preprocessed as described in (Hinault et al., 2021) using the temporal signal-space separation approach (tSSS): 0.98 correlation, 10-s window; bad channel correction: ON; motion correction: OFF; and 50 Hz +harmonics (mains) notch. Afterwards, artifact rejection, filtering (0.3-100 Hz bandpass), temporal segmentation into epochs, averaging and source estimation were performed using Brainstorm (Tadel et al., 2011). In addition, physiological artefacts (e.g. blinks, saccades) were identified and removed using spatial space projection of the signal. In order to improve the accuracy of the source reconstruction, the FreeSurfer (Fischl, 2012) software was used to generate cortical surfaces and automatically segment them from the cortical structures from each participant's T1-weighted anatomical MRI. The advanced MEG model was obtained from a symmetric boundary element method (BEM model, OpenMEEG; Gramfort et al., 2010; Kybic et al., 2005), fitted to the spatial positions of each electrode (Huang et al., 1999). A cortically constrained sLORETA procedure (Pascual-Marqui, 2002) was applied to estimate the cortical origin of the scalp MEG signals.
The two dimensions of the kernel matrix used to perform the inverse model are the number of MEG channels and the number of reconstructed sources, here equal to 338 and 9001 respectively. The 68 time series used to estimate FC were obtained averaging the sources according to the Desikan-Killiany atlas (Desikan et al., 2006).

Measures of statistical dependency

To assess FC in frequency domain we used the corrected imaginary part of the phase locking value (ciPLV; Bruña et al., 2018) and the amplitude-envelope correlation (AEC; Hipp et al., 2012), with and without orthogonalization to remove the signal components with the same phase. The ciPLV and the AEC with orthogonalization are designed to be less sensitive to volume conduction. The relations between these measures, also including coherence, are described in previous instructive papers (Nolte et al., 2020; Pascual-Marqui, 2007).

Measures of fingerprinting

The identifiability matrix is a square, asymmetric matrix, of size determined by the number of subjects. It contains the correlations between the vectorized upper (or lower) half of the functional connectivity matrices of every single participant at time point T1 (y axis) and time point T2 (y axis).

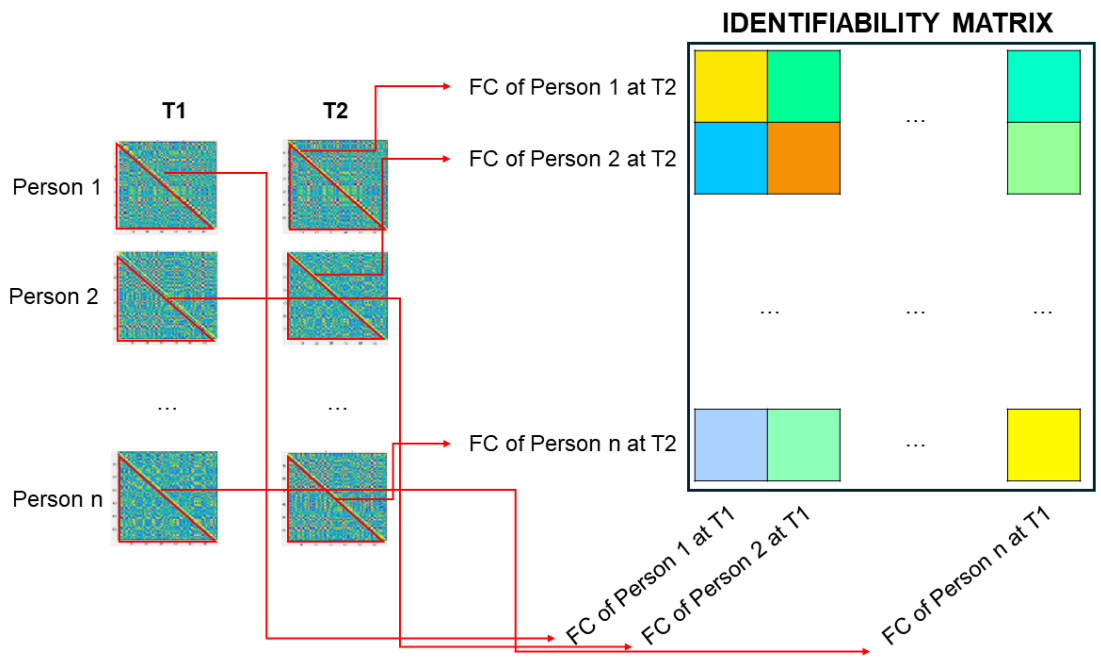

Figure 1: From the individual correlation matrices at time points T1 and T2 to the identifiability matrix.

From this identifiability matrix, two measures can be computed to assess identifiability and differentiability.

The Equal Error Rate (EER) is a standard identifiability measure introduced to summarise the performance of a biometric system. It relies on the basic accuracy measures for biometric verification: the False Reject Rate (FRR), that is the percentage of times that a subject is incorrectly perceived as an imposter (not themselves) by the system, and the False Accept Rate (FAR), that is the percentage of imposters which are incorrectly recognized as the original subject. The EER represents the system error when the FRR equals the FAR. Lower values of EER indicate better classification performance.

Self-differentiability (D_{self}) was introduced as the correlation of one participant with themselves over different timepoints with respect to this participant's correlation to all other

participants (da Silva Castanheira et al., 2021). In mathematical terms this becomes $D_{self,IJ} = (Corr_{II} - \mu_{IJ})/\sigma_{IJ}$ where $Corr_{II}$ is the participant's correlation with themselves, $\mu_{IJ})$ is the mean of the correlations of the participant with all other participants, and σ_{IJ} is the empirical standard deviation. The higher the D_{self}, the better this participant can be differentiated from all the other participants. With respect to other previously introduced measures for global accuracy in differentiability such as I_{self} and I_{diff} (Amico & Goñi, 2018), D_{self} characterizes the accuracy of differentiability of one single participant in comparison to all the others.

Our strategies for mixing/decoupling brain data and head models

We used five different strategies to elucidate and disambiguate the role of the head model in fingerprinting:

1. **Matched head model:** this is the default setting, where the head model of the same subject is used to project the sensor data to the sources, from which the functional connectivity for the subject is obtained. This is the sole case for which a "subject" in the identifiability matrix is always the same human being.
2. **Same brain data:** sensor data from a subject, not further used in the fingerprinting, are projected to the cortex according to their own head model.These source reconstructed data for an external subject would represent the "brain activity" that we expect to be transferred to the sensors when recording. The projection to the sensors is done according to the head model of each of the subjects. Starting from this point, the procedure is the same as described in point 1. If "brain activity" was the sole responsible of brain FC fingerprinting, this strategy should lead to complete lack of differentiation.
3. **Same head model:** sensor data for each subject are projected to the source level via a single head model (of a subject not used in the fingerprinting procedure). From these sources, FCs are derived. If the head model had no effect at all, this strategy would give the same results as the matched head model.
4. **Randomized head model:** sensor data from each subject are projected to the sources through a head model randomly selected (without repetitions) from the whole pool of subjects. From these sources, FCs are derived.

5. **Sensor data FC:** The source reconstruction step is omitted, and FC for each subject is obtained from the sensor data. The FC matrices have in this case a different dimensionality, determined by the number of sensors.

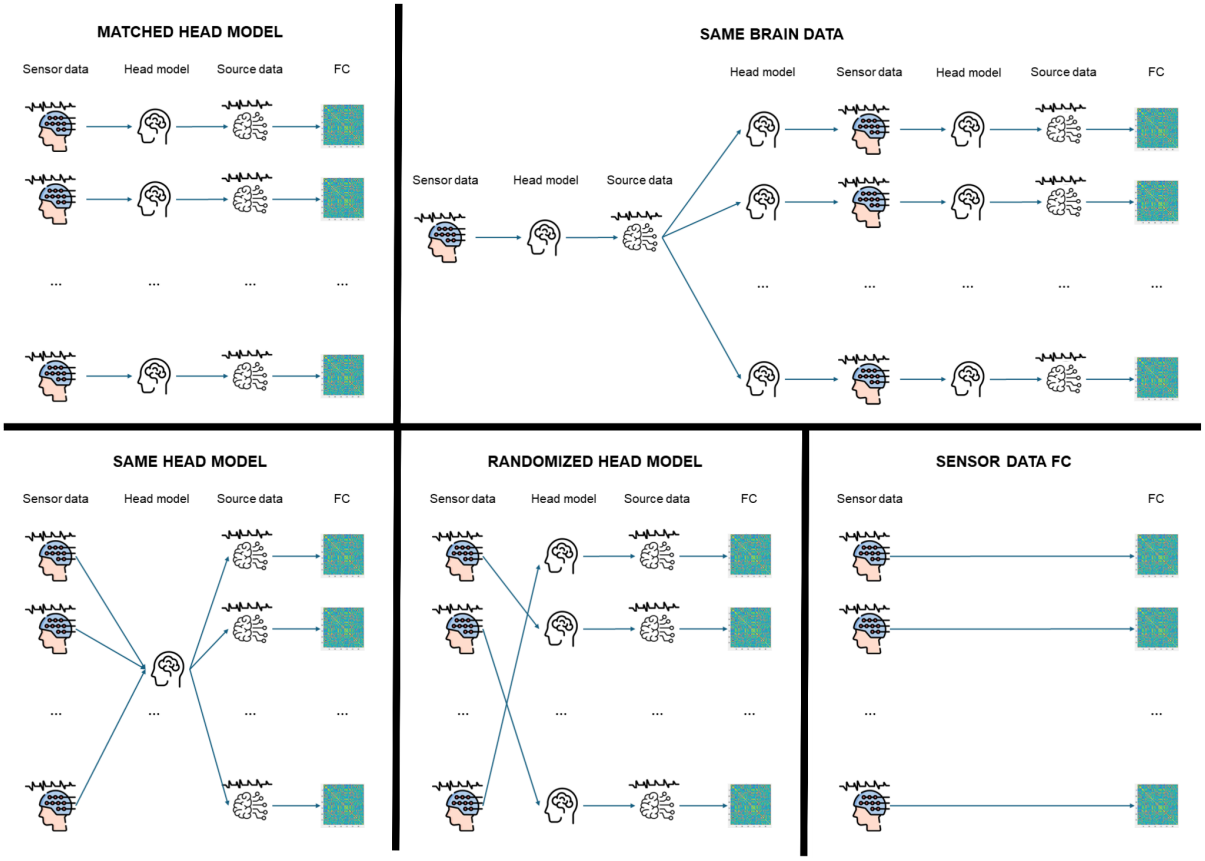

Figure 2. The different combinations of sensor data, head model, and source data used to obtain the Functional Connectivity (FC) matrices to be used in the fingerprinting.

Results

EER

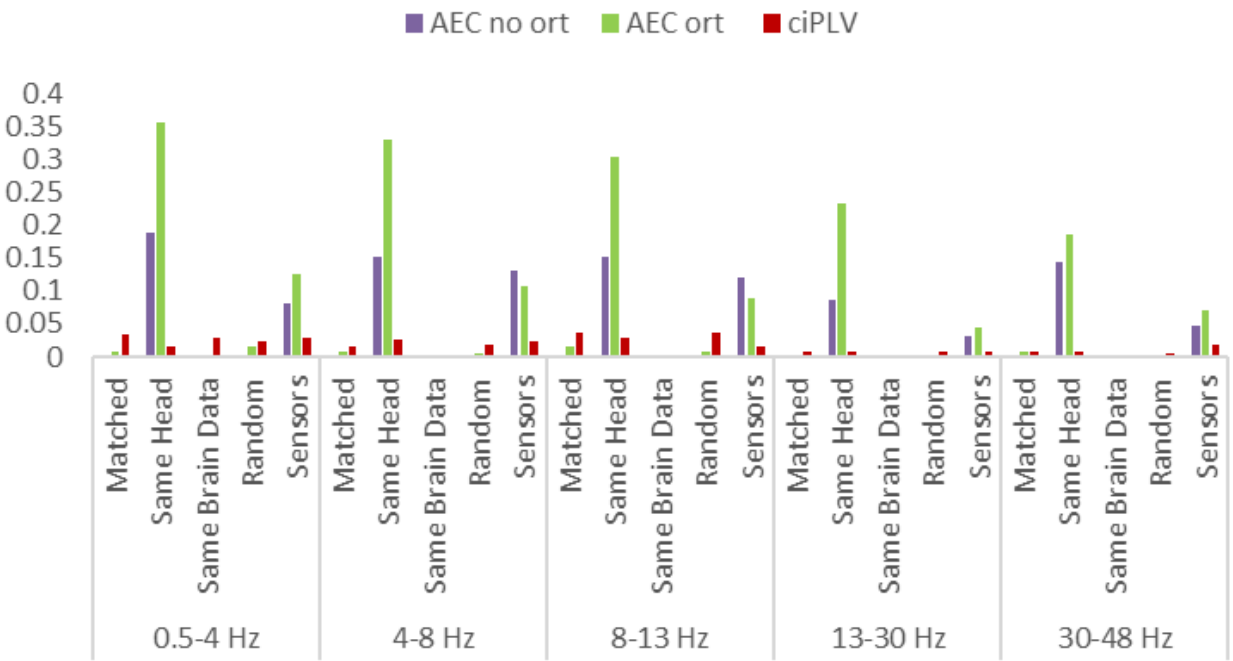

Figure 3. Equal Error Rate (EER) for Amplitude Envelope Correlation (AEC) with and without orthogonalization, and corrected, imaginary part of the Phase Locking Value (ciPLV), for different frequency bands and different matches between sensors and sources.

Figure 3 displays the EER for the three measures, in five different frequency bands, for each of the five strategies depicted in Figure 2.

The results are qualitatively similar across bands, with values decreasing overall with increasing frequency; we will then just proceed to the description of any of the bands.

The Matched case results, as expected, in perfect recognition for the AEC without orthogonalization, very good to perfect recognition for AEC with orthogonalization, and slightly worse performance with ciPLV.

The performances drop dramatically for AEC in the Same Head Model case. This is not the case for ciPLV. A possible explanation, also for the nonzero EER in the Matched case, is that ciPLV is based on the phase and by construction less sensitive to volume conduction issues.

The most striking results are those for the Same Brain Data scenario. Here the “neural data”, the thing that “should make us unique” is the same. Yet, the identification is even better than in the matched case, extending to perfect identification for ciPLV in all bands except theta.

This “better than the real thing” performance could be due to the fact that the “ground truth”

brain activity, consisting of reconstructed source activity from a subject chosen at random, is particularly stable between the two sessions.
The Randomized Head Model case acts as a sort of control against the hypotheses that the success of the default “Matched” strategy is due to a sort of “perfect match” between the data and head model of the same subject. The results here do not suggest evident differences in performance in the two cases.

D_{self}

For this measure, which is defined for each participant to indicate its individual differentiability, we report in Figure 4 the scatter plots of the value obtained with the different “tweaked” combinations in figure 2 against the default “Matched” setting. The results show that for AEC the Same Head approach significantly reduces differentiability, similarly for what happened with fingerprinting as measured by EER. Also FC in sensor space significantly reduces differentiability, but less than the Same Head approach.
Also similarly with what observed with EER, and clearer here, the values for ciPLV are overall lower, and more similar in all cases, with the Sensors and Same Head providing higher differentiability than the Matched case.
For the AEC measures, the “Same Head” case yields also negative values, as fluctuations around a small mean value.

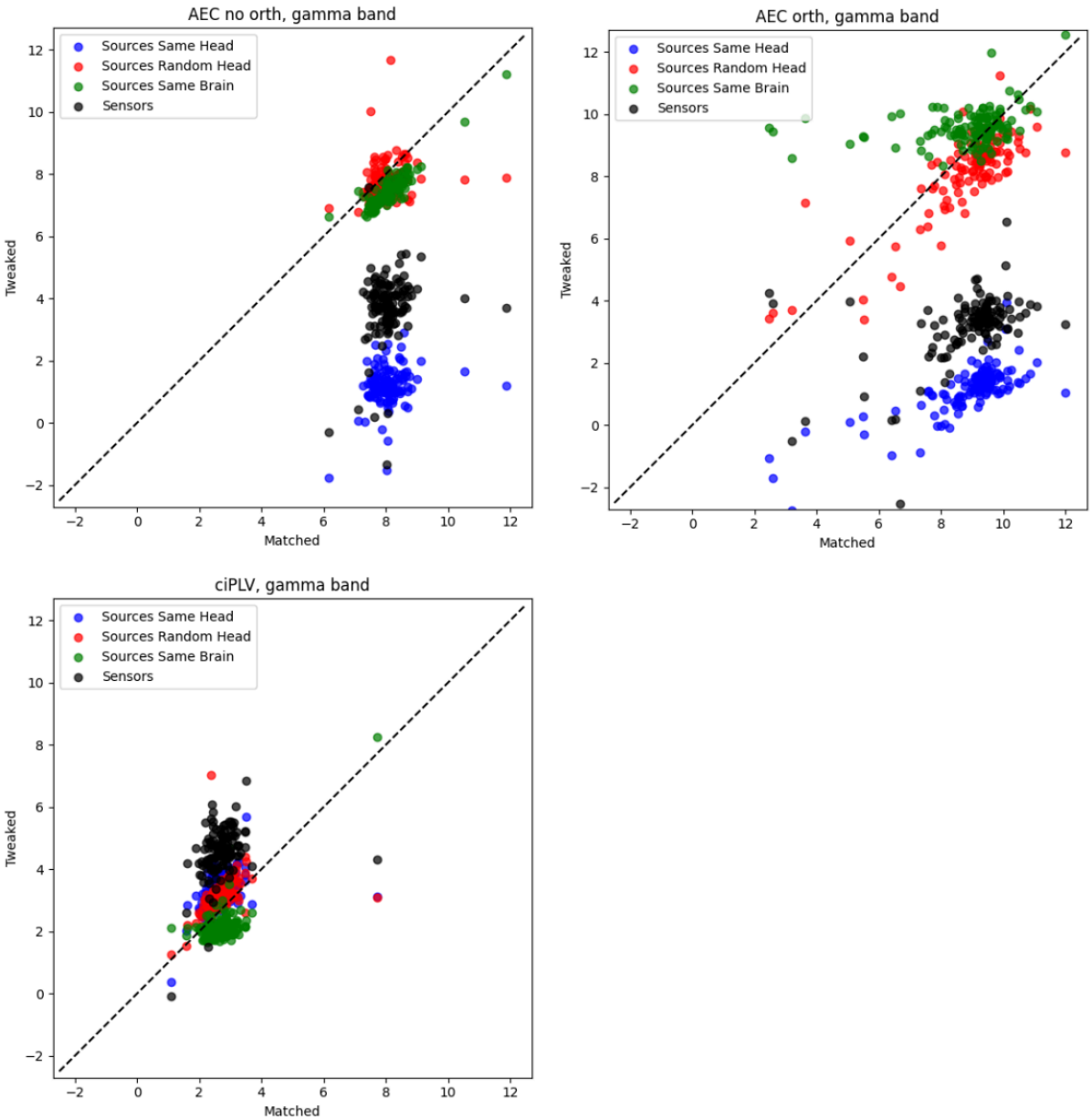

Figure 4. Scatter plots, one for each connectivity measure, of the values of D_{self} for the different manipulations of the inverse model (Tweaked) against the Matched case. Each point represents a subject.

The full results, as Supplementary Material, also include Pearson correlation in the time domain as FC measure and metrics such as the Correct Recognition Rate (CRR) and I_{diff}, providing a different flavor on identifiability and differentiability respectively. The results all point in the same direction.

Brainstorm tutorial

For improved clarity and reproducibility we modified the brain fingerprinting tutorial presenting a reduced version of the results in (da Silva Castanheira et al., 2021) using five subjects from the OMEGA dataset available in Brainstorm to replicate the Same Head, Random Head, Same Brain cases, reporting the results in Figure 5. The results are only indicative since this is an example with only five subjects (that become 4 in the Same Head and Same Brain cases). The participant similarity matrices for Same Head and Random Head are qualitatively similar to the original (Matched) case. For the Same Brain case the cross-subject similarity increases, but identifiability is still clear.

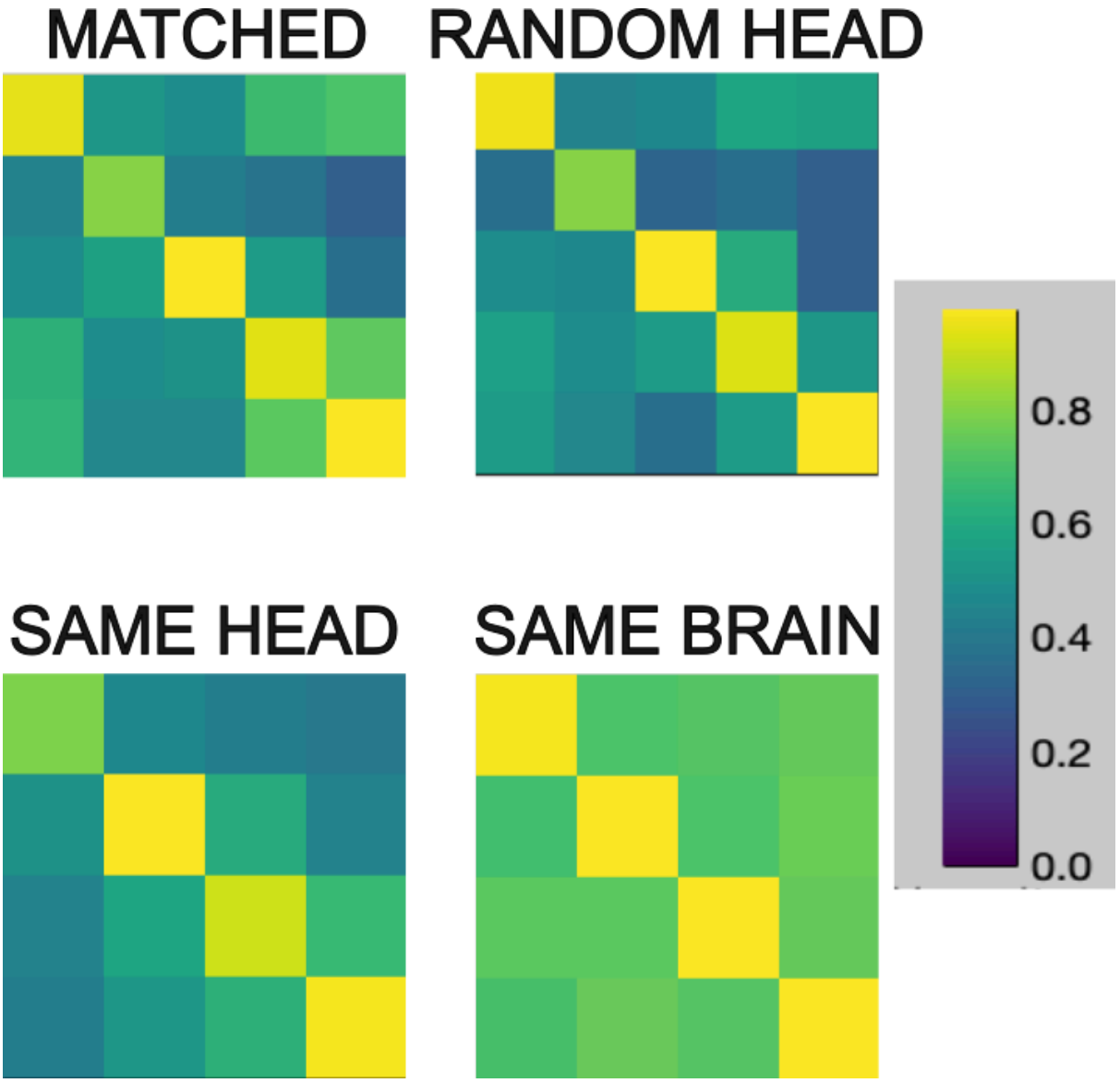

Figure 5. Participant similarity matrices from the Brainstorm Brain Fingerprinting tutorial, in the original (Matched) case and in the modified ones.

Discussion

There was no particular reason why we chose to work with the CAM/CAN dataset for our main results, beyond the fact that it's of good quality and publicly available, and we already had processed and analysed it in other occasions. The points that we made in this study are in our opinion general and easily exportable to other datasets. The two timepoints we considered here belong to the same session, and are spaced by 16 minutes only (as it is also the case for the Brainstorm tutorial on brain fingerprinting using the OMEGA dataset). This is something that, if anything, should favour the role of brain activity over the role of the head model, since the latter is likely more stable in time for a single subject.

We have shown that the head model (likely through the leakage associated with both the forward and the inverse problem) is a major player in determining identifiability and differentiability of a single subject. A previous seminal study on MEG-based brain fingerprinting (da Silva Castanheira et al., 2021) had excluded a strong effect of anatomy mainly through a test consisting in projecting empty-room sensor recordings through the kernel reflecting the subject anatomy. Our hypothesis on the reasons behind this discrepancy is that leakage and mixing depending on the anatomy are induced in the data already at the stage of forward modelling. We also think that starting from the same source level data (our Same Brain data case) represents a more appropriate counterexample for the question "are subjects differentiable by means of their brain activity?".
This problem is not specific to MEG/EEG. A recent study showed that brain anatomy is relevant also in shaping surface fMRI connectivity and its applications, including fingerprinting (Jeganathan et al., 2024). Some issues related to normalization to a common template were found to be of minor importance in volumetric fMRI (Finn et al., 2015).
The effect of the anatomy when fingerprinting is computed on reconstructed sources from MEG reported here should not be surprising, or not even necessarily be a bad thing. Neural activity can definitely play a role in fingerprinting, and task-induced modulations happen while the anatomy is fixed, but one cannot forget that neural activity is linked to anatomy, and some anatomical features or locations also influence the dynamics and its relevance for fingerprinting (Jeganathan et al., 2024). Not to forget that anatomy alone is itself a primary tool for fingerprinting, not only of the brain. Consequently, some interpretations in terms of "unique signature components of fast neurophysiological brain dynamics" (da Silva Castanheira et al., 2021) or along similar lines should be weighted against this evidence. Similarly, in case of twins (da Silva Castanheira et al., 2024; Demuru et al., 2017), what is

heritable and common is primarily the head shape, eventually followed by the dynamics of brain activity.
Finally, together with the caveats exposed above, we should always be careful and align nomenclature and measurement, using consolidated performance metrics (the Equal Error Rate) when the goal is identifiability and other measures when the question is a different one (e.g. difference/separability between distributions). These two concepts are different, and both affected by anatomy.

Data and code availability

The raw data are available at https://cam-can.mrc-cbu.cam.ac.uk/dataset/.
Code is available at https://github.com/MatthiasSchelf/brain-fingerprinting.
Results and identifiability matrices are available at https://zenodo.org/records/12795882.

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Citation Diversity Statement

Recent work in several fields of science has identified a bias in citation practices such that papers from women and other minority scholars are under-cited relative to the number of such papers in the field. Here we sought to check whether our references reflect the diversity of the field in thought, form of contribution, gender, race, ethnicity, and other factors, using the tool available at https://github.com/dalejn/cleanBib. First, we obtained the predicted gender of the first and last author of each reference by using databases that store the probability of a first name being carried by a woman. By this measure and excluding self-citations to the first and last authors of our current paper), our references contain 12.22% woman(first)/woman(last), 22.52% man/woman, 22.64% woman/man, and 42.62% man/man. This method is limited in that a) names, pronouns, and social media profiles used to construct the databases may not, in every case, be indicative of gender identity and b) it cannot account for intersex, non-binary, or transgender people. Second, we obtained predicted racial/ethnic category of the first and last author of each reference by databases

that store the probability of a first and last name being carried by an author of color. By this measure (and excluding self-citations), our references contain 18.57% author of color (first)/author of color(last), 12.13% white author/author of color, 30.46% author of color/white author, and 38.85% white author/white author. This method is limited in that a) names and Florida Voter Data to make the predictions may not be indicative of racial/ethnic identity, and b) it cannot account for Indigenous and mixed-race authors, or those who may face differential biases due to the ambiguous racialization or ethnicization of their names. We look forward to future work that could help us to better understand how to support equitable practices in science.

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