

**Towards Scalable, Flexible, and Interpretable
Self-Supervised Learning for Multiview
Biomedical Data**

by

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Declaration

I, James Chapman, confirm that the work presented in my thesis is my own. Where information has been derived from other sources, I confirm that this has been indicated in the thesis.

Abstract

Biomedical data are essential for advancing our knowledge and practice of medicine and healthcare. However, biomedical data are also challenging to analyze due to their complexity, heterogeneity, high-dimensionality, and scarcity of labels. To overcome these challenges, self-supervised learning (SSL) has emerged as a promising paradigm for learning from unlabeled data by leveraging inherent structures or patterns in the data. SSL methods can exploit different forms of supervision signals derived from the data itself, such as contrastive learning, reconstruction, prediction, or clustering. SSL methods can also benefit from deep neural networks that can learn expressive and flexible representations from complex and high-dimensional data.

In this thesis, we focus on a specific type of SSL problem, namely multiview SSL, where data are represented by multiple distinct feature groups or modalities that describe the same phenomenon or entity. Each feature group or modality is referred to as a view, and different views may provide complementary or redundant information. Multiview SSL aims to learn useful representations from multiview data by exploiting the inherent structures or patterns across views. Multiview SSL has a wide range of applications in biomedical domains, such as integrating multiple types of genomic data for disease diagnosis or prognosis, generating natural language descriptions from brain images, and understanding human behaviors during social interactions based on multimodal signals.

In this thesis, we propose novel approaches to multiview SSL that are scalable, flexible, and interpretable. We address the following research questions: How can we reformulate classical subspace learning methods as unconstrained optimization problems that can be solved by gradient descent? How can we extend classical subspace learning methods to nonlinear functions using deep neural networks? How can we incorporate different forms of regularization or prior knowledge into subspace learning methods to improve their quality or robustness?

To answer these questions, we develop novel methods for multiview subspace learning that leverage mathematical optimization techniques, deep neural networks, regularization techniques. We evaluate our methods on various real-world biomedical datasets and demonstrate their effectiveness and advantages over existing methods.

Impact Statement

This thesis contributes to the advancement of machine learning and biomedical data analysis by developing novel methods for multiview self-supervised learning that are scalable, flexible, and interpretable. The proposed methods can help researchers and practitioners to analyze complex and high-dimensional biomedical data more efficiently and effectively, and to discover new insights and opportunities for improving health outcomes. The proposed methods can also be applied to other domains where multiview data are available or desirable, such as natural language processing, computer vision, multimedia analysis, and social network analysis. This thesis also provides a valuable reference for future research on multiview self-supervised learning and related topics.

List of Publications

First Author Peer Reviewed Conference Proceedings

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James Chapman Janaina Mourao-Miranda, John Shawe-Taylor (n.d.). *A Framework for Regularised Canonical Correlation Analysis by Alternating Least Squares*.

First Author Pre-Print

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Lawry Aguila, Ana, James Chapman, Mohammed Janahi, et al. (2022). "Conditional VAEs for Confound Removal and Normative Modelling of Neurodegenerative Diseases". In: *International Conference on Medical Image Computing and Computer-Assisted Intervention*. Springer Nature Switzerland Cham, pp. 430–440.

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Acronyms

ADNI Alzheimer's Disease Neuroimaging Initiative. 8, 14, 16, 39–41, 53, 54, 57, 58, 60, 89, 91–93, 130

CCA Canonical Correlation Analysis. 13, 14, 21, 29–34, 37, 38, 40, 43, 69–76, 78, 79, 82–85, 87–89, 91, 93, 96, 100, 101

DCCA Deep Canonical Correlation Analysis. 30

FRALS Flexible Regularised Alternating Least Squares. 50–52

GFA Group Factor Analysis. 14, 69, 72–74, 76, 87–89

HCP Human Connectome Project. 8, 14, 16, 39–41, 53, 54, 57, 60, 89, 91–93, 128

KCCA Kernel Canonical Correlation Analysis. 101

MCCA Multiset Canonical Correlation Analysis. 31

MRI Magnetic Resonance Imaging. 49

PCA Principal Component Analysis. 25–27, 99–101

PLS Partial Least Squares. 27–31, 84, 85, 87, 93, 96, 100

RCCA Regularized Canonical Correlation Analysis. 87, 93

sPLS Sparse Partial Least Squares. 85, 87

Glossary

latent variables Latent variables are variables that are not observed. They are also called hidden variables. Latent variables are used to model the relationship between the observed variables.. 25

loadings The loadings of a latent variable or representation are the correlations between the latent variable or representation and the observed variables.. 8, 9, 25, 71, 73–76, 78–83, 85, 89, 91, 93–97, 129, 131

representations Representations are the latent variables in a multiview dataset. They can be either the same or different types of data. The key assumption of multiview learning is that the views are related to each other in some sense. For example, in a dataset of images and text, the images and text are related because they describe the same object. We could also have a dataset containing images of the same object taken from different angles, in which case the images are still related because they describe the same object.. 7, 8, 25, 56, 58, 63, 67, 93

views Views are the observed variables in a multiview dataset. They can be either the same or different types of data. The key assumption of multiview learning is that the views are related to each other in some sense. For example, in a dataset of images and text, the images and text are related because they describe the same object. We could also have a dataset containing images of the same object taken from different angles, in which case the images are still related because they describe the same object.. 21–24, 27, 29, 37

weights The weights of a latent variable or representation are the coefficients of the linear combination of the observed variables that make up the factor.. 7–10, 25, 41, 43, 44, 49, 55–58, 61–63, 65, 67, 85, 87, 91, 93, 95–97, 131

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Chapter I

Introduction

In the middle of my PhD journey, in June 2021, I self-referred to the Community Living Well service in London, UK, for help with my mental health. I was assigned a therapist, who I met with weekly for 12 weeks. During our sessions, we discussed my mental health and the challenges I was facing. I was also asked to complete a questionnaire at the beginning and end of each session, which asked me to rate my mood and answer questions about my mental health. Each time I did this, I questioned how well these subjective numbers truly represented my feelings.

A keen sportsperson, I also wear a Garmin watch that tracks my heart rate, my sleep, and my activity levels. I use this data to monitor my health and fitness, and I have found it to be a useful tool in my training. Using a physical ‘stress level’ metric based on Heart Rate Variability (HRV), I can see how alcohol affects my sleep¹, how well I have slept, and I know I am about to get sick before I feel it.

As a type 1 diabetic, I rely on a continuous glucose monitor for my blood sugar levels. This device measures my blood sugar every five minutes, and I can see the results on my phone. I can also see how my blood sugar changes over time, and I can use this information to adjust my insulin doses and improve my control.

This thesis stems from a simple idea: What if we could combine different kinds of health data to get a clearer, more complete picture of a person’s health?

¹badly

1 Thesis Structure and Contributions

This thesis presents innovative methodologies for scaling multiview data fusion to massive datasets, aiming to transform the way biomedical data is analyzed and understood. By leveraging advancements in self-supervised learning and multiview learning, the research herein explores the integration of diverse data sources, similar to how my mental health, physical activity, and diabetes data each provide unique insights into my well-being.

The overarching aim is to develop methodological improvements that are practical and user-friendly. We strive to create tools and methods that are theoretically robust yet intuitive and straightforward to use in real-life scenarios. The goal is to empower practitioners in biomedical research and other fields to fully leverage their data, without requiring deep technical expertise in data analysis algorithms.

This thesis offers three primary contributions:

- Developing a regularization method for CCA using structured priors, including the Elastic Net, to improve interpretability.
- Proposing the use of loadings over weights in CCA for better interpretability and relevance to biomedical data generation processes.
- Creating a new gradient descent-based formulation for CCA and generalized eigenvalue problems, suitable for large datasets.

1.1 Chapter Summaries

Chapter II reviews multiview and self-supervised learning techniques, focusing on their application in biomedical data.

Chapter III introduces a method to regularize CCA using structured priors, demonstrated with Human Connectome Project and Alzheimer's Disease Neuroimaging Initiative data.

Chapter IV examines the relationship between loadings and weights in CCA, using simulated data to show the advantages of loadings for interpretability.

Chapter V presents a new loss function for generalized eigenvalue problems, applicable to CCA and SSL methods, and demonstrates its effectiveness with various benchmarks.

Chapter ?? introduces CCA-Zoo, a Python package implementing the methodologies of this thesis, and discusses its role in the Python ecosystem and biomedical research.

Chapter 7 discusses the implications, challenges, and future directions for the research presented in this thesis.

I hope that this thesis and the work it represents will help to bridge the gap between the potential of biomedical data and the capabilities of current analytical methods.

Chapter II

Background: Multiview Machine Learning: Concepts, Methods, and Limitations

Principal Component Analysis is a dimensionally invalid method that gives people a delusion that they are doing something useful with their data. If you change the units that one of the variables is measured in, it will change all the “principal components”! It’s for that reason that I made no mention of PCA in my book. I am not a slavish conformist, regurgitating whatever other people think should be taught. I think before I teach.

Professor David MacKay

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1 Introduction to Machine Learning and Multiview Learning

In this chapter, we gather the necessary background knowledge needed to motivate and understand the contributions of this thesis.

Machine learning enables models to automatically learn patterns and make decisions from data. Machine learning comprises three primary paradigms: supervised, self-supervised (in the past called unsupervised), and reinforcement learning, each distinct in its approach to learning from data. This thesis focuses on *multiview self-supervised machine learning*, which aims to develop robust representations by uncovering associations between various data types within datasets. These data types, known as views may include distinct sources of information such as MRI images, genomic data, and clinical records in the context of patient data analysis.

1.1 Multiview Machine Learning

Multiview machine learning encompasses a variety of techniques aimed at learning from data that have multiple sources or modalities, also known as views. These techniques can be broadly classified into supervised and self-supervised (or sometimes, equivalently, unsupervised) multiview learning, with some algorithms straddling the boundary between the two.

1.1.1 Supervised Multiview Learning

In supervised multiview learning, one view serves as the input while the other view is treated as the target label. The algorithm learns to predict the target view based on the input view, leveraging the information from both to enhance the predictive performance (Zong, Mac Aodha, and T. Hospedales, 2023).

1.1.2 Self-Supervised Multiview Learning

Self-Supervised Learning (SSL) is a paradigm where the training signal is derived from the data itself, rather than relying on external labels (Balestrieri, Ibrahim, et al., 2023). The cornerstone of SSL is the concept of a ‘pretext task,’ a learning task created from the data that trains the model to capture useful features or representations. In the context of multiview machine learning, self-supervised learning often operates under the assumption that different views are generated from a common source. A natural pretext task, in this case, is to predict or estimate this source from the given views. In the prediction setting, we might mask the source and train the model to predict it from the remaining views, closer to supervised learning. In the estimation setting, we never directly observe the source, but we train the model to estimate it from the views. In this case, the model is forced to learn the underlying structure of the data without any direct supervision. This not only enables the model to learn associations between views but also allows it to derive robust and informative representations for subsequent tasks like classification or regression. This is particularly true if the source is unavailable at test time when an application must rely on the views alone to make predictions. In the case of latent variables, where the assumed source is unobserved, the model learns to estimate latent variables from the views which are unavailable even at training time. These are usually much lower-dimensional than the original views, and therefore provide a more compact and informative representation of the data. The models we deal with in this thesis are generally of this type.

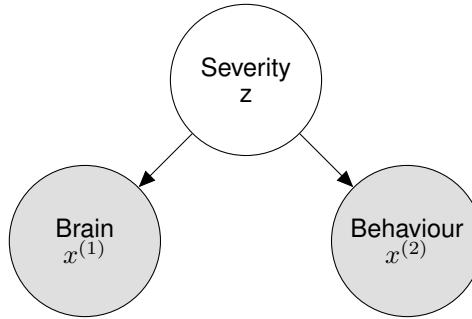


Figure II.1: Latent Variable Model of Mental Health: From this perspective the neuroimaging modality and behavioural data are both considered to have been generated with distributions conditioned on the severity of a mental health condition

1.2 Conditional Independence, Causality, and Multiview Learning

Consider the graphical model depicted in Figure II.1. It comprises two distinct observed views: a brain modality and a behavioral modality. The graph represents the assumption that the brain and behaviour are conditionally independent given the severity of an unobserved ‘latent’ mental health condition.

In multiview machine learning, the relationship between conditional independence and causality is nuanced but crucial. When examining dependencies between events, such as those observed between brain activity and behavior, several scenarios emerge:

- direct causation (brain influencing behavior or vice versa or even both)
- both being influenced by a common, possibly unobserved, cause
- no direct causal link between them

Importantly, if a common cause does exist, conditioning on it renders brain and behavior independent; this ‘screens off’ their dependence, revealing key insights for our models (Reichenbach, 1956). However, it is essential to recognize that the presence of a common latent variable, inferred from these views, does not automatically imply causality in the observed data.

1.2.1 Complementary and Redundant Information

The nature of the information provided by different views (such as neuroimaging and behavioral data) is important for understanding multiview learning models. A particularly useful distinction is between *complementary* and *redundant* information (Nguyen and D. Wang, 2020). When views contain complementary information, they provide different perspectives on the same subject or sample. For example, we can understand different aspects of a mental health condition by examining both neuroimaging and behavioral data. On the other hand, when views contain redundant information about the latent variables, they provide the same information from different perspectives. For example, a disease diagnosis might be encoded in both neuroimaging and blood test results. This does not make the views useless, however, because they can be used to denoise each other, enhancing the clarity and reliability of the data. We can be more confident that a diagnosis is correct if it is supported by both neuroimaging and blood test results. A particularly famous example of this principle is the ‘Wisdom of Crowds’ effect, where the average of multiple noisy estimates is more accurate than any individual estimate (Galton, 1907). This process exploits the overlap in information to correct or reduce noise and errors, a principle fundamental to many denoising techniques in machine learning.

In this thesis we will work with Canonical Correlation Analysis, a multiview learning method which assumes that the views contain complementary information about latent variables. The next section builds a formal understanding of the principles behind Canonical Correlation Analysis and its variants.

2 Learning Representations: Definitions and Notation

Suppose we have a sequence of vector-valued random variables $X^{(i)} \in \mathbb{R}^{D_i}$ for $i \in \{1, \dots, I\}$. We want to learn meaningful K -dimensional representations

$$Z^{(i)} = f^{(i)}(X^{(i)}; \theta^{(i)}). \quad (\text{II.1})$$

For convenience, define $D = \sum_{i=1}^I D_i$ and $\theta = (\theta^{(i)})_{i=1}^I$. Without loss of generality take $D_1 \geq D_2 \geq \dots \geq D_I$. We will consistently use the subscripts $i, j \in [I]$ for views; $d \in [D_i]$ for dimensions of input variables; and $l, k \in [K]$ for dimensions of representations - i.e. to subscript dimensions of $Z^{(i)}, f^{(i)}$. Later on we will introduce total number of samples N .

In this report, when the functions f are linear, we will typically refer to u_k as *weights*, $Z_k = X_k u_k$ as *representations* or *latent variables*, depending on the context. We will sometimes consider a matrix $U = (u_1, \dots, u_K) \in \mathbb{R}^{D \times K}$ of weights, and a matrix $Z = (Z_1, \dots, Z_K) \in \mathbb{R}^{N \times K}$ of representations. We will refer to the Pearson correlation between features and their respective latent variable $\text{Corr}(X_j^{(i)}, Z_k)$ as the *loadings* of $X_j^{(i)}$ on Z_k (Rosipal and Krämer, 2005; Alpert and Peterson, 1972), noting that the same concept has also been referred to as *structure correlations* (Meredith, 1964).

2.1 Background: GEPs in linear algebra

A Generalized Eigenvalue Problem (GEP) is defined by two symmetric matrices $A, B \in \mathbb{R}^{D \times D}$ (Stewart and J.-G. Sun, 1990)¹. They are usually characterized by the set of solutions to the equation:

$$Au = \lambda Bu \quad (\text{II.2})$$

with $\lambda \in \mathbb{R}$, $u \in \mathbb{R}^D$, called (generalized) eigenvalue and (generalized) eigenvector respectively. We shall only consider the case where B is positive definite to avoid degeneracy. Then the GEP becomes equivalent to an eigen-decomposition of the symmetric matrix $B^{-1/2}AB^{-1/2}$. This is key to the proof of our new characterization. In addition, one can find a basis of eigenvectors spanning \mathbb{R}^D . We define a *top-K subspace* to be one spanned by some set of eigenvectors u_1, \dots, u_K with the top- K associated eigenvalues $\lambda_1 \geq \dots \geq \lambda_K$. We say a matrix $U \in \mathbb{R}^{D \times K}$ defines a top- K subspace if its columns span one.

Uniqueness In GEPs, the eigenvectors u are not in general unique, but the canonical correlations $1 \geq \rho_1 \geq \rho_2 \geq \dots \geq 0$ are unique (Mills-Curran, 1988).

2.2 Principal Components Analysis

Principal Components Analysis (Hotelling, 1933) (PCA) is a classical method in unsupervised machine learning for representation learning. It is widely used for dimensionality reduction and feature extraction. The primary goal of PCA is to transform the original high-dimensional data into a new coordinate system defined by orthogonal axes, capturing the most relevant aspects of the data.

¹more generally, A, B can be Hermitian, but we are only interested in the real case

In PCA, the representations are constrained to be linear transformations of the form:

$$Z_k = X u_k, \quad (\text{II.3})$$

where u_k are the orthonormal basis vectors such that:

$$u_k^\top u_k = 1, \quad u_k^\top u_l = \delta_{kl} \text{ for } k \neq l. \quad (\text{II.4})$$

The primary goal of PCA is to maximize the variance of the representations Z_k .

2.2.1 Optimization and Solution

Mathematically, for the first principal component, this can be formulated as:

$$u_{\text{opt}} = \underset{u}{\operatorname{argmax}} (u^\top \Sigma u) \quad (\text{II.5})$$

subject to:

$$u^\top u = 1$$

Where $\Sigma = \mathbb{E}[X^\top X]$ is the covariance matrix of the data.

The Lagrangian for this problem is:

$$f(u, \lambda) = u^\top \Sigma u + \lambda(1 - u^\top u), \quad (\text{II.6})$$

where λ is the Lagrange multiplier. Differentiating the Lagrangian yields the first-order conditions:

$$\Sigma u = \lambda u, \quad (\text{II.7})$$

$$u^\top u = 1. \quad (\text{II.8})$$

Eigenvalue Problem This transforms the problem into an eigenvalue equation for the covariance matrix Σ , which can be efficiently solved using standard libraries such as scikit-learn (Pedregosa et al., 2011).

The first principal component therefore corresponds to the eigenvector associated with the largest eigenvalue λ . Subsequent components are the remaining eigenvectors ordered by their corresponding eigenvalues.

2.2.2 Limitations

However, when applying PCA to datasets such as high-dimensional neuroimaging and behavioral data, PCA's main limitation arises: it only accounts for variance within a single dataset, so it cannot take advantage of the redundancy in multiview data.

2.3 Partial Least Squares

Partial Least Squares (PLS) (**wold1975path**) aims to maximize the shared covariance between two paired sets of data, referred to as views. PLS can be seen as a generalization of PCA, where PCA becomes a special case when the two views are identical.

2.3.1 Optimization and Solution

The optimization problem for PLS can be formulated as:

$$u_{\text{opt}}^{(1)} = \underset{u^{(1)}}{\operatorname{argmax}} \{ u^{(1)T} \Sigma_{12} u^{(2)} \} \quad (\text{II.9})$$

subject to:

$$u^{(1)T} u^{(1)} = 1$$

$$u^{(2)T} u^{(2)} = 1$$

where $X^{(1)} \in \mathbb{R}^{n \times p_1}$ and $X^{(2)} \in \mathbb{R}^{n \times p_2}$, meaning we have two views with the same number of samples but potentially different number of features.

The Lagrangian for this optimization problem can be formulated as:

$$f(u^{(1)}, \lambda) = u^{(1)T} \Sigma_{12} u^{(2)} + \lambda_1 (1 - u^{(1)T} u^{(1)}) + \lambda_2 (1 - u^{(2)T} u^{(2)}) \quad (\text{II.10})$$

Upon deriving the first order conditions, we get:

$$\Sigma_{21}u^{(1)} = \lambda_2 u^{(2)} \quad (\text{II.11})$$

$$\Sigma_{12}u^{(2)} = \lambda_1 u^{(1)} \quad (\text{II.12})$$

$$u^{(1)T}u^{(1)} = 1 \quad (\text{II.13})$$

$$u^{(2)T}u^{(2)} = 1 \quad (\text{II.14})$$

By substituting the constraint conditions into these equations, we find that $\lambda_1 = \lambda_2 = \lambda$ by symmetry. Further simplification yields:

$$\Sigma_{21}\Sigma_{12}u^{(2)} = \lambda^2 u^{(2)} \quad (\text{II.15})$$

$$\Sigma_{12}\Sigma_{21}u^{(1)} = \lambda^2 u^{(1)} \quad (\text{II.16})$$

Eigenvalue Problem Once again, we see that solving these equations will yield the $u^{(1)}$ and $u^{(2)}$ vectors as eigenvectors, this time of $\Sigma_{12}\Sigma_{21}$ and $\Sigma_{21}\Sigma_{12}$, respectively (Höskuldsson, 1988).

Generalized Eigenvalue Problem We can also represent the system of equations in matrix form as follows:

$$\begin{pmatrix} 0 & \Sigma_{12} \\ \Sigma_{21} & 0 \end{pmatrix} \begin{pmatrix} u^{(1)} \\ u^{(2)} \end{pmatrix} = \lambda I \begin{pmatrix} u^{(1)} \\ u^{(2)} \end{pmatrix} \quad (\text{II.17})$$

Which is of the form $Av = \lambda Bv$. PLS is therefore also defined by the solution to a single generalized eigenvalue problem.

