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# Population shrinkage of covariance (PoSCE) for better individual brain functional-connectivity estimation

Mehdi Rahim, Bertrand Thirion, Gaël Varoquaux

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## Abstract

Estimating covariances from functional Magnetic Resonance Imaging at rest (r-fMRI) can quantify interactions between brain regions. Also known as brain functional connectivity, it reflects inter-subject variations in behavior and cognition, and characterizes neuropathologies. Yet, with noisy and short time-series, as in r-fMRI, covariance estimation is challenging and calls for penalization, as with shrinkage approaches. We introduce population shrinkage of covariance estimator (PoSCE) : a covariance estimator that integrates prior knowledge of covariance distribution over a large population, leading to a non-isotropic shrinkage. The shrinkage is tailored to the Riemannian geometry of symmetric positive definite matrices. It is coupled with a probabilistic modeling of the individual and population covariance distributions. Experiments on two large r-fMRI datasets (HCP n=815, CamCAN n=626) show that PoSCE has a better bias-variance trade-off than existing covariance estimates: this estimator relates better functional-connectivity measures to cognition while capturing well intra-subject functional connectivity.

*Keywords:* Covariance, functional connectivity, shrinkage, population models

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## 1. Introduction

Functional magnetic resonance imaging (fMRI) reflects neural activity in the brain through the blood-oxygen-level-dependent (BOLD) signal. Task-free or resting-state experiments (r-fMRI) are used to estimate brain functional connectivity between brain structures or regions. These pairwise interactions capture patterns that can be linked to the cognitive, psychiatric, or neurological status of individuals. With the advent of large cohort studies, functional connectivity has been used in neuroimaging population analyses to study cognitive differences between individuals (Smith et al., 2015; Finn et al., 2015). In clinical studies, functional connectivity can extract biomarkers related to neurological (Varoquaux et al., 2010b; Richiardi et al., 2012), neurodegenerative (Challis et al., 2015), or neuropsychiatric disorders (Zeng et al., 2012; Abraham et al., 2017).

These studies describe individuals by a *connectome*: a matrix of interactions between pairs of brain regions. Connectome matrices are typically based on the covariance of the signal: empirical covariance or Pearson correlation (i.e. normalized covariance). For estimated covariances to capture brain connectivity, they have to overcome the limitations of r-fMRI: low signal-to-noise ratio and short time-series. These limitations can easily lead to unreliable estimates with high within-subject variance, in particular when the number of regions is large. Regularized covariance estimators are used to reduce the variance of the estimates (Smith et al., 2011; Varoquaux et al., 2010a). They rely on injecting a prior on the covariance. For example,

sparse inverse covariance models enforce zeros on some partial-correlation coefficients. Sparsity, while very useful for interpretation purpose, entails costly optimizations. Additionally, it has been criticized as an oversimplification of brain connectivity (Markov et al., 2012; Ercsey-Ravasz et al., 2013).

*Covariance shrinkage* is another class of biased estimators that have appealing theoretical properties in high dimension (Ledoit and Wolf, 2004; Chen et al., 2010). These estimators rely on a convex combination between the empirical covariance and a target matrix –usually the identity. The resulting well-conditioned estimators come with reduced variance at little computational cost. Shrinkage-based covariance estimators have wide applications, such as genomics (Schäfer and Strimmer, 2005) or signal processing (Chen et al., 2010). Current solutions for functional-connectivity estimation shrink the covariance towards the identity matrix (Brier et al., 2015). This prior seems modest and over-biased compared to the information provided by the large cohorts of modern population neuroimaging. Indeed, as suggested in Crimi et al. (2011); Mejia et al. (2016), shrinkage towards population average yields more stable and more accurate functional-connectivity estimates. However, taking into account the variability of the population, beyond its mean, is likely to inject pertinent information and could lead to more useful priors.

In this paper, we introduce Population Shrinkage Covariance Estimator (PoSCE), a covariance shrinkage that uses as a prior a probabilistic distribution of the covariances calculated on a population. The resulting estimator shrinks toward the population mean, but additionally it accounts for the population dispersion, hence uses a non-isotropic shrinkage.

PoSCE uses a Riemannian parametrization of covariances,

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60 tailored to the information geometry and the positive-definite-110  
 constraint of covariance matrices (Lenglet et al., 2006; Fletcher  
 and Joshi, 2007). Riemannian frameworks for covariances have  
 been successfully applied for testing differences (Varoquaux  
 et al., 2010b), classification (Ng et al., 2014), or regression  
 65 Qiu et al. (2015) with functional connectivity. Mathemati-115  
 cally, we rely on the fact that an information-geometric Rie-  
 mannian metric gives local Euclidean approximations of the  
 maximum-likelihood risk, and makes it possible to use an ef-  
 ficient minimum-mean-squared-error estimation.

70 We demonstrate the efficiency of PoSCE through extensive  
 experimental validations on r-fMRI data from large cohorts:  
 815 healthy subjects from the Human Connectome Project  
 (HCP) dataset (Van Essen et al., 2013); and 626 subjects from  
 the Cambridge Center (CamCAN) dataset (Taylor et al., 2017).  
 75 Results show that PoSCE offers better bias-variance trade-off  
 compared to state-of-the-art estimators. PoSCE leads to very  
 efficient shrinkage algorithms that makes it usable routinely in  
 any functional-connectivity analysis with a small computation  
 cost. In particular, it does only one pass over the population,  
 80 avoiding any iterative optimization.

The paper is organized as follows: section 2 gives the mathe-  
 matical background of the shrinkage and the Riemannian man-  
 ifold of covariances. Section 3 introduces PoSCE and its imple-  
 85 mentation. Experimental results are discussed in section 4.  
 Section 5 concludes the paper.

## 2. Background: shrinkage and manifolds for covariances 125

*Notations.*  $n$  and  $p$  denote the number of samples and vari-  
 ables, respectively. In our case, r-fMRI time-points are the sam-  
 ples and ROIs’ signals are the variables. We use boldface up-  
 90 percase letters for matrices,  $\mathbf{A}$ . We work on two spaces: the  
 ambient space of covariances  $\mathbb{R}^{p \times p}$  and a tangent space. To  
 distinguish from the ambient space, we write  $\vec{a}$  for vectors in  
 tangent space and  $\vec{\mathbf{A}}$  for matrices in tangent space.

### 2.1. Prior art: shrinkage and covariances

#### 2.1.1. Shrinkage and James-Stein estimators 95

A *risk* –or a loss– function characterizes the efficiency of an  
 estimator. An estimator strives to minimize a given risk be-  
 100 tween the estimator and the true parameter. A typical risk is  
 the mean squared error (MSE) in regression. Unbiased esti-  
 mators, such as the empirical mean and variance, are not the  
 best estimators in term of MSE: while their *empirical* risk –the  
 MSE on the observed data– is minimum, their *expected* risk of  
 105 the population can be improved. Shrinkage estimators such as  
 James-Stein (JS) estimators (James and Stein, 1961) are biased  
 estimators of the mean. This bias improves the estimation of the  
 mean by giving a lower expected MSE risk. The fact that the  
 empirical mean is not the best estimator of the population mean  
 is sometimes known as Stein’s paradox (Stein, 1956). Yet, deci-  
 sion making when faced with small data intuitively leads to

slightly conservative choices that match Stein’s paradox (Efron  
 and Morris, 1977) 1. <sup>1</sup>

From a Bayesian stand-point, the shrinkage can be seen as an  
 empirical Bayes estimation. The overall distribution of the data  
 is the prior used to estimate individual parameters (Efron and  
 Morris, 1973). The posterior mean –conditional on the data–  
 gives the minimum MSE estimator (Lehmann and Casella,  
 2006, Corollary 4.1.2.). We use this result in the proposed co-  
 variance shrinkage model.

#### 2.1.2. Application of shrinkage to covariances

Maximum-likelihood estimates for covariances –empirical  
 covariances– are unstable when the number of variables is large  
 and the sample size is small. Many prior works have used  
 shrinkage as a regularization of the covariance estimation (Dey  
 and Srinivasan, 1985; Daniels and Kass, 2001; Chen et al.,  
 2010). Ledoit and Wolf (2003, 2004) propose a shrinkage  
 estimator of covariances that is optimal in high-dimensional  
 asymptotics with regards to the Frobenius risk –MSE for ma-  
 trices. The Ledoit-Wolf estimator  $\hat{\Sigma}_{LW}$  shrinks the empirical  
 covariance  $\mathbf{S}$  towards a target  $\mathbf{T}$  with a convex combination

$$\hat{\Sigma}_{LW} = (1 - \lambda)\mathbf{S} + \lambda\mathbf{T}. \quad (1)$$

Ledoit and Wolf (2003) use the identity matrix as a uniform  
 shrinkage target. They propose an analytical calculation of the  
 amount of shrinkage  $\lambda$  such that the Frobenius risk is mini-  
 mized. As a JS-type estimator, the Ledoit-Wolf estimator is  
 simple and fast to compute. It yields biased estimates that  
 are more stable than the empirical covariance and often recom-  
 mended for functional connectivity (Varoquaux and Craddock,  
 2013; Brier et al., 2015). However, when the covariance has  
 a reproducible strong off-diagonal structure, as with functional  
 brain networks, identity-based shrinkage is arguably subopti-  
 mal, i.e. induces high bias.

Beyond JS-type estimators, another approach to covariance  
 regularization uses sparsity on the inverse covariance as zeros in  
 the inverse covariance denote conditional independence. Sev-  
 eral works rely on the graphical Lasso (Friedman et al., 2007)  
 135 to estimate a sparse covariance for r-fMRI (Smith et al., 2011).  
 For example, Varoquaux et al. (2010a) use a group-level esti-  
 mator of sparse covariance. Yet, such models may not yield  
 stable covariance coefficients: the  $\ell_1$  penalty used for sparsity  
 often leads to unstable selection. In addition, they lead to costly  
 optimization and are not tractable on large scale datasets. Dif-  
 ferent formulations of a sparsity prior on conditional dependen-  
 cies, e.g. using Bayesian approaches (Hinne et al., 2014), give  
 more stable estimates, but come with an even greater cost. Our  
 approach to covariance estimation with good bias-variance and  
 stability properties relies not on sparsity, but on leveraging the  
 structure of the data.

<sup>1</sup> Efron and Morris (1977) showed a simple, yet famous, baseball-related  
 example that highlights JS estimator efficiency over empirical average. They  
 estimated batting abilities of players over a season from few observations (45 at-  
 tempts of 18 players). Results shows that JS shrinkage estimator yields smaller  
 mean squared errors w.r.t the season batting average of each player, compared  
 to simple averages.

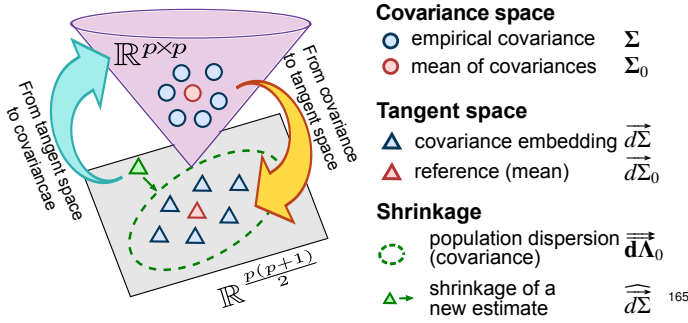


Figure 1: **Tangent embedding and population prior modeling.**  $\Sigma_0$  is the mean covariance from a train set of covariances. It is the reference point in the tangent space. The population prior is defined as a Gaussian multivariate distribution centered on  $\overline{d\Sigma_0}$ .  $\overline{d\Lambda_0}$  is the covariance dispersion over the population. The arrows depict the mapping between the non-Euclidean covariance space and the tangent space.

## 2.2. Statistics on Riemannian manifolds for covariances

Information geometry (Amari and Nagaoka, 2007) analyzes families of distributions with Riemannian geometry. When used to parametrize multivariate normal distributions, it describes a manifold structure for covariance matrices. It defines from the Fisher information matrix a Riemannian metric that coincides locally with the KL-divergence. Pennec et al. (2006) and Lenglet et al. (2006) introduce theoretically these geometric concepts on the manifold of normal distributions, with applications to diffusion-MRI tensors.

The space of valid covariances matrices  $\mathbb{R}^{p \times p}$  is the set of symmetric positive definite (SPD) matrices. Thus, covariance matrices live on the positive definite cone. Endowed with the Fisher-Rao metric, it defines Riemannian manifold that is well-suited for statistical modeling of covariances. In our case, the r-fMRI time-series for a given subject  $s$  are drawn from a Gaussian distribution:  $\mathbf{X}_s \sim \mathcal{N}(\mu_s, \Sigma_s)$ . For centered data the mean  $\mu_s$  is 0. The covariance  $\Sigma$  captures functional connectivity<sup>2</sup>.

As shown in Fig.1, the cone of SPD matrices, endowed with an affine-invariant metric –as the Fisher-Rao metric–, is a Riemannian manifold. This metric is well suited to invariances of the Gaussian model (Pennec et al., 2006; Varoquaux et al., 2010b). The manifold can be projected onto a vector space where Euclidean distances approximate locally Riemannian distances on the manifold. The covariance matrices of a group of subjects can be modeled as drawn from a generalized Gaussian distribution on the manifold, centered on a representative covariance  $\Sigma_0$ . Statistical model of a covariance  $\Sigma$  is then naturally performed by projecting it to  $\mathbb{R}^{p \times p}$ , using the tangent space representation at  $\Sigma_0$  (Varoquaux et al., 2010b). The tangent-space vector  $\mathbf{d}\Sigma \in \mathbb{R}^{p \times p}$  is then:

$$\mathbf{d}\Sigma = \log_m(\Sigma_0^{-\frac{1}{2}} \Sigma \Sigma_0^{-\frac{1}{2}}), \quad (2)$$

<sup>2</sup>Note that this approach does not model the auto-correlations of time series. This could be handled in future work as a generalization of the model discussed here.

where  $\frac{1}{2}$  denotes the matrix square root<sup>3</sup> and  $\log_m$  is the matrix logarithm.  $\mathbf{d}\Sigma$  stands for the tangent space of  $\Sigma$  at the reference covariance  $\Sigma_0$ . A convenient parametrization  $\overline{d\Sigma} \in \mathbb{R}^d$  with  $d = p(p+1)/2$  removes repeated entries while preserving the norm:

$$\overline{d\Sigma} = \text{vec}(\mathbf{d}\Sigma) = \{\sqrt{2} \mathbf{d}\Sigma_{i,j}, j < i, \mathbf{d}\Sigma_{i,i}, i = 1 \dots p\}. \quad (3)$$

– From Kullback-Leibler divergence to squared error

The Kullback-Leibler (KL) divergence is a probabilistic measure of the discrepancy between two distributions. On the information geometric manifold, the  $\ell_2$  distance in the tangent space approximates the KL divergence:

*Lemma 1.* The squared Euclidean distance between the tangent-space embeddings of two covariance matrices is a second-order approximation of the KL divergence between the two corresponding Gaussian distributions.

