

# Supplementary Information

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## 1 Details of simulation study

To generate the cost function depicted in Figure 1a, we draw  $n = m = 1000$  points from mean-zero 3-dimensional Gaussian distributions with the following respective covariance matrices:

$$\Sigma_X = \begin{bmatrix} 1 & 0.2 & 0.4 \\ 0.2 & 1 & 0 \\ 0.4 & 0 & 1 \end{bmatrix} \quad \Sigma_Y = \begin{bmatrix} 1 & -0.9 & 0 \\ -0.9 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

Due to the large sample sizes, the empirical distributions accurately represent the underlying populations, and thus the projection produced by the tightening procedure (in green) is significantly inferior to the projection produced by the RELAX algorithm (in red) in terms of actual divergence captured. Note that only dimensions 2 and 3 of the projection-space are plotted in the figure since  $\beta_1 = \sqrt{1 - \sum_{\ell=2}^d \beta_\ell^2}$  is fixed for the unit-norm projections of interest.

Next, we detail the process by which the data are generated for the two-sample problems depicted in Figure 1c. We set the features of the underlying  $X$  and  $Y$  to mean-zero multivariate Gaussian distributions in blocks of 3, where within each block, (common) covariance parameters are sampled from the  $\text{Wishart}(\mathbf{I}_{3 \times 3})$  distribution with 3 degrees of freedom. Only for the first block of 3 features do we sample a separate covariance matrix for  $X$  and a separate covariance matrix for  $Y$ , so all differences between the two distributions lie in the first 3 features. To generate a dataset with  $d = 3 \times \ell$ , we simply concatenate  $\ell$  of our blocks together (always including the first block with the

underlying difference) and draw  $n = m = 100$  points from each class. We generate 20 datasets by increasing  $\ell$  (so the largest  $d = 60$ ), and repeat this entire experiment 10 times reporting the average  $p$ -values in Figure 1c.

Each  $p$ -value is obtain by randomly permuting the class labels and recomputing the test statistic 100 times (where we use the same permutations between all datasets). In SPARDA, regularization parameter  $\lambda$  is re-selected using our cross-validation technique in each permutation. The overall Wasserstein distance in the ambient space is computed by solving a transportation problem [1], and we note the similarity between this statistic and the cross-match test [2]. A popular kernel method for testing high-dimensional distribution equality, the mean map discrepancy, is computed using the Gaussian kernel with bandwidth parameter chosen by the “median trick” [3] (this is very similar to the energy test of [4]). Finally, we also compute the DiProPerm statistic, employing the the DWD- $t$  variant recommended for testing general equality of distributions [5].

## 2 Single cell gene expression in cortex vs. hippocampus

Playing critical roles in the brain, the somatosensory cortex (linked to the senses) and hippocampal region (linked to memory regulation and spatial coding) contain a diversity of cell types [6]. It is thus of great interest to identify how cell populations in these regions diverge in developing brains, a question we address by applying SPARDA to single cell RNA-seq data from these regions. Following [7], we represent gene expression by log-transformed FPKM computed from the sequencing read counts<sup>1</sup>, so values are directly comparable between genes. Because expression measurements from individual cells are poorer in quality than transcriptome profiles obtained in aggregate across tissue samples (due to a drastically reduced amount of available RNA), it is important to filter out poorly measured genes and we retain a set of 10,305 genes that are measured with sufficient accuracy for informative analysis [7].

Table 1 and Figure 1 demonstrate that SPARDA discovers many interesting genes which are already known to play important functional roles in these regions of the brain. For comparison, we also run LIMMA, a standard method for differential expression analysis which tests for marginal mean-differences on a gene-by-gene basis [8]. Ordering the significant genes under LIMMA by magnitude of their mean expression difference, we find that 3 of the top 10 genes identified by SPARDA also appear in this top 10 list (*Crym*, *Spink8*, *Neurod6*), demonstrating SPARDA’s implicit attraction toward large first-order differences over more nuanced changes in practice. Because only few genes can feasibly be considered for subsequent experimentation in these studies, a good tool for differential expression analysis must rank the most relevant genes very highly in order for researchers to take note.