Given the notions of uniqueness in GEPs, the weights u are not in general unique but we can write the vector of generalized eigenvalues, here representing covariances, as

$$\text{PLS}_K(X^{(1)}, X^{(2)}) := (\rho_k)_{k=1}^K \quad (\text{II.18})$$

2.3.2 Limitations

The problem with applying PLS to neuroimaging and behavioural modalities is that PLS is not scale invariant and is therefore biased towards the largest principal components in the data (Helmer et al., 2020). This is particularly problematic when

there is a low signal to noise ratio since PLS may find directions in either dataset which correspond to the largest directions of noise in the other. Additionally, PLS assumes that the structures contributing to variance in both datasets are linearly related, which may not be the case in complex biological systems like the brain or in intricate behavioral patterns (Rosipal and Krämer, 2005). The linearity assumption can sometimes be overly restrictive, failing to capture more complicated, nonlinear relationships between the data modalities. Another issue is the lack of sparsity in the PLS solution. Traditional PLS methods do not provide sparse weight vectors, which makes the interpretation of results challenging in high-dimensional settings such as neuroimaging where only a subset of features might be relevant. There are sparse variants of PLS available, but these typically introduce additional complexity and may require fine-tuning of regularization parameters (Chun and Keleş, 2010; D. M. Witten, Tibshirani, and Hastie, 2009). Furthermore, PLS can be sensitive to outliers, which are not uncommon in neuroimaging data due to motion artifacts or other sources of noise. Since the method aims to maximize covariance, extreme values in one dataset can disproportionately affect the resulting latent variables (Wold, 1973).

2.4 Canonical Correlation Analysis

In Canonical Correlation Analysis (CCA), we aim to find the directions that maximize correlation, as opposed to maximizing covariance between two views of a dataset. This nuance renders CCA invariant to feature scale.

2.4.1 Optimization and Solution

The optimization problem for CCA can be expressed as:

$$u_{\text{opt}} = \underset{u}{\operatorname{argmax}} \{ u^{(1)T} X^{(1)T} X^{(2)} u^{(2)} \} \quad (\text{II.19})$$

subject to:

$$u^{(1)T} \Sigma_{11} u^{(1)} = 1$$

$$u^{(2)T} \Sigma_{22} u^{(2)} = 1$$

Although non-convex, numerous methods exist for solving the CCA problem, including eigendecomposition and generalized eigendecomposition solvers(Uurtio et al., 2017) and block coordinate descent via alternating least squares regressions

(Golub and Zha, 1995; L. Sun, Ji, and Ye, 2008).

The first-order conditions derived in the same manner as the PLS case are:

$$\Sigma_{21}u^{(1)} = \lambda^{(2)}\Sigma_{22}u^{(2)} \quad (\text{II.20})$$

$$\Sigma_{12}u^{(2)} = \lambda^{(1)}\Sigma_{11}u^{(1)} \quad (\text{II.21})$$

$$u^{(1)T}\Sigma_{11}u^{(1)} = 1 \quad (\text{II.22})$$

$$u^{(2)T}\Sigma_{22}u^{(2)} = 1 \quad (\text{II.23})$$

Eigenvalue Problems Substituting the second two conditions into the first two, we get $\lambda^{(1)} = \lambda^{(2)} = \lambda$. Then, recognizing $X_i^\top X_i$ as the covariance matrix Σ_{ii} and $X_i^\top X_j$ as the cross-covariance matrix Σ_{ij} , we obtain another pair of eigenvalue problems:

$$\Sigma_{11}^{-1}\Sigma_{12}\Sigma_{22}^{-1}\Sigma_{21}u^{(1)} = \lambda^2 u^{(1)}$$

$$\Sigma_{22}^{-1}\Sigma_{21}\Sigma_{11}^{-1}\Sigma_{12}u^{(2)} = \lambda^2 u^{(2)}$$

An alternative form of the CCA problem can be developed by reparameterizing $u^{(i*)} = \Sigma_{ii}^{-\frac{1}{2}}u^{(i)}$. The optimization problem then becomes:

$$u_{\text{opt}} = \underset{u}{\operatorname{argmax}} \{u^{(1)T}\Sigma_{11}^{-\frac{1}{2}}\Sigma_{12}\Sigma_{22}^{-\frac{1}{2}}u^{(2)}\} \quad (\text{II.24})$$

subject to:

$$u^{(1)T}u^{(1)} = 1$$

$$u^{(2)T}u^{(2)} = 1$$

This reparameterized form will later underpin Deep Canonical Correlation Analysis (DCCA).

This form also shows that PLS and CCA can be made equivalent by whitening the data matrices before constructing the covariance matrix. When the number of features exceeds the number of samples ($p > n$), CCA becomes degenerate because the within-view covariance matrices cannot be inverted—contrasting with PLS, which is always computable.

Generalized Eigenvalue Problem We can also represent the system of equations in equation II.20 as a matrix equation:

$$\begin{pmatrix} 0 & \Sigma_{12} \\ \Sigma_{21} & 0 \end{pmatrix} \begin{pmatrix} u^{(1)} \\ u^{(2)} \end{pmatrix} = \lambda \begin{pmatrix} \Sigma_{11} & 0 \\ 0 & \Sigma_{22} \end{pmatrix} \begin{pmatrix} u^{(1)} \\ u^{(2)} \end{pmatrix} \quad (\text{II.25})$$

Which is once again of the form $Av = \lambda Bv$. CCA, like PLS, is therefore also defined by the solution to a single generalized eigenvalue problem.

Given the notions of uniqueness in GEPs, the weights u are not in general unique but we can write the vector of generalized eigenvalues, here representing covariances, as

$$\text{CCA}_K(X^{(1)}, X^{(2)}) := (\rho_k)_{k=1}^K \quad (\text{II.26})$$

2.5 Multiview CCA

Multiview CCA or MCCA is a straightforward extension of CCA to the case of 3-or more datasets. The goal is to find a set of directions $u^{(i)}$ such that the pairwise correlations between the views are maximized.

2.5.1 Optimization and Solution

The optimization problem for MCCA can be stated as:

$$u_{\text{opt}} = \underset{u}{\operatorname{argmax}} \sum_{i=1}^m \sum_{j=1, j \neq i}^m u^{(i)T} \Sigma_{ij} u^{(j)} \quad (\text{II.27})$$

subject to:

$$\sum_{i=1}^m u^{(i)T} \Sigma_{ii} u^{(i)} = 1$$

Generalized Eigenvalue Problem The generalized eigenvalue problem (GEP) for MCCA can be written in matrix form as follows:

$$\begin{pmatrix} 0 & \Sigma_{12} & \cdots & \Sigma_{1m} \\ \Sigma_{21} & 0 & \cdots & \Sigma_{2m} \\ \vdots & \vdots & \ddots & \vdots \\ \Sigma_{m1} & \Sigma_{m2} & \cdots & 0 \end{pmatrix} \begin{pmatrix} u^{(1)} \\ u^{(2)} \\ \vdots \\ u^{(m)} \end{pmatrix} = \lambda \begin{pmatrix} \Sigma_{11} & 0 & \cdots & 0 \\ 0 & \Sigma_{22} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & \Sigma_{mm} \end{pmatrix} \begin{pmatrix} u^{(1)} \\ u^{(2)} \\ \vdots \\ u^{(m)} \end{pmatrix}. \quad (\text{II.28})$$

This GEP formulation of MCCA can be presented in a unified framework generalizing CCA and ridge-regularized extensions. Indeed, we now take $A, B_\alpha \in \mathbb{R}^{D \times D}$ to be block matrices $A = (A^{(ij)})_{i,j=1}^I, B_\alpha = (B_\alpha^{(ij)})_{i,j=1}^I$ where the diagonal blocks of A are zero, the off-diagonal blocks of B_α are zero, and the remaining blocks are defined by:

$$A^{(ij)} = \text{Cov}(X^{(i)}, X^{(j)}) \text{ for } i \neq j, \quad B_\alpha^{(ii)} = \alpha_i I_{D^{(i)}} + (1 - \alpha_i) \text{Var}(X^{(i)}) \quad (\text{II.29})$$

Where $\alpha \in [0, 1]^I$ is a vector of ridge penalty parameters: taking $\alpha_i = 0 \forall i$ recovers CCA and $\alpha = 1 \forall i$ recovers PLS. We may omit the subscript α when $\alpha = 0$ and we recover the ‘pure CCA’ setting; in this case, following Equation (II.26) we can define $\text{MCCA}_K(X^{(1)}, \dots, X^{(I)})$ to be the vector of the top- K generalized eigenvalues.

2.6 Linear Discriminant Analysis LDA

Linear Discriminant Analysis (LDA) can be viewed as a special case of Canonical Correlation Analysis (CCA) where $X^{(2)}$ is a one-hot encoded matrix representing the class labels. This allows us to draw a connection between the unsupervised learning framework of CCA and the supervised framework of LDA, thus expanding the understanding of both algorithms.

Intuition: In LDA, the aim is to find a lower-dimensional subspace where the classes are maximally separated. This objective can be viewed through the lens of CCA, where the optimal directions $u^{(1)}$ and $u^{(2)}$ in the original and one-hot encoded spaces aim to maximize correlation. In the LDA context, $u^{(1)}$ would maximize the separation between classes.

2.6.1 Optimization and Solution

Mathematically, LDA is reduced to solving a generalized eigenvalue problem involving the between-class scatter matrix S_B and the within-class scatter matrix S_W :

$$\hat{S}_B = \sum_{i=1}^c n_i(\mu_i - \mu)(\mu_i - \mu)^\top$$

$$\hat{S}_W = \sum_{i=1}^c \sum_{x \in X_i} (x - \mu_i)(x - \mu_i)^\top$$

Connection to CCA: When $X^{(2)}$ is the one-hot encoded matrix of class labels, the CCA problem effectively tries to maximize the correlation between the feature vectors and their corresponding labels. This turns out to be equivalent to maximizing the between-class variance in LDA while minimizing the within-class variance. Thus, LDA can be thought of as a constrained form of CCA, tailored to classification tasks.

This perspective unifies the two algorithms and shows that the core objective—finding meaningful relationships or directions in the data—is shared between both CCA and LDA.

2.7 Sample Covariance and Population Covariance

In the previous sections, the methods were described in terms of population covariance matrices such as $\Sigma_{11} = \mathbb{E}[X^{(1)T}X^{(1)}]$, $\Sigma_{22} = \mathbb{E}[X^{(2)T}X^{(2)}]$, and $\Sigma_{12} = \mathbb{E}[X^{(1)T}X^{(2)}]$. These population covariances assume an underlying probability distribution from which the data are drawn.

Sample Covariance: In practical settings, we often do not have access to the entire population but only to a sample. Hence, we can utilize the Sample Average Approximation to estimate these covariances:

$$\hat{\Sigma}^{(12)} = \frac{1}{b-1} \bar{\mathbf{X}}^{(1)} \bar{\mathbf{X}}^{(2)T}$$

Here, b denotes the size of the minibatch, and $\mathbf{X}^{(1)} \in \mathbb{R}^{p \times b}$ and $\mathbf{X}^{(2)} \in \mathbb{R}^{q \times b}$ are the data matrices for the samples from $X^{(1)}$ and $X^{(2)}$, respectively. The bar over $\mathbf{X}^{(1)}$ and $\mathbf{X}^{(2)}$ signifies that these are centered versions of the matrices, i.e., the mean has been subtracted from each column.

Practical Implications: Using sample covariance matrices introduces some estimation error but allows us to apply the methods in real-world scenarios where population-level data are unattainable. Additionally, the use of minibatches provides a computationally efficient way to estimate these covariances in large-scale problems, at the cost of some additional statistical noise.

Connection to Previous Methods: The use of sample covariance matrices

is directly applicable to algorithms like CCA and LDA. When replacing the population covariances $\Sigma^{(ij)}$ with sample estimates, the optimization problems remain structurally similar but are solved using the sample data.

This dual perspective—considering both population and sample covariance matrices—enables a more robust and flexible approach to the methods discussed, bridging the gap between theoretical analysis and practical application. It will be particularly useful in the context of chapter IV where we will use population variables as ground truth while estimating the models using sample data.

3 Practical Frameworks for Multiview Learning

At this point, we have introduced the theoretical foundations of multiview learning, including CCA and its variants. However, it is not yet clear how we should apply these methods to real-world datasets.

3.1 Machine Learning and Statistical Inference

Canonical Correlation Analysis (CCA) has been studied from both machine learning and statistical inference perspectives. In this section, we will explore the differences between these two approaches and their implications for multiview learning.

3.1.1 Statistical Inference Evaluation Framework

Statistical inference approaches provide a contrasting perspective to machine learning methods, focusing on understanding and quantifying the underlying data structure:

Parameter Estimation In statistical inference, parameter estimation involves estimating model parameters and their uncertainties. This process is fundamental to understanding the data and the model's fit.

Hypothesis Testing Hypothesis testing assesses the statistical significance of the relationships found by the model. It tests whether the observed data patterns are likely to have occurred under the null hypothesis.

Confidence Intervals Confidence intervals provide ranges within which the true parameter values are likely to fall, considering uncertainty. They are essential for understanding the reliability of parameter estimates.

Permutation Testing Permutation testing is a non-parametric method that evaluates the significance of models. It compares model performance on the original data with performance on randomly shuffled data, helping to ascertain the results' robustness.

3.1.2 Machine Learning Evaluation Framework

Training, Validation, and Test Sets In machine learning, data is typically partitioned into training, validation, and test sets, each serving a specific purpose in the model development process:

- Training Set: Used for fitting the model.
- Validation Set: Assists in model parameter tuning.
- Test Set: Evaluates the model's generalization capability.

Cross-Validation A fundamental technique in machine learning, cross-validation involves dividing the training dataset into smaller subsets for training and validation. This approach provides insights into the model's performance across different data segments.

Holdout Method The holdout method involves using a separate dataset, not involved in training or validation, for final model assessment. This ensures an unbiased performance evaluation.

Out of Sample Correlation Specific to canonical correlation analysis, this involves measuring the correlation between latent variables in new datasets, assessing the model's ability to uncover relationships in unseen data.

Downstream Tasks Evaluating model performance on downstream tasks like classification or prediction can offer practical insights into the utility of the learned representations.

3.2 Components and Subspaces in CCA: A Subspace Perspective

3.2.1 Context: Eigenvalue Problems in CCA

While our focus so far has primarily been on the top-1 eigenvector-eigenvalue pair, it's important to note that the methodology also extends to the top-k subspace problem. This broader approach involves identifying the top-k eigenvectors and their corresponding eigenvalues.

3.2.2 Addressing the Top-k Problem

Transitioning from a focus on the top-1 component to exploring the top-k subspace introduces additional complexities. One common method to solve the top-k problem is to identify the top-1 component and then apply a deflation process to find subsequent orthogonal components. Deflation involves removing the top-1 component from the data and then repeating the process to find the next top-1 component. This process is repeated until the desired number of components is found. For instance, Hotelling's Deflation (Hotelling, 1933) involves removing the top-1 component from the data, while Projection Deflation (Mackey, 2008) involves projecting the data onto the orthogonal complement of the top-1 component. Different deflation methods enforce different forms of orthogonality, which can impact the resulting components and their interpretation, particularly when the first component is not a true eigenvector.

3.2.3 Non-Uniqueness of Components

Furthermore, non-uniqueness is a significant challenge in CCA, particularly when eigenvectors have repeated eigenvalues. Imagine a scenario where the top-1 eigenvalue is repeated k times. In this case, there are k possible eigenvectors that can be associated with the top-1 eigenvalue. While this is unlikely to occur in practice, the eigenvalues can in practice be very close to each other, leading to numerical instability and non-uniqueness in the components. Particularly true in cross-validation settings, this non-uniqueness can lead to instability in the components, complicating their interpretation and comparison. For example, the top-1 component in one analysis might be the second component in another analysis, making it difficult to compare the results.

This non-uniqueness also has a grounding in the probabilistic perspectives on PCA and CCA, where the latent variables are considered unique only up to a

rotation. This perspective further reinforces the subspace approach, emphasizing the identification of a subspace rather than specific directions within it.

Thesis Approach: Concentrating on the Top-1 Component In this thesis, we focus on the top-1 component in CCA to align with and facilitate comparison with typical componentwise studies in brain-behavior research. This choice is driven by the complexity associated with the top-k problem and the variety of methods available to address it. Under the assumption of a significant eigengap², the first component can be considered equivalent to the top-1 subspace. This equivalence allows for a clear and interpretable analysis, making the top-1 subspace a straightforward and reliable choice for studying multivariate data. It's important to note that while we focus on the top-1 component, the later sections of the thesis introduce a method for simultaneously solving the complete subspace, addressing broader subspace analyses.

4 Multiview Learning in Neuroimaging

There have been a number of applications of CCA and related methods to multiview problems in neuroimaging. Using resting state fMRI data, modes of correlation have been found that relate to differences in sex and age relating to drug and alcohol abuse, depression and self harm (Mihalik, Ferreira, Rosa, et al., 2019). A similar mode relating to ‘positive-negative’ wellbeing has been found across studies (Stephen M Smith et al., 2015) suggesting that mental wellbeing has a relationship (though not necessarily causally) with functional connectivity between networks in the brain. Later in this dissertation we will replicate and build on the findings from this paper by using regularised and non-linear CCA methods.

CCA has also been used as a preprocessing step in order to identify groups of subjects in the latent variable space. In particular, CCA and clustering have been used to identify depression using fMRI data (Dinga et al., 2019; Drysdale et al., 2017). CCA has also been used in the manner we described to denoise two views of a dataset such as separate measures of neuroimaging data (Zhuang, Yang, and Cordes, 2020) to remove artefacts. Deep CCA has recently been used to extract features for the diagnosis of schizophrenia(Qi and Tejedor, 2016).

²An ‘eigengap’ refers to the difference in magnitude between consecutive eigenvalues in an eigenvalue problem. A significant eigengap between the first and second eigenvalues suggests that the first eigenvalue (and its corresponding eigenvector) is distinctly more significant than the next, lending credence to its uniqueness and importance.

5 Open challenges in Multiview Learning and CCA

This thesis has been motivated by a number of open challenges in multiview learning and canonical correlation analysis. Chapter III and IV will address the first challenge, which is the regularisation of CCA in high dimensional settings and the interpretation of the resulting components. Chapter ?? and ?? will address the second challenge, the efficient application of CCA to big data. Finally ?? will also address the third challenge, extending CCA to Deep Self-Supervised Learning.

5.1 Interpretability and Regularization

TODO: Add a paragraph on interpretability and regularization

5.2 Efficient Algorithms for High-Dimensional Data

TODO: Add a paragraph on efficient algorithms for high-dimensional data

5.3 Non-linear CCA and Joint Embedding Self-Supervised Learning

TODO: Add a paragraph on non-linear CCA and Joint Embedding Self-Supervised Learning

Chapter III

Regularization of CCA Models

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Preface

This chapter expands on my work previously showcased at the OHBM conference and draws connections to a tutorial paper I co-authored, where I contributed a number of simulations (Mihalik, Chapman, et al., 2022).

This chapter explores the role of regularization in improving the performance and interpretation of CCA using simulated and brain-behaviour data. We develop a framework for regularized CCA which allows us to incorporate any regularized least squares solver to efficiently implement a wide range of regularization functions using any scikit-learn compatible solver, but in particular allows us to efficiently implement the elastic net penalty with controllable L2 and L1 penalties so that we can control the bias towards the largest principal components while still encouraging sparsity in the weights in contrast to most previous work on sparse Brain-Behavior analysis which has used a PLS objective with lasso constraints (SPLS), which inherits a bias towards the largest principal components from PLS.

1 Introduction

Large datasets neuroimaging datasets including the Human Connectome Project (HCP) and Alzheimer's Disease Neuroimaging Initiative (ADNI) datasets as well as the UK Biobank and Adolescent Brain Cognitive Development (ABCD) datasets¹ appear to offer unprecedented opportunities for understanding the relationship between brain structure and function and behavior (Stephen M. Smith and Thomas E. Nichols, 2018; Bzdok and B.T. Thomas Yeo, 2017; H.-T. Wang et al., 2020). Despite the impressive scale of these modern neuroimaging studies, the number of subjects is still often orders of magnitude smaller than the number of features in the data; the ADNI dataset we use in this chapter, for example, has 592 subjects and 168,130 structural MRI voxels. In this context, CCA models are prone to overfitting, leading to spurious correlations and poor generalization (Helmer et al., 2020; Mihalik, Ferreira, Moutoussis, et al., 2020). But given the reproducibility crisis in neuroscience (Button et al., 2013), it is important to ensure that our models generalize well to new data.

Regularization, having been extensively studied and well-understood in the contexts of Linear Regression and Inverse Problems (Engl, Hanke, and Neubauer,

¹Not covered in this chapter

1996), introduces a deliberate bias to guide models towards more generalizable solutions, can be a powerful tool for addressing these problems. Furthermore, regularization can help us improve the interpretability of the results by imposing structure on the solutions, perhaps most obviously by encouraging sparsity(Bzdok, Thomas E Nichols, and Stephen M Smith, 2019). However, due to the complexity of the CCA problem, regularization is not as straightforward as in Linear Regression. The most popular approaches to ‘sparse CCA’ have, in practice, been based on Partial Least Squares (PLS), which simplifies the optimization problem but, as we shall see, causes the model to inherit a bias towards the largest principal components from PLS.

With this perspective in mind, we propose a flexible regularized alternating least squares (FRALS) framework for CCA which allows us to incorporate any regularized least squares solver to efficiently implement a wide range of regularization functions, but in particular allows us to efficiently implement the elastic net penalty with controllable L2 and L1 penalties so that we can control the bias towards the largest principal components while still encouraging sparsity in the weights. This is in contrast to much of the previous work on sparse Brain-Behavior analysis which has used a PLS objective with lasso constraints (SPLS), which inherits a bias towards the largest principal components from PLS.