*Proof:* The divergence between two centered Gaussian distributions  $\mathcal{N}_1, \mathcal{N}_2$  characterized by their covariance  $\Sigma_1$  and  $\Sigma_2$  respectively, is

$$D_{\text{KL}}(\mathcal{N}_1, \mathcal{N}_2) = \frac{1}{2} \left( \text{tr}(\Sigma_2^{-1} \Sigma_1) - \log |\Sigma_2^{-1} \Sigma_1| - p \right)$$

Then, writing  $\Sigma_1 = \Sigma_2 + \mathbf{d}\Sigma$ :

$$\begin{aligned} D_{\text{KL}}(\mathcal{N}_1, \mathcal{N}_2) &= \frac{1}{2} \left( \text{tr}(\mathbf{I} + \Sigma_2^{-1} \mathbf{d}\Sigma) - \log |\mathbf{I} + \Sigma_2^{-1} \mathbf{d}\Sigma| - p \right) \\ &= \frac{1}{2} \left( \text{tr}(\Sigma_2^{-1} \mathbf{d}\Sigma) - \log |\mathbf{I} + \Sigma_2^{-1} \mathbf{d}\Sigma| \right). \end{aligned}$$

The second-order expansion of the determinant is written:

$$|\mathbf{I} + \mathbf{dA}| = 1 + \text{tr}(\mathbf{dA}) + \frac{\text{tr}^2(\mathbf{dA}) - \text{tr}(\mathbf{dA}^2)}{2} + o(\|\mathbf{dA}\|^2).$$

An important intermediate step is the second-order expansion of  $\log(|\mathbf{I} + \mathbf{dA}|)$ :

$$\log(|\mathbf{I} + \mathbf{dA}|) = \text{tr}(\mathbf{dA}) - \frac{1}{2} \text{tr}(\mathbf{dA}^2) + o(\|\mathbf{dA}\|^2).$$

Using these two expressions in the KL formula:

$$\begin{aligned} D_{\text{KL}}(\mathcal{N}_1, \mathcal{N}_2) &= \frac{1}{4} \text{tr} \left( (\Sigma_2^{-1} \mathbf{d}\Sigma)^2 \right) + o(\|\Sigma_2^{-1} \mathbf{d}\Sigma\|^2) \\ &= \frac{1}{4} \text{tr} \left( (\Sigma_2^{-\frac{1}{2}} \mathbf{d}\Sigma \Sigma_2^{-\frac{1}{2}})^2 \right) + o(\|\Sigma_2^{-1} \mathbf{d}\Sigma\|^2). \quad (4) \end{aligned}$$

This second order expansion corresponds to a squared error of the tangent space embedding that will be used for the covariance shrinkage.

<sup>3</sup>Computed with an eigenvalues decomposition, taking the square roots of the eigenvalues.

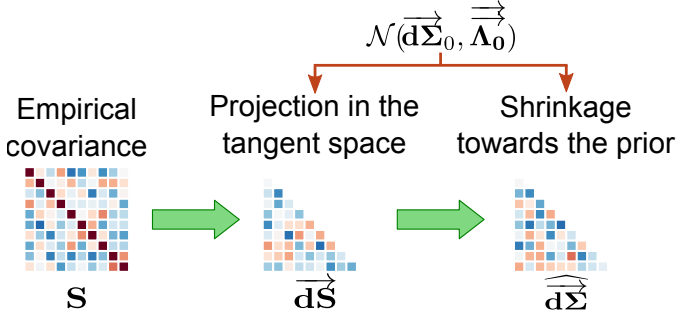


Figure 2: **PoSCE estimation workflow.** The empirical covariance is projected in the tangent space at  $\Sigma_0$  defined previously. This projected covariance is shrunk towards the population prior.

### 3. Population shrinkage covariance embedding (PoSCE)

Our contribution relies on adapting James-Stein shrinkage theory to the geometry of covariances, using the Riemannian formulation to turn a KL-divergence risk to an MSE risk. We propose a population shrinkage estimator of the tangent parametrization of covariance matrices. This estimator shrinks the covariance estimates toward a prior distribution of covariances, rather than using a constant target as in Ledoit and Wolf (2003). The prior can be seen as a generative model of covariances from which each individual covariance is drawn.

Fig.2 gives an overview of the method : *i*) a prior distribution for covariances is estimated over a training dataset; *ii*) each subject covariance is shrunk according to the prior in the tangent space at  $\Sigma_0$ .

#### 3.1. Prior construction from population distribution

We consider the prior as a generative model of the embeddings of the observed covariance models. To define the population prior, we use as inputs a set of covariances  $\mathbf{S}_i$  from an r-fMRI dataset. We use the tangent space parameterization of these covariances, by applying formulas (2) and (3). The generative model is then a multivariate Gaussian distribution  $\vec{d}\Sigma \sim \mathcal{N}(\vec{d}\Sigma_0, \vec{\Lambda}_0)$ . The prior is centered at the reference point of the tangent space  $\vec{d}\Sigma_0 = \vec{0}$ . The prior covariance  $\vec{\Lambda}_0$  measures the element-wise dispersion of connectivity matrices in the tangent space. The dispersion with respect to the reference point is given by the mean outer product of the tangent embedding over the train set (Pennec et al., 2006):

$$\vec{\Lambda}_0 = \frac{1}{N_{\text{train}} - 1} \sum_{i=1}^{N_{\text{train}}} \vec{d}\mathbf{S}_i \otimes \vec{d}\mathbf{S}_i, \quad (5)$$

where  $\vec{\Lambda}_0 \in \mathbb{R}^{d \times d}$  with  $d = p(p+1)/2$ .  $\vec{d}\mathbf{S}_i = \text{vec}(\mathbf{d}\mathbf{S}_i)$  is the parametrized tangent space transform of the empirical covariance  $\mathbf{S}_i$ .

#### 3.2. Population prior-based shrinkage

We use the prior distribution  $\mathcal{N}(\vec{d}\Sigma_0, \vec{\Lambda}_0)$  for optimal shrinkage of  $\vec{d}\Sigma$  in the tangent space. As mentioned in section 2.1.1, JS-type shrinkage can be expressed in a Bayesian framework:

$$p(\vec{d}\Sigma | \vec{D}\mathbf{S}) \propto p(\vec{D}\mathbf{S} | \vec{d}\Sigma) p(\vec{d}\Sigma), \quad (6)$$

where  $p(\vec{d}\Sigma)$  is the population prior and  $\vec{D}\mathbf{S}$  is the embedded empirical covariance (the embedding of the observed sample covariance).  $p(\vec{D}\mathbf{S} | \vec{d}\Sigma)$  is the likelihood of the observed data  $\vec{D}\mathbf{S}$  given  $\vec{d}\Sigma$ . The log-likelihood is also the cross-entropy between the prior and the data, a key component of the KL divergence between both models: For  $p(\vec{D}\mathbf{S} | \vec{d}\Sigma)$ , the KL divergence is a natural loss on covariances. We then use the second order expansion to approximate the KL by a quadratic loss in the tangent space, as mentioned in Lemma 1. The posterior mean  $p(\vec{d}\Sigma | \vec{D}\mathbf{S})$  –conditional on the data– gives the minimum MSE shrinkage estimator of  $\vec{d}\Sigma$  (see 2.1.1 and Lehmann and Casella 2006, Corollary 4.1.2.). Thus,

$$\widehat{\vec{d}\Sigma} = \mathbb{E}[\vec{d}\Sigma | \vec{D}\mathbf{S}] = \underset{\vec{d}\Sigma}{\text{argmin}} \text{MSE}(\vec{d}\Sigma, \vec{D}\mathbf{S}). \quad (7)$$

To compute this expectancy we use in Equation 6:

- *Population prior:*  $p(\vec{d}\Sigma) = \mathcal{N}(\vec{d}\Sigma_0, \vec{\Lambda}_0)$  where  $(\vec{d}\Sigma_0, \vec{\Lambda}_0)$  are estimated as in section 3.1.
- *Data likelihood:*  $p(\vec{D}\mathbf{S} | \vec{d}\Sigma) = \mathcal{N}(\vec{D}\mathbf{S}, \vec{\Lambda})$ , the likelihood of the observed data  $\vec{D}\mathbf{S}$  given  $\vec{d}\Sigma$ . It is a Gaussian distribution centered on  $\vec{d}\mathbf{S}$ , the tangent-space projection of the empirical covariance  $\mathbf{S}$ , and a covariance  $\vec{\Lambda}$  which is a hyper-parameter of the algorithm discussed below.

Figure 1 depicts both likelihood and prior distributions.

Population prior-based shrinkage (PoSCE) relies on Bayes rule for multivariate Gaussian distributions (Bishop, 2006, Section 2.3.6.). The posterior is  $p(\vec{d}\Sigma | \vec{D}\mathbf{S}) = \mathcal{N}(\vec{d}\Sigma, \vec{\mathbf{C}})$ , where the inverse posterior covariance is  $\vec{\mathbf{C}}^{-1} = \vec{\Lambda}^{-1} + \vec{\Lambda}_0^{-1}$ , and the posterior mean  $\widehat{\vec{d}\Sigma}$  is:

$$\widehat{\vec{d}\Sigma} = (\vec{\Lambda}^{-1} + \vec{\Lambda}_0^{-1})^{-1} (\vec{\Lambda}^{-1} \vec{d}\mathbf{S} + \vec{\Lambda}_0^{-1} \vec{d}\Sigma_0). \quad (8)$$

As the prior mean  $\vec{d}\Sigma_0$  is null, we have:

$$\text{PoSCE: } \widehat{\vec{d}\Sigma} = (\vec{\Lambda}^{-1} + \vec{\Lambda}_0^{-1})^{-1} \vec{\Lambda}^{-1} \vec{d}\mathbf{S}. \quad (9)$$

A fully-fledged estimate of the covariance can be computed by inverting formulas (3) and (2) to go from the tangent space back to the covariance manifold:

$$\hat{\Sigma}_{\text{PoSCE}} = \Sigma_0^{\frac{1}{2}} \text{expm}(\widehat{\vec{d}\Sigma}) \Sigma_0^{\frac{1}{2}} \quad (10)$$

#### 3.3. Implementation details

We detail in this section the steps to compute PoSCE. As depicted in figure 2, PoSCE takes as input the empirical covariance  $\mathbf{S}$ . Then, it uses multivariate Gaussian distributions on the tangent space parameterization of the covariance.

Algorithm 1 summarizes the tangent space parameterization used for population-based covariance shrinkage. It relies on the population reference  $\Sigma_0$ . There are several ways to calculate the population reference  $\Sigma_0$ . We use the Euclidean mean, since it yields more stable estimations than Fréchet mean, as mentioned in Ng et al. (2014). For a given set of  $N$  covariances  $\{\Sigma_i\}$ ,

$$\Sigma_0 = \frac{1}{N} \sum_{i=1}^N \Sigma_i \quad (11)$$

210 As depicted in [algorithm 3](#), the population prior is modeled as a Gaussian distribution from a set of covariances. Since the population reference  $\Sigma_0$  is the population mean, the prior is centered at  $\vec{d\Sigma}_0 = \vec{0}$ .  $\vec{\Lambda}_0$  is the dispersion (covariance) of the prior distribution. In practice,  $\vec{\Lambda}_0$  is very high dimensional and is learned from a finite population of subjects. Rather than the scatter matrix  $\vec{\Lambda}_*$ , that corresponds to the maximum likelihood estimate, we use for  $\vec{\Lambda}_0$  a low-rank approximation which corresponds to regularizing with a PCA decomposition (see [algorithm 2](#)). Let  $\vec{\Lambda}_* = \Delta L \Delta^T$  and  $\mathbf{D} = \Delta_{[1..r]} \sqrt{\mathbf{L}_{[1..r]}}$ , where  $_{[1..r]}$  denotes the selection of the first  $r$  components; in practice  $r$  is set such that the captured variance ratio is above 70%. Finally  $\vec{\Lambda}_0 = \alpha \mathbf{I} + \mathbf{D}\mathbf{D}^T$ , where  $\alpha$  is set such that  $Tr(\vec{\Lambda}_0) = Tr(\vec{\Lambda}_*)$ .

225 PoSCE is described in [algorithm 4](#). For a given subject covariance, it uses the prior distribution from [algorithm 3](#).  $\vec{\Lambda}$  cannot be fully estimated from limited data, hence we take  $\vec{\Lambda} = \lambda \mathbf{I}$ , where  $\lambda$  acts as a shrinkage control parameter. In our experiments, we set  $\lambda$  with a cross-validation on a subset of the train dataset. The optimal  $\lambda$  is chosen to maximize the log-likelihood of the test set data, for an estimator calculated on the train set. 235

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#### Algorithm 1: Tangent embedding parametrization

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**Input:** Covariance  $\Sigma$ , reference  $\Sigma_0$   
 /\* Project covariance in tangent space \*/  
 1  $\mathbf{d}\Sigma = \text{logm}(\Sigma_0^{-\frac{1}{2}} \Sigma \Sigma_0^{-\frac{1}{2}})$   
 2  $\vec{d\Sigma} = \text{vec}(\mathbf{d}\Sigma) = \{\sqrt{2} \mathbf{d}\Sigma_{i,j}, j < i, \mathbf{d}\Sigma_{i,i}, i = 1..p\}$   
**Output:** Covariance embedding  $\vec{d\Sigma}$

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#### Algorithm 2: Low-rank approximation

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**Input:** Matrix  $\vec{\Lambda}_*$   
 1  $\vec{\Lambda}_* = \Delta \mathbf{L} \Delta^T$  // eigenvalue decomposition  
 2 Select  $r$  components such that variance ratio  $\geq 70\%$   
 3  $\mathbf{D} = \Delta_{[1..r]} \sqrt{\mathbf{L}_{[1..r]}}$   
 4  $\vec{\Lambda}_0 = \alpha \mathbf{I} + \mathbf{D}\mathbf{D}^T$ ,  $\alpha$  is set such that  $Tr(\vec{\Lambda}_0) = Tr(\vec{\Lambda}_*)$   
**Output:** Approximated matrix  $\vec{\Lambda}_0$

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#### Algorithm 3: Population prior estimation

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**Input:** Set of  $N$  covariances  $\{\mathbf{S}_i\}$ , reference  $\Sigma_0$   
 /\* Set embedding parametrization \*/  
 1 **forall** covariance  $\mathbf{S}_i$  **do**  
 2 |  $\vec{dS}_i \leftarrow$  Embedding of  $\mathbf{S}_i$  according to [algorithm 1](#)  
 3 **end**  
 /\* Build prior distribution  $\mathcal{N}(\vec{d\Sigma}_0, \vec{\Lambda}_0)$  \*/  
 4  $\vec{d\Sigma}_0 = \vec{0}$  // prior mean  
 5  $\vec{\Lambda}_0 = \frac{1}{N-1} \sum_{i=1}^N \vec{dS}_i \otimes \vec{dS}_i$  // prior dispersion  
 6  $\vec{\Lambda}_0 \leftarrow$  low-rank approximation according to [algorithm 2](#)  
**Output:** Population prior distribution  $\mathcal{N}(\vec{d\Sigma}_0, \vec{\Lambda}_0)$

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#### Algorithm 4: Population shrinkage covariance embedding (PoSCE)

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**Input:** covariance  $\mathbf{S}$ , population prior  $\mathcal{N}(\vec{d\Sigma}_0, \vec{\Lambda}_0)$ , shrinkage parameter  $\lambda$   
 /\* Build covariance distribution  $\mathcal{N}(\vec{dS}, \vec{\Lambda})$  \*/  
 1  $\vec{dS} \leftarrow$  Embedding of  $\mathbf{S}$  according to [algorithm 1](#)  
 2  $\vec{\Lambda} = \lambda \mathbf{I}$  // likelihood covariance  
 /\* Shrink towards population distribution \*/  
 3  $\widehat{\vec{d\Sigma}} = (\vec{\Lambda}^{-1} + \vec{\Lambda}_0^{-1})^{-1} \vec{\Lambda}^{-1} \vec{dS}$   
**Output:** Shrunk covariance embedding  $\widehat{\vec{d\Sigma}}$

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### 3.4. Relating PoSCE to standard linear shrinkage

We observe that [Equation 9](#) is a generalization of classic shrinkage estimators ([Ledoit and Wolf, 2004](#); [Schäfer and Strimmer, 2005](#)) that relies on a convex combination of a prior with the empirical covariance matrix. Below we make that link explicit and show that with  $\vec{\Lambda}_0 = \lambda_0 \mathbf{I}$  and  $\vec{\Lambda} = \lambda \mathbf{I}$  we recover classic shrinkage.

In PoSCE, the shrinkage is in the tangent space and the amount of shrinkage is controlled by the likelihood covariance parameter  $\lambda$ . [Equation 9](#) summarizes the shrinkage. It can be seen as a generalization of covariance shrinkage as in [Ledoit and Wolf \(2004\)](#) where the target is the average covariance. Indeed, considering uniform prior covariance  $\vec{\Lambda}_0 = \lambda_0 \mathbf{I}$  and  $\vec{\Lambda} = \lambda \mathbf{I}$  in [Eq.\(9\)](#) leads to:

$$\begin{aligned} \widehat{\vec{d\Sigma}} &= \left(\frac{1}{\lambda} \mathbf{I} + \frac{1}{\lambda_0} \mathbf{I}\right)^{-1} \left(\frac{1}{\lambda} \mathbf{I} \vec{dS} + \frac{1}{\lambda_0} \mathbf{I} \vec{d\Sigma}_0\right), \\ &= \left(1 - \frac{\lambda}{\lambda_0 + \lambda}\right) \vec{dS} + \frac{\lambda}{\lambda_0 + \lambda} \vec{d\Sigma}_0. \end{aligned}$$

By taking  $\lambda' = \frac{\lambda}{\lambda_0 + \lambda}$ , we have:

$$\widehat{\vec{d\Sigma}} = (1 - \lambda') \vec{dS} + \lambda' \vec{d\Sigma}_0. \quad (12)$$

To *back-project*  $\widehat{\vec{d\Sigma}}$  –with  $\widehat{\vec{d\Sigma}} = \text{vec}(\widehat{\mathbf{d\Sigma}})$ – into the ambient space, we choose any reference point  $\mathbf{R}$ , such that  $\vec{dS}$  and  $\vec{d\Sigma}_0$  are small. For any matrix  $\mathbf{A}$  in the vicinity, we have  $\mathbf{dA} = \text{logm}(\mathbf{R}^{-\frac{1}{2}} \mathbf{A} \mathbf{R}^{-\frac{1}{2}})$ .

Hence,  $\mathbf{A} = \mathbf{R}^{\frac{1}{2}} \text{expm}(\mathbf{dA}) \mathbf{R}^{\frac{1}{2}} \approx \mathbf{R}^{\frac{1}{2}} (\mathbf{dA} + \mathbf{I}) \mathbf{R}^{\frac{1}{2}}$ . In particular,  $\mathbf{S} \approx \mathbf{R}^{\frac{1}{2}} (\mathbf{dS} + \mathbf{I}) \mathbf{R}^{\frac{1}{2}}$  and  $\Sigma_0 \approx \mathbf{R}^{\frac{1}{2}} (\mathbf{d\Sigma}_0 + \mathbf{I}) \mathbf{R}^{\frac{1}{2}}$ , using first-order approximations.

We apply this to  $\widehat{\vec{d\Sigma}}$ :

$$\begin{aligned} \widehat{\Sigma} &\approx \mathbf{R}^{\frac{1}{2}} (\widehat{\mathbf{d\Sigma}} + \mathbf{I}) \mathbf{R}^{\frac{1}{2}}, \\ &\approx \mathbf{R}^{\frac{1}{2}} ((1 - \lambda') \mathbf{dS} + (\lambda' \mathbf{d\Sigma}_0 + \mathbf{I})) \mathbf{R}^{\frac{1}{2}}, \\ &\approx \mathbf{R}^{\frac{1}{2}} ((1 - \lambda') \mathbf{dS} + (1 - \lambda') \mathbf{I} + \lambda' \mathbf{d\Sigma}_0 + \lambda' \mathbf{I}) \mathbf{R}^{\frac{1}{2}}, \\ &\approx (1 - \lambda') \mathbf{S} + \lambda' \Sigma_0, \end{aligned} \quad (13)$$

which corresponds to a linear shrinkage of covariance  $\mathbf{S}$  towards the target  $\Sigma_0$  (formula (1) and [Ledoit and Wolf 2003](#)).

## 4. Experimental validation

In this section, we compare PoSCE to state-of-the-art estimators and show that it achieves a better bias-variance trade-off than current alternatives for various applications. Ideally, an estimator should be stable to sampling noise, e.g. have high test-retest reproducibility, yet it should retain key inter-subject differences. Hence, we specifically probe these differences as they are of direct interest for applications. With four different experiments, we assess: *i*) predicting subject age from its connectivity profile; *ii*) capturing functional connectivity similarities within twins, siblings and unrelated subjects; *iii*) characterizing multi-dimensional cognitive and behavioral phenotypes based on functional connectivity; *iv*) reproducibility of connectivity estimates across two sessions of the same subject. In all experiments, covariances are estimated on signals from 64 brain regions from bootstrap analysis of stable clusters (BASC) atlas (Bellec et al., 2010).

We use two distinct datasets in our experiments, namely the Human Connectome Project (HCP) dataset and the Cambridge Center for Ageing and Neuroscience (CamCAN) dataset. In each experiment, the dataset is split in two subsets. The first subset –200 randomly selected subjects– is used for population prior estimation. The second subset is used for the validation.

### 4.1. Performance in across-subject prediction

We assess the capacity of PoSCE to provide relevant connectivity features for out-of-sample prediction. Predicting subject phenotype or clinical status from neuroimaging data helps to identify brain biomarkers of a physiological or mental state. Several studies have highlighted the impact of the age on the brain. They rely on a regression model to predict subject age from r-fMRI (Liem et al., 2017) or anatomical MRI (Franke et al., 2010; Cole et al., 2017).

In this experiment, we consider the accuracy of age prediction from functional connectivity as a measure to benchmark different connectivity estimators. We use the CamCAN dataset, a publicly available dataset for brain ageing. It includes around 700 healthy subjects aged from 18 to 88 years. The dataset is presented in Taylor et al. (2017). Selected subjects and preprocessing steps are detailed in the appendix. We compare three age-prediction models based on three functional connectivity estimators as subject descriptors : correlation matrix, the tangent space embedding of the covariance, and the proposed PoSCE. We use a linear support vector machine regressor with the same parameters ( $C = 1$ ). Predictive models are compared through 100 randomized cross-validations on left out data (10% of the dataset). At each iteration, the prediction accuracy is measured with the mean absolute error (MAE). It measures the average discrepancy in years of the predicted age compared to the true age. Learning curves in Figure 3 correspond to the three age-prediction models. The learning curves are obtained by varying the number of subjects included in the train set while keeping the test set fixed.

The results show that the PoSCE estimator systematically outperforms other functional connectivity estimators. Shrinking towards the population prior improve age-prediction accu-

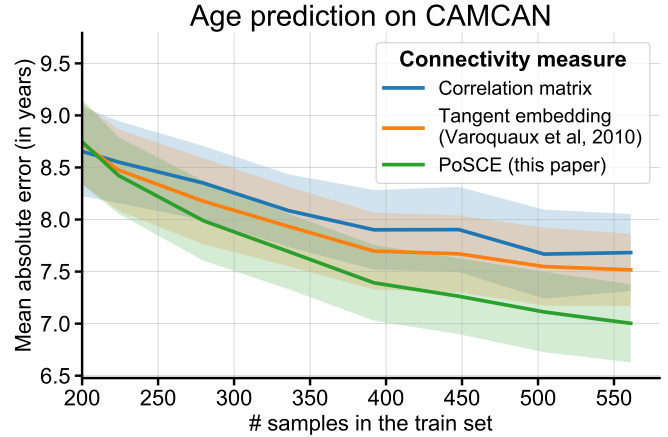


Figure 3: Estimator performance for age prediction. Learning curves shows that tangent space-based estimators decrease age overall error. The population-shrinkage estimator yields better age predictions.

racy, including in small sample-size setting. The results also demonstrate the benefits of using the tangent space parametrization rather than correlation matrices. This corroborates previous studies comparing different functional connectivity estimators for disease prediction (Abraham et al., 2017; Dadi et al., 2016).