One particularly relevant gene in this data is *Snca*, a presynaptic signaling and membrane trafficking gene whose defects are implicated in both Parkinson and Alzheimer’s disease [9, 10]. While *Snca* is ranked 11<sup>th</sup> highest under SPARDA, it only ranks 349 according to LIMMA  $p$ -values and 95 based on absolute mean-shift. Figure 2 shows that the primary change in *Snca* expression between the cell types is not a shift in the distributions, but rather the movement of a large fraction of low (1-2.5 log-FPKM) expression cells into the high-expression ( $> 2.5$  log-FPKM) regime. As this type of change does not match the restrictive assumptions of LIMMA’s  $t$ -test, the method fails to highly-rank this gene while the Wasserstein distance employed by SPARDA is perfectly suited for measuring this sort of effect.

### 2.1 Identifying genes whose interactions differ between cortex vs. hippocampus cells

After restricting our analysis to only the top 500 genes with largest average expression (since genes playing important roles in interactions must be highly expressed), we normalize each gene’s expression values to have mean zero and unit variance within in the cells of each class. Subsequent application of SPARDA reveals that most of the genes corresponding to the ten greatest values of the resulting  $\hat{\beta}$  are known to play important roles in in signaling and regulation (see Table 2).

<sup>1</sup>available in NCBI’s Gene Expression Omnibus (under accession GSE60361)

GENE	WEIGHT	DESCRIPTION
Cck	0.0593	Primary distinguishing gene between distinct interneuron classes identified in the cortex and hippocampus [11]
Neurod6	0.0583	General regulator of nervous system development whose induced mutation displays different effects in neocortex vs. the hippocampal region [12]
Stmn3	0.0573	Up-expressed in hippocampus of patients with depressive disorders [13]
Plp1	0.0570	An oligodendrocyte- and myelin-related gene which exhibits cortical differential expression in schizophrenia [14]
Crym	0.0550	Plays a role in neuronal specification [15]
Spink8	0.0536	Serine protease inhibitor specific to hippocampal pyramidal cells [6]
Gap43	0.0511	Encodes plasticity protein important for axonal regeneration and neural growth
Cryab	0.0500	Stress induction leads to reduced expression in the mouse hippocampus [16]
Mal	0.0494	Regulates dendritic morphology and is expressed at lower levels in cortex than in hippocampus [17]
Tspan13	0.0488	Membrane protein which mediates signal transduction events in cell development, activation, growth and motility

Table 1: Genes with the greatest weight in the projection  $\hat{\beta}$  produced by SPARDA analysis of the mouse brain single cell RNA-seq data. Where not cited, the description of the genes are taken from the standard ontology annotations.

GENE	WEIGHT	DESCRIPTION
Thy1	0.1245	Plays a role in cell-cell & cell-ligand interactions during synaptogenesis and other processes in the brain
Vsnl1	0.1245	Modulates intracellular signaling pathways of the central nervous system
Stmn3	0.1222	Stathmins form important protein complex with tubulins
Stmn2	0.1188	Note: Tubulins Tubb3 and Tubb2 are ranked 20 <sup>th</sup> and 25 <sup>th</sup> by weight in $\hat{\beta}$
Tmem59	0.1176	Fundamental regulator of neural cell differentiation. Knock out in the hippocampus results in drastic expression changes of many other genes [18]
Baspl	0.1171	Transcriptional cofactor which can divert the differentiation of cells to a neuronal-like morphology [19]
Snhg1	0.1166	Unclassified non-coding RNA gene
Mllt11	0.1145	Promoter of neurodifferentiation and axonal/dendritic maintenance [20]
Uchl1	0.1137	Loss of function leads to profound degeneration of motor neurons [21].
Cck	0.1131	Targets pyramidal neurons and enables neocortical plasticity allowing for example the auditory cortex to detect light stimuli [22, 23]

Table 2: Genes with the greatest weight in the projection  $\hat{\beta}$  produced by SPARDA analysis of the marginally normalized expression data.

gene ontology term	category, level	set size	candidates contained	p-value	q-value
GO:0019226 transmission of nerve impulse	BP 4	490	18 (3.7%)	5.46e-11	1.31e-08
GO:0007268 synaptic transmission	BP 4	391	13 (3.3%)	1.04e-07	1.02e-05
GO:0055082 cellular chemical homeostasis	BP 4	632	16 (2.5%)	1.27e-07	1.02e-05
GO:0032051 clathrin light chain binding	MF 4	3	3 (100.0%)	1.33e-07	4.66e-06
GO:0048666 neuron development	BP 4	646	16 (2.5%)	1.87e-07	1.09e-05
GO:0022008 neurogenesis	BP 4	1029	20 (1.9%)	2.28e-07	1.09e-05
GO:0032846 positive regulation of homeostatic process	BP 4	57	6 (10.5%)	4.72e-07	1.89e-05
GO:0048878 chemical homeostasis	BP 4	838	17 (2.0%)	1.12e-06	3.82e-05
GO:0007399 nervous system development	BP 4	1486	23 (1.6%)	1.31e-06	3.93e-05
GO:0030182 neuron differentiation	BP 4	854	17 (2.0%)	1.57e-06	4.18e-05
GO:0031175 neuron projection development	BP 4	529	13 (2.5%)	3.21e-06	7.7e-05
GO:0051969 regulation of transmission of nerve impulse	BP 4	194	8 (4.1%)	7.32e-06	0.00016
GO:0048858 cell projection morphogenesis	BP 4	516	12 (2.3%)	1.37e-05	0.000275
GO:0032990 cell part morphogenesis	BP 4	542	12 (2.2%)	2.19e-05	0.000405
GO:0007010 cytoskeleton organization	BP 4	763	14 (1.8%)	3.33e-05	0.000571
GO:0048168 regulation of neuronal synaptic plasticity	BP 4	38	4 (10.5%)	4.29e-05	0.000686
GO:0000902 cell morphogenesis	BP 4	814	14 (1.7%)	6.91e-05	0.00093
GO:0050877 neurological system process	BP 4	2024	24 (1.2%)	6.97e-05	0.00093
GO:0044057 regulation of system process	BP 4	427	10 (2.3%)	7.09e-05	0.00093
GO:0008366 axon ensheathment	BP 4	84	5 (6.0%)	7.36e-05	0.00093
GO:0008344 adult locomotory behavior	BP 4	86	5 (5.8%)	8.23e-05	0.000988
GO:0007611 learning or memory	BP 4	151	6 (4.0%)	0.000131	0.0015
GO:0006900 membrane budding	BP 4	21	3 (14.3%)	0.000165	0.0018
GO:0071822 protein complex subunit organization	BP 4	900	14 (1.6%)	0.000192	0.00201
GO:0001662 behavioral fear response	BP 4	27	3 (11.1%)	0.000356	0.00341
GO:0002209 behavioral defense response	BP 4	27	3 (11.1%)	0.000356	0.00341
GO:0030913 paranodal junction assembly	BP 4	6	2 (33.3%)	0.00039	0.0036
GO:0007626 locomotory behavior	BP 4	188	6 (3.2%)	0.000405	0.0036

Figure 1: Biological process terms most significantly enriched in the annotations of the top 100 genes identified by SPARDA.

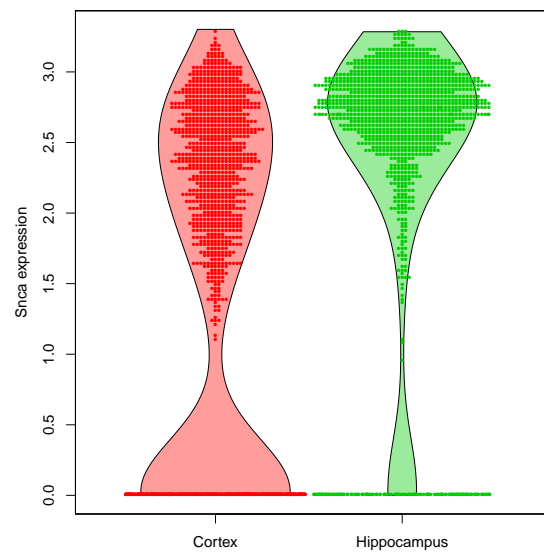


Figure 2: Distribution of *Snca* expression across cells of the somatosensory cortex and hippocampus.

### 3 Proofs and Auxiliary Lemmas

Throughout this section, we use  $C$  to denote absolute constants whose value may change from line to line.  $F$  is defined the cdf of a random variable, and the corresponding quantile function is  $F^{-1}(p) := \inf\{x : F(x) \geq p\}$ . Note our assumptions (A1)-(A3) ensure the quantile function equals the unique inverse of any projected cdf. Hat notation is used to represent the empirical versions of all quantities, and recall that  $D$  denotes the *squared* Wasserstein distance.

#### 3.1 Proof of Theorem 1

*Proof.* Since  $\hat{\beta}$  maximizes the empirical divergence, we have:

$$\begin{aligned} & \Pr(D(\hat{\beta}^T \hat{X}^{(n)}, \hat{\beta}^T \hat{Y}^{(n)}) > \Delta - \epsilon) \\ & \geq \Pr(D(\beta^{*T} \hat{X}^{(n)}, \beta^{*T} \hat{Y}^{(n)}) > \Delta - \epsilon) \\ & \geq \Pr(D(\beta^{*T} \hat{X}^{(n)}, \beta^{*T} X) + D(\beta^{*T} \hat{Y}^{(n)}, \beta^{*T} Y) \leq \epsilon) \\ & \geq 1 - 4 \exp\left(-\frac{n\epsilon^2}{16R^4}\right) \text{ applying Lemma 1 and the union bound.} \end{aligned}$$

□

**Lemma 1.** *For bounded univariate random variable  $Z \in [-R, R]$  with nonzero continuous density in this region, we have*

$$D(\hat{Z}^{(n)}, Z) > \epsilon$$

*with probability at most  $2 \exp\left(-\frac{n\epsilon^2}{8R^4}\right)$*

*Proof.* On the real line, the (squared) Wasserstein distance is given by:

$$\begin{aligned} D(\hat{Z}^{(n)}, Z) &= \int_0^1 \left( \hat{F}_Z^{-1}(p) - F_Z^{-1}(p) \right)^2 dp \\ &= 4R^2 \int_0^1 \left( \frac{\hat{F}_Z^{-1}(p) - F_Z^{-1}(p)}{2R} \right)^2 dp \quad \text{where } \left| \frac{\hat{F}_Z^{-1}(p) - F_Z^{-1}(p)}{2R} \right| \leq 1 \text{ for each } p \in (0, 1) \\ &\leq 4R^2 \int_0^1 \left| \frac{\hat{F}_Z^{-1}(p) - F_Z^{-1}(p)}{2R} \right| dp \\ &= 2R \int_0^1 \left| \hat{F}_Z^{-1}(p) - F_Z^{-1}(p) \right| dp \\ &= 2R \int_{-\infty}^{\infty} \left| \hat{F}_Z(z) - F_Z(z) \right| dz \quad \text{by the equivalence of the (empirical) quantile function and inverse (empirical) cdf} \\ &\leq 4R^2 \cdot \sup_z \left| \hat{F}_Z(z) - F_Z(z) \right| \\ &\leq \epsilon \text{ with probability } \geq 1 - 2 \exp\left(-\frac{n\epsilon^2}{8R^4}\right) \text{ by the Dvoretzky-Kiefer-Wolfowitz inequality [24].} \end{aligned}$$

□

### 3.2 Proof of Theorem 2

*Proof.* We first construct a fine grid of points  $\{\alpha_1, \dots, \alpha_S\}$  which form an  $(\epsilon/R^2)$ -net covering the surface of the unit ball in  $\mathbb{R}^d$ . When  $\mathbb{P}_X = \mathbb{P}_Y$ , the Cramer-Wold device [25] implies that for any point in our grid:  $D(\alpha_s^T X, \alpha_s^T Y) = 0$ . A result analogous to Theorem 1 implies  $D(\alpha_s^T \hat{X}^{(n)}, \alpha_s^T \hat{Y}^{(n)}) > \epsilon$  with probability  $< C_1 \exp(-\frac{C_2}{R^4} n \epsilon^2)$ .

Subsequently, we apply the union bound over the finite set of all grid points. The total number of points under consideration is the covering number of the unit-sphere which is  $\left(1 + \frac{2R^2}{\epsilon}\right)^d$ . Thus, the probability that  $D(\alpha_s^T \hat{X}^{(n)}, \alpha_s^T \hat{Y}^{(n)}) < \epsilon$  simultaneously for all points in the grid is at least

$$C_1 \left(1 + \frac{2R^2}{\epsilon}\right)^d \exp\left(-\frac{C_2}{R^4} n \epsilon^2\right)$$

By construction, there must exist grid point  $\alpha_0$  such that  $\|\hat{\beta} - \alpha_0\|_2 < \epsilon/R^2$ . By Lemma 2

$$D(\hat{\beta}^T \hat{X}^{(n)}, \hat{\beta}^T \hat{Y}^{(n)}) \leq D(\alpha_0^T \hat{X}^{(n)}, \alpha_0^T \hat{Y}^{(n)}) + C\epsilon$$

thus completing the proof.  $\square$

**Lemma 2.** For  $\alpha, \beta \in \mathcal{B}$  such that  $\|\alpha - \beta\|_2 < \epsilon$ , we have:

$$|D(\alpha^T \hat{X}^{(n)}, \alpha^T \hat{Y}^{(n)}) - D(\beta^T \hat{X}^{(n)}, \beta^T \hat{Y}^{(n)})| \leq C\epsilon R^2 \quad (1)$$

*Proof.* We assume that the  $\alpha$ -projected divergence is larger than the  $\beta$ -projected divergence, and write:

$$D(\beta^T \hat{X}^{(n)}, \beta^T \hat{Y}^{(n)}) = \min_{M \in \mathcal{M}} \sum_{i=1}^n \sum_{j=1}^m (\beta^T x^{(i)} - \beta^T y^{(j)})^2 M_{ij}$$

recalling that  $\mathcal{M}$  is the set of matching matrices defined in the main text. Let  $M(\beta)$  denote the matrix which is used in the computation of the  $\beta$ -projected empirical Wasserstein distance (the minimizer of the righthand side of the above expression). Thus, we can express (1) as:

$$\begin{aligned} & \sum_{i=1}^n \sum_{j=1}^m (\alpha^T x^{(i)} - \alpha^T y^{(j)})^2 M(\alpha)_{ij} - \sum_{i=1}^n \sum_{j=1}^m (\beta^T x^{(i)} - \beta^T y^{(j)})^2 M(\beta)_{ij} \\ & \leq \sum_{i=1}^n \sum_{j=1}^m (\alpha^T x^{(i)} - \alpha^T y^{(j)})^2 M(\beta)_{ij} - \sum_{i=1}^n \sum_{j=1}^m (\beta^T x^{(i)} - \beta^T y^{(j)})^2 M(\beta)_{ij} \\ & \leq \sum_{i=1}^n \sum_{j=1}^m \left[ (\alpha^T (x^{(i)} - y^{(j)}))^2 - (\beta^T (x^{(i)} - y^{(j)}))^2 \right] M(\beta)_{ij} \\ & = \sum_{i=1}^n \sum_{j=1}^m \left[ (\alpha - \beta)^T (x^{(i)} - y^{(j)}) \cdot (\alpha + \beta)^T (x^{(i)} - y^{(j)}) \right] M(\beta)_{ij} \\ & \leq \sum_{i=1}^n \sum_{j=1}^m C\epsilon R^2 M(\beta)_{ij} = C\epsilon R^2 \end{aligned}$$

$\square$

### 3.3 Proof of Theorem 3

*Proof.* Our proof relies primarily on a quantitative form of the Cramer-Wold result presented in [26]. We adapt Theorem 3.1 [26] in its contrapositive form: If  $\exists a \geq 0$  such that  $T_a(X, Y) > h(g(\Delta))$ , then  $\exists \beta \in \mathcal{B}$  such that

$$\sup_{z \in \mathbb{R}} \left| \Pr(\beta^T X \leq z) - \Pr(\beta^T Y \leq z) \right| > g(C\Delta) \quad (2)$$

Subsequently we leverage a number of well-characterized relationships between different probability metrics (cf. [27]) to lower bound the projected (squared) Wasserstein distance (of the underlying random variables).

Letting  $K_\beta$  denote the projected Kolmogorov distance in (2), we have that the  $\beta$ -projected Lévy-distance,  $L_\beta$  satisfies:

$$K_\beta \leq (1 + \Phi)L_\beta \quad \text{where } \Phi := \sup_{\alpha \in \mathcal{B}} \left\{ \sup_y |f_{\alpha^T Y}(y)| \right\} \quad (3)$$

and  $f_{\alpha^T Y}(y)$  is the density of the projection of  $Y$  in the  $\alpha$  direction.

In turn the projected Lévy  $L_\beta$  is bounded above by the Prokhorov metric which itself is bounded above by the square root of the  $\beta$ -projected Wasserstein distance. Following the chain of inequalities, we obtain:  $D(\beta^T X, \beta^T Y) \geq C\Delta$ , to which we can apply Theorem 1 to obtain the desired probabilistic bound on the empirical projected divergence.  $\square$

### 3.4 Proof of Theorem 4

*Proof.* Theorem 2 implies that with high probability, any  $\beta_{S^C} \in \mathbb{R}^{d-k}$  has  $D(\beta_{S^C}^T \hat{X}_{S^C}^{(n)}, \beta_{S^C}^T \hat{Y}_{S^C}^{(n)}) < \epsilon$ , while Theorem 3 specifies the probability that there exists  $\beta_S \in \mathbb{R}^k$  such that  $D(\beta_S^T \hat{X}_S^{(n)}, \beta_S^T \hat{Y}_S^{(n)}) > d \cdot \epsilon$ .

A bound for the probability that both theorems' conclusions hold may be obtained by the union bound. When this is the case, it is clear that the optimal  $k$ -sparse  $\hat{\beta} \in \mathbb{R}^d$  must obey the sparsity pattern specified in the statement of Theorem 4. To see this, consider any  $\beta \in \mathcal{B}$  with  $\beta_j \neq 0$  for some  $j \in S^C$  and note that it is always possible to produce a strictly superior projection by setting  $\beta_j = 0$  and distributing the additional weight  $|\beta_j|$  among the features in  $S$  in an optimal manner.  $\square$

## 4 Derivation of semidefinite relaxation properties

Here, we provide some intuitive arguments for the conclusions in §4.3, regarding some conditions under which our semidefinite relaxation is nearly tight.

Condition (i) derives from the fact that (5) has rank one solution when the objective is approximately linear in  $B$ .

(ii) and (iii) are derived by noting that (5) is the Wasserstein distance between random variables  $B^{1/2}X$  and  $B^{1/2}Y$  where  $AX$  follows a  $N(A\mu_X, A\Sigma_X A^T)$  distribution when  $X$  is Gaussian. Furthermore, the Wasserstein distance between (multivariate) Gaussian distributions can be analytically written as

$$W(X, Y) = \|\mu_X - \mu_Y\|_2^2 + \|\Sigma_X^{1/2} - \Sigma_Y^{1/2}\|_F^2$$



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