We apply FRALS with Elastic Net regularization to the HCP and ADNI datasets. We show that it outperforms other CCA models in terms of out-of-sample canonical correlation. We also show that the identified mode of variation is distinct from previous work which identified latent variables with weights related to cognitive tests and negatively related to cigarette, tobacco or alcohol(Stephen M Smith et al., 2015). FRALS has stronger correlations with the Line Orientation test, which measures visuospatial abilities, and the parietal lobe, which is known to be involved in visuospatial processing.

2 Background: Regularization for High-Dimensional and Structured Data

In this section, we review a number of regularization techniques that have been applied to CCA and related methods.

2.1 The Bias-Variance Tradeoff

A key principle in machine learning is the bias-variance tradeoff. This concept posits that a tradeoff exists between the bias and variance of a model: high-bias models typically exhibit low variance, and vice versa. High-bias models are generally simpler and more stable, but they might oversimplify the problem, leading to underfitting. Conversely, low-bias, complex models are sensitive to data changes and prone to overfitting. As the number of features increases, there are more parameters to estimate, and models tend to become more complex, leading to higher variance and lower bias. This relationship highlights the importance of balancing model complexity to avoid overfitting, particularly in high-dimensional scenarios with a low signal-to-noise ratio (McIntosh, 2021)². Regularization can be understood as a method for reducing the variance of a model by introducing a bias towards simpler models. This means regularization can improve the generalizability of models in high-dimensional settings.

Implicit and Explicit Regularization We can implement regularization in two different ways. *Explicit* regularization is achieved by adding a penalty term to the objective function. Weights the objective function against a term that penalizes complexity.

Implicit regularization is achieved by changing the optimization algorithm.

2.2 Shrinkage Regularization

Shrinkage regularization is a form of regularization that penalizes the magnitude of the model parameters. This technique is particularly effective in enhancing the performance of linear models in situations characterized by high dimensionality, multicollinearity, or low signal-to-noise ratios.

In high-dimensional situations where the number of features exceeds the number of observations in either view, Like Linear Regression, Canonical Correlation Analysis is non-identifiable, meaning there is no unique solution. This is because we can find perfectly correlated latent variables using a linear combination of the features, but there are many different linear combinations that will achieve this. Some of these linear combinations will generalize better than others, but there is no way to distinguish between them using the training data alone.

²It's worth noting that the number of model parameters, often used as a proxy for complexity, does not always directly correlate with model behavior, as illustrated by the 'double descent' phenomenon.

Even in low-dimensional situations, if features exhibit multicollinearity, they can also be non-identifiable or, at best, estimates of the parameters are unstable. Mathematically, this is because in both cases the covariance matrix of the features is not full rank and therefore is not invertible (non-identifiable) or ill-conditioned (matrix inversion is unstable). To capture this intuition, if two features are perfectly correlated, the model is not identifiable (has no unique solution) because we can arbitrarily swap the weights between the two features without changing the latent variables (CCA) or the predictions (regression). In practice, features are rarely perfectly correlated, but even when features are highly correlated, the model can be unstable (Mihalik, Ferreira, Moutoussis, et al., 2020), and small changes in the data can lead to large changes in the model parameters. Once again, some of these linear combinations will generalize better than others, but we might expect a model to generalize better if it spreads the weights across the correlated features rather than concentrating them on a single feature.

Finally, even in low-dimensional settings with little multicollinearity, the model parameters can sensitive to noise in the data, and once again small changes in the data can lead to large changes in the model parameters. For example, parameters associated with noisy features might ‘cancel out’ in the training set, but not in the test set, leading to poor generalization.

The premise of shrinkage regularization in all these cases is that the latent variables or predictions are too sensitive to small changes in the data because the model parameters are too large. Shrinkage regularization works by shrinking the model parameters towards zero, so that small changes in the data do not lead to large changes in the model estimates.

PLS as Shrinkage Regularization PLS can be interpreted as a form of shrinkage regularization applied to CCA. We can explain this by considering an analogy between CCA and *Linear Regression*³.

In Linear Regression, the ridge regression solution is given by:

$$\hat{\beta}_{\text{ridge}} = ((1 - c)\Sigma_{X,X} + cI)^{-1}\Sigma_{X,y} \quad (\text{III.1})$$

Where c is the regularization parameter between 0 and 1⁴. The ridge penalty acts in three important ways:

³indeed Linear Regression is a special case of CCA where $X^{(2)}$ has one feature

⁴It is more common to see $(\Sigma_{X,X} + cI)^{-1}\Sigma_{X,y}$ but these are equivalent up to a scalar factor and this form helps us later on

- It shrinks the weights towards zero.
- It shrinks the weights of correlated features towards each other.
- It biases the solution to high covariance directions rather than high correlation directions.

As c becomes large, $\lim_{c \rightarrow \infty} (\Sigma_{X,X} + cI)^{-1} = (cI)^{-1}$, so that $\hat{\beta}_{\text{ridge}} = \frac{\Sigma_{X,Y}}{c}$, which is precisely the covariance of the features of X with Y scaled by c (and shrunk towards zero for $c \geq 1$). Notice that the ridge regression solution is no longer sensitive to the correlation of features in X . Additionally, notice that for sufficiently large c , $(\Sigma_{X,X} + cI)$ is invertible even if $\Sigma_{X,X}$ is not invertible, so that ridge regression is always identifiable even when the number of features exceeds the number of observations.

Now consider the CCA problem. Firstly, recall that PLS and CCA are equivalent up to a scaling when the covariance matrices are identity matrices, a similar relationship to the relationship between Linear and Ridge Regression. Consider the well-known form of CCA given in equation III.2 (Mihalik, Chapman, et al., 2022) (formed by reparameterizing $u^{(i)} = (\Sigma_{ii})^{-\frac{1}{2}} u^{(i)}$):

$$u_{\text{opt}} = \underset{u}{\operatorname{argmax}} \{u^{(1)T} (\Sigma_{11} + cI)^{-\frac{1}{2}} \Sigma_{12} (\Sigma_{22} + cI)^{-\frac{1}{2}} u^{(2)}\} \quad (\text{III.2})$$

subject to:

$$u^{(1)T} u^{(1)} = 1, u^{(2)T} u^{(2)} = 1$$

As we increase c , $\lim_{c \rightarrow \infty} (\Sigma_{ii} + cI)^{-\frac{1}{2}} = (cI)^{-1}$ so that the objective approaches:

$$u_{\text{opt}} = \underset{u}{\operatorname{argmax}} \{u^{(1)T} (cI)^{-1} \Sigma_{12} (cI)^{-1} u^{(2)}\} \quad (\text{III.3})$$

subject to:

$$u^{(1)T} u^{(1)} = 1, u^{(2)T} u^{(2)} = 1$$

Which is precisely the PLS objective and constraints with an arbitrary scaling of the covariance matrix Σ_{12} by $\frac{1}{c^2}$. For this reason, we can consider PLS as an explicit shrinkage method for CCA, equivalent to adding a maximal ridge regularization term. The downside of using PLS as a regularised CCA is precisely its very

high bias. By strongly guiding the model towards high covariance solutions, it strongly biases the solution towards only the largest principal components. But what if the correlation between the views is not concentrated in the largest principal components? Although one would rarely resort to maximally regularized ridge regression except in extremely low sample sizes or high-dimensional data, it has become almost standard practice to use PLS in neuroimaging and genetics (Cruciani et al., 2022; Krishnan et al., 2011). One of the core contributions of this chapter will be to demonstrate that PLS is usually a poor choice for regularization even in these very high-dimensional settings and that more nuanced regularization methods can offer significant improvements in performance and interpretability. PLS is evidently not a nuanced tool for regularization because it offers no control over the degree of regularization applied.

Ridge Regularization For this reason, Vinod (1976) proposed the *Canonical Ridge* or *Ridge CCA*, which combined the PLS and CCA constraints in a single constrained optimization:

$$u_{\text{opt}}^{(1)} = \underset{u^{(1)}}{\operatorname{argmax}} \{u^{(1)T} \hat{\Sigma}_{12} u^{(2)}\} \quad (\text{III.4})$$

subject to:

$$(1 - c_1)u^{(1)T} \hat{\Sigma}_{11} u^{(1)} + c_1 u^{(1)T} u^{(1)} = 1$$

$$(1 - c_2)u^{(2)T} \hat{\Sigma}_{22} u^{(2)} + c_2 u^{(2)T} u^{(2)} = 1$$

Where c_1 and c_2 are the ridge regularization parameters for the first and second views respectively. By tuning these parameters, we can control the degree of regularization applied to each view independently. If we set c_1 and c_2 to zero, we recover the standard CCA objective while if we set c_1 and c_2 to one, we recover the PLS objective. This allows us to interpolate between the two extremes, allowing us to control the level of shrinkage and therefore the level of bias towards the largest principal components

PCA-CCA PCA can be used as an implicit regularization method for CCA.

Most obviously, by using only the first k principal components of each view as the input to CCA, we can reduce the dimensionality of the data and therefore reduce the number of parameters in the model. Moreover, by working with the principal components, we remove the correlation between the features, which can improve

the conditioning of the problem.

A Visual Comparison of Shrinkage Techniques The distinct effects of Ridge and PCA on the eigenvalues of the effective covariance matrices can be clearly visualized with a simple visualisation. We plot the eigenvalues of covariance matrices as perceived by models with different regularization techniques⁵. As shown in Figure III.1, Ridge regularization reduces the magnitude of the largest eigenvalues in the effective covariance matrix towards 1, and increases the magnitude of the smallest eigenvalues towards 1. On the other hand, PCA-CCA, leaves the largest eigenvalues unchanged, and ignores the smallest eigenvalues (we could have represented this by setting them to infinity).

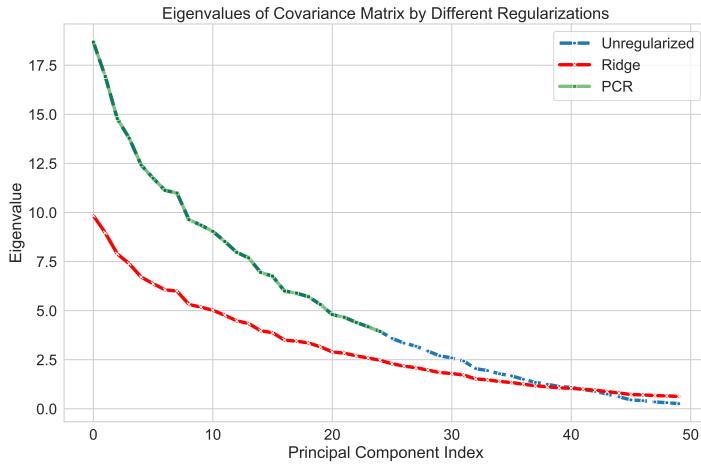


Figure III.1: Comparison of the effect of OLS, Ridge, and PCA regularization on the eigenvalues of the covariance matrix.

When these effective covariance matrices are inverted to form the CCA objective, these effects are reversed. Ridge regularization increases the magnitude of the weights associated with the largest eigenvalues and decreases the magnitude of the smallest eigenvalues. PCA maintains the weights associated with the largest eigenvalues and sets the weights associated with the smallest eigenvalues to zero. The visualization underscores the intrinsic nature of each regularization method:

- **Unregularized:** Presents the unaltered spectrum, making it susceptible to noise but preserving potential subtle patterns.

⁵e.g. the eigenvalues of $(1 - c_i)\hat{\Sigma}_{ii} + c_i I$ for ridge and $\hat{\Sigma}_{ii}$ truncated to include only the largest k principal components for PCA

- **Ridge:** Warps the spectrum, shrinking the largest eigenvalues and expanding the smallest eigenvalues, potentially missing subtle patterns but offering a cleaner representation of stronger associations.
- **PCA:** Truncates the spectrum, ignoring the smallest eigenvalues and preserving the largest eigenvalues, potentially missing subtle patterns but offering a cleaner representation of stronger associations.

However, while these shrinkage techniques can improve the performance of CCA, they do not obviously improve the interpretability of the results. Weights are shrunk towards zero, but they are not set to zero. This means that the model still uses all the features, and the results are not sparse.

2.3 Sparse Regularization

Sparse regularization is a powerful tool for improving the performance and interpretability of linear models. Sparse regularization encourages the model to use only a subset of the features, which can both help to avoid overfitting and improve the interpretability of the model. Sparse regularization works on the premise that only a subset of the features are relevant to the model. Sparsity is typically achieved by adding either an L1 penalty or constraint⁶. The L1 penalty is defined as:

$$\|u\|_1 = \sum_i |u_i| \quad (\text{III.5})$$

Intuitively, this is the sum of the absolute values of the elements of the vector. Now, with a foundational understanding of sparse regularization, we review a number of approaches to adding sparsity to the CCA problem.

Sparse PLS: Penalized Matrix Decomposition Penalized Matrix Decomposition (PMD) (D. M. Witten, Tibshirani, and Hastie, 2009) provides an approximate solution to the sparse CCA problem by altering the constraints of the classical CCA formulation. Specifically, PMD replaces the constraints $u^{(i)T} \hat{\Sigma}_{ii} u^{(i)} = 1$ with the PLS constraints $u^{(i)T} u^{(i)} = 1$ and additionally imposes $\|u^{(i)T}\|_1 \leq \tau$. The optimization problem for PMD is then given by:

⁶The L0 norm of the weight vector is the number of non-zero elements in the vector and is arguably a closer match to the goal, but the L0 norm is (a) not a proper norm in the mathematical sense and (b) not convex and so is difficult to optimize.

$$u^{opt} = \underset{u}{\operatorname{argmax}} \{ u^{(1)T} \hat{\Sigma}_{12} u^{(2)} \} \quad (\text{III.6})$$

subject to:

$$u^{(1)T} u^{(1)} = 1, u^{(2)T} u^{(2)} = 1$$

$$\|u^{(1)}\|_1 \leq \tau_1, \|u^{(2)}\|_1 \leq \tau_2$$

This Sparse PLS (SPLS) approximation has been highly influential as a form of Sparse CCA because it is extremely computationally efficient method⁷. There are a number of other sparse CCA methods that employ the PLS approximation (Parkhomenko, Tritchler, and Beyene, 2009; Waaijenborg, Witt Hamer, and Zwinderman, 2008; Lindenbaum et al., 2021). However, while the PLS approximation is efficient, it means these methods inherit a bias towards the largest principal components from PLS.

To address these problems and truly tackle the sparse CCA optimization, another class of approaches have adopted a penalized least squares approach.

Sparse CCA: Least Squares Approaches It is well known that the CCA problem can be formulated as a constrained least squares problem with the intuition that for $X^{(1)T} u^{(1)} = 1$ and $X^{(2)T} u^{(2)} = 1$, correlation is maximized when the squared distance between $X^{(1)T} u^{(1)}$ and $X^{(2)T} u^{(2)}$ is minimized. (Golub and Zha, 1995) proved the convergence of a simple algorithm which alternates between solving the least squares problem for $u^{(1)}$ and $u^{(2)}$ while keeping the other fixed.

With this intuition, Wilms and Croux, 2015 and Mai and Zhang, 2019 separately proposed iterative penalized least squares methods for sparse CCA.

$$u^{opt} = \underset{u}{\operatorname{argmin}} \left\{ \|X^{(1)T} u^{(1)} - X^{(2)T} u^{(2)}\|_2^2 + P(u) \right\} \quad (\text{III.7})$$

subject to:

$$u^{(1)T} \hat{\Sigma}_{11} u^{(1)} = 1$$

$$u^{(2)T} \hat{\Sigma}_{22} u^{(2)} = 1$$

Where $P(u)$ is a penalty function. The penalty term can be any function that penalizes the norm of the vector u . (Mai and Zhang, 2019) proved that solving

⁷it can be solved by a variant of the power method; iteratively multiplying $u^{(1)}$ by $\hat{\Sigma}_{12}$ and soft-thresholding

the subproblems where one of $u^{(i)}$ is fixed is easy for one-homogenous P where $P((\mu + 1)\theta) = (\mu + 1)P(\theta)$ which notably includes the lasso penalty. This means a sparse CCA based on alternating lasso regressions can be solved relatively efficiently using existing solvers. However, the one homogenous penalty in practice limits the flexibility of the method. For example, the elastic net penalty is not one-homogenous and therefore cannot be used with this method. Chi et al. (2013) and Mullins et al., 2021 added ridge penalties to the subproblems to improve the conditioning of the problem in a way that could be considered a form of elastic net regularization but the subproblems no longer correctly optimize the global objective⁸.

Sparse CCA: Proximal Gradient Descent and ADMM Kanatsoulis et al. (2018) proposed solving equation III.7 for more general classes of P using the alternating direction method of multipliers (ADMM) (Boyd et al., 2011). Fu et al., 2017 propose a regularized CCA based on an alternative classical CCA formulation, sometimes called the MAXVAR formulation, which views the problem as a constrained least squares with an auxiliary representation T (Carroll, 1968; Kettenring, 1971).

$$\operatorname{argmin}_{U,T} \left\{ \sum_i \|X^{(i)}U^{(i)} - T\|_F^2 \right\} \quad (\text{III.8})$$

$$\text{subject to: } T^\top T = I \quad (\text{III.9})$$

$$(\text{III.10})$$

In this formulation, $U^{(i)}$ represents the weights for the i^{th} view, and T denotes the latent variable matrix. The premise is that when T closely mirrors $X^{(i)}U^{(i)}$ across all i , the scores correlate. Notably, this method is adaptable to multiple views. The authors employed proximal gradient descent for regularization, specifically suited for penalties like the lasso. While these methods are flexible, they don't have the plug-and-play nature of the penalized least squares methods. Not just a matter of convenience, this means that these methods are not compatible with existing solvers for regularized least squares problems like for example total variation regularisation solvers in nilearn, which are often highly optimized for specific problems and modalities.

Structured Regularization As highly structured data, linear models using both Structural and Functional MRI data have been shown to benefit from structured

⁸when rescaling the penalized solutions back to unit variance

regularization methods but notably these methods have not been applied to CCA. Total variation regularization, which biases spatially neighboring weights to be similar, has been shown to improve the performance of PCA (De Pierrefeu et al., 2017) and regression (Michel et al., 2011; Dohmatob et al., 2014; Baldassarre, Mourao-Miranda, and Pontil, 2012). Similarly, Laplacian (or *GraphNet*) regularization, which induces a similar spatial bias with additional smoothness, has been shown to improve the performance of CCA on functional MRI data (Groenick et al., 2013).

Having discussed the benefits of both shrinkage (e.g., PCA-CCA, Ridge CCA, PLS), sparsity (SPLS, Sparse CCA), and structure (Total Variation, Laplacian) in handling high-dimensional, noisy, and structured data, a natural progression is to integrate these advantages. Specifically, the challenge lies in creating a framework that allows for users to match the regularization method to their data and research question, enhancing the interpretability and performance of Brain-Behaviour association models. The solution? A method that employs readily available regularized regression solvers, allowing for flexible and tunable regularization in CCA. This leads us to propose the Flexible Regularized Alternating Least Squares (FRALS).

3 Methods - Flexible Regularized Alternating Least Squares (FRALS)

The primary goal of our Flexible Regularized Alternating Least Squares framework is to provide a versatile and user-friendly interface for Canonical Correlation Analysis (CCA). This is achieved by designing the framework to be compatible with any scikit-learn compatible regularized least squares solver. This compatibility is pivotal as it allows researchers and practitioners to leverage the extensive range of solvers available in scikit-learn, a popular machine learning library in Python.

This approach marks a significant departure from traditional methodologies in CCA, which often focused on developing or utilizing specific solvers tailored for particular types of data or computational constraints. By contrast, FRALS democratizes access to advanced CCA techniques, allowing users to select solvers that best fit their specific data characteristics, computational needs, or familiarity. Such flexibility is particularly advantageous in interdisciplinary fields like neuroimaging, where diverse datasets and varying levels of technical expertise are common.

For example, users dealing with high-dimensional, sparse neuroimaging data could opt for solvers optimized for such datasets, while those needing parallel computation for large data sets might choose solvers with GPU acceleration capabilities.

In principle, FRALS can even be used with Neural Network-based solvers, which are becoming increasingly popular in machine learning⁹. This adaptability enhances FRALS' accessibility and future-proofs the framework against evolving computational technologies and data analysis needs.

In the FRALS framework, we consider the formulation for a single latent variable t with regularization $\lambda_i P_i$ on the weights $u^{(i)}$:

$$\begin{aligned} \operatorname{argmin}_u & \left\{ \sum_i \|X^{(i)} u^{(i)} - t\|_2^2 + \lambda_i P_i(u^{(i)}) \right\} \\ & \text{subject to: } t^\top t = 1 \end{aligned} \quad (\text{III.11})$$

This problem can be decomposed into three subproblems. The first subproblem for the auxiliary variable t :

$$\begin{aligned} \operatorname{argmin}_t & \left\{ \sum_i \|X^{(i)} u^{(i)} - t\|_2^2 \right\} \\ & \text{subject to: } t^\top t = 1 \end{aligned} \quad (\text{III.12})$$

is a standard least squares problem and can be solved in closed form by averaging $X^{(i)} u^{(i)}$ and normalizing i.e. $t = \frac{\sum_i X^{(i)} u^{(i)}}{\|\sum_i X^{(i)} u^{(i)}\|_2}$. As shown earlier this makes t an estimate of the latent variables of a generative CCA model.

The subproblems for the weights $u^{(i)}$:

$$\operatorname{argmin}_{u^{(i)}} \left\{ \|X^{(i)} u^{(i)} - t\|_2^2 + \lambda_i P_i(u^{(i)}) \right\} \quad (\text{III.13})$$

are regularized least squares problems that can be solved using any suitable regularized least squares solver¹⁰.