### 4.2. Agreement with phenotype similarities

We evaluate the extent to which PoSCE estimator captures phenotype similarities between subjects. Recent studies investigate the link between phenotype similarity and brain connectivity. Colclough et al. (2017) measure the heritability of the functional connectivity on the Human Connectome Project dataset (HCP) (Van Essen et al., 2012). These studies show that twins have closer functional-connectivity profiles compared to other subjects. We perform a similar experiment on the same dataset, by comparing connectivity profiles of 815 subjects from HCP. First, we compute the connectivity profile for each subject using either PoSCE or the correlation matrix. Then, we compare the pairwise euclidean distances between the connectivity profiles of twins, siblings, and unrelated subjects.

Figure 4 shows the distribution of the distances for the three groups with PoSCE and the correlation matrix. PoSCE-based distances of twins are significantly smaller than siblings and unrelated subjects. On the opposite, distances based on correlation matrices do not capture significant differences between group: they show a wider spread and a smaller group effect. Figure B.7 in the appendix shows that PoSCE also significantly improves upon standard shrinkage or sparse covariance estimators. Overall, the results reproduce the findings of Colclough et al. (2017). They show the benefit of using a good covariance estimator using the population prior to characterize phenotypical differences.

### 4.3. Association with behavioral scores

We measure the correlation of PoSCE with multi-dimensional description of subjects demographics, psychomet-

## Connectivity-based similarities between subjects

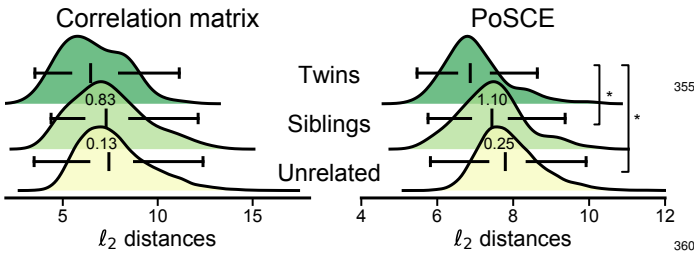


Figure 4: **Similarities between HCP subjects based on functional connectivity profiles.** Plots represent distributions of pairwise distances between connectivity profiles of each two twins, siblings and unrelated subjects. Digits represent differences between each two distributions. Group comparisons show higher differences of twins compared to siblings and unrelated subjects. Such differences are highlighted by the PoSCE estimator (\*:  $p < 0.001$ , 10 000 permutations), whereas Pearson correlation does not capture twins specific similarities: the distributions overlap and there are no significant differences.

rics, and lifestyle. This type of analysis is popular in population neuroimaging (Smith et al., 2015; Miller et al., 2016; Xia et al., 2017). Smith et al. (2015) investigate the relationship between behavior and brain connectivity on the Human Connectome Project dataset. They apply a canonical correlation analysis (CCA) with 100 components on 158 selected behavioral scores and subjects functional connectivity profiles. We replicate this analysis on 615 subjects from HCP (we use 200 separate subjects to build the population prior). We compare PoSCE and the correlation matrix as functional connectivity features from r-fMRI scans. We first measure canonical correlation modes within sample, then –more importantly– the correlation of this mode on unseen data.

Figure 5 shows the principal CCA mode scatter plot. This mode relates functional connectivity to behavioral assessments. As expected from Smith et al. (2015), both PoSCE and corre-

## CCA modes of connectivity and behavioral scores

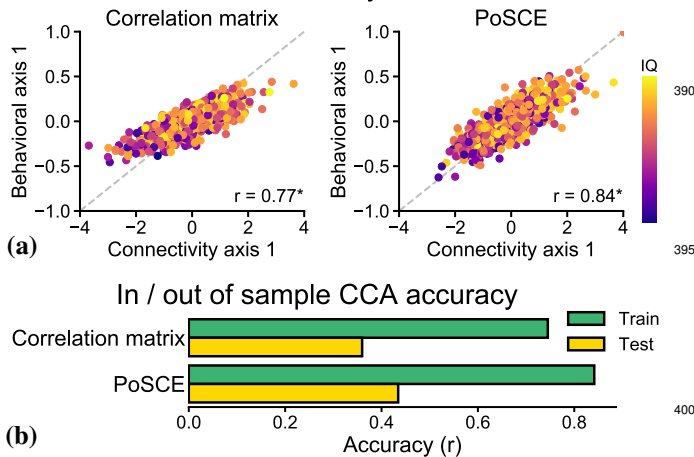


Figure 5: **Relating functional connectivity with behavior on HCP.** Subjects distribution over the first CCA connectivity-behavior mode shows higher correlation when using PoSCE as a connectivity descriptor (a). First CCA mode with PoSCE has a better out-of-sample generalization compared to Pearson correlation (b).

lation matrix estimators yield significant canonical correlation (\*:  $p < 10^{-3}$ , 10 000 permutations). Yes, the PoSCE estimator yields more significant co-variations between functional connectivity and behavioral assessments. PoSCE also gives better accuracy on out-of-sample data. To illustrate correlations between connectivity and behavior, we represent the fluid intelligence (IQ) of each subject on the scatter plot in Figure 5 by a purple-to-yellow colormap. This shows consistent correlation between IQ and the first functional connectivity mode.

## 4.4. Reproducibility within subjects

Finally, we study the reproducibility of PoSCE within each subject across sessions. For each subject of the HCP dataset (815 subjects), we use two r-fMRI scans acquired at different sessions (rest1, rest2). We measure the fidelity of an estimator by the log-likelihood of the data from a r-fMRI session –rest2– in a model estimated on a previous session –rest1– from the same subject. For a covariance model  $\Sigma$  estimated on rest1, and observed data from rest2 characterized by the correlation matrix  $S$ , the log-likelihood of the data observed from rest2 is:  $1/2(-\text{tr}(S\Sigma^{-1}) + \det(\Sigma^{-1}) - p \log(2\pi))$ .

We compare six covariance models for each subject: 1) the correlation matrix without any regularization; 2) the graphical Lasso –GraphLassoCV from scikit-learn (Pedregosa et al., 2011)–, where a sparse precision matrix is estimated with an  $\ell_1$  penalty (Friedman et al., 2007; Smith et al., 2013); 3) the Ledoit-Wolf estimator, that shrinks to the identity with an analytically set shrinkage parameter (Ledoit and Wolf, 2004); 4) shrinkage to the identity in the tangent space with a shrinkage set by cross-validation (Identity shrinkage CV); 5) the estimator with isotropic shrinkage towards the population mean (Prior shrinkage CV); 6) the proposed PoSCE, with non-isotropic shrinkage towards the population mean, controlled by the population distribution (PoSCE). For the estimators with cross-validation, the optimal shrinkage is set such that it maximizes the log-likelihood on a separate subject session rest3.

Figure 6 summarizes the subject-wise dispersion of the log-likelihoods of each estimator, relative to the mean. The results demonstrate that shrinking the covariance towards the prior produces the highest likelihood values, and outperforms shrinkage to identity. There is a systematic gain with PoSCE compared to only using the mean covariance as target of the shrinkage model, as in Crimi et al. (2011). This suggests that the population distribution is useful to regularize connections that exhibit more variability across subjects. We also observe that the optimal shrinkage is better estimated with cross-validation than with the Ledoit-Wolf method. Indeed, the Ledoit-Wolf estimator strives to minimize a squared-error risk, and not a likelihood risk. Further comparisons show that the results are consistent across different brain atlases (see appendix, Figure C.8).

## 5. Conclusion

We introduced PoSCE, a covariance model that integrates the knowledge of population distribution for an optimal shrinkage of the covariance.



PoSCE belongs to James-Stein estimators family ensuring lower error than maximum-likelihood estimators. It relies on a parametrization of covariances that enables approximating KL divergences between covariances as Euclidean distances. Hence, it can use shrinkage results for squared error, namely the equivalence between minimum mean squared error and Bayesian analysis of Gaussian models. Our Bayesian formulation integrates not only a shrinkage target, but also the variability of covariance over a reference population for non isotropic shrinkage. It yields straightforward closed-form equations, and is thus computational cheap even on very large cohorts. Yet, PoSCE scalability can be improved to better approximate population-level variability matrix, since it depends on the number of brain regions used in the analysis.

Empirically, PoSCE shows an excellent bias-variance trade-off for brain functional connectivity: it reduces estimator variance (intra-subject variability) while highlighting more accurately co-variations between connectivity profiles and subjects behavioral assessments. Further work should study the transfer of the population prior, for instance across distinct brain-imaging datasets. Ideally, the definition of a *universal* prior to compute connectivity matrices could be used in all functional connectivity analyses, provided they rely on the same initial region definition.

Our extensive experimental results show that PoSCE captures better connectivity-phenotype covariation than all alternative estimators. Hence, it can be used to learn better biomarkers based on functional connectivity. Indeed, there is important ongoing research that builds prediction models of various neurological or psychiatric disorders as well as health outcomes from clinical r-fMRI data.

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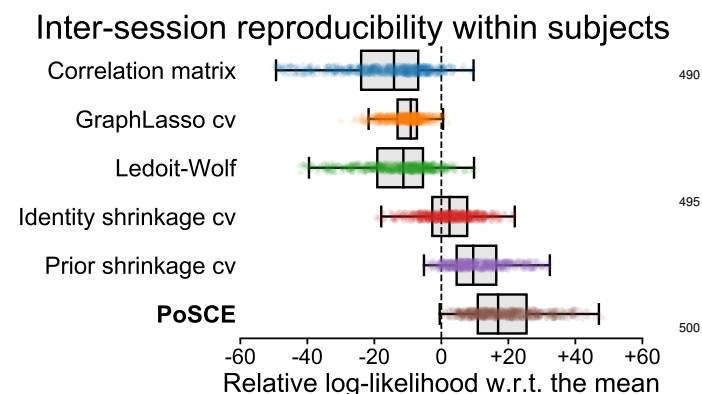


Figure 6: **Fidelity to subject data.** Boxplots represent the average log-likelihood of the data in a second session, which quantifies the relative similarities between respective sessions of 615 subjects from HCP. Shrinking the covariance towards population prior improves reproducibility compared with Pearson correlation, Ledoit-Wolf, and  $\ell_1$  penalized estimators. PoSCE outperforms all other estimators.

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## Appendix A. R-fMRI datasets

We detail in this section the r-fMRI datasets used in our experiments. For each dataset, r-fMRI timeseries are extracted from a set of ROIs corresponding to a brain atlas. We use the Nilearn library (Abraham et al., 2014) for the temporal pre-processing. It includes linear detrending, motion confounds re-

gression, CompCor (Behzadi et al., 2007), and band filtering (0.01–0.1Hz).

– *The Human Connectome Project dataset*

We use r-fMRI scans from the 900-subjects release of the Human Connectome Project dataset (HCP), to assess estimator reproducibility and phenotype characterization. As summarized in table A.1, 815 quality-checked subjects are selected, including twins, siblings, and unrelated subjects. Each subject has four r-fMRI scans that have been already spatially preprocessed and normalized to the MNI space. Each r-fMRI scan is around 15 min-long comprising 1 200 time-points.

– *The Cambridge Center for Ageing Neuroscience dataset*

This dataset is used to highlight the interest of using PoSCE to predict subject age. The dataset comprises 626 healthy subjects equally distributed over age ranges. We apply a standard spatial preprocessing pipeline using SPM12. (motion correction, coregistration to T1-MRI, normalization to the MNI space).

Table A.1: **Datasets description.**

– The HCP dataset

| N   | Gender  | Zygoty          | Age     |
|-----|---------|-----------------|---------|
| 815 | F : 462 | Twins : 181     | 22 – 37 |
|     | M : 353 | Siblings : 100  |         |
|     |         | Unrelated : 214 |         |
|     |         |                 |         |

– The CamCAN dataset

| N   | Gender  | Age     |
|-----|---------|---------|
| 626 | F : 318 | 18 – 88 |
|     | M : 308 |         |

## Appendix B. Comparing PoSCE with other estimators

We provide in this section full comparisons between PoSCE and other covariance estimators, by comparing experimental results of different regularizations and shrinkage targets.

– *Age prediction*

Table B.2 shows accuracies of CamCAN age prediction from brain connectivity extended to other estimators. We use the same setting as explained in section 4.1 : 100 randomized cross-validations on 10% left out data using support vector regression. Cross-validation mean absolute deviation and r-squared values suggest that PoSCE-based connectivity features better capture age-related variations. While shrinkage-based estimators results are similar to those from correlation matrix,  $\ell_1$  penalized connectivity has the lowest accuracy. It is less suited for inter-individual functional connectivity characterization.

Table B.2: **Estimator performance for age prediction.** Model accuracies (mean  $\pm$  standard deviation) over 100 randomized train-test splits show better age prediction with PoSCE.

| Connectivity measure  | MAD                               | r-squared                         |
|-----------------------|-----------------------------------|-----------------------------------|
| Correlation matrix    | 7.63 $\pm$ 0.73                   | 0.73 $\pm$ 0.05                   |
| GraphLasso cv         | 8.23 $\pm$ 0.68                   | 0.69 $\pm$ 0.05                   |
| Ledoit-Wolf           | 7.54 $\pm$ 0.73                   | 0.73 $\pm$ 0.05                   |
| Identity shrinkage cv | 7.77 $\pm$ 0.73                   | 0.72 $\pm$ 0.05                   |
| Prior shrinkage cv    | 7.77 $\pm$ 0.73                   | 0.72 $\pm$ 0.05                   |
| <b>PoSCE</b>          | <b>6.88 <math>\pm</math> 0.69</b> | <b>0.76 <math>\pm</math> 0.06</b> |

Table B.3: **CCA performances** on train and test set.

| Connectivity measure  | r (train set)                     | r (test set)                      |
|-----------------------|-----------------------------------|-----------------------------------|
| Correlation matrix    | 0.78 $\pm$ 0.01                   | 0.36 $\pm$ 0.09                   |
| GraphLasso cv         | 0.77 $\pm$ 0.01                   | 0.10 $\pm$ 0.08                   |
| Ledoit-Wolf           | 0.78 $\pm$ 0.01                   | 0.31 $\pm$ 0.07                   |
| Identity shrinkage cv | 0.78 $\pm$ 0.01                   | 0.32 $\pm$ 0.07                   |
| Prior shrinkage cv    | 0.77 $\pm$ 0.01                   | 0.35 $\pm$ 0.08                   |
| <b>PoSCE</b>          | <b>0.82 <math>\pm</math> 0.01</b> | <b>0.43 <math>\pm</math> 0.05</b> |

– *Phenotype similarities*

Figure B.7 shows additional functional connectivity comparisons within similar phenotype groups on HCP. Results sustain the fact that PoSCE highlights better phenotype similarities, while graphical Lasso estimates yield more overlapping distributions of pairwise distances within twins and non-twins.

– *Canonical brain-behavior correlations*

Table B.3 summarizes the CCA performances on HCP from all connectivity estimators on in-sample (train) and out-of-sample (test) settings. Similarly to age prediction results, PoSCE connectivity features give better CCA generalization whereas graphical Lasso features have the lowest accuracies.

## Appendix C. Impact of the brain atlas on PoSCE

In all previous experiments, covariances are estimated on 64 brain regions from bootstrap analysis of stable clusters (BASC) atlas (Bellec et al., 2010). To assess brain atlas impact on connectivity estimation, we compare connectivity estimators reproducibility within subjects as in section 4.4 by choosing different brain atlases. We include two publicly available brain atlases :

- Multi-scale dictionary learning atlas (MSDL) (Varoquaux et al., 2011) with 39 regions.
- Harvard-Oxford atlas from FSL software (Jenkinson et al., 2012) with 96 regions.

Figure C.8 shows estimator reproducibility results on HCP using MSDL and Harvard-Oxford atlas. These two atlases yield comparable results to those observed in section 4.4 where the prior has similar contribution to the covariance stability when increasing or decreasing the number of regions.

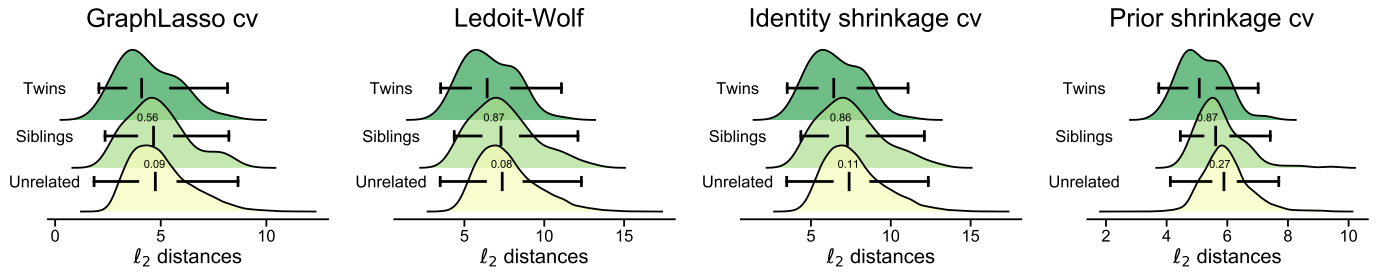


Figure B.7: **Within phenotype similarities.** Plots represent pairwise distance distributions. Digits represent differences between each two distributions. Distances between functional connectivity profiles are better highlighted with PoSCE. Overall, shrinkage yield better similarities compared to  $\ell_1$  penalized covariance.

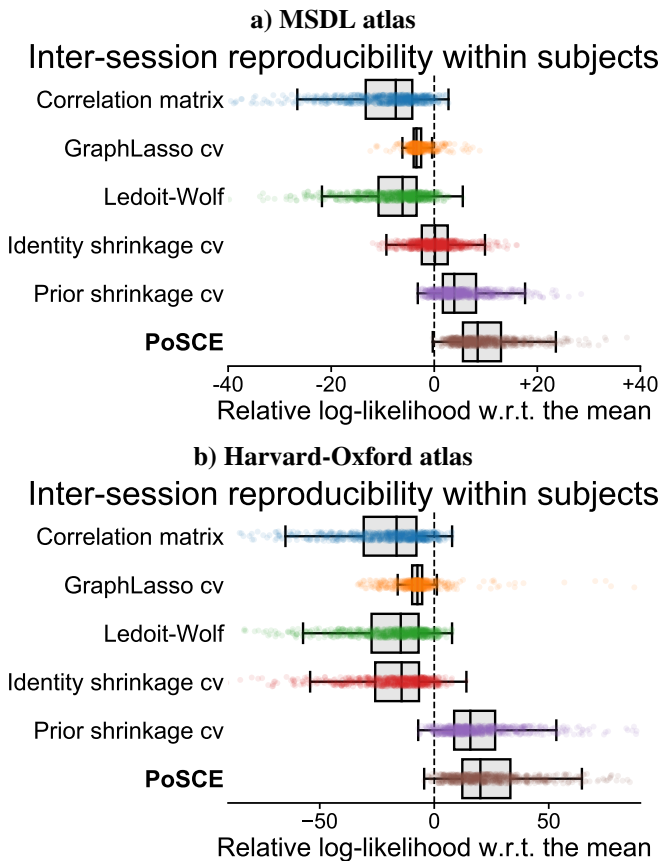


Figure C.8: **Fidelity to subject data.** Using different brain atlases yield similar results : the population prior gives more stable within-subject estimates.

## Appendix D. Prior visualization

710 We provide visualizations of the calculated population distributions. Figure D.9 shows population distribution characteristics of HCP and CamCAN. It depicts the mean  $\vec{d}\Sigma_0$  and the first two principal component analysis (PCA) modes of the covariance  $\vec{\Lambda}$ . We note that the mean matrices are similar for HCP  
 715 and CamCAN datasets where pairwise connectivities are dense and stronger within each functional network (auditory, default mode network, attention, ...).

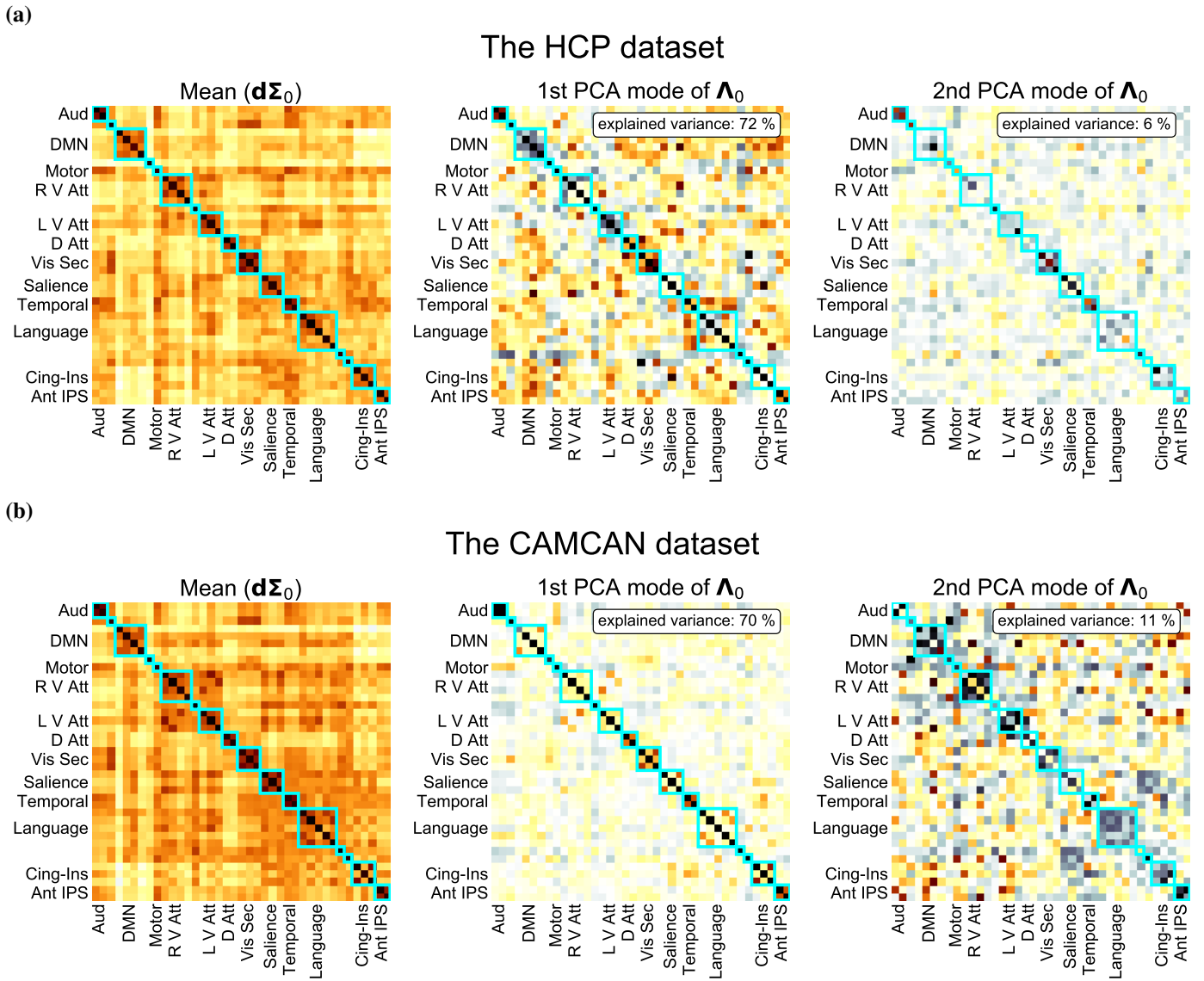


Figure D.9: **Population prior distributions.** Mean and covariance modes of the HCP and the CamCAN datasets.