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Local functional connectivity abnormalities in mild cognitive impairment and Alzheimer's disease: A meta-analytic investigation using minimum Bayes factor activation likelihood estimation

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ABSTRACT

Functional magnetic resonance imaging research employing regional homogeneity (ReHo) analysis has uncovered aberrant local brain connectivity in individuals with mild cognitive impairment (MCI) and Alzheimer's disease (AD) in comparison with healthy controls. However, the precise localization, extent, and possible overlap of these aberrations are still not fully understood. To bridge this gap, we applied a novel meta-analytic and Bayesian method (minimum Bayes Factor Activation Likelihood Estimation, mBF-ALE) for a systematic exploration of local functional connectivity alterations in MCI and AD brains. We extracted ReHo data via a standardized MEDLINE database search, which included 35 peer-reviewed experiments, 1,256 individuals with AD or MCI, 1,118 healthy controls, and 205 x-y-z coordinates of ReHo variation. We then separated the data into two distinct datasets: one for MCI and the other for AD. Two mBF-ALE analyses were conducted, thresholded at "very strong evidence" (mBF \geq 150), with a minimum cluster size of 200 mm 3 . We also assessed the spatial consistency and sensitivity of our Bayesian results using the canonical version of the ALE algorithm. For MCI, we observed two clusters of ReHo decrease and one of ReHo increase. Decreased local connectivity was notable in the left precuneus (Brodmann area – BA 7) and left inferior temporal gyrus (BA 20), while increased connectivity was evident in the right parahippocampal gyrus (BA 36). The canonical ALE confirmed these locations, except for the inferior temporal gyrus. In AD, one cluster each of ReHo decrease and increase were found, with decreased connectivity in the right posterior cingulate cortex (BA 30 extending to BA 23) and increased connectivity in the left posterior cingulate cortex (BA 31). These locations were confirmed by the canonical ALE. The identification of these distinct functional connectivity patterns sheds new light on the complex pathophysiology of MCI and AD, offering promising directions for future neuroimaging-based interventions. Additionally, the use of a Bayesian framework for statistical thresholding enhances the robustness of neuroimaging meta-analyses, broadening its applicability to small datasets.

1. Introduction

Mild cognitive impairment (MCI) can be considered as an intermediate state between normal aging and Alzheimer's Disease (AD) and it is mostly characterized by memory deficits, but with normal activities of daily living [\(Klekociuk](#page-10-0) et al., 2016). Considering the growing field of potential disease-modifying treatments, it is mandatory to elucidate the neurobiology of MCI, to obtain the greatest likelihood to modify the natural history of the disease with pharmacological (or non-pharmacological) interventions (Márquez and Yassa, 2019). Over the past 30 years, significant advancements in technology related to functional magnetic resonance imaging (fMRI) have provided an unparalleled environment for in-vivo assessment of the neurobiological substrate of dementias. Notably, resting-state fMRI (rs-fMRI), a

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well-established set of methods capable of detecting spontaneous low-frequency regional temporal correlations in the Blood Oxygen Level-Dependent (BOLD) signal, has emerged as a valuable tool for investigating the disrupted brain functional connectivity of the pathological human brain. Previous rs-fMRI research has predominantly concentrated on abnormalities in long-range connectivity using predetermined regions-of-interest, revealing patterns of hypo-connectivity in distinct cohorts of individuals with MCI and AD ([Badhwar](#page-10-0) et al., [2017;](#page-10-0) Brier et al., [2014](#page-10-0); [Ibrahim](#page-10-0) et al., 2021). By contrast, the establishment of local (or short-range) functional connectivity abnormalities remains less robust, primarily due to the absence of sound fMRI-based metrics. Nevertheless, exploring local functional connectivity aberrations for neurodegenerative conditions holds promise for providing a precise definition of candidate diagnostic and prognostic biomarkers at the brain level (Liu et al., [2021](#page-11-0); [Wang](#page-12-0) et al., 2021).

Independent research endeavors have been dedicated to unveiling atypical local functional connectivity in MCI through the application of regional homogeneity (ReHo). ReHo, a voxel-wise rs-fMRI technique, utilizes Kendall's coefficient of concordance to examine the coherence of time series of the BOLD signal amplitude within small clusters of neighboring voxels [\(Jiang](#page-10-0) and Zuo, 2016; Zang et al., [2004\)](#page-12-0). The data-driven whole-brain nature of the method and its demonstrated high test-retest reliability (Zuo et al., [2013\)](#page-12-0) have contributed valuable insights into the spatial distribution of aberrant local connectivity in MCI, appearing to be concentrated in diverse brain regions associated with visual, default mode, attentional, and sensorimotor networks [\(Cha](#page-10-0) et al., [2015;](#page-10-0) Min et al., [2019;](#page-11-0) [Yuan](#page-12-0) et al., 2016; Yue et al., [2023](#page-12-0)). Notwithstanding the significance of these findings, it is imperative to recognize the inherent inconsistency observed in the outcomes of research efforts. Recent neuroimaging meta-analyses (C. [Yang](#page-12-0) et al., 2023; X. [Yang](#page-12-0) et al., [2023;](#page-12-0) [Zhen](#page-12-0) et al., 2018) have successfully identified consistent changes in ReHo among individuals with MCI in comparison to healthy controls (HCs), encompassing prefrontal, temporo-parietal, limbic, and cerebellar regions. However, the specific localization of these changes varies markedly across different studies (refer to **Fig. S1** for the neuroanatomical distribution of observed ReHo variations in previous meta-analyses conducted on MCI).

Somewhat unexpectedly, the exploration of ReHo in AD has been relatively limited to date. Part of this body of research has revealed concurrent patterns of both local hypo- and hyper-connectivity, spanning neocortical, limbic, and cerebellar territories (He et al., [2007](#page-10-0); [Peraza](#page-11-0) et al., 2016). Other discrepancies emerge in this literature, as certain studies singularly point to either decreased or increased ReHo aberrations in AD when compared to HCs (Liao et al., [2022;](#page-11-0) [Marchitelli](#page-11-0) et al., [2018](#page-11-0)). Finally, conflicting effects have been observed in hub nodes of the human connectome, such as the cingulate cortex, precuneus, and superior temporal cortex (Cha et al., [2015](#page-10-0); He et al., [2007;](#page-10-0) [Peraza](#page-11-0) et al., [2016\)](#page-11-0). Hence, there exists a compelling interest in addressing the prevailing inconsistency and systematically characterizing ReHo alterations in individuals with AD by quantitatively aggregating the existing studies. To date, no comprehensive study has undertaken this endeavor. This gap in the literature underscores a critical need, as such an investigation holds potential significance for the advancement of neuroimaging-based interventions. Additionally, it may contribute to delineating the specific or shared local functional alterations occurring in MCI and AD, a matter of particular importance given the scarcity of direct comparisons and the inherent inconsistencies in the available findings [\(Zhang](#page-12-0) et al., 2021, [2012](#page-12-0)).

Within the context delineated, the primary objective of this study is to conduct a comprehensive meta-analysis using the most extensive compilation of ReHo studies in MCI and AD available to date. This investigation is designed to achieve two principal goals: firstly, to elucidate consistent changes in local brain connectivity in MCI and AD when compared to HCs; and secondly, to discern functional distinctions and commonalities between the conditions, shedding light on potential shared and/or distinct neuropathological pathways throughout the AD

continuum. To this end, we employed the minimum Bayes Factor version of the activation likelihood estimation (ALE) algorithm [\(Costa](#page-10-0) et al., [2023\)](#page-10-0), a recently developed Bayesian implementation of the most widely utilized neuroimaging meta-analytic method globally. This updated statistical threshold not only assesses the spatial convergence of functional variations among the outcomes of previously published studies, but also offers several advantages over traditional thresholding ALE procedures. Distinctive features include its capacity to provide informative insights into the probabilities associated with the validity of considered hypotheses, unlike conventional approaches that solely offer a rejection criterion for the null hypothesis based on a critical p-value ([Liloia](#page-11-0) et al., 2023). Still, it eliminates the prerequisite for a minimum number of studies in the ALE environment to generate unbiased results, enhancing the robustness of the findings [\(Costa](#page-10-0) et al., 2021; [Eickhoff](#page-10-0) et al., [2016](#page-10-0)). To enhance the elucidation of the neurophysiological foundation underlying ReHo aberrations in MCI and AD, we also conducted an examination of large-scale network functional connectivity and cognitive processes statistically associated with the observed ReHo clusters of variation. This analysis was facilitated through the utilization of the Neurosynth database ([Yarkoni](#page-12-0) et al., 2011), providing an interpretation of our findings from an observer-independent and unbiased perspective.

2. Materials and methods

2.1. Search strategy and data selection

The study design adhered to established guidelines for neuroimaging meta-analyses [\(Manuello](#page-11-0) et al., 2022; [Müller](#page-11-0) et al., 2018) and followed PRISMA statement quality criteria (Page et al., [2021](#page-11-0)). A systematic literature search was conducted in the PubMed database using these two sets of keywords: (search a) "*mild cognitive impairment*" OR "*MCI*" OR "*aMCI*" AND "*regional homogeneity*" OR "*ReHo*" OR "*local connectivity*"; (search b) "*Alzheimer's disease*" OR "*AD*" AND "*regional homogeneity*" OR "*ReHo*" OR "*local connectivity*". Furthermore, reference lists of pertinent reviews and meta-analyses ([Badhwar](#page-10-0) et al., 2017; X. Yang et al., [2023;](#page-12-0) [C.](#page-12-0) Yang et al., [2023;](#page-12-0) Zhen et al., [2018\)](#page-12-0) were scrutinized to identify eligible articles. The search was updated until December 2023, without imposing restrictions on publication years.

Screening identified records based on the following inclusion criteria: (i) original peer-reviewed English-language journal articles; (ii) experiments investigating ReHo voxel-wise differences between subjects with MCI or AD and HCs at the whole-brain level; (3) experiments reporting significant results and coordinates (x–y-z foci) of clusters of ReHo changes using a stereotactic space. Records exclusion was based on: (i) case report, conference abstract, or review articles; (ii) animal model investigations; (iii) absence of between-group comparison with HCs; (iv) sample sizes *<* 7 participants per group; (v) experiments focused on specific brain regions (i.e., region-of-interest and/or small volume correction analyses); (vi) analysis of no resting-state fMRI data (i.e., ReHo data derived from task-based fMRI experiments). Ultimately, to mitigate the risk of spurious results stemming from population overlap, multiple ReHo experiments within a single article were taken into account only when reporting on independent clinical groups ([Liloia](#page-11-0) et al., [2024a\)](#page-11-0).

The articles were first extracted by two authors (LD and CT). The fulltexts of the relevant articles were then independently evaluated by three authors (LD, CT, and EP). Disagreements were resolved by unanimous consensus. Peak coordinates of abnormal ReHo clusters were extracted from all included ReHo experiments. Our analyses were carried out in MNI space. To enhance the spatial accuracy of the meta-analysis, we employed the icbm2tal algorithm [\(Laird](#page-11-0) et al., 2010). This algorithm facilitated the conversion of experimental result coordinates initially reported in Talairach space to the MNI space.

2.2. Data analysis

To ascertain the presence of consistent patterns of ReHo variation in individuals with MCI and AD, as well as to determine the force of evidence of our findings, we used both Bayesian-based and canonical versions of the activation likelihood estimation (ALE) method.

Specifically, we firstly adopted the recent version of the ALE algorithm using a minimum Bayes Factor (mBF) thresholding ([Costa](#page-10-0) et al., [2023\)](#page-10-0) as implemented in the MATLAB® script available at [https:](https://figshare.com/articles/software/minimum_bayes_factor_script/17023931) [//figshare.com/articles/software/minimum_bayes_factor_script](https://figshare.com/articles/software/minimum_bayes_factor_script/17023931)

[/17023931](https://figshare.com/articles/software/minimum_bayes_factor_script/17023931). Following the distribution of the evidence categories for the Bayes Factor proposed by Kass and Raftery (Kass and [Raftery,](#page-10-0) 1995), the mBF-ALE threshold was set at strong evidence (i.e., $BF \geq 20$) and very strong evidence (i.e., BF \geq 150), with a cluster size \geq 200 mm $^3.$ Thus, we also evaluated the spatial consistency and sensitivity of our primary findings using the canonical version of the ALE algorithm implemented in the GingerALE software package (v.3.0.2; [https://brainmap.](https://brainmap.org/software.html#GingerALE) [org/software.html#GingerALE\)](https://brainmap.org/software.html#GingerALE) [\(Eickhoff](#page-10-0) et al., 2012) re-analyzing the same data set. Following the recently recommended ALE setting ([Eickhoff](#page-10-0) et al., 2016), ALE results were family-wise error-corrected (FWE-c) for multiple comparisons, with a cluster-level inference of *p <* .05, a cluster-forming threshold of $p < .001$ on the voxel-level (1000). permutation runs), and a with a cluster size ≥ 200 mm 3 .

2.2.1. Anatomical likelihood estimation (canonical version)

The ALE technique furnishes insights into the spatial convergence of coordinates across the selected neuroimaging literature. In this context, each reported coordinate in a neuroimaging experiment is regarded as the center of a Gaussian probability distribution, defined as:

$$
p(d)=\frac{1}{\sigma^2\;\sqrt{\left(2\pi\right)^3}}e^{-\frac{d^2}{2\sigma^2}}
$$

Here, *d* represents the Euclidean distance between the coordinate and the surrounding voxels, while σ signifies the spatial uncertainty. For each selected experiment, a modeled alteration (MA) map is computed, representing the union of all Gaussian distributions associated with that experiment. The integration of all MA maps produced the final ALE map. The significance of each voxel was assessed against a null-hypothesis derived from an iterative random distribution of the coordinates. The cluster-level threshold was hence established through a Monte Carlo simulation of a cluster size distribution. For detailed technical information about the method, consult [Eickhoff](#page-10-0) et al. (2009).

2.2.2. Activation likelihood estimation (minimum Bayes factor version)

The mBF-ALE technique offers insights into the spatial convergence of coordinates across the chosen neuroimaging literature. Importantly, it possesses the capability to furnish informative perspectives on the probabilities associated with the validity of considered hypotheses, even in the context of small meta-analytic datasets. The computation of the mBF relies on Bayes' theorem. In accordance with this theorem, the probability linked to two simultaneous hypotheses, denoted as H_0 and *H*1, can be formally expressed as follows:

$$
P(H_0|D) = \frac{P(D|H_0)}{P(D)}P(H_0)
$$

and, correspondingly

$$
P(H_1|D) = \frac{P(D|H_1)}{P(D)}P(H_1)
$$

where *D* is the measured effect for each brain voxel. Their quotient represents the Bayes' theorem in terms of relative belief:

$$
\frac{P(H_0|D)}{P(H_1|D)} = \frac{P(D|H_0)}{P(D|H_1)} \frac{P(H_0)}{P(H_1)}
$$

Derived from the preceding formulas, the expression for BF_{01} can be articulated as follows:

$$
BF_{01} = \frac{P(D|H_0)}{P(D|H_1)}
$$

The *BF*₀₁ value quantifies the strength of evidence for two concurrent hypotheses: a $BF_{01} > 1$ supports the evidence favoring H_0 , while a BF_{01} < 1 supports H_1 . Traditionally, using the Bayes Factor to gauge evidence for a composite hypothesis involves averaging all potential distinct alternative values. However, in scenarios where infinite alternative values exist, such as the hypothesis "the mean is different from zero", a method is required to address this. To overcome this challenge, the approach involves selecting the alternative value with the most substantial effect against the null hypothesis. This value is considered a summary of evidence across all possible distinct values within the composite alternative hypothesis and is termed the minimum Bayes Factor (mBF). The mBF, therefore, represents the most compelling evidence against the null hypothesis.

Now, consider the hypothesis as the probability of a generic observed effect *x* modeled through a Gaussian distribution with mean *μ* and variance *σ*² :

$$
p(x|\mu,\sigma) = \frac{1}{\sigma\sqrt{2\pi}}e^{-\frac{(x-\mu)^2}{2\sigma^2}}
$$

the BF for the null-hypothesis versus the supported hypothesis ($\mu = x$) is the mBF:

$$
mBF_{01}=e^{-\frac{x^2}{2\sigma^2}}
$$

Upon utilizing the Z map derived from the unthresholded ALE map, the computation of the mBF can be achieved by applying the following formula:

$$
mBF_{01}=e^{-\frac{Z^2}{2}}
$$

by applying a simple exponentiation. This signifies the strength of evidence supporting the null-hypothesis H_0 over the alternative hypothesis *H*1.

The mBF varies across a range from 0 to ∞. As per Kass and Raftery (Kass and [Raftery,](#page-10-0) 1995), the interpretation of values can be delineated as illustrated in Table 1.

2.2.3. Amnestic mild cognitive impairment sub-analysis

A subgroup meta-analytic investigation was undertaken to elucidate consistent patterns of ReHo variation specifically observed in ReHo experiments analyzing individuals with MCI who have an explicitly reported amnestic phenotype (i.e., amnestic mild cognitive impairment; aMCI). This analysis is particularly pertinent as aMCI is characterized by prominent memory impairment and is associated with a heightened risk of progression to AD neuropathology compared to non-amnestic MCI presentations ([Dubois](#page-10-0) and Albert, 2004; [Forlenza](#page-10-0) et al., 2009; [Petersen](#page-11-0) et al., [2014\)](#page-11-0).

2.2.4. Meta-regression analysis

We employed the seed-based d mapping software (v.6.21) ([Albaje](#page-10-0)[s-Eizagirre](#page-10-0) et al., 2019) to perform a series of voxel-wise meta-regression

Table 1 The evidence categories for the Bayes Factor (BF). Adapted from Kass & Raftery.

BF_{10} value	Force of evidence
$1 - 3$	Very weak
$3 - 20$	Positive
$20 - 150$	Strong
>150	Very strong

analyses. These post-hoc analyses aimed to investigate the potential influence of socio-demographic, clinical, and methodological variables on both MCI and AD meta-analytic ReHo findings. Specifically, we assessed the impacts of mean age at the scan session, sex distribution (i. e., percentage of males), mean years of education, sample size, and cognitive impairment (i.e., mean score of the mini-mental state examination test). Details of the data included in these analyses are summarized in [Table](#page-4-0) 2. We also evaluated the effects of MRI field strength and image smoothing level. Details of the data included in these analyses are summarized in **Table S1**. ReHo experiments missing these measures were excluded from the analysis. To achieve an optimal balance between specificity and sensitivity [\(Radua](#page-11-0) et al., 2012), we adopted a voxel-level threshold of *p <* .0005 and a minimum cluster size of 150 $mm³$.

2.2.5. Contrast data analysis

A comprehensive whole-brain voxel-wise comparison analysis was performed to identify shared regions exhibiting ReHo variations between MCI and AD. This involved the comparison of canonical ALE maps, as well as mBF-ALE maps for MCI and AD, with thresholds set at strong evidence (BF > 20) and very strong evidence (BF > 150), along with a minimum cluster size of ≥ 10 mm³.

2.2.6. Cognitive association analysis

The NeuroSynth meta-analytic tool was used to estimate the association between regions with significant ReHo variations and relevant cognitive terms. By utilizing high-frequency keywords associated with functional MRI stereotactic coordinates, NeuroSynth taps into findings from over 15,000 published fMRI studies ([https://github.com/neurosyn](https://github.com/neurosynth) [th\)](https://github.com/neurosynth). This estimation is grounded in the likelihood of a given cognitive function being mentioned alongside the activation of a specific regionof-interest (ROI). In our study, ROIs were defined as 10-mm radius areas surrounding the local peak of each altered ReHo cluster. The values used are derived from quantitative estimates of spatial uncertainty associated with stereotactic coordinates in the ALE environment, indicating a mean spatial uncertainty of 10.2 mm (StDev $= 0.4$ mm) ([Eickhoff](#page-10-0) et al., 2009; [Liloia](#page-11-0) et al., 2021). The estimate from NeuroSynth offers a quantitative measure of the relationship between abnormal brain areas and cognitive processes. Following prior studies ([Hansen](#page-10-0) et al., [2021](#page-10-0); Liloia et al., [2024b,](#page-11-0) [2024a](#page-11-0)), we exclusively focused on concepts from the Cognitive Atlas [\(Poldrack](#page-11-0) et al., 2011) (i.e., 886 concepts at the time of analysis).

2.2.7. Large-scale functional networks decomposition

To quantitatively delineate the functional localization of identified ReHo variations in MCI and AD, we delved into their impact on largescale functional networks. Specifically, we examined the distribution of ReHo variation voxels from mBF-ALE analyses across different brain networks. We adopted the network parcellation introduced by Yeo et al. (Yeo et al., [2011\)](#page-12-0), which delineates the human brain cortex into seven functionally distinct networks based on resting-state fMRI data from 1000 healthy human subjects.

3. Results

The literature searches identified 1374 articles. After the title/abstract screening, 124 records were evaluated at the full-text level. A total of 35 ReHo experiments coming from 27 different articles were included in the quantitative synthesis. PRISMA flow charts are reported in **Fig. S2**. In detail, the MCI group included 28 ReHo experiments, for a total of 1010 subjects compared with 954 HCs and 143 coordinates of alteration (78 of ReHo decrease and 65 of ReHo increase; [Fig.](#page-5-0) 1**A**). The aMCI sub-group included 16 ReHo experiments, for a total of 600 subjects compared with 622 HCs and 99 coordinates of alteration (59 of ReHo decrease and 40 of ReHo increase). The AD group included seven ReHo experiments, for a total of 246 subjects compared with 229 HCs

and 62 coordinates of alteration (50 of ReHo decrease and 12 of ReHo increase; [Fig.](#page-6-0) 2**A**). Detailed clinical and methodological information about the MCI and AD groups are summarized in [Table](#page-4-0) 2 and **Table S1**.

3.1. Local connectivity changes in mild cognitive impairment

mBF-ALE (thresholded at strong evidence). Compared to HCs, subjects with MCI showed seven clusters of ReHo decrease and 14 clusters of ReHo increase, respectively (**Fig. S3A** and **Table S2**). Local peaks of decreased local connectivity were found in the left precuneus (Brodmann area – BA 7), right supramarginal gyrus (BA 40), left inferior temporal gyrus (ITG; BA 20), right globus pallidus, right posterior cingulate cortex (PCC; BA 30), right middle frontal gyrus (BA 46), and left precentral gyrus (BA 6). By contrast, increased local connectivity was found in the right parahippocampal gyrus (BA 36), left lingual gyrus (BA 18), left inferior parietal lobule (BA 39), right postcentral gyrus (BA 40), left cuneus (BA 17), left inferior frontal gyrus (IFG; BAs 9 and 44), right paracentral lobule (BA 5), right culmen of the cerebellum, bilateral putamen, left caudate body, right anterior cingulate cortex (ACC; BA 24), and left precuneus (BA 7). Sub-analysis of the aMCI phenotype revealed statistically significant clusters that largely overlapped with those identified in the main MCI analysis (**Table S2**).

mBF-ALE (thresholded at very strong evidence). Compared to HCs, subjects with MCI showed two clusters of ReHo decrease and one cluster of ReHo increase, respectively [\(Fig.](#page-5-0) 1**B** and [Table](#page-7-0) 3). Local peaks of decreased local connectivity were found in the left precuneus (BA 7) and left ITG (BA 20). By contrast, increased local connectivity was found in the right parahippocampal gyrus (BA 36). The analysis of the aMCI sub-group revealed statistically significant clusters that overlapped with those identified in the primary MCI analysis, except for the cluster located in the left BA 20 [\(Table](#page-7-0) 3).

Canonical ALE (thresholded at cluster-level). Compared to HCs, subjects with MCI showed one cluster of ReHo decrease and one cluster of ReHo increase, respectively [\(Fig.](#page-5-0) 1**C** and [Table](#page-7-0) 3). Local peak of decreased local connectivity was found in the left precuneus (BA 7). By contrast, increased local connectivity was found in the right parahippocampal gyrus (BA 36). The analysis of aMCI sub-group revealed statistically significant clusters that overlapped with those identified in the primary MCI analysis.

3.2. Local connectivity changes in Alzheimer's disease

mBF-ALE (thresholded at strong evidence). Compared to HCs, subjects with AD showed 17 clusters of ReHo decrease and 10 clusters of ReHo increase, respectively (**Fig. S3B** and **Table S3**). Local peaks of decreased local connectivity were found in the bilateral PCC (BAs 23, 30, and 31), left medial frontal gyrus (BA 10), left superior parietal lobule (BA 40), left precuneus (BA 7), left cuneus (BA 17), right middle occipital gyrus (BA 18), right precentral gyrus (BA 4), left ACC (BA 24), left superior temporal gyrus (BAs 22), left postcentral gyrus (BA 2), bilateral middle temporal (BA 39) and left supramarginal gyrus (BA 40). By contrast, increased local connectivity was found in the left ITG (BA 19), right declive of the cerebellum, left PCC (BA 31), left precuneus (BA 7), left IFG (BA 44), and in the bilateral cuneus (BA 18) and lingual gyrus (BA 19).

mBF-ALE (thresholded at very strong evidence). Compared to HCs, subjects with AD showed one cluster of ReHo decrease and one cluster of ReHo increase, respectively [\(Fig.](#page-6-0) 2**B** and [Table](#page-7-0) 4). The peak of decreased local connectivity was found in the right PCC (BA 30 extending to BA 23). By contrast, increased local connectivity was found in the left PCC (BA 31).

Canonical ALE (thresholded at cluster-level). Compared to HCs, subjects with AD showed one cluster of ReHo decrease and one cluster of ReHo increase, respectively [\(Fig.](#page-6-0) 2**B** and [Table](#page-7-0) 4). The peak of decreased local connectivity was found in the right PCC (BA 30 extending to BA 23). Increased local connectivity was found in the left PCC (BA 31).

Table 2

Regional homogeneity experiments included in the activation likelihood estimation meta-analyses of mild cognitive impairment (A) and Alzheimer's disease (B): demographic and clinical details.

AD, Alzheimer's Disease; aMCI, amnestic mild cognitive impairment; HC, healthy control group; MCI, mild cognitive impairment; N/A, data not associated; PAT, patients; SD, standard deviation.

(caption on next page)

A) ReHo changes in Mild Cognitive Impairment

Fig. 1. Results of mild cognitive impairment (MCI) meta-analysis. (A) Neuroanatomical distribution of regional homogeneity variation findings selected from included experiments. Brain clusters of regional homogeneity decrease (red) and increase (blue) in subjects with mild cognitive impairment compared to healthy controls using the minimum Bayes Factor version of the activation likelihood estimation thresholded at very strong evidence (A) and using the cluster-level familywise error rate (FWE) version of the activation likelihood estimation (B). Findings are visualized as coronal/axial/sagittal slices (2-D cortical, subcortical, and cerebellar view) in neurological convention. Below, the functional network decomposition results (bar charts represent the number of mm³ of regional homogeneity variation in subjects with mild cognitive impairment compared to healthy controls) and the cognitive processes statistically related to the ALE findings according to the Neurosynth database (font sizes represent the magnitude of the associated Z-scores). ALE = activation likelihood estimation; mBF = minimum Bayes Factor; VA = ventral Attention network; DM = default mode network; FP = frontoparietal network; SM = somatomotor network; DA = dorsal attention network; VIS = visual network; LIM = limbic network.

Fig. 2. Results of Alzheimer's disease (AD) meta-analysis. (A) Neuroanatomical distribution of regional homogeneity variation findings selected from included experiments. (B) Brain clusters of regional homogeneity decrease (red) and increase (blue) in subjects with Alzheimer's disease compared to healthy controls using both the minimum Bayes Factor version of the activation likelihood estimation thresholded at very strong evidence and using the cluster-level family-wise error rate (FWE) version of the activation likelihood estimation. Findings are visualized as coronal/axial/sagittal slices (2-D cortical, subcortical, and cerebellar view) in neurological convention. Below, the functional network decomposition results (bar charts represent the number of mm³ of regional homogeneity variation in subjects with Alzheimer's compared to healthy controls) and the cognitive processes statistically related to the ALE findings according to the Neurosynth database (font sizes represent the magnitude of the associated Z-scores). ALE = activation likelihood estimation; mBF = minimum Bayes Factor; VA = ventral Attention network; DM = default mode network; FP = frontoparietal network; SM = somatomotor network; DA = dorsal attention network; VIS = visual network; LIM = limbic network.

Table 3

Clusters of regional homogeneity variation in mild cognitive impairment compared with healthy controls.

BA = Brodmann area; ITG = inferior temporal gyrus; MNI = Montreal Neurological Institute; mBF = minimum Bayes Factor; ALE = activation likelihood estimation. * = brain cluster also identified via canonical ALE algorithm with a cluster-level inference of *p <* .05, and a cluster-forming threshold of *p <* .001 on the voxel-level.

 $\frac{8}{3}$ = brain cluster also identified for the amnestic mild cognitive impairment (aMCI) sub-group using the mBF-ALE algorithm and thresholded at very strong evidence.

Table 4

BA = Brodmann area; PCC = posterior cingulate cortex; MNI = Montreal Neurological Institute; mBF = minimum Bayes Factor; ALE = activation likelihood estimation. * = brain cluster also identified via canonical ALE algorithm with a cluster-level inference of *p <* .05, and a cluster-forming threshold of *p <* .001 on the voxel-level.

3.3. Effects of clinical, socio-demographic, and methodological variables

Several moderators were examined to understand their betweenexperiment influence on published ReHo findings in MCI and AD. No significant linear associations were found with age, sex distribution, education, sample size, cognitive impairment, smoothing, and MRI field strength at $p < .0005$ and a minimum cluster size of 150 mm $^3.$

3.4. Local connectivity changes in Alzheimer's disease vs. mild cognitive impairment

Using voxel-wise maps coming from canonical ALE and mBF-ALE thresholded at very strong evidence analyses, no voxels of overlap were identified between the two primary data sets for both ReHo decreases and increases. Contrariwise, findings coming from the mBF-ALE thresholded at strong evidence revealed a spatial convergence of ReHo decrease in the right PCC (BA 30) and bilateral precuneus (BA 7). One cluster of convergence of ReHo increase was also identified in the left IFG (BA 44) **(Fig. S3C** and **Table S4**).

3.5. Cognitive associations

NeuroSynth association analyses uncovered quantitative associations between ReHo changes in MCI/AD and a diverse array of cognitive processes. Utilizing both canonical and mBF-ALE algorithms, we identified cognitive functions linked to peaks of ReHo variation in MCI, including learning and memory domain, such as navigation, episodic memory, memory retrieval, encoding, and spatial ability. Although both algorithms highlighted the same overall functions, a notable difference emerged in the language domain associated with the left ITG. Specifically, the mBF-ALE algorithm revealed significant associations with orthographic lexicon and phonological retrieval. Further details on the cognitive terms associated with MCI are presented in [Fig.](#page-5-0) 1 and **Table S5**. In AD, ReHo alterations were characterized by the involvement of different cognitive processes within the learning and memory and social function domains, encompassing navigation, memory, autobiographical memory, social cognition, social norm processing, and mentalization [\(Fig.](#page-6-0) 2 and **Table S6**).

3.6. Large-Scale functional networks decomposition

The results of the functional large-scale network decomposition analysis for MCI and AD are illustrated in [Figs.](#page-5-0) 1 and 2, respectively. In AD, the entire pattern of variation was associated with the default mode network (DMN), regardless of whether there was an increase or decrease in ReHo changes. In MCI, a distinct pattern emerged with the DMN prominently implicated in ReHo decreases, while the limbic network was exclusively involved in ReHo increases.

4. Discussion

To the best of our knowledge, this study offers a unique quantitative synthesis of aberrant local functional connectivity in MCI and AD compared with HCs. By employing both novel Bayesian-based and canonical versions of the ALE method, we provided evidence about the presence of consistent patterns of ReHo variation in these clinical populations, mainly localized within certain hub areas of the functionally defined default mode network. However, when stringent statistical thresholds were applied, our data-driven approach did not uncover spatial overlap of alterations between MCI and AD for both decreased and increased ReHo data. Additionally, cognitive large-scale analysis of the identified brain areas unveiled observer-independent associations with memory, language, and social functioning domains commonly impaired starting from the predementia stage of AD spectrum disease.

4.1. Altered reho in mci

The bilateral precuneus and left ITG revealed very strong evidence of local hypo-connectivity in MCI, while the right parahippocampal gyrus reported very strong evidence of local hyper-connectivity. Current findings only partially corroborate with those of the previous metaanalyses on the topic, while also introduce novel insights into the functional pathophysiology of this clinical entity. Specifically, we confirmed previous observations of ReHo decrease in the bilateral precuneus, as reported by C. Yang et al. [\(2023\)](#page-12-0) and X. Yang et al. [\(2023\)](#page-12-0), alongside identifying a significant ReHo increase in the right parahippocampus, a phenomenon previously highlighted solely by X. [Yang](#page-12-0) et al. [\(2023\).](#page-12-0) In contrast, our findings diverge from the early heterogeneous observations regarding ReHo alterations in several brain regions

(C. Yang et al., [2023;](#page-12-0) X. Yang et al., [2023;](#page-12-0) Zhen et al., [2018](#page-12-0)). We did not replicate, at least at very strong evidence and cluster-level FWE thresholding, patterns of increased/decreased ReHo changes in ACC, insular cortex, lingual gyrus, cerebellum, superior temporal gyrus, inferior parietal lobule, and prefrontal areas. These discrepancies may be attributed to a number of methodological factors. For example, our study leveraged the rapid expansion of the field, allowing us to integrate the largest available dataset on the topic; therefore, we optimized the balance between sensitivity and susceptibility to false positive effects, increasing the statistical power of our analysis [\(Eickhoff](#page-10-0) et al., 2016; [Manuello](#page-11-0) et al., 2022; [Müller](#page-11-0) et al., 2018). Moreover, in light of evidence from recent simulation and experimental efforts [\(Albajes-Eiza](#page-10-0)girre et al., [2019;](#page-10-0) [Albajes-Eizagirre](#page-10-0) and Radua, 2018; [Eickhoff](#page-10-0) et al., [2016\)](#page-10-0), it is plausible to hypothesize that the statistical thresholding procedures and multiple comparisons correction utilized in early meta-analyses are susceptible to insufficient control over type I errors within the neuroimaging coordinate-based meta-analytic domain.

Precuneus (BA 7) has been mentioned in previous MCI research, showing gray matter atrophy [\(Nickl-Jockschat](#page-11-0) et al., 2012), cortical thickness reduction ([Haussmann](#page-10-0) et al., 2017), accumulation of amyloid-β plaque (Mak et al., [2023](#page-11-0)), as well as reduced connectivity ([Drzezga](#page-10-0) et al., 2011). Moreover, in line with our cognitive association analysis, studies have found that this area can be associated with spatial ability and egocentric navigation impairment in aMCI populations (Vlček and Laczó, 2014; [Weniger](#page-12-0) et al., 2011). Independent efforts have indicated an intricate large-scale functional organization linked to the human precuneus, dividing it into anterior, central, and posterior parts ([Margulies](#page-11-0) et al., 2009; [Zhang](#page-12-0) and Li, 2012). Intriguingly, our decomposition analysis demonstrated that the identified cluster of local hypo-connectivity predominantly resides in the central portion of the BA 7, known for its hub role within the DMN [\(Cunningham](#page-10-0) et al., 2016). Therefore, this result confirms the notion that such a network is functionally impaired in MCI ([Eyler](#page-10-0) et al., 2019; Joo et al., [2016](#page-10-0)) and underscores that the decreased short-range functionality of BA 7 stands out as a robust pathophysiological indication, plausibly representing effects of ongoing early neurodegeneration (Sorg et al., [2007](#page-11-0)).

We have identified voxels of ReHo decrease in the left ITG, an associative region recently found hypoperfused via arterial spin labeling in MCI patients ([Thomas](#page-11-0) et al., 2021) and known to be involved in high-cognitive functions, including learning tasks and semantic language processing (Lin et al., [2020\)](#page-11-0). However, it is worth noting that this finding has not been replicated in the sub-analysis focused on individuals with aMCI, even though aMCI and prodromal stages of AD are known to have a specific involvement of the inferior temporal gyrus, also with an increased synaptic loss [\(Scheff](#page-11-0) et al., 2011). The different sample size of the studies in MCI and aMCI as well as the clinical heterogeneity could at least partially explain this discrepancy.

Both Bayesian and canonical versions of the ALE method have revealed a statistically significant ReHo increase at the level of the right parahippocampal gyrus. This is not a surprising result, given that many studies revealed higher cortical thickness (Fernández et al., 2020), increased long-range (Penalba-Sánchez et al., 2023) and short-range (Yue et al., [2023\)](#page-12-0) connectivity of this memory-related region. Previous research suggests that the ReHo increase of the BA 36 may be explained by a mechanism of compensation for the neurodegeneration of other temporo-limbic regions recruited in memory processing [\(Bai](#page-10-0) et al., [2008;](#page-10-0) X. Yang et al., [2023;](#page-12-0) [Zhang](#page-12-0) et al., 2012) and for the functional disruption of the DMN (C. Yang et al., [2023;](#page-12-0) Zhou et al., [2014\)](#page-12-0). Other authors have proposed that this phenomenon, in the context of aging and neurodegeneration, could be a temporary reorganization of regional neural activity of the connectome hub nodes due to neuroanatomical damage localized elsewhere [\(Damoiseaux](#page-10-0) et al., 2012; [Dolcos](#page-10-0) et al., [2002;](#page-10-0) [Hillary](#page-10-0) et al., 2014), followed by a structural morphometric decrease with progression of behavioral deficits [\(Mancuso](#page-11-0) et al., 2020; [Manuello](#page-11-0) et al., 2018; [Montal](#page-11-0) et al., 2018). While it is tempting to speculate about the biological meaning of the identified abnormal

patterns of local connectivity, our non-invasive meta-level approach cannot directly address this issue, which remains a subject of ongoing debate ([Jiang](#page-10-0) et al., 2015). In other words, the biological implications of ReHo variations in the neurological context remain unclear, emphasizing the critical need to investigate the histological and physiological basis of abnormal connectivity for distinct clinical entities.

4.2. Altered ReHo in AD

The PCC was the focus of perturbed connectivity in AD, with a concordance between mBF-ALE at very strong evidence and canonical ALE. As reported, one cluster of reduced connectivity on the right side of the PCC and one contralateral cluster of increased connectivity were evident. PCC is commonly affected in neurodegenerative diseases and particularly in AD ([Zhang](#page-12-0) et al., 2024). This involvement can be seen in a more complex picture of amyloid deposition and brain atrophy spatially resembling the pattern of DMN [\(Buckner](#page-10-0) et al., 2005). Interestingly, PCC functional connectivity is also related to the APOE genetic status, with young healthy E4 carriers showing an increased DMN functional connectivity, as a coping strategy to overcome network inefficiency related to the at-risk APOE genotype [\(Filippini](#page-10-0) et al., 2009). Furthermore, considering the integrated model of PCC function (i.e., Arousal, Balance, and Breadth of Attention model; ABBA) [\(Leech](#page-11-0) and [Sharp,](#page-11-0) 2014) a dynamic system approach can help in the understanding of the complex functioning of PCC. From this point of view, dynamic functional connectivity recently demonstrated a fine-grained fluctuation of PCC connectivity in the AD spectrum, in particular for the right PCC dynamic ReHo variability (Liao et al., [2022\)](#page-11-0). Taken together, these data can partially account for the differential left/right involvement of PCC in our analysis, as a result of different pathological and compensatory mechanisms still in action in AD spectrum and potentially captured by this methodological approach.

We have observed a more circumscribed patterning of ReHo variation in AD compared to MCI. This is an unexpected result given the numerous pieces of evidence suggesting network-based damage spread in the AD course [\(Cauda](#page-10-0) et al., 2020; [Fornari](#page-10-0) et al., 2019; Li et al., [2022](#page-11-0); Raj and [Powell,](#page-11-0) 2018). Probably, moot points are the left medial frontal gyrus, right precentral gyrus, left IFG, and bilateral temporal areas that, although found aberrant with a more liberal threshold (i.e., mBF-ALE at strong evidence), did not survive our most rigorous statistical thresholding procedures. One possible methodological explanation for this result is that the exact loci of local maximum in these brain areas differed considerably across experiments. This, and the fact that our design used x–y-z coordinates instead of three-dimensional parametric maps, could explain why no significant spatial convergences survived in this study. We also note, however, that peaks of ReHo variation in AD tend to concentrate in ventral and dorsal PCC across independent studies (Cha et al., [2015](#page-10-0); He et al., [2007](#page-10-0); Liao et al., [2022;](#page-11-0) [Marchitelli](#page-11-0) et al., [2018;](#page-11-0) [Zhang](#page-12-0) et al., 2012). In light of this, we speculate that short-range local functional connectivity aberrations may not follow the same transneural spread and connectome-based mechanisms linked to volumetric degeneration and long-range functional connectivity impairments. Future multidisciplinary research is sorely needed to disentangle this issue and to further elucidate the mechanisms underlying ReHo variations in the AD continuum.

4.3. Altered ReHo in MCI vs. AD

Patients diagnosed with MCI and AD did not exhibit voxel of alteration overlap for both decreased and increased ReHo data. This result remains consistent when conservative thresholding procedures are employed at Bayesian and FWE levels of inference, as well as when the aMCI sub-group was compared with the AD group. However, using a more liberal Bayesian force of evidence (i.e., $BF \geq 20$) we found common clusters of local hypo-connectivity in the right PCC and bilateral precuneus. It is essential to highlight that our meta-level finding aligns with the only two extant cross-sectional reports addressing directly this topic ([Zhang](#page-12-0) et al., 2021, [2012](#page-12-0)). Interestingly, previous literature data partially support the idea of a differential involvement of precuneus and PCC in the different stages of AD pathology, with the former more involved in MCI and the latter progressively impaired in AD ([Benzinger](#page-10-0) et al., [2013;](#page-10-0) Liu et al., [2008;](#page-11-0) [Miners](#page-11-0) et al., 2016; [Thomas](#page-12-0) et al., 2015). Beside this, we cannot also rule out a diagnostic heterogeneity in the reported clinical diagnosis across studies, as well as the inclusion of a portion of patients with an official diagnosis of AD but with a clinical picture more resembling atypical presentation of AD pathology like posterior cortical atrophy or dementia with Lewy body. Interestingly, these clinical entities are often characterized by a relative sparing of posterior cingulate/precuneus regions, defined as cingulate island sign ([Whitwell](#page-12-0) et al., 2017), which can play a role in the aforementioned discrepancy among MCI and AD.

4.4. Limitations and future challenges

The current findings should be considered in light of several limitations, primarily stemming from the coordinate-based approach employed. Whether in its Bayesian or canonical form, the ALE method selectively examined local maxima of functional variation [\(Costa](#page-10-0) et al., [2023;](#page-10-0) [Eickhoff](#page-10-0) et al., 2009), thereby overlooking other significant voxels within clusters of hypo/hyperconnectivity. While the rigorous standardization of this methodology minimizes the likelihood of spatial errors, original image-based analyses utilizing statistical parametric mapping offer superior spatial resolution and signal-to-noise ratio ([Manuello](#page-11-0) et al., 2023, [2022](#page-11-0); [Müller](#page-11-0) et al., 2018). Therefore, future research endeavors could expand upon our findings by replicating them using multi-site mega-analysis designs.

Our meta-level design is also cross-sectional; thus, our short-range functional connectivity evaluation was circumscribed to a group categorization of published data about MCI/aMCI and AD. In this regard, we note that the MCI label encompasses subjects in the prodromal dementia stage but also with stable cognitive functions (Mitchell and [Shiri-Feshki,](#page-11-0) [2009\)](#page-11-0). While we found that patterns of variation in the aMCI subgroup largely overlapped with those of the overall MCI group, the existing literature did not allow us to fully resolve this issue due to the unavailability of biological marker analyses for detecting prodromal Alzheimer's disease in the considered cohorts. De facto, only etiological characterization utilizing biological and imaging markers, or follow-up evaluations, can reliably predict the development of Alzheimer's disease or other neurodegenerative dementias. However, follow-up studies have consistently reported a high conversion rate to AD among individuals who meet the clinical criteria for MCI. The annual conversion rate from MCI to dementia ranges from 15 % to 40 %, with those diagnosed with aMCI being at the most and closest risk of conversion [\(Espinosa](#page-10-0) et al., [2013;](#page-10-0) [Farias](#page-10-0) et al., 2009; [Geslani](#page-10-0) et al., 2005; [McGrattan](#page-11-0) et al., 2022; [Tabert](#page-11-0) et al., 2006; [Thaipisuttikul](#page-11-0) et al., 2022). Among these individuals, approximately 80 % tend to progress to AD ([Schmidtke](#page-11-0) and [Hermeneit,](#page-11-0) 2008; Tábuas-Pereira et al., 2016; Visser and [Verhey,](#page-12-0) 2008). Further primary research incorporating longitudinal follow-up analyses is essential to identify distinctive short-range functional connectivity profiles. Future cohorts should therefore include subjects with MCI who have undergone biological characterization and for whom ReHo data are available.

Future investigations could enhance this methodological issue by incorporating longitudinal follow-up analyses to gain deeper insights into the dynamic trajectories of ReHo aberrations in the AD continuum, particularly concerning the transition from aMCI to AD. Also, it can be argued that in analyzing the AD dataset we cannot ensure an adequate type I error control due to the limited availability of published data. While we aspire that future AD fMRI research will place greater emphasis on ReHo analyses, it is important to note that previous empirical tests have shown that the mBF-ALE algorithm effectively minimizes this type of error in such scenarios ([Costa](#page-10-0) et al., 2023). Lastly,

while we were able to reveal consistent and reproducible findings across the published literature, it is crucial to acknowledge the limitations of our group-level design in discerning the influence of specific critical variables (i.e., sex, level of cognitive performance or education, and sample size) that could potentially affect the replicability of functional connectivity brain research in MCI/AD [\(Mohtasib](#page-11-0) et al., 2022; [Passa](#page-11-0)[monti](#page-11-0) et al., 2019; [Williamson](#page-12-0) et al., 2022; Zhu et al., [2021](#page-12-0)). We note that our post hoc meta-regression analyses did not find a significant impact of these socio-demographic and clinical variables on ReHo findings in both clinical conditions of interest. However, it is crucial to recognize that these results are derived from mean group values that may include considerable variability among subjects, especially in multicenter contexts. Therefore, these findings should be interpreted cautiously and warrant further investigation in primary ReHo research studies.

5. Conclusions

This meta-analysis provides a first quantitative synthesis about regional homogeneity aberrations in MCI and Alzheimer's disease identified over the last two-decades, providing valuable insights into a relatively underexplored area of research. Despite the heterogeneity in the literature, our meta-level approach has uncovered compelling evidence for consistent patterns of local hypo/hyperconnectivity variation in these clinical populations, predominantly localized within specific hub nodes of the human connectome. These findings represent a provisional yet insightful step toward a deeper understanding of the complex pathophysiology of these clinical entities and present promising avenues for future neuroimaging-based interventions and diagnostic MRI-based approaches.

Ethics approval and consent to participate

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Data and code availability statements

Data were analyzed using the minimum-Bates Factor activation likelihood estimation as implemented in the MATLAB® script available at [https://figshare.com/articles/software/minimum_bayes_factor_script](https://figshare.com/articles/software/minimum_bayes_factor_script/17023931) [/17023931](https://figshare.com/articles/software/minimum_bayes_factor_script/17023931). Data were analyzed using the GingerALE software package (version 3.0.2) that can be freely downloaded from [https://www.](https://www.brainmap.org/ale/) [brainmap.org/ale/](https://www.brainmap.org/ale/). Functional parcellations can be freely downloaded from [https://surfer.nmr.mgh.harvard.edu/fswiki/CorticalParcellatio](https://surfer.nmr.mgh.harvard.edu/fswiki/CorticalParcellation_Yeo2011) [n_Yeo2011.](https://surfer.nmr.mgh.harvard.edu/fswiki/CorticalParcellation_Yeo2011) Foci and functional maps are available upon reasonable request.

CRediT authorship contribution statement

Tommaso Costa: Writing – review & editing, Writing – original draft, Validation, Supervision, Software, Resources, Project administration, Methodology, Investigation, Funding acquisition, Data curation, Conceptualization. **Enrico Premi:** Writing – review & editing, Writing – original draft, Methodology. **Barbara Borroni:** Writing – review & editing, Writing – original draft, Methodology. **Jordi Manuello:** Writing – review & editing. **Franco Cauda:** Writing – review & editing. **Sergio Duca:** Writing – review & editing, Supervision. **Donato Liloia:** Writing – review & editing, Writing – original draft, Visualization, Validation,

Software, Methodology, Investigation, Formal analysis, Data curation, Conceptualization.

Declaration of competing interest

The authors report no declarations of interest.

Data availability

Data will be made available on request.

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Supplementary materials

Supplementary material associated with this article can be found, in the online version, at [doi:10.1016/j.neuroimage.2024.120798](https://doi.org/10.1016/j.neuroimage.2024.120798).

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