In this chapter, we illustrate the power of the FRALS framework by implementing the well-tested Elastic Net solver from the `scikit-learn` package (Pedregosa et al., 2011), where $P_i = \alpha_i \times \text{l1_ratio} \|u^{(i)}\|_1 + \alpha_i \times (1 - \text{l1_ratio}) \|u^{(i)}\|_2^2$, allowing for independent tuning of shrinkage and sparsity of the weights in both views.

In summary, the FRALS framework is a flexible and user-friendly interface for

⁹Though for reasons that will later become clear, we do not recommend this!

¹⁰We could also in principle replace $X^{(i)} u^{(i)}$ with $f(X^{(i)})$ for any function f including kernels, neural networks, or random forests

CCA that allows users to combine scikit-learn compatible regularized least squares solvers to solve regularized CCA problems.

4 Experiments

In this section, we outline the methodologies employed in our study of FRALS and related techniques.

4.1 The predictive framework for CCA

To evaluate the performance of CCA models, we employ a standard predictive framework. We split the data into training and test sets using a 80:20 split, and use the training set to fit the model. We then use the test set to evaluate the model's performance. Where relevant, pre-processing is performed on the training set and the same pre-processing is applied to the test set. This is important to avoid data leakage, where information from the test set is used to fit the model.

4.1.1 Model Comparisons

In the experiments in this section, we are interested in illustrating the effects of tunable shrinkage and sparsity on the performance and interpretability of CCA models, enabled by the FRALS framework. To this end, we compare the performance of Elastic Net FRALS with other CCA variants, including PCA, PLS, Ridge CCA, Sparse PLS, and Elastic Net CCA.

Table 4.1: Employed CCA Variants

Model	Abbreviation	Hyperparameters	Hyperparameter Range
Principal Component Analysis	PCA	-	-
Regularized CCA	RCCA	c_1, c_2	0-1 (log scaled)
FRALS - Elastic	Elastic	$\alpha_1, \alpha_2, l1_1, l1_2$	(1e-5, 1e-1), (0-1)
Partial Least Squares	PLS	-	-
Sparse PLS	SPLS	τ_1, τ_2	0-1 ¹¹ (log scaled)

4.1.2 Model Selection

For the models that require hyperparameter tuning, we use a grid search to find the best hyperparameters. Specifically, we use 5-fold cross-validation to evaluate the performance of a model with a given set of hyperparameters on 5 different

Table 4.2: HCP Data Parameters

Parameter	Value
Number of samples (n)	1003
Number of features in View 1 (p)	19900
Number of features in View 2 (q)	145

splits of the training data with non-overlapping validation sets. We optimise for the hyperparameters that give the best average out of sample correlation.

4.2 Datasets

For this chapter, we chose the HCP and the ADNI datasets to facilitate comparison with two influential brain-behaviour studies (Stephen M Smith et al., 2015; João M Monteiro et al., 2016) as well as the tutorial paper that this chapter is loosely related to (Mihalik, Chapman, et al., 2022).

4.2.1 The Human Connectome Project (HCP)

The HCP offers publicly available resting-state functional MRI (rs-fMRI) and non-imaging measures like demographics, psychometrics, and other behavioral measures. Specifically, we sourced data from 1003 subjects out of the 1200-subject data release of the HCP. This dataset is constructed using brain connectivity features of the thoroughly processed rs-fMRI data. This processing results in 19,900 brain connectivity variables for every subject. Additionally, there are 145 non-imaging measures employed. Notably, nine confounding variables were regressed out from both data modalities. Each variable was standardized for zero mean and unit variance. More details can be found in Stephen M Smith et al., 2015; Mihalik, Chapman, et al., 2022. We summarize the parameters of the HCP data in table 4.2.

4.2.2 The Alzheimer's Disease Neuroimaging Initiative (ADNI)

The ADNI database is found at adni.loni.usc.edu. Launched in 2003, ADNI's main objective is to assess the combination of serial MRI, PET (Positron emission tomography), biological markers, and clinical and neuropsychological assessment in tracking the progression of Mild Cognitive Impairment (MCI) and early Alzheimer's disease. For our experiments, we used a subset of 592 unique subjects from the ADNI. The MRI scans underwent a series of processing stages, yielding a grey matter probability map. The Mini-Mental State Examination (MMSE) scores were

Table 4.3: ADNI Data Parameters

Parameter	Value
Number of samples (n)	592
Number of features in View 1 (p)	168130
Number of features in View 2 (q)	31

employed to investigate the association with the grey matter maps. Composed of a series of brief tasks, the MMSE evaluates various cognitive domains including memory, attention, language, and visuospatial skills. The MMSE is a widely used test for assessing cognitive impairment. The MMSE scores range from 0 to 30, with lower scores indicating more severe cognitive impairment. We summarize the parameters of the ADNI data in table 4.3.

5 Results

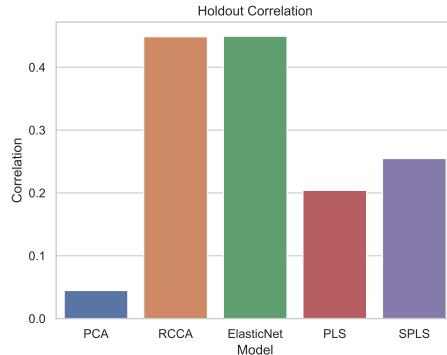
5.1 HCP Results

Next, we consider the results of applying the various CCA variants to the HCP data. Since the HCP data is high-dimensional, we drop CCA from the analysis since it would produce random results.

5.1.1 Out of Sample Correlation

Both Ridge CCA and Elastic Net outperformed PLS and SPLS in terms of holdout correlation captured (Figure III.7). This suggests that tunable L2 regularization is important, even for very high-dimensional data, and that resorting to PLS is suboptimal. On the other hand, while the additional sparsity improved SPLS over PLS (consistent with previous work João M Monteiro et al., 2016), it did not improve the performance of the Elastic Net model over Ridge CCA.

Nonetheless, the Elastic Net model did produce sparser weights than the Ridge CCA model (Figure ??) with the Elastic Net model using 241 and 96 non-zero weights for the brain and behaviour views respectively. This is compared to 300 and 145 non-zero weights for the brain and behaviour views respectively for the Ridge CCA model. The SPLS model used even fewer variables with 118 and 56 non-zero weights for the brain and behaviour views respectively. Given that the Elastic Net model can produce the same performance as the Ridge CCA model with fewer variables, we might then be inclined to prefer the Elastic Net model.

**Figure III.2: HCP:** Out-of-sample canonical correlations for each model.**Table 5.1: HCP:** Number of non-zero weights for each model.

Model	Brain Weights	Behaviour Weights
PCA	300	145
RCCA	300	145
Elastic Net	241	96
PLS	300	145
SPLS	118	56

5.1.2 Behaviour Weights

FigureIII.3 plots the top 8 positive and negative non-imaging weights for each model. This is to illustrate some of the effects we have observed in the previous section. PCA finds a mode of variation in the behavioural data that is positively correlated with psychiatric and life function tests and negatively correlated with a number of emotion and personality tests. The RCCA and Elastic Net models find a mode of variation in the behavioural data that is negatively correlated with the Line Orientation test and to a lesser extent smoking and positively correlated with a number of other cognitive tests. The PLS model finds a mode of variation in the behavioural data that is somewhat similar to the 'positive-negative' mode in Stephen M Smith et al. (2015) with a positive correlation with agreeableness, vocabulary tests, and feelings about ones' life and a strong negative correlation with smoking, rule-breaking, and antisocial personality traits. The SPLS mode is similar but selects out the rule-breaking and antisocial personality traits in favour of the vocabulary tests and smoking. This appears consistent with the additional preprocessing steps in Stephen M Smith et al. (2015), which included a top-100 PCA projection of both the brain and behaviour data.

5.1.3 Brain Connectivity Weights

In this section, we use two different methods to visualize the brain connectivity weights. The first method is to use chord diagrams to visualize the top 8 positive and negative brain weights for each model. This approach is inspired by the chord diagrams used in Stephen M Smith et al., 2015. The second method is to use surface maps to visualize the brain connectivity weights. This approach has been used by both Ferreira et al., 2022 and Stephen M Smith et al., 2015.

Chord Diagrams We grouped the nodes of the connectivity matrix of our data into 7 parcels according to the Yeo 7 network parcellation BT Thomas Yeo et al., 2011. These are then arranged around the circumference of the chord diagram using the Nichord package(Bogdan et al., 2023). The plots then show the 8 strongest positive and negative weights for each model as ‘chords’. The chord diagrams in Figure III.4 show the top 8 positive and negative brain weights for each model.

5.1.4 Model Similarity

In this section, we compare the models in terms of their similarity. We can measure the pairwise similarity between two models by comparing their weights and their representations. We can compare the weights by computing the correlation between the weights of the two models and we can compare the representations by computing the correlation between the representations of the two models.

In Figure IV.11, we plot the correlation between the brain and behaviour representations for each model. We can see clearly that both PCA, PLS, and SPLS are all highly correlated in terms of their brain representations, revealing the bias of PLS towards the largest principal components. On the other hand, in the behaviour space, the models are less correlated, with the exception of PLS and SPLS which are highly correlated with one another. There is however still substantial correlation between the PCA and PLS models. The very low correlation between the Ridge CCA and Elastic Net models with the PCA model is evidence that there are stronger correlations outside of the first principal components.

In Figure III.6, we similarly plot the correlation between the brain and behaviour weights for each model. The story is similar, albeit with marginally lower correlations between the PLS and PCA-based models. Finally, in the weights space, the Ridge CCA and ElasticNet models are even less correlated with the PCA model.

Table 5.2: ADNI: Number of non-zero weights for each model.

Model	Brain Weights	Behaviour Weights
PCA	168130	31
RCCA	168130	31
Elastic Net	59617	17
PLS	168130	31
SPLS	74995	10

5.2 ADNI Results

We now turn to the ADNI data.

5.2.1 Out of Sample Correlation

In this experiment, the Elastic Net model outperformed all other models in terms of out-of-sample correlation (Figure III.7). The RCCA model also outperformed the PLS and SPLS models while SPLS outperformed PLS. Surprisingly, PCA performed almost as well as PLS. This suggests that there is value in both tunable shrinkage and sparsity in this dataset. It also reveals that the correlated signal between the brain structure and behavioural data is relatively much stronger than in the HCP data.

5.2.2 Sparsity of Weights

Table 5.2 once again shows the number of non-zero weights for each model. We can see that tuned SPLS and Elastic Net once again identify sparse weights. In this case, the difference in performance is more convincing and suggests that this sparsity is less spuriously induced than for the HCP data. This is supported by the fact that Elastic Net and SPLS models find a similar level of sparsity in the brain weights. On the other hand SPLS finds a much sparser set of behavioural weights.

5.2.3 Behaviour Weights

As for the HCP data, Figure III.8 plots the top 8 positive and negative non-imaging weights for each model. Some of the identified behavioural weights including a number of orientation tests are similar across all of the models, including even PCA. This is indicative of the strong shared signal between the behavioural data and the brain structure data. SPLS and Elastic Net both hone in on the orientation and recall tests in the weight space. The RCCA and Elastic Net models are surprisingly

different in the weight space, with the RCCA weights on a couple of attention and calculation tests in addition to the ubiquitous orientation and recall tests.

5.2.4 Brain Structure Weights

We plot the weights as a mosaic plot with 3 slices in each direction in Figure .5. Previous work using SPLS with the ADNI dataset identified the same striking pattern of weights with the model strikingly selecting the hippocampal weights João M Monteiro et al., 2016. The Elastic Net has a less visually appealing selection of weights, with a honeycomb pattern near the edges of the brain and likewise for RCCA. It is noticeable that PCA, PLS and SPLS both weights in the same direction whereas RCCA and Elastic Net weight different regions with opposite signs.

5.2.5 Model Similarity

In this section, we once again compare the models in terms of their similarity. In Figure III.10, we can see that all of the models are highly correlated in terms of their behaviour representations. The brain representations are less correlated, but once again PCA, PLS, and SPLS are highly correlated with one another and less correlated with the Ridge CCA and Elastic Net models.

Surprisingly, in Figure III.11, we can see that the weights in both views are less correlated. This is particularly true for the brain weights where PCA exhibits a very low correlation with Ridge CCA and Elastic Net.

5.3 Timings

Finally, we consider the timings of the different models. This is an important metric because one of the main reasons for the popularity of SPLS is its speed and therefore convenience. Figure III.12 shows an estimate of the time taken to fit each model for each complete training dataset over 10 runs. We can see clearly that the Elastic Net is much slower than the other models when using the high dimensional ADNI data. Despite also being an iterative algorithm, the SPLS model is much faster than the Elastic Net and only slightly slower than the PLS and RCCA models which call optimised solvers in C. Since PLS and RCCA both use PCA preprocessing for efficiency, it is unsurprising that PCA is the fastest model.

6 Discussion and Limitations

In this section, we discuss the implications of our findings as well as the limitations of our study and the proposed FRALS method, some of which we address in later chapters of this thesis.

6.1 Discussion

Ridge CCA is typically much better than PLS across datasets: Our results show that Ridge CCA is typically much better than PLS across datasets. Much like regularised regression, it is unusual to need to use maximal ridge regularization even in high dimensions. This means that while PLS might be more stable for a given dataset, it is not necessarily more stable across random samples from the same population.

6.2 FRALS Limitations

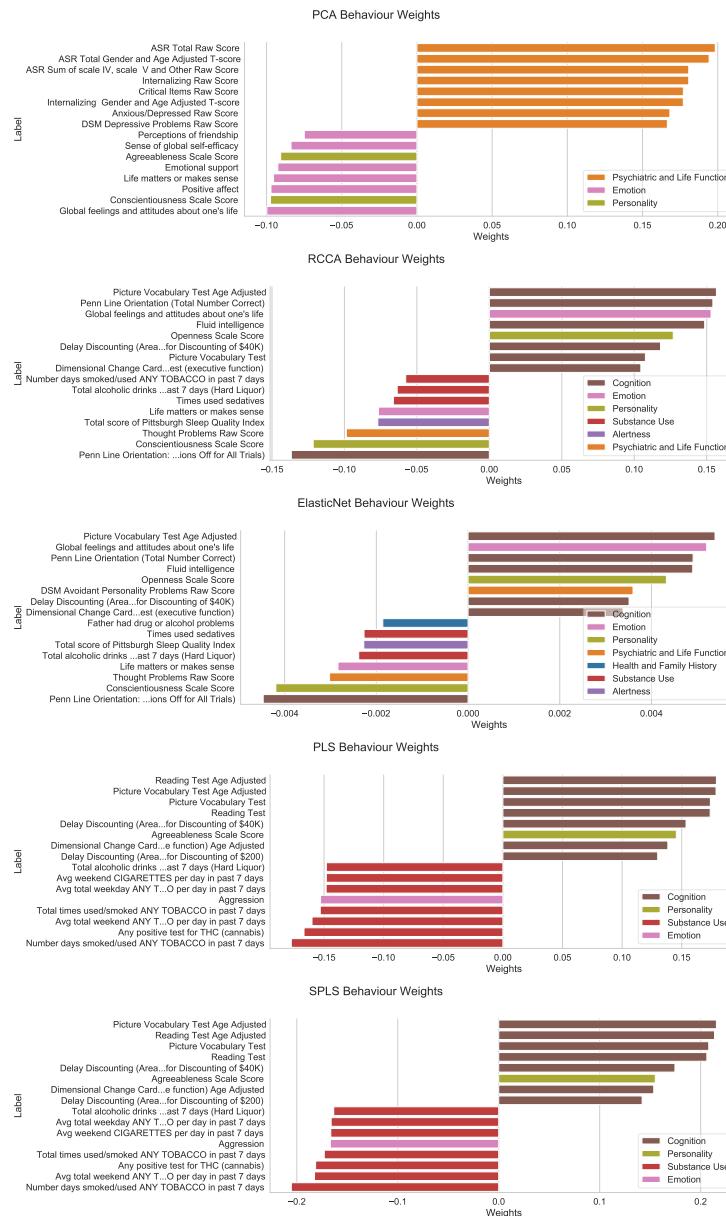
While FRALS offers promising performance in terms of out-of-sample correlation, it does come with significant drawbacks, the most noteworthy being its computational inefficiency. Below, we outline the primary factors contributing to the slow speed of FRALS and provide some insights into the computational bottlenecks.

Changing Regression Targets Adding to the computational burden is the fact that the regression targets, i.e., the projections of the other view, are not static but change dynamically throughout the algorithm's run. Each update to the least squares solution consequently alters the global objective, leading to a constantly shifting landscape that the algorithm needs to navigate. This also leads to a significant amount of redundant computation, as the algorithm needs to recompute the least squares solution for each view at each iteration.

Computational Time The primary bottleneck in FRALS is the computation of the least squares solution. For each iteration of the algorithm, we need to compute the least squares solution for each view. This is a computationally expensive operation. It is the primary factor contributing to the slow speed of FRALS (depending on the experiment around 10 times slower than Ridge CCA).

7 Conclusion

In this chapter, we introduced the Flexible Regularized Alternating Least Squares (FRALS) framework for CCA. We used the FRALS framework to implement Elastic Net CCA. We then compared the performance of Elastic Net CCA with other CCA variants on two datasets: the HCP and ADNI. We found that Elastic Net CCA outperformed other CCA variants on both datasets but that the performance of Elastic Net CCA was similar to Ridge CCA on the HCP dataset. However we found that Elastic Net CCA was much slower than other CCA variants.

**Figure III.3: HCP: Top 8 positive and negative non-imaging weights for each model**

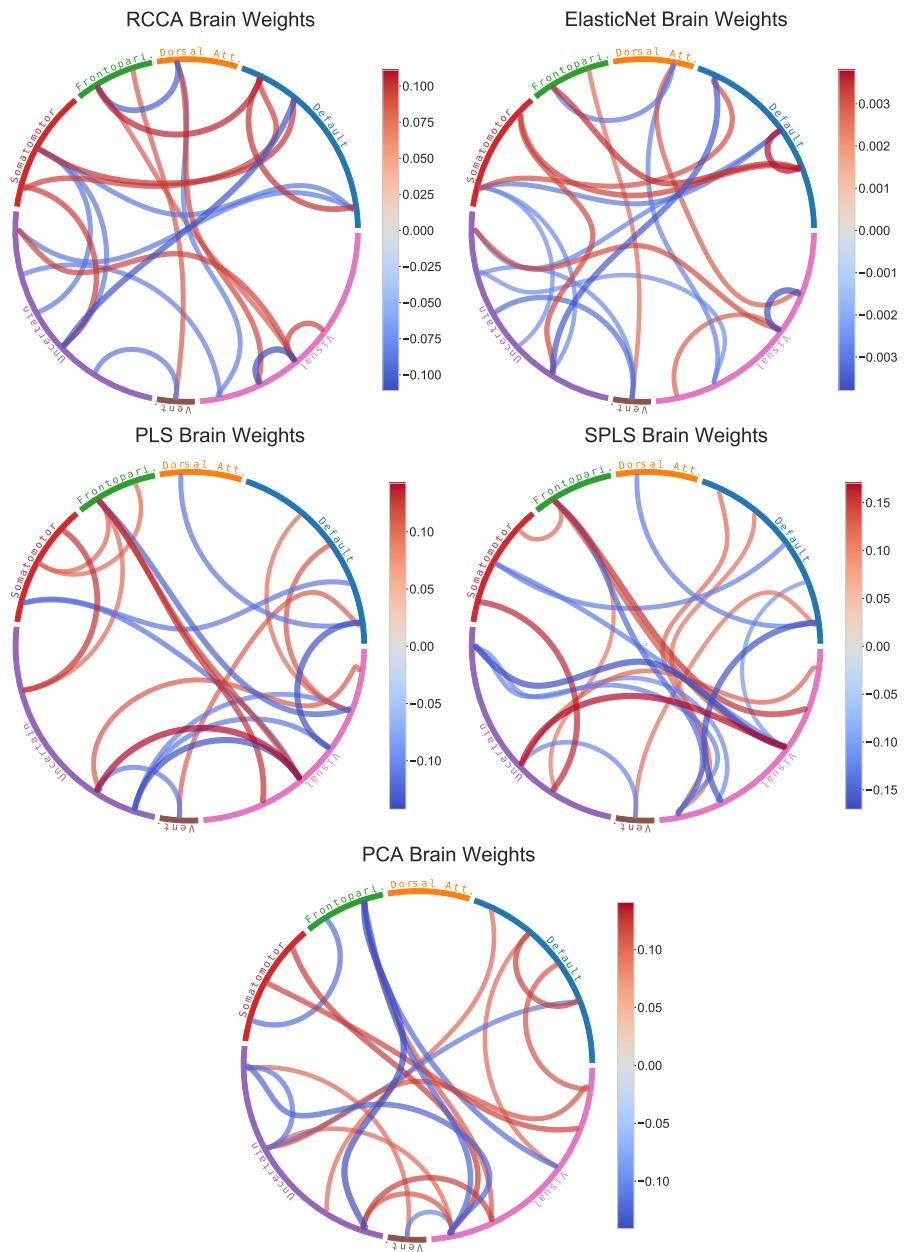


Figure III.4: HCP: Chord diagrams of the top 8 positive and negative brain weights for each model.

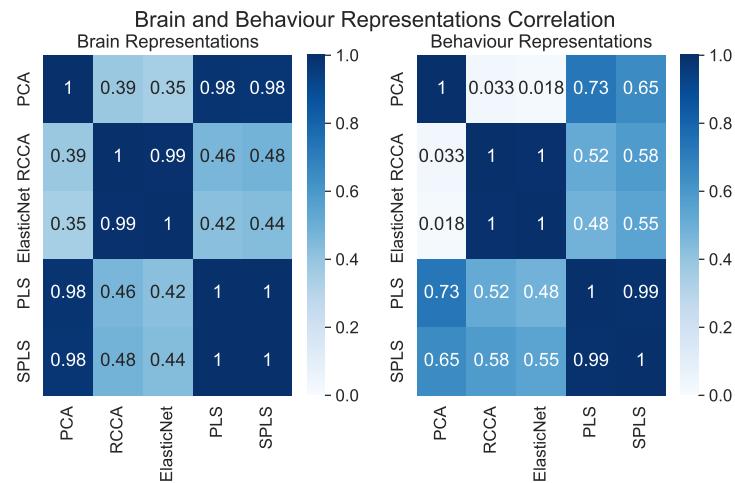


Figure III.5: HCP: Correlation between the brain and behaviour representations for each model.

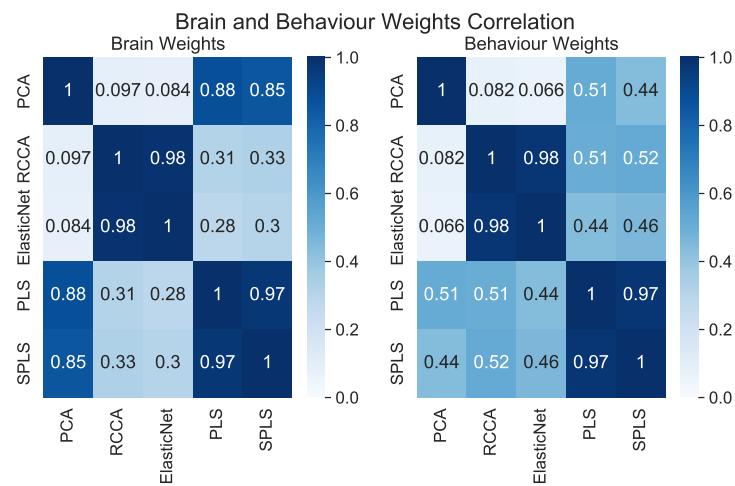


Figure III.6: HCP: Correlation between the brain and behaviour weights for each model.

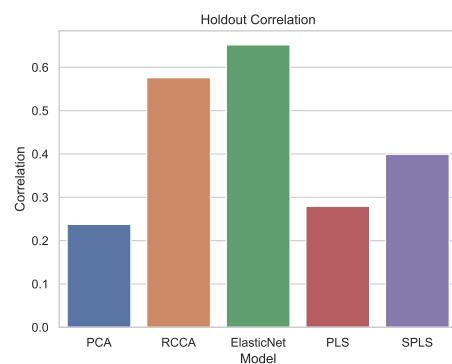
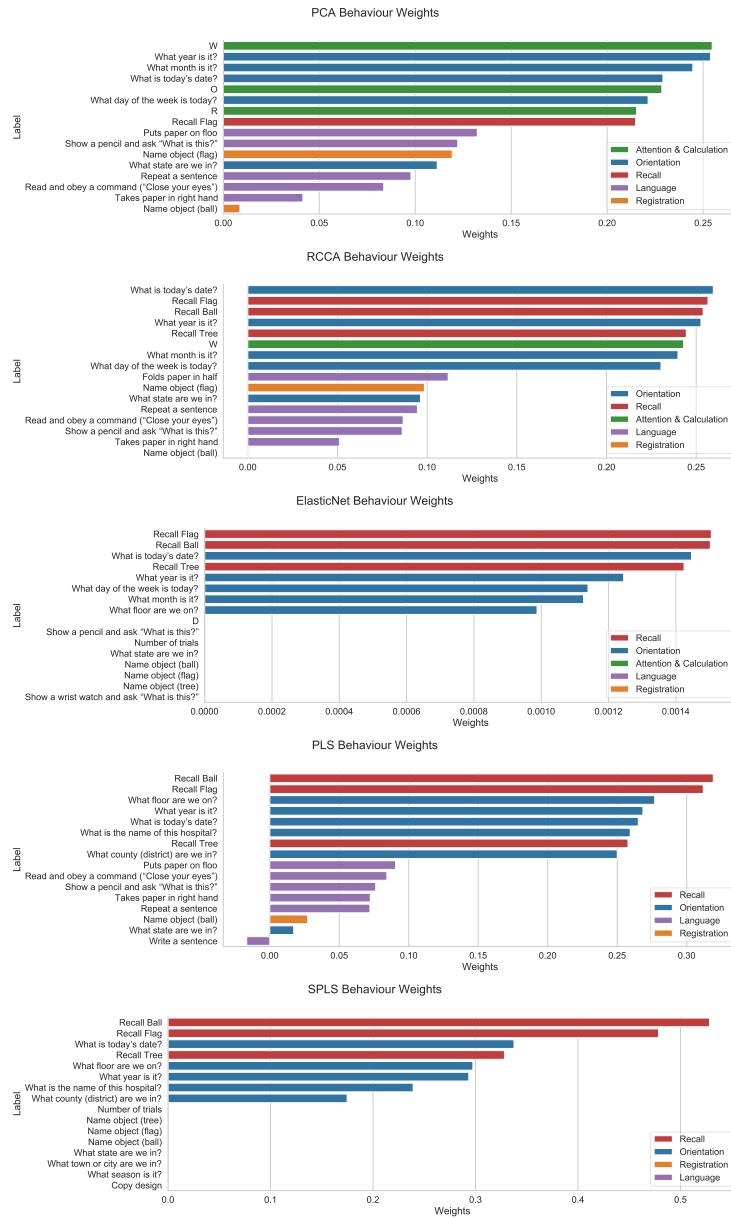


Figure III.7: ADNI: Out-of-sample canonical correlations for each model.

**Figure III.8: ADNI:** Bar plots of the behaviour weights for each model.

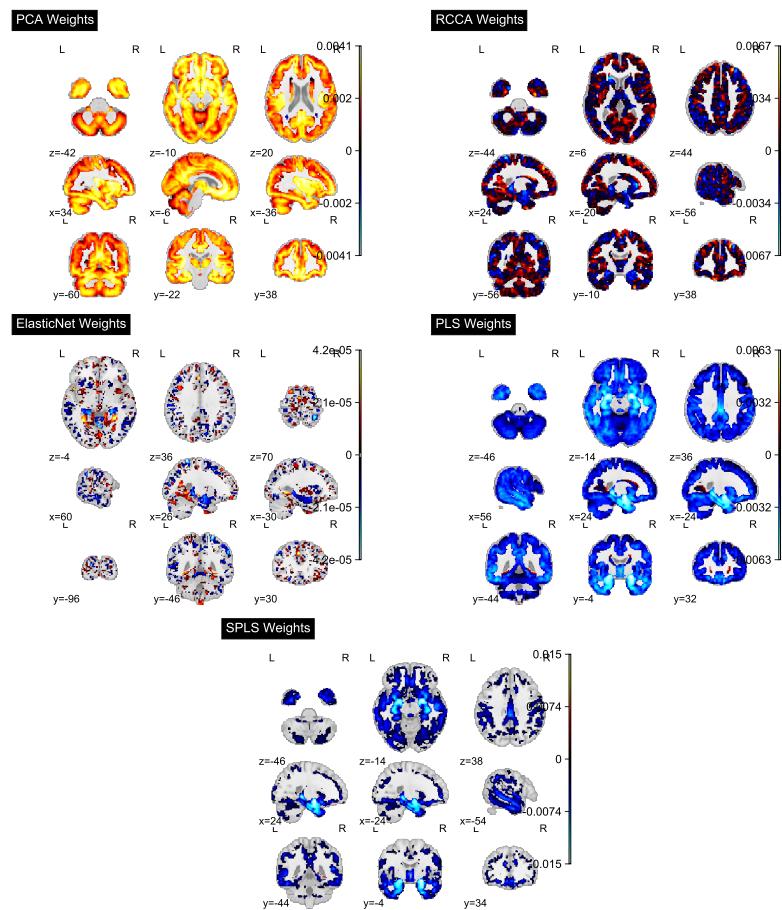


Figure III.9: ADNI: Statistical maps of brain structure weights for each model.

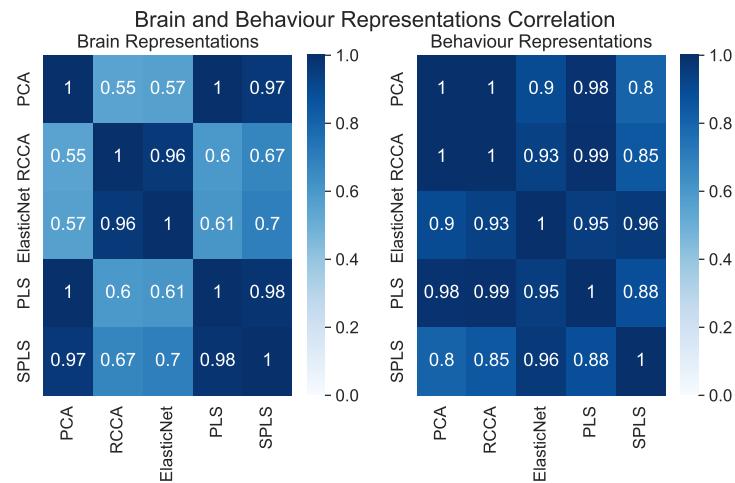


Figure III.10: ADNI: Correlation between the brain and behaviour representations for each model.

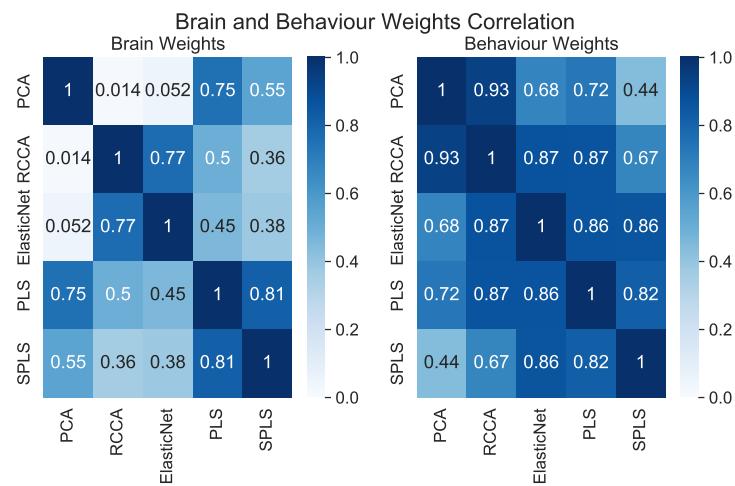


Figure III.11: ADNI: Correlation between the brain and behaviour weights for each model.

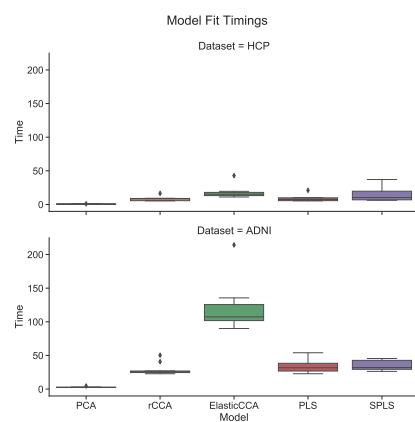


Figure III.12: Time taken to fit each model.

Chapter IV

Insights From Generating Simulated Data for CCA: Loadings not Weights

Correlation does not imply causation.

Anon.

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Preface

This chapter, deriving insights from various projects, primarily unpublished, delves into the application of loadings over weights for model interpretation in CCA models. The simulated data generation methods were used to generate simulated data in Mihalik, Chapman, et al. (2022). The arguments for the use of loadings influenced our choice of loadings for the interpretation of the results in <empty citation>

1 Introduction

There remains a substantial debate in the CCA literature about the relative merits of interpreting models in terms of weights or loadings (Gu and Wu, 2018). Simulated data has also been used extensively to understand the properties of CCA models for high-dimensional data (M. Chen et al., 2013; Suo et al., 2017; Helmer et al., 2020) including the recovery of sparse weights.

In this chapter, we first review the generative perspectives on CCA and show that they can be categorized into two groups: explicit latent variable models and implicit latent variable models, in particular by reformulating the joint covariance matrix perspective used by Suo et al. (2017), M. Chen et al. (2013), and Helmer et al. (2020) as an implicit latent variable model.

This rigorous categorization of generative approaches to CCA is novel and gives both a unique perspective on both the merits of weights and loadings, and understanding the properties of CCA models in high-dimensional simulations. We

also make a mathematical argument for the use of loadings over weights for the interpretation of CCA models, showing that the loadings are invariant to columnwise transformations of the data matrix, while the weights are not.

We illustrate these arguments with simulated data and revisit the results from chapter III through the lens of loadings.

2 Background

In practical applications, (CCA) has two aspects: estimating latent variables associated with different views, and exploring the expression of these latent variables in each view, ideally providing insight into biomedical mechanisms. These aspects correspond to the motivation behind discriminative and generative approaches in machine learning.

Generative approaches in CCA seek to understand the data generation process. They are concerned with the joint distribution $P(X^{(1)}, X^{(2)})$ and the conditional distribution $P(X^{(1)}, X^{(2)}|Z)$. We will refer to this conditional distribution as the ‘forward model’, since it describes how the observed data are generated from the latent variables. This model is parameterized by ‘loadings’ which describe the relationship between the latent variables and the observed data.

Discriminative approaches in CCA prioritize estimating latent variables from observed data, typically employing ‘weights’ as parameters. In the context of the graphical model of CCA in Figure IV.1, discriminative approaches estimate the distribution $P(Z|X^{(1)}, X^{(2)})$. We will refer to this conditional distribution as the ‘backward model’, since it describes how we can infer the latent variables from the observed data.

Gu and Wu (2018) noted that there appear to be two schools of thought in the CCA literature: one that focuses on the weights and one that focuses on the loadings. The former group argues both that the weights provide a measure of the contribution of each feature holding other features constant, and that weights are multivariate. The latter group argues that the loadings are more interpretable because they measure how much each feature is represented by the latent variable. Haufe et al. (2014) argued for the use of loadings for interpretability in the context of linear models like SVM and Lasso in neuroimaging. Alpert and Peterson (1972) also highlighted the problem with interpreting weights in the backward model, noting that they inherit all of the problems of interpreting regression coefficients. They

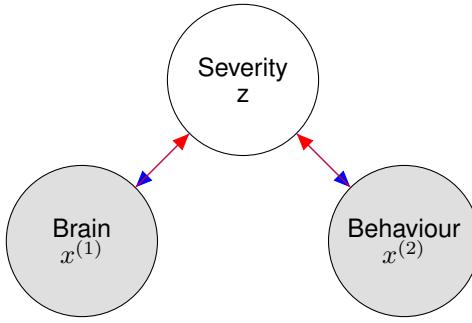


Figure IV.1: Forward and Backward Multiview Models: The generative approach to CCA focuses on the forward model from latent variables to observed data, while the machine learning approach focuses on the backward model from observed data to latent variables.

conclude that weights appear more suitable for prediction, while correlations may better explain underlying (although interrelated) constructs.

In this chapter, we are interested in generating insights to the interpretability of CCA models in the context of simulated data where we know precisely how the data were generated. The most important argument we will make is that all generative approaches to CCA are implicitly latent variable models, so that loadings are the natural parameters for interpretation.

3 Unifying Generative Perspectives on CCA

In this section, we review the generative perspectives on CCA and show that they can be categorized into two groups: explicit latent variable models and implicit latent variable models.

3.1 Probabilistic CCA and GFA (Explicit Latent Variable Models)

Let's reconsider the graphical model depicted in Figure IV.1. Now we further assume that the brain is generated via a linear model with added noise, while the behavioural modality similarly arises from a linear model with noise. Once again they are conditionally independent, given the latent variable.

The distributions of the two views are given by:

$$z \sim \mathcal{N}(0, I) \quad (\text{IV.1})$$

$$x^{(i)} \sim \mathcal{N}(W^{(i)}z + \mu^{(i)}, \Psi^{(i)}) \quad (\text{IV.2})$$

Where z represents the latent variable (disease severity), $x^{(i)}$ represents the i^{th} view, $W^{(i)}$ represents the model loadings, $\mu^{(i)}$ represents the mean, and $\Psi^{(i)}$ represents the noise covariance matrix for the i^{th} view. Notice that if it were not for the view-specific noise, the two views would be perfectly correlated subject to a linear transformation.

Bach and Jordan (2005) showed that the maximum likelihood solution for this model is equivalent to the solution of the CCA problem in the sense that the loadings are the same as the CCA weights multiplied by the covariance:

$$\hat{W}^{(i)} = \Sigma_{ii} \hat{U}^{(i)} R \quad (\text{IV.3})$$

Where R is an arbitrary rotation matrix and $\hat{U}^{(i)}$ is the matrix of CCA weights for the i^{th} view. This implies that for invertible covariance matrices, we can access the ‘true’ CCA weights associated with the top-k subspace by multiplying the loadings by the inverse of the covariance matrix:

$$\hat{U}^{(i)} R = \Sigma_{ii}^{-1} \hat{W}^{(i)} \quad (\text{IV.4})$$

In practice we do not have access to the covariance matrices Σ_{ii} , so we must estimate them from the data using the sample covariance matrices $\hat{\Sigma}_{ii}$.

Notice that for Identity covariance matrices, the CCA weights are the same as the loadings. Otherwise, there is a linear transformation between the two. For singular covariance matrices, the CCA weights are not uniquely defined.

Moreover, the mean of the posterior distribution of the latent variables is proportional to the mean of the CCA scores (Klami, Virtanen, and Kaski, 2013). Group Factor Analysis (GFA) is a closely related model that assumes diagonal covariance in $\Psi^{(i)}$:

$$z \sim \mathcal{N}(0, I) \quad (\text{IV.5})$$

$$x^{(i)} \sim \mathcal{N}(W^{(i)}z, \sigma^{(i)}I) \quad (\text{IV.6})$$

An interesting feature of the GFA model is that as the noise level approaches zero, the marginal distribution of the views is the same as the probabilistic PCA model for each view (Tipping and Bishop, 1999). This suggests that for small noise levels, we should in fact be able to recover much of the mutual information between the views by using PCA on each view separately. For this reason, we will use and recommend PCA as a baseline in our later experiments. Because the diagonal covariance assumption makes inference computationally cheaper, this line of work has been able to extend to incorporate sparsity on the loadings (Virtanen, Klami, and Kaski, 2011) as well as missing data (Ferreira et al., 2022).

By marginalizing out the latent variables of the generative CCA and GFA models, we can write down the joint distribution of the two views:

$$\begin{bmatrix} X^{(1)} \\ X^{(2)} \end{bmatrix} \sim \mathcal{N}\left(\begin{bmatrix} \mu^{(1)} \\ \mu^{(2)} \end{bmatrix}, \begin{bmatrix} W^{(1)}W^{(1)T} + \Psi_1 & W^{(1)}W^{(2)T} \\ W^{(2)}W^{(1)T} & W^{(2)}W^{(2)T} + \Psi_2 \end{bmatrix}\right) \quad (\text{IV.7})$$

Importantly, this shows us that the true covariance in each view is a function of the loadings and the noise covariance matrix. Specifically, the covariance matrix of the i^{th} view is given by:

$$\Sigma_{ii} = W^{(i)T}W^{(i)} + \Psi_i \quad (\text{IV.8})$$

While these generative models are provide a clear interpretation of the data generation process and possible biological processes, their application in practice is limited compared to classical CCA. This is primarily due to their computational intensity and the need for a careful selection of priors. Moreover, while these models can generate data with sparse loadings, generating data with sparse weights is challenging due to the dependence of CCA weights on the covariance matrices of the views.

3.2 Joint Covariance Matrix Perspective (Implicit Latent Variable Model)

In contrast to the explicit latent variable models discussed earlier, the joint covariance matrix perspective Suo et al., 2017; M. Chen et al., 2013 offers an implicit approach to understanding the data generation process. This method focuses on the covariance matrices of the views, rather than directly modeling latent variables. A key advantage of this perspective, particularly noted in the sparse CCA literature, is its ability to generate data with known sparse weights and or known canonical correlations. This is achieved by constructing the joint covariance matrix of the distribution $P(X^{(1)}, X^{(2)})$:

$$\begin{bmatrix} X^{(1)} \\ X^{(2)} \end{bmatrix} \sim \mathcal{N} \left(\begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} \Sigma_{11} & \Sigma_{12} \\ \Sigma_{21} & \Sigma_{22} \end{bmatrix} \right) \quad (\text{IV.9})$$

Where Σ_{11} and Σ_{22} are the within-view covariance matrices and Σ_{12} and Σ_{21} are the between-view covariance matrices.

This has the advantage of allowing us to control the within-view covariance and therefore test the methods under specific conditions. The process was first described by Chen (M. Chen et al., 2013) and further explained by (Suo et al., 2017) and has been the basis behind findings in Helmer et al. (2020) and Matković et al. (2023).

We can control the true signal by setting the active variables and correlations in the between-view covariance matrices Σ_{12} and Σ_{21} . Specifically we construct the between-view covariance matrices as follows:

$$\Sigma_{12} = \sum_{k=1}^K \rho_k \Sigma_{11} u_k^{(1)} u_k^{(2)T} \Sigma_{22} \quad (\text{IV.10})$$

Where ρ_k is the k^{th} canonical correlation and $u_k^{(i)}$ is the k^{th} column of the matrix of weights $U^{(i)}$.

We can still access the true loadings of the implied latent variable model by using the relationship in IV.3 and multiplying the weights $u^{(i)}$ by the within-view covariance matrix Σ_{ii} .

3.3 Summary of Data Generation Methods

Comparison of Joint Covariance Matrices To understand the distinct approaches of each data generation method, we present a comparison of their covariance structures. This comparison highlights the differences in how these methods model the relationship within and between views.

Table 3.1: Covariance Structures in Data Generation Methods

	Method	Within-view Covariance Σ_{ii}	Between-view Covariance Σ_{12}
Explicit	Probabilistic CCA	$W^{(i)}W^{(i)\top} + \Psi_i$	$W^{(1)}W^{(2)\top}$
	GFA	$W^{(1)}W^{(1)\top} + \sigma^{(1)}I$	$W^{(1)}W^{(2)\top}$
Implicit	Joint Covariance	Σ_{ii}	$\sum_{k=1}^K \rho_k \Sigma_{11} u_k^{(1)} u_k^{(2)\top} \Sigma_{22}$
	Joint Covariance (Identity)	I	$\sum_{k=1}^K \rho_k u_k^{(1)} u_k^{(2)\top}$

Comparison of True Weights and Loadings We summarize the relationship between the weights and loadings in each data generation method, distinguishing between population and sample cases. This distinction is crucial, especially in scenarios where the population covariance matrix Σ is identity, but the sample covariance matrix $\hat{\Sigma}$ is only an approximation.

Table 3.2: Relationship Between Weights and Loadings in Population and Sample Cases

	Method	Case	Weights	Loadings
Explicit	Probabilistic CCA	Population	$(W^{(i)}W^{(i)\top} + \Psi_i)^{-1}W^{(i)}$	$W^{(i)}$
		Sample	$\hat{\Sigma}_{ii}^{-1}W^{(i)}$	$W^{(i)}$
Implicit	GFA	Population	$(W^{(i)}W^{(i)\top} + I)^{-1}W^{(i)}$	$W^{(i)}$
		Sample	$\hat{\Sigma}_{ii}^{-1}W^{(i)}$	$W^{(i)}$
Implicit	Joint Covariance (Non-Identity)	Population	$U^{(i)}$	$\Sigma_{ii} U^{(i)}$
		Sample	$U^{(i)}$	$\hat{\Sigma}_{ii} U^{(i)}$
Implicit	Joint Covariance (Identity)	Population	$U^{(i)}$	$U^{(i)}$
		Sample	$U^{(i)}$	$\hat{\Sigma}_{ii} U^{(i)}$

3.4 Efficient Sampling of Simulated CCA Data

Efficient sampling from high-dimensional multivariate normal distributions is a critical step in simulating data for Canonical Correlation Analysis (CCA). Traditional methods can be computationally intensive and storage-demanding, especially for large datasets. To address these challenges, we leverage low-rank and sparse covariance matrices, along with Singular Value Decomposition (SVD), to facilitate efficient and feasible sampling procedures.

3.4.1 Challenges with High-Dimensional Data

In the context of high-dimensional data, direct sampling from a multivariate normal distribution and storing the full covariance matrix ($p \times p$ for p dimensions) become impractical. High computational cost and substantial storage requirements necessitate more efficient approaches.

3.4.2 Utilizing Low-Rank Covariance Matrices

A practical solution is to use low-rank approximations of covariance matrices. Instead of storing the entire covariance matrix, we store only the significant components, specifically the matrices U and S from the SVD of the covariance matrix ($\Sigma = USU^T$). Sampling then involves generating samples from a standard univariate normal distribution and transforming them using these SVD components.

3.4.3 Sparse Covariance Matrices

For certain applications, sparse covariance matrices offer an additional avenue for efficiency. These matrices, with many zero entries, reduce both computational complexity and storage requirements, allowing for faster processing and less memory usage.

3.4.4 Explicit Latent Variable Models

In explicit latent variable models, we generate orthogonal latent variables from a low-dimensional multivariate normal distribution. These are then transformed using the loading matrices to create the signal component of the data. Noise is added by sampling from a univariate normal distribution and multiplying by a factorized (low-rank or sparse) covariance matrix. This method allows for precise control over the signal-to-noise ratio in the simulated data.

3.4.5 Implicit Latent Variable Models

Implicit latent variable models pose a greater challenge as they typically require storing the full covariance matrix. However, we can improve the efficiency by employing the SVD of the covariance matrix. This approach involves decomposing the covariance matrix and then using the resulting components to transform samples from a standard multivariate normal distribution, thereby generating samples that conform to the desired high-dimensional distribution with reduced computational overhead.

These methods collectively enhance the feasibility and efficiency of simulating CCA data, especially in high-dimensional scenarios, providing a robust framework for research and analysis in various fields.

4 A Mathematical Argument for Using Loadings not Weights for Interpretation of CCA Models

In this section, we make a mathematical argument for the use of loadings over weights for the interpretation of CCA models. In particular, we show that the loadings are invariant to columnwise transformations of the data matrix, while the weights are not.

CCA can be solved in the principal component space. Consider the singular value decomposition (SVD) of the data matrices:

$$X^{(i)} = U^{(i)} \Sigma^{(i)} V^{i\top} \quad (\text{IV.11})$$

Here, $U^{(i)}$ and $V^{(i)}$ are the left and right singular vectors of $X^{(i)}$ respectively, and $\Sigma^{(i)}$ is a diagonal matrix of singular values. The intuition behind this decomposition is that we are representing the data matrix in terms of its fundamental components: the directions of maximum variance (captured by $V^{(i)}$), the scale of these directions (captured by $\Sigma^{(i)}$), and the projections of the data onto these directions (captured by $U^{(i)}$). $U^{(i)}$ are the principal components of $X^{(i)}$.

Substituting Equation IV.11 into the CCA objective function, we have:

$$\max_{U^{(1)}, u^{(2)}} \text{Corr}(X^{(1)}U^{(1)}, X^{(2)}u^{(2)}) = \max_{U^{(1)}, u^{(2)}} \text{Corr}(U^{(1)}\Sigma^{(1)}V^{1\top}U^{(1)}, U^{(2)}\Sigma^{(2)}V^{2\top}u^{(2)}) \quad (\text{IV.12})$$

Reparameterizing the weights as $v^{(i)} = \Sigma^{(i)} V^{i\top} u^{(i)}$, we obtain:

$$\max_{v^{(1)}, v^{(2)}} \text{Corr}(U^{(1)} v^{(1)}, U^{(2)} v^{(2)}) \quad (\text{IV.13})$$

This reparameterization simplifies the optimization problem in two ways. Firstly, if the data matrices are low rank (which is guaranteed if the number of samples is less than the number of features), then the matrix of principal components $U^{(i)}$ is lower dimensional than the data matrix $X^{(i)}$, reducing the number of parameters in the optimization problem. Secondly, the reparameterization ensures that $v^{(1)\top} U^{(1)\top} U^{(1)} v^{(1)} = v^{(1)\top} v^{(1)}$, making the constraints independent of the data. We can therefore solve the CCA problem by solving the simpler PLS problem in the principal component space, which is computationally more feasible but also gives us a convenient way to understand how the weights and loadings of CCA models change under different transformations of the data.

Definition: *Loadings* are defined using the reparameterized weights as follows:

$$w_j^{(i)} = \text{Corr}(X_j^{(i)}, U^{(i)} v^{(i)}) = \frac{\text{Cov}(X_j^{(i)}, U^{(i)} v^{(i)})}{\sqrt{\text{Var}(X_j^{(i)})} \sqrt{\text{Var}(U^{(i)} v^{(i)})}} \quad (\text{IV.14})$$

By convention, and without loss of generality, we standardize the latent variables to have unit variance so that:

$$w_j^{(i)} = \frac{\text{Cov}(X_j^{(i)}, U^{(i)} v^{(i)})}{\sqrt{\text{Var}(X_j^{(i)})}} \quad (\text{IV.15})$$

Intuitively, loadings measure how much each original feature contributes to the latent variables, providing insight into the structure of the data.

4.1 Invariance to Scale

First, we show that the loadings are invariant to column-wise scaling of the data matrix whereas the weights are not.

Lemma 4.1. *Scaling the columns of the data matrix does not affect the left singular vectors $U^{(i)}$.*

Proof. Scale the columns of the data with a matrix C :

$$C = \begin{pmatrix} c_{11} & 0 & \cdots & 0 \\ 0 & c_{22} & \cdots & 0 \\ \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & c_{nn} \end{pmatrix} \quad (\text{IV.16})$$

where c_{ii} represents the scaling factor for the i -th column of the data matrix. For columns that are not scaled, $c_{ii} = 1$. This means that the corresponding column remains unchanged.

Since C is diagonal it can be represented by a diagonal matrix $S = C$ and an orthogonal matrix (the identity matrix) R . The transformed dataset is therefore $X^{(1')} = X^{(1)}C$:

$$X^{(1')} = U^{(i)}\Sigma^{(i)}V^{i\top}C = U^{(i)}(\Sigma^{(i)}S^{(i)})(V^{i\top}I) = \quad (\text{IV.17})$$

which makes clear that the left and right singular vectors $U^{(i)}$ and $V^{(i)}$ right remain unchanged. Therefore, the modified equation can be represented as:

$$X^{(1')} = U^{(i)}\Sigma^{(i')}(V^{(i)})^T \quad (\text{IV.18})$$

where $\Sigma^{(i')} = \Sigma^{(i)}S^{(i)}$. □

Intuition Scaling the data is like changing the units of measurement. It stretches or compresses the data but does not change the relationships between the samples.

Noting that the CCA optimisation problem remains the same as in Equation IV.13, we can now show that the weights are not invariant to scaling of the data matrix but the loadings are.

Weights change From the earlier reparameterization, and given that $v^{(i')} = v^{(i)}$, the weights post-scaling are:

$$u^{(i')} = V^{(i)}(\Sigma^{(i')})^{-1}v^{(i)} = V^{(i)}(\Sigma^{(i')})^{-1}v^{(i)} = C^{(i)-1}u^{(i)} \quad (\text{IV.19})$$

which are the original weights scaled by the inverse of the scaling matrix C . This means that the weights are not invariant to scaling of the data matrix. Furthermore

it means we can set the weights to arbitrary values by scaling the data matrix. While we can build pipelines with standardized data, there is no a priori reason to do so.

Loadings are invariant Since loadings are correlations between the original features and the latent variables, they are invariant to scaling of the data. This follows from the definition of correlation and the unchanged latent variables:

$$w_j^{(i)} = \text{Corr}(X_j^{(i')}, U^{(i)}v^{(i)}) = \text{Corr}(c_{jj}X_j^{(i)}, U^{(i)}v^{(i)}) = \text{Corr}(X_j^{(i)}, U^{(i)}v^{(i)}) \quad (\text{IV.20})$$

Intuition The loadings remain the same because scaling the data does not change the relative contributions of each feature to the latent variables.

4.2 Invariance to Repeated Linear Combinations of Columns

We can also prove a more general result that the loadings are invariant to repeated linear combinations of columns of the data matrix. This is not as contrived as it sounds, since we often need to decide which features to include or exclude in a model, and when we work with highly correlated variables like survey questions, we may choose to use summary scores instead of individual questions.

Lemma 4.2. *Adding linear combinations of columns to the data matrix does not affect the left singular vectors $U^{(i)}$.*

Proof. Now, consider adding columns that are linear combinations of existing columns in $X^{(i)}$ to form $X^{(i'')}$. We can represent this using a transformation matrix A such that $X^{(i'')} = X^{(i)}A$:

$$A = \begin{pmatrix} 1 & 0 & \cdots & 0 & a_{11} & a_{12} & \cdots & a_{1m} \\ 0 & 1 & \cdots & 0 & a_{21} & a_{22} & \cdots & a_{2m} \\ \vdots & \vdots & \ddots & \vdots & \vdots & \vdots & \ddots & \vdots \\ 0 & 0 & \cdots & 1 & a_{n1} & a_{n2} & \cdots & a_{nm} \end{pmatrix} \quad (\text{IV.21})$$

where a_{ij} represents the weight of the j -th column in the i -th linear combination. The key is that we can still represent the transformed dataset as a product of the original left singular vectors $U^{(i)}$ and a new diagonal matrix $\Sigma^{(i'')}$ and right singular vectors $V^{(i'')}$.

$$X^{(i'')} = U^{(i)}(\Sigma^{(i)}V^{i\top}A) = U^{(i)}(\Sigma^{(i')}V^{(i')\top}) \quad (\text{IV.22})$$

Where we know that the transformation is rank preserving because the first n columns of A are the identity matrix. The left singular vectors $U^{(i'')}$ therefore remain the same as $U^{(i)}$. \square

Weights are Underdetermined The weights $u^{(i'')}$ are underdetermined in the transformed space due to the added linear dependencies in the columns. The specific weights will depend on the SVD computation approach.

$$u^{(i'')} = V^{(i)}(\Sigma^{(i'')})^{-1}v^{(i)} \quad (\text{IV.23})$$

Intuition In the extreme case, if we have two identical columns in the data matrix, then we can use any weights we like for these columns provided that their sum is the same.

Loadings Remain Invariant The loadings, as before, remain unchanged because the original columns are unchanged and the latent variables are unchanged.

4.3 Summary

We have shown that the loadings are invariant to columnwise transformations of the data matrix, while the weights are not. This is a key advantage of loadings over weights for the interpretation of CCA models. We might even be inclined to state this even more strongly: **the loadings are the true parameters of the model, while the weights are not.**

5 Experiments

Having given a mathematical argument for the use of loadings over weights for the interpretation of CCA models, we now motivate a number of experiments demonstrating the relationship between loadings and weights in CCA models.

The first set of experiments illustrates the relationship between weights and loadings in simulated data from explicit and implicit latent variable models with identity and non-identity covariance matrices.

The second set of experiments illustrates the power of the less popular explicit latent variable models for studying the properties of CCA and PLS models in high dimensional settings.

5.1 The Relationship Between Weights and Loadings

This experiment uses simulated data to illustrate the relationship between weights and loadings in CCA models. Given the thrust of this chapter, we are particularly interested in scenarios where the model weights are uninformative, but the loadings are informative.

We generate data with 100 samples and 10 features in each view. We then generate data under two implicit latent variable models and two explicit latent variable models.

Implicit Latent Variable Models The implicit latent variable approach allows us to choose the true weights. We ensure that the true weights are sparse with 5 non-zero entries in each view. We use a true correlation of 1.0 between the views at the population level.

We generated data under two scenarios:

- Using identity within-view covariance matrices, such that the true weights are equivalent to true loadings.
- Using random covariance matrices, where true weights differ from true loadings, usually resulting in non-sparse loadings.

Explicit Latent Variable Models and Sparse Loadings: The explicit latent variable approach allows us to choose the true loadings. We ensure that the true loadings are sparse with 5 non-zero entries in each view. The signal-to-noise ratio was set so that the sum of the signal's eigenvalues was half that of the noise. We generate data under two scenarios:

- GFA (identity noise covariance matrices)
- Probabilistic CCA (random covariance matrices)

For the two models with random covariance matrices, we also duplicate each column of the data matrix and add a small amount of noise to illustrate the effect of repeated linear combinations of columns on the weights and loadings.

Table 5.1: Simulated Data Parameters for Weight and Loadings Recovery Experiments

Parameter	Value
Number of samples (n)	100 train, 500 test
Number of features in View 1 (p)	10-20 (10 repeated)
Number of features in View 2 (q)	10-20 (10 repeated)
True Latent dimensions	1
Fraction of active features View 1	0.5
Fraction of active features View 2	0.5

Table 5.2: Simulated Data Parameters for Brain-Behaviour Simulations

Parameter	Value
Number of features in View 1 (p)	100-10000
Number of features in View 2 (q)	100-10000
True Latent dimensions	1
Fraction of active features View 1	1.0
Fraction of active features View 2	1.0
Signal-to-noise ratio	0.001-1

5.2 Varying the Signal-to-Noise Ratio

Our next experiment was motivated by the observation that PLS models (including sparse PLS) often exhibit low but non-zero out of sample correlations in real high-dimensional data. We want to understand how much of this is due to the fact that PLS models optimize covariance rather than correlation, and how much is due to the fact that the signal-to-noise ratio is too low. In order to understand this, we simulated data with varying signal-to-noise ratios and compared the out of sample correlations of PLS models with the out of sample correlations of Ridge CCA models with varying regularization. We simulated data with 1000 samples and between 100 and 10,000 features in one view and 100 features in the other. These are of the same order of magnitude as typical brain-behaviour datasets. We summarise these data properties in table 5.2.

6 Results

6.1 The Relationship Between Weights and Loadings

6.1.1 Implicit Latent Variables (Sparse Weights)

For this data, we estimated model loadings using the product of the model weights and the sample within-view covariance matrix. Note that because we multiply model weights by the sample covariance matrix to estimate the loadings, the estimated loadings are sometimes not sparse even when both the model weights are sparse and the true covariance matrix is identity.

Figure IV.2 shows the true and estimated weights and loadings for the implicit latent variable models. Figure IV.2a) shows the results for the identity covariance scenario, while Figure IV.2b) shows the results for the random covariance scenario.

Elastic regularization sets true zero weights close to zero and accurately retrieves true weights in both the identity (Figure IV.2a) and non-identity (Figure IV.2b) scenarios.

PCA performs badly across both scenarios. This is unsurprising because the implicit latent variable model does not assume that the latent variables are the principal components of the data.

It is clear that the PLS and sPLS models have been skewed by the principal components. Furthermore, the sPLS does not result in appropriate shrinkage and identifies a number of false negatives. This is perhaps surprising because all three problems are equivalent in the population setting (due to identical view covariances).

Interestingly, all the models seem to give more accurate estimates of the true loadings in the random covariance scenario (Figure IV.2b) than in the identity covariance scenario (Figure IV.2a). In particular, even when the true covariance is identity, the estimated loadings are not sparse even when the model weights are sparse because the estimated loadings are the product of the model weights and the sample covariance matrix rather than the population covariance matrix.

Recovery of Latent Variables Unregularized CCA and Ridge CCA are comparable to Elastic Net regularization but slightly worse in both scenarios (Figure IV.3)

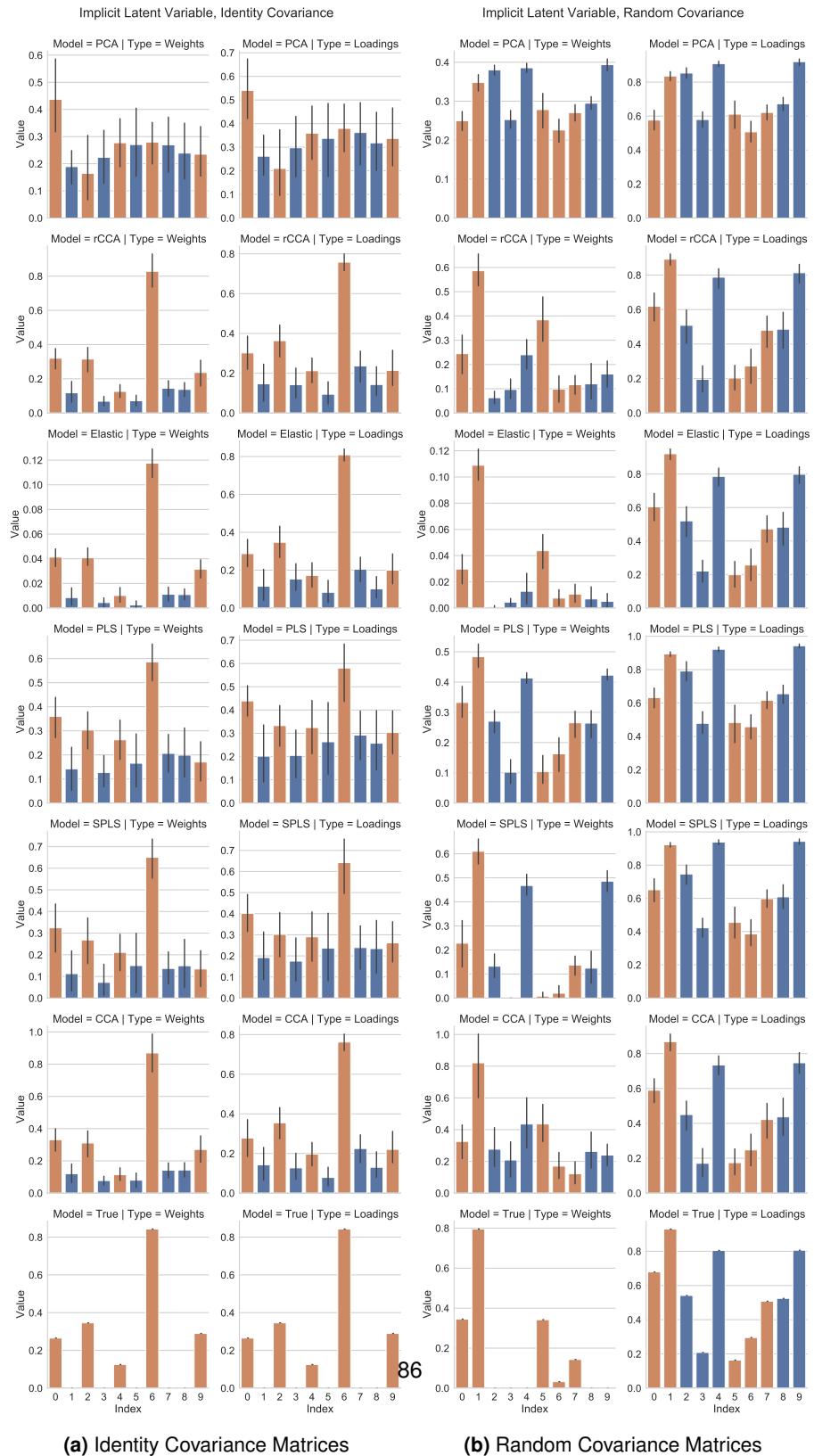
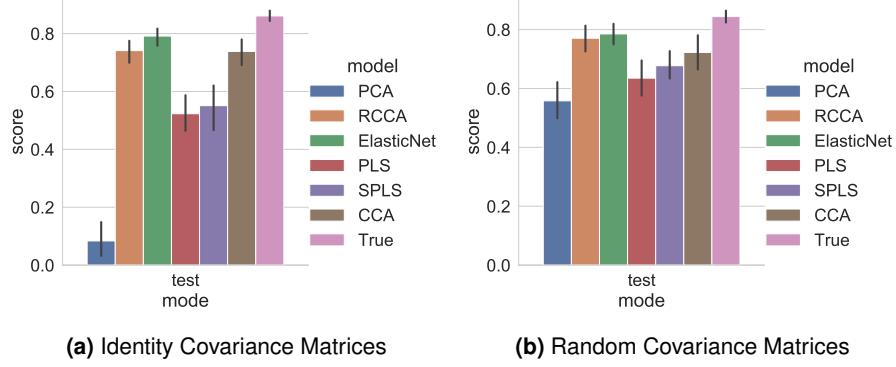


Figure IV.2: Implicit Latent Variable: Weights and Loadings. Blue signifies true zero weights and loadings, while Orange indicates estimated true non-zero weights and loadings.

**Figure IV.3: Implicit Latent Variable:** Test Scores.

6.1.2 Explicit Latent Variables (Sparse Weights)

Recovery of Weights and Loadings A striking observation, though theoretically consistent, from Figure IV.4a is that PCA almost perfectly recovers the true weights and loadings for the GFA model with identity noise covariance. Admittedly, we have chosen a reasonably high signal-to-noise ratio for this experiment, but this nonetheless demonstrates that PCA can be a useful baseline for multiview data under an isotropic latent variable noise model. Figure IV.4b indicates that with anisotropic noise covariance, PCA no longer captures the true loadings. There is no strong evidence that sPLS or Elastic Net regularization outperform PLS or RCCA, respectively, in this setting. This is unsurprising because the true weights are not sparse, and so the additional sparsity constraints do not help. However, this does illustrate that priors on weights do not translate well to priors on loadings.

Recovery of Latent Variables Indeed, in the identity noise covariance scenario, all the models perform similarly (Figure IV.5a) with the exception of CCA which appears to be unstable in this setting (Figure IV.4a). In the random noise covariance scenario, PCA performs poorly, and CCA now performs well (Figure IV.5b).

6.1.3 Measuring the Identitiness of the Covariance Matrices

The theory we developed in section 3 suggests that the identitiness of the covariance matrices is crucial for understanding how imposing sparsity on the weights imposes a prior belief in sparsity on the more biologically interesting loadings. We can measure the identitiness of the covariance matrices by looking at the eigenvalues of the covariance matrices. If the eigenvalues of the sample covariance matrix are

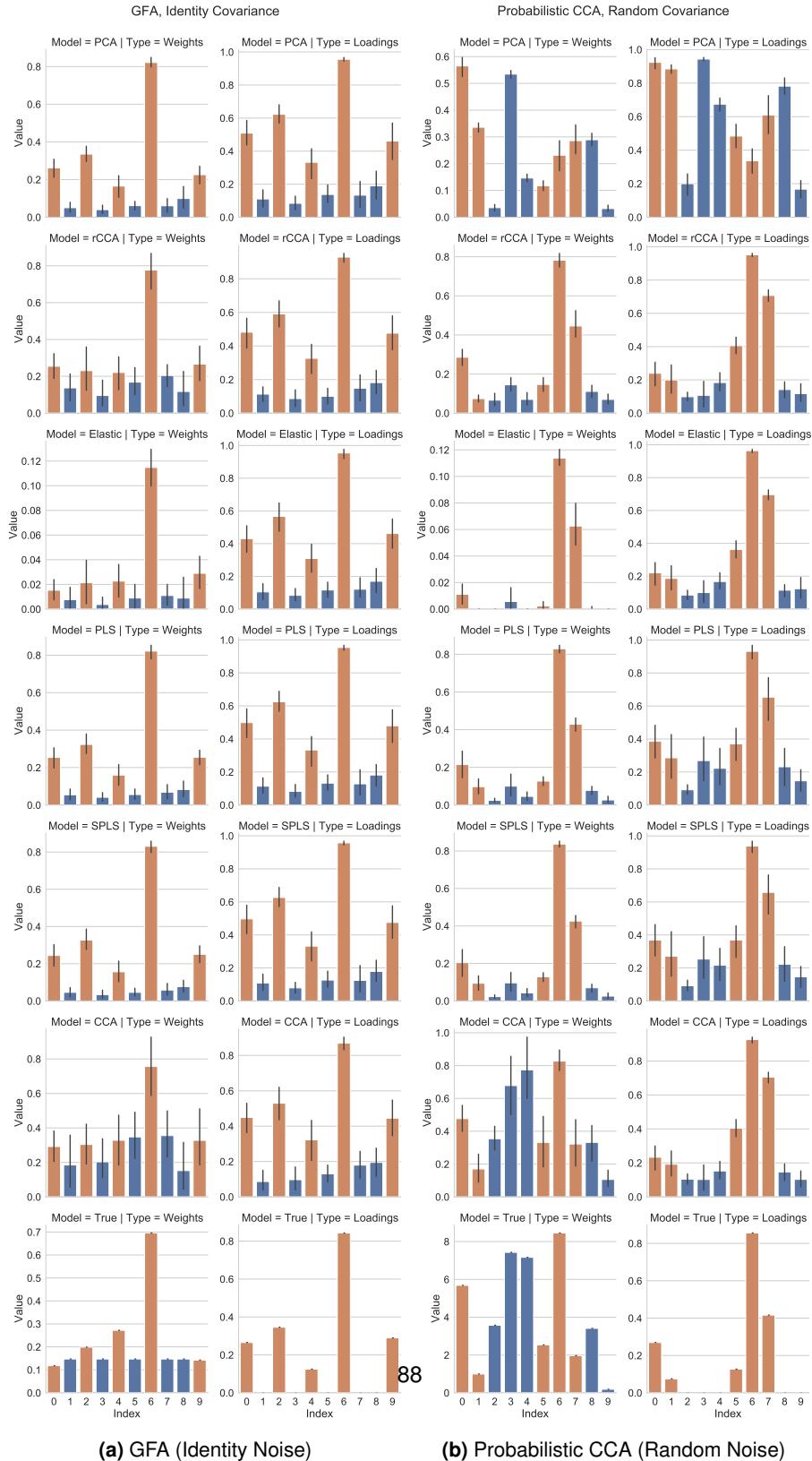
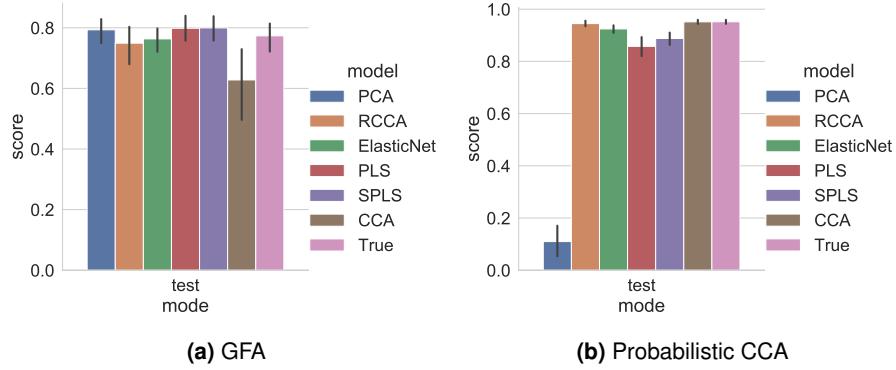


Figure IV.4: Explicit Latent Variable: Weights and Loadings. Blue signifies true zero weights and loadings, while Orange indicates estimated true non-zero weights and loadings.

**Figure IV.5: Explicit Latent Variable:** Test Scores.

all close to 1, then the sample covariance matrix is close to identity. Departures from 1 indicate that the sample covariance matrix is not close to identity and imply multicollinearity in the data.

In the simulated data, we can see that the data generation models with identity noise covariance matrices, have eigenvalues closer to one than (Figure IV.6). On the other hand, these plots (shown for 10 random samples) show that all of the sample covariance matrices depart from the ideal case, *even when the true covariance matrices are identity*.

6.2 Varying the Signal-to-Noise Ratio

In Figures IV.7 and IV.8 we plot the test correlation (score) varying the signal-to-noise ratio and the number of features. Figure

7 Revisiting Brain-Behaviour Results

In this section, we revisit the results from the brain-behaviour experiments in Chapter III by comparing the weights and loadings of the HCP and ADNI datasets.

7.1 Identitiness of Covariance Matrices

In this section, we consider the identitiness of the covariance matrices for the HCP and ADNI datasets. Figure IV.9 shows the eigenvalues of the covariance matrices for the HCP and ADNI datasets while Figure IV.10 shows the covariance matrices themselves (with the ADNI brain covariance matrix left out due to its size). From

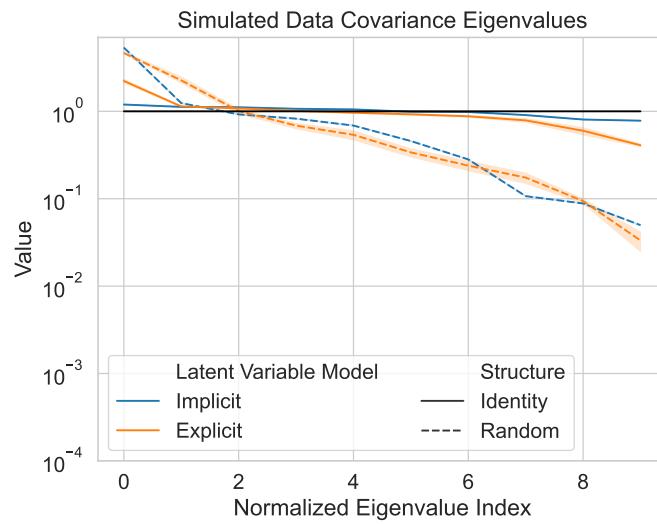


Figure IV.6: Eigenvalues of the covariance matrices for the simulated datasets.

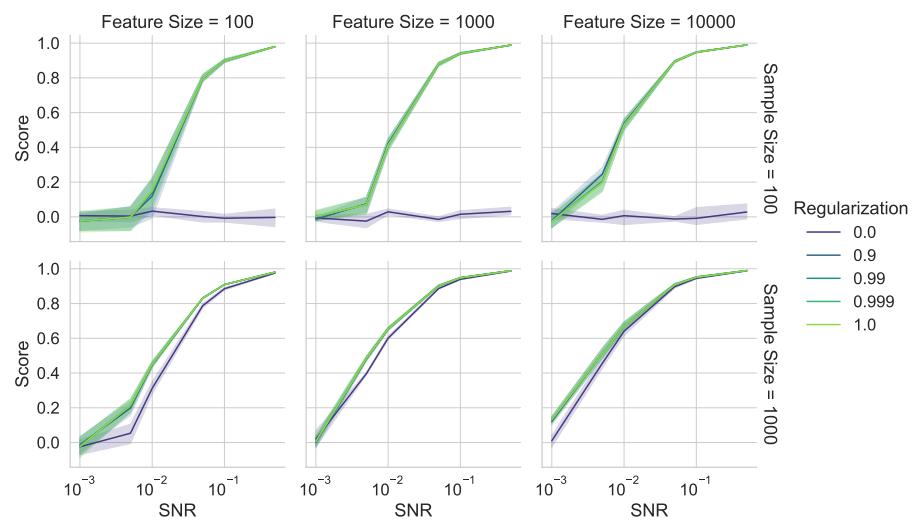


Figure IV.7: Identity Covariance Matrices

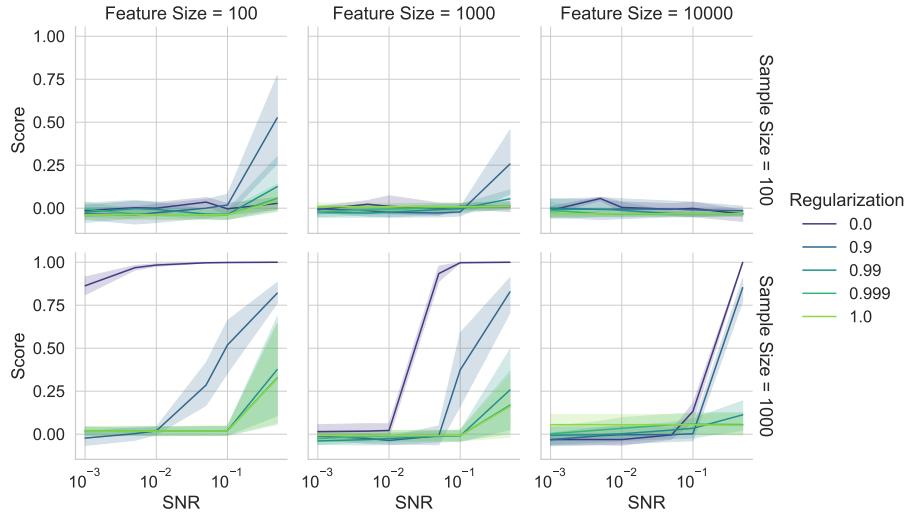
**Figure IV.8:** Random Covariance Matrices

Figure IV.9, we can see that the eigenvalues of the covariance matrices for the ADNI data are much closer to the ideal for identity covariance than for the HCP data.

From Figure IV.10, we can see the block structure of the covariance matrices.

7.2 Loading Similarity

7.3 Comparing Behaviour Weights and Loadings

7.3.1 Human Connectome Project (HCP) Data

7.3.2 Alzheimer's Disease Neuroimaging Initiative (ADNI) Data

8 Discussion

In this section, we discuss the implications of our findings.

Interpreting the Forward and Backward Models of CCA: Consistent with Haufe et al., 2014, we have shown that assumptions imposed on the weights of a model do not in general transfer to the loadings. This is because the weights and loadings are only equivalent when the covariance matrices are identity. We have gone a step further than Haufe et al., 2014 by showing that the identititess of the covariance

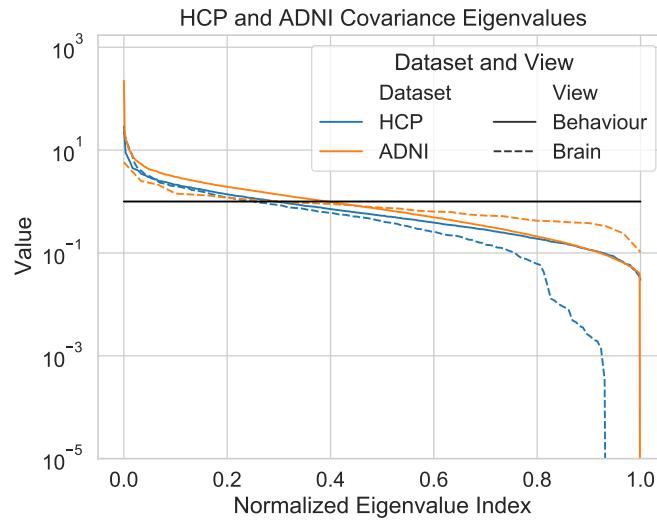


Figure IV.9: Eigenvalues of the covariance matrices for the HCP and ADNI datasets.

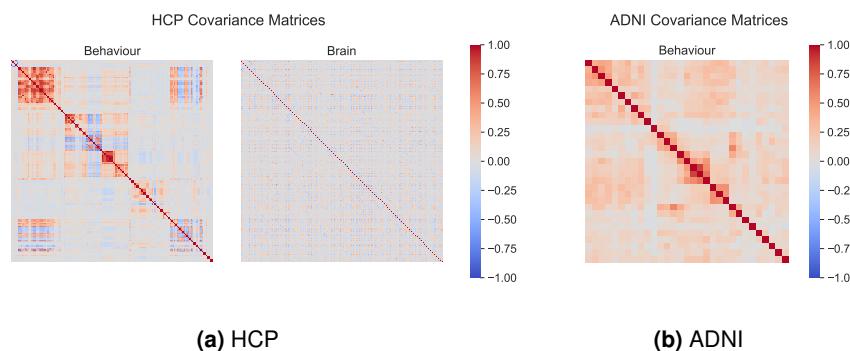


Figure IV.10: Covariance matrices for the HCP and ADNI datasets.

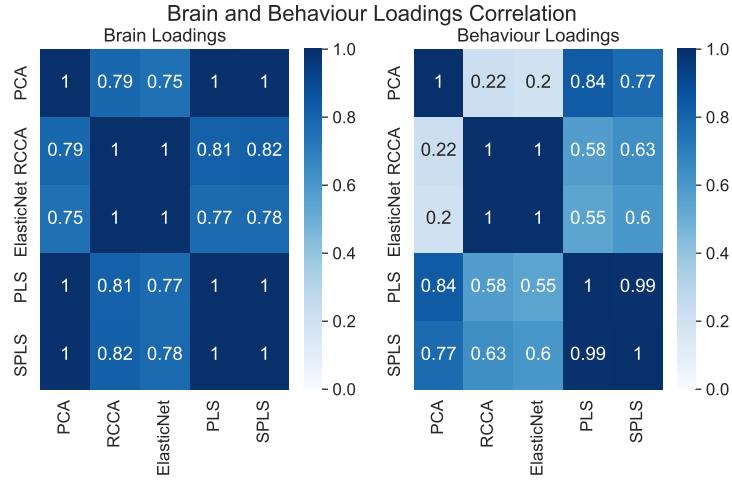
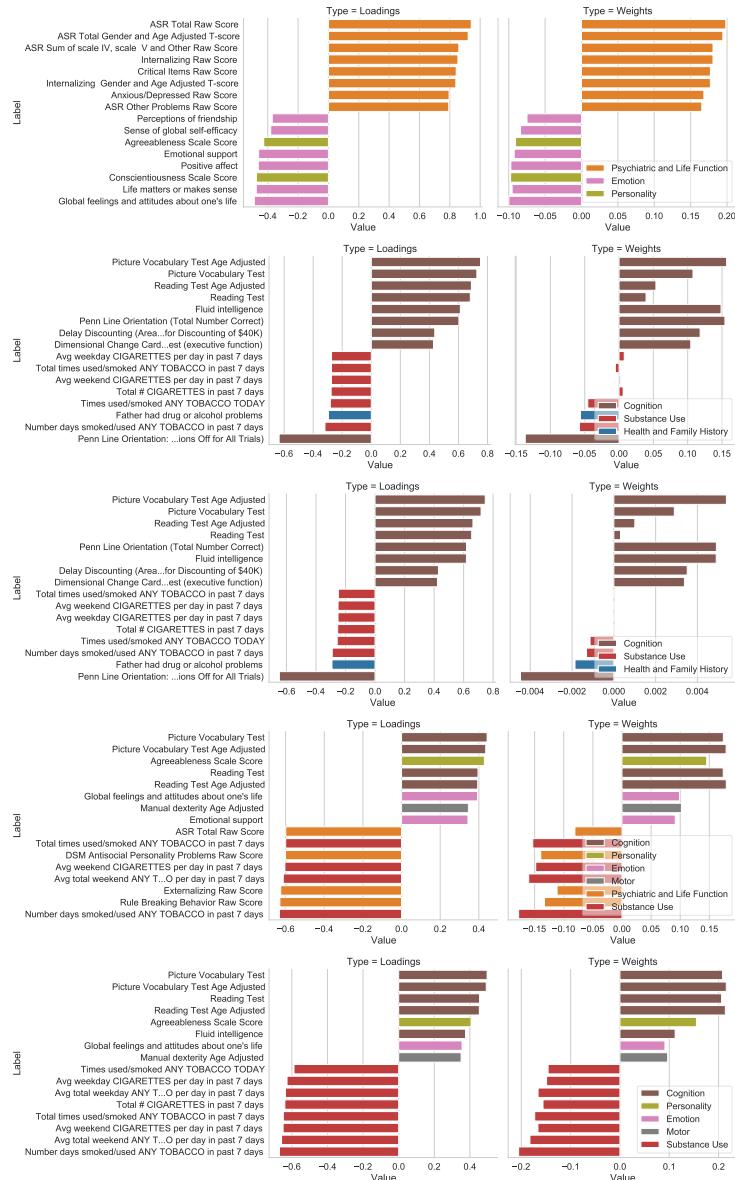


Figure IV.11: HCP: Correlation between the brain and behaviour representations for each model.

matrices is crucial for understanding how imposing sparsity on the weights imposes a prior belief in sparsity on the more biologically interesting loadings.

Identitiness of real covariance matrices: Between the HCP and ADNI datasets, only the ADNI data had eigenvalue spectra that were reasonably close to those of an identity matrix. This suggests that the only dataset and view where we can expect sparsity on the weights to imply sparsity on the loadings is the ADNI data. This is consistent with the results we have seen in the previous section, that sparsity improves performance in the ADNI data but not in the HCP data. Furthermore, the loadings and weights are much more similar to each other in the ADNI data than in the HCP data, supporting the idea that the ADNI weights are themselves somewhat interpretable as estimates of the biologically relevant loadings. Finally, in the well understood Alzheimer's disease data, we know that the identified weights (and loadings) are consistent with the known biology of the disease.

Sample versus Population Setting: The results from the simulated data illustrate the disparities that can arise between population and sample settings. Although PLS, RCCA, and CCA are equivalent under isotropic noise in a population framework, experiments showed that their performance can vary substantially in a sample setting. In particular, this manifested as PLS underperforming RCCA and CCA under isotropic noise *even though this is exactly the scenario where covariance identity*

**Figure IV.12:** Top 8 positive and negative non-imaging loadings for each model

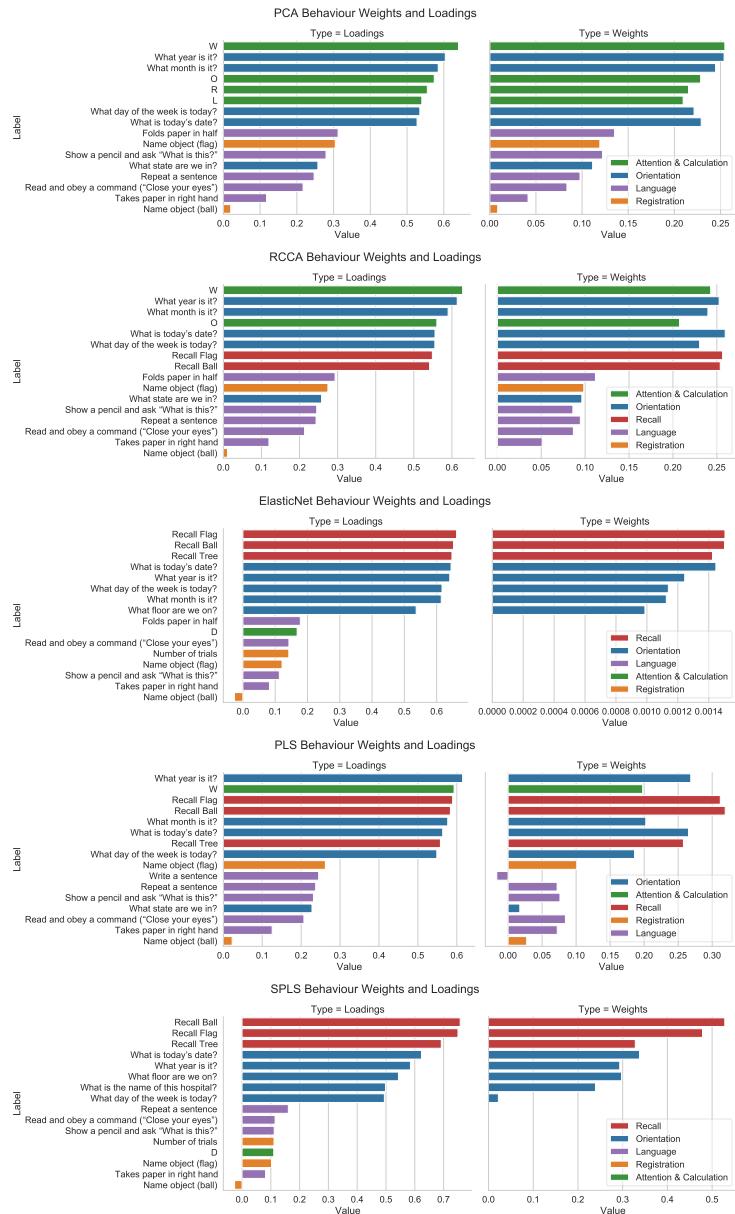


Figure IV.13: Bar plots of the behaviour weights and loadings for each model.

holds and covariance thus equals correlation. This is because the sample covariance matrix is not the same as the population covariance matrix and PLS is sensitive to even small differences in the principal components of the sample covariance matrix. Furthermore, in limited sample sizes, our estimations of the covariance matrices are not accurate, and so the identitiness of the covariance matrices is not guaranteed. This generally resulted in poor estimation of loadings from model weights *even when the weights themselves were estimated almost perfectly.* Therefore, it's crucial for researchers to recognize these nuances and adopt appropriate measures when extrapolating results, especially in brain-behaviour studies where typically only one sample is available and often limited in size.

Can We Construct a Regularization Functional that Imposes Sparsity on the Loadings? Finally, given our observations, a natural question to ask is whether we can construct a regularization functional that imposes sparsity on the loadings (instead of the weights). The answer is yes, but it is not straightforward and in the small sample setting, it is not clear that it is a good idea. The principle would be much the same as the Lasso, but we would need to use the sample covariance matrix to define the norm:

$$P(W) = \|W\|_1 \quad (\text{IV.24})$$

$$P(L) = \|\hat{\Sigma}U\|_1 \quad (\text{IV.25})$$

Which imposes an L1 penalty on the loadings via an L1 penalty on the weights multiplied by the sample covariance matrix. We could in principle apply the soft-thresholding operator to the estimated loadings. However we would need to be careful to ensure that the sample covariance matrix is invertible in order to get back to the weights. This is of course not guaranteed in the small sample setting.

9 Conclusion

In this chapter, we have shown that the loadings are of critical importance for the interpretation of CCA models. We have shown that the loadings are invariant to columnwise transformations of the data matrix, while the weights are not. Through a series of experiments, we have demonstrated that the loadings are more stable than the weights across datasets and samples. We have also shown that regularisation of the weights does not imply regularisation of the loadings. Finally, we have shown

that the identitiness of the covariance matrices is crucial for understanding whether imposing sparsity on the weights imposes a prior belief in sparsity on loadings. We revisited the results of chapter ?? and showed that our interpretations would be different if we used loadings instead of weights.

Chapter V

Efficient Algorithms for the CCA Family: Unconstrained Losses with Unbiased Gradients

It seems easier to train a
bi-directional LSTM with attention
than to compute the SVD of a large
matrix

Chris Ré

I. Gemp, McWilliams, et al., 2021

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Preface

The content of this chapter is based on a series of papers (Chapman, Aguila, and Wells, 2022; Chapman, Wells, and Aguila, 2023) as well as a NeurIPS workshop paper (**chapman2023neurips**). I am grateful to my co-authors Lennie Wells and Ana Lawry Aguila for their contributions to this work. In particular, Lennie’s mathematical expertise improved the theoretical grounding of the idea greatly and Ana’s access to the UK Biobank dataset enabled the application of our methods to a real-world biomedical dataset. In this thesis I include much of the work from these papers, but I exclude many of Lennie’s extensive proofs where I can make no claim to have contributed beyond proofreading.

1 Introduction

There are significant computational challenges when applying these CCA methods to large scale data.

Classical algorithms for linear CCA methods require computing full covariance matrices and so scale quadratically with dimension, becoming intractable for many large-scale datasets of practical interest. There is therefore great interest in approximating solutions for CCA in stochastic or data-streaming settings (Arora et al., 2012).

2 Background: Efficient CCA

2.0.1 Challenges in Solving Generalized Eigenvalue Problems

The GEP is often represented as $Ax = \lambda Bx$, where A and B are matrices. To generalize the dimensions of these matrices, let’s denote them as $m \times m$. This dimension m can vary based on the specific method in use. For instance, in Principal Component Analysis (PCA), represented as PCA, m would be equal to p since A and B are $p \times p$ matrices. In methods like Partial Least Squares (PLS) and

Canonical Correlation Analysis (CCA), represented as PLS and CCA respectively, m would be $p + q$, as A and B in these cases are $(p + q) \times (p + q)$.

Method	A	B	x	Dimensions
PCA	Σ_{11}	I	$u^{(1)}$	$p \times p$
LDA	S_B	S_W	$u^{(1)}$	$p \times p$
CCA	$\begin{pmatrix} \Sigma_{11} & \Sigma_{12} \\ \Sigma_{21} & \Sigma_{22} \end{pmatrix}$	$\begin{pmatrix} \Sigma_{11} & 0 \\ 0 & \Sigma_{22} \end{pmatrix}$	$\begin{pmatrix} u^{(1)} \\ u^{(2)} \end{pmatrix}$	$(p + q) \times (p + q)$
PLS	$\begin{pmatrix} 0 & \Sigma_{12} \\ \Sigma_{21} & 0 \end{pmatrix}$	I	$\begin{pmatrix} u^{(1)} \\ u^{(2)} \end{pmatrix}$	$(p + q) \times (p + q)$

Table 2.1: Definitions and dimensions of A and B for different subspace learning methods.

To solve the GEP, one common technique is to transform it into a standard eigenvalue problem $B^{-\frac{1}{2}}AB^{-\frac{1}{2}}y = \lambda y$, followed by eigendecomposition. However, this approach has computational complexity $O(m^3)$ and may suffer from numerical instability.

2.0.2 PCA-CCA

One way to reduce the complexity of solving GEPs is to use the PCA-CCA method, which first applies PCA to the data and then solves the GEP in the reduced space. An important advantage of using PCA-CCA is computational efficiency, especially for high-dimensional data. The overall complexity of PCA-CCA involves two main steps. First, applying PCA has a complexity of $O(\max(p^3, q^3))$, dominated by the larger of the two matrices. Second, solving the generalized eigenvalue problem in the reduced space with K components in each view leads to a complexity of $O((2K)^3)$. Thus, the overall complexity of PCA-CCA is $O(\max(p^3, q^3) + (2K)^3)$, which is significantly lower than the complexity of solving the GEP directly. Since CCA, ridge CCA, and PLS can all be solved in the principal component space, PCA-CCA can be used to compute solutions efficiently *even if we keep all the principal components*. Most obviously, this is the case when the number of samples n is smaller than either of the number of features p or q , i.e. $n < p$ or $n < q$. In this case the maximum number of principal components is $K = n$, and the complexity of PCA-CCA is thus $O(n^3)$, which is significantly lower than the complexity of solving the GEP directly. This approach has been employed to great effect in neuroimaging but surprisingly is not used even in the scikit-learn implementation of CCA (Pedregosa et al., 2011). Nonetheless, for the large sample sizes (desirable for machine learning

frameworks as well as statistical power), the complexity of even PCA-CCA can render the problems nearly intractable.

Kernel CCA (KCCA) also offers computational efficiency for high-dimensional data ($p > n$) as its complexity scales with the number of samples n , not the number of features p . It casts the CCA optimisation as a dual problem:

$$\alpha_{\text{opt}} = \underset{\alpha_{\text{opt}}}{\operatorname{argmax}} \{ \alpha^{(1)} K^{(1)T} K^{(2)} \alpha^{(2)} \} \quad (\text{V.1})$$

subject to:

$$\alpha^{(1)} K^{(1)T} K^{(1)} \alpha^{(1)} = 1$$

$$\alpha^{(2)} K^{(2)T} K^{(2)} \alpha^{(2)} = 1$$

Where $\alpha^{(1)} =$

The kernel function in KCCA can be computed iteratively on pairwise comparisons of samples, allowing for memory efficiency by not requiring the entire dataset to be loaded into RAM. This iterative approach uses slow hard drive memory access instead of RAM, making KCCA RAM memory-efficient but slower. However, a significant drawback of KCCA is the need for access to all training data at test time, which raises concerns about efficiency and scalability.

2.1 Stochastic PLS and CCA

To the best of our knowledge, the state-of-the-art in Stochastic PLS and CCA are the subspace Generalized Hebbian Algorithm (**SGHA**) of Z. Chen et al., 2019 and γ -**EigenGame** from I. M. Gemp et al., 2020; I. Gemp, McWilliams, et al., 2021. Specifically, SGHA utilizes a Lagrange multiplier heuristic along with saddle-point analysis, albeit with limited convergence guarantees. EigenGame focuses on top-k subspace learning but introduces an adaptive whitening matrix in the stochastic setting with an additional hyperparameter. Both methods set the benchmarks we aim to compare against in the subsequent experimental section. Like our method, both can tackle other symmetric Generalized Eigenvalue Problems in principle.

3 Novel Objectives and Algorithms

3.1 Unconstrained objective for GEPs

First, we present proposition 3.1, a formulation of the top- K subspace of GEP problems, which follows by applying the Eckhart–Young–Minsky inequality (Stewart and J.-G. Sun, 1990) to the eigen-decomposition of $B^{-1/2}AB^{-1/2}$. However, making this rigorous requires some technical care which we defer to the proof in supplement ??.

Proposition 3.1 (Eckhart–Young inspired objective for GEPs). *The top- K subspace of the GEP (A, B) can be characterized by minimizing the following objective over $U \in \mathbb{R}^{D \times K}$:*

$$\mathcal{L}_{EY-GEP}(U) := \text{trace}(-2U^T AU + (U^T BU)(U^T BU)) \quad (\text{V.2})$$

Moreover, the minimum value is precisely $-\sum_{k=1}^K \lambda_k^2$, where (λ_k) are the generalized eigenvalues.

This objective also has appealing geometrical properties. It is closely related to a wide class of unconstrained objectives for PCA and matrix completion which have no spurious local optima (Ge, Jin, and Zheng, 2017), i.e. all local optima are in fact global optima. This implies that certain local search algorithms, such as stochastic gradient descent, should indeed converge to a global optimum.

Proposition 3.2. [No spurious local minima] *The objective \mathcal{L}_{EY-GEP} has no spurious local minima. That is, any matrix \bar{U} that is a local minimum of \mathcal{L}_{EY-GEP} must in fact be a global minimum.*

It is also possible to make this argument quantitative by proving a version of the strict saddle property from Ge, Jin, and Zheng, 2017; Ge, Huang, et al., 2015; we state an informal version here and give full details in ??.

Corollary 3.1 (Informal: Polynomial-time Optimization). *Under certain conditions on the eigenvalues and generalized eigenvalues of (A, B) , one can make quantitative the claim that: any $U_K \in \mathbb{R}^{D \times K}$ is either close to a global optimum, has a large gradient $\nabla \mathcal{L}_{EY-GEP}$, or has Hessian $\nabla^2 \mathcal{L}_{EY-GEP}$ with a large negative eigenvalue.*

Therefore, for appropriate step-size sequences, certain local search algorithms, such as sufficiently noisy SGD, will converge in polynomial time with high probability.

3.2 Corresponding Objectives for the CCA family

For the case of linear CCA we have $U^T A U = \sum_{i \neq j} \text{Cov}(Z^{(i)}, Z^{(j)})$, $U^T B U = \sum_i \text{Var}(Z^{(i)})$. To help us extend this to the general case of nonlinear transformations, Equation (II.1), we define the analogous matrices of total between-view covariance and total within-view variance

$$C(\theta) = \sum_{i \neq j} \text{Cov}(Z^{(i)}, Z^{(j)}), \quad V(\theta) = \sum_i \text{Var}(Z^{(i)}) \quad (\text{V.3})$$

In the case of linear transformations, ??, it makes sense to add a ridge penalty so we can define

$$V_\alpha(\theta) = \sum_i \alpha_i U^{(i)T} U^{(i)} + (1 - \alpha_i) \text{Var}(Z^{(i)}) \quad (\text{V.4})$$

This immediately leads to following unconstrained objective for the CCA-family of problems.

Definition 3.1 (Family of EY Objectives). *Learn representations $Z^{(i)} = f^{(i)}(X^{(i)}; \theta^{(i)})$ minimizing*

$$\mathcal{L}_{\text{EY}}(\theta) = -2 \text{trace } C(\theta) + \|V_\alpha(\theta)\|_F^2 \quad (\text{V.5})$$

Unbiased estimates: since empirical covariance matrices are unbiased, we can construct unbiased estimates to C, V from a batch of transformed variables \mathbf{Z} .

$$\hat{C}(\theta)[\mathbf{Z}] = \sum_{i \neq j} \widehat{\text{Cov}}(\mathbf{Z}^{(i)}, \mathbf{Z}^{(j)}), \quad \hat{V}(\theta)[\mathbf{Z}] = \sum_i \widehat{\text{Var}}(\mathbf{Z}^{(i)}) \quad (\text{V.6})$$

In the linear case we can construct $\hat{V}_\alpha(\theta)[\mathbf{Z}]$ analogously by plugging sample covariances into Equation (V.4). Then if \mathbf{Z}, \mathbf{Z}' are two independent batches of transformed variables, the batch loss

$$\hat{\mathcal{L}}_{\text{EY}}[\mathbf{Z}, \mathbf{Z}'] := -2 \text{trace } \hat{C}[\mathbf{Z}] + \langle \hat{V}_\alpha[\mathbf{Z}], \hat{V}_\alpha[\mathbf{Z}'] \rangle_F \quad (\text{V.7})$$

gives an unbiased estimate of $\mathcal{L}_{\text{EY}}(\theta)$. This loss is a differentiable function of \mathbf{Z}, \mathbf{Z}' and so also of θ .

Simple algorithms: We first define a very general algorithm using these estimates in Algorithm 1. In the next section we apply this algorithm to multi-view stochastic CCA and PLS.

Algorithm 1: GEP-EY: General algorithm for learning correlated representations

Input: data stream of mini-batches $(\mathbf{X}(b))_{b=1}^{\infty}$ where each consists of M samples from the original dataset. Learning rate $(\eta_t)_t$. Number of time steps T . Class of functions $f(\cdot; \theta)$ whose outputs are differentiable with respect to θ .

Initialize: $\hat{\theta}$ with suitably random entries

for $t = 1$ **to** T **do**

- Obtain two independent mini-batches $\mathbf{X}(b), \mathbf{X}(b')$ by sampling b, b' independently
- Compute batches of transformed variables
- $\mathbf{Z}(b) = f(\mathbf{X}(b); \theta), \mathbf{Z}(b') = f(\mathbf{X}(b'); \theta)$
- Estimate loss $\hat{\mathcal{L}}_{\text{EY}}(\theta)$ using Equation (V.7)
- Obtain gradients by back-propagation and step with your favourite optimizer.

end for

3.3 Applications to (multi-view) stochastic CCA and PLS

Lemma 3.1 (Objective recovers GEP formulation of linear (multi-view) CCA). *When the $f^{(i)}$ are linear, as in ??, the population loss from Equation (V.5) recovers MCCA as defined in ??.*

Proof. By construction, for linear MCCA we have $C = U^T A U$, $V_\alpha = U^T B_\alpha U$, where (A, B_α) define the GEP for MCCA introduced in Equation (II.29). So $\mathcal{L}_{\text{EY}}(U) = \mathcal{L}_{\text{EY-GEP}}(U)$ and by Proposition 3.1 the optimal set of weights define a top- K subspace of the GEP, and so is a MCCA solution. \square

Moreover, by following through the chain of back-propagation, we obtain gradient estimates in $\mathcal{O}(MKD)$ time. Indeed, we can obtain gradients for the transformed variables in $\mathcal{O}(MK^2)$ time so the dominant cost is then updating U ; we flesh this out with full details in ??.

4 Experiments

4.1 Stochastic CCA

First, we compare our proposed method, CCA-EY, to the baselines of γ -EigenGame and SGHA. Our experimental setup is almost identical to that of Z. Meng, Chakraborty, and Singh, 2021; I. Gemp, C. Chen, and McWilliams, 2022; unlike I. Gemp, C. Chen, and McWilliams, 2022 we do not simplify the problem by first performing PCA on

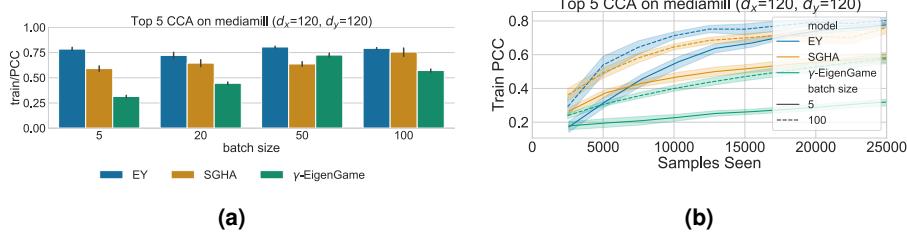


Figure V.1: Stochastic CCA on MediaMill using the Proportion of Correlation Captured (PCC) metric: (a) Across varying mini-batch sizes, trained for a single epoch, and (b) Training progress over a single epoch for mini-batch sizes 5, 100. Shaded regions signify \pm one standard deviation around the mean of 5 runs.

the data before applying the CCA methods, which explains the decrease in performance of γ -EigenGame compared to their original work. All models are trained for a single epoch with varying mini-batch sizes ranging from 5 to 100. We use Proportion of Correlation Captured (PCC) as our evaluation metric, defined as $PCC = (\sum_{i=k}^K \rho_k) / (\sum_{k=1}^K \rho_k^*)$ where ρ_k are the full batch correlations of the learnt representations, and ρ_k^* are the canonical correlations computed numerically from the full batch covariance matrices.

Parameters: For each method, we searched over a hyperparameter grid using Biewald (2020).

Parameter	Values
minibatch size	5,20,50,100
components	5
epochs	1
seed	1, 2, 3, 4, 5
lr	0.01, 0.001, 0.0001
γ^1	0.01, 0.1, 1, 10

Observations: Figure V.1 compares the algorithms on the MediaMill dataset. Figure V.1a shows that CCA-EY consistently outperforms both γ -EigenGame and SGHA in terms of PCC across all evaluated mini-batch sizes. Figure V.1b examines the learning curves for batch sizes 5 and 100 in more detail; CCA-EY appears to learn more slowly than SGHA at the start of the epoch, but clearly outperforms SGHA as the number of samples seen increases. γ -EigenGame significantly underperforms SGHA and CCA-EY, particularly for small batch sizes.

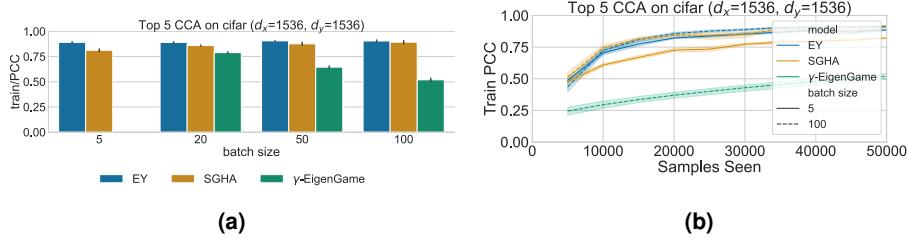


Figure V.2: Stochastic CCA on CIFAR using the Proportion of Correlation Captured (PCC) metric: (a) Across varying mini-batch sizes, trained for a single epoch, and (b) Training progress over a single epoch for mini-batch sizes 5, 100. Shaded regions signify \pm one standard deviation around the mean of 5 runs.

4.2 Stochastic PLS UK Biobank

Next, we demonstrate the scalability of our methods to extremely high-dimensional data by applying stochastic PLS to imaging genetics data from the UK Biobank (Sudlow et al., 2015). PLS is typically used for imaging-genetics studies owing to the extremely high dimensionality of genetics data requiring lots of regularisation. PLS can reveal novel phenotypes of interest and uncover genetic mechanisms of disease and brain morphometry. Previous imaging genetics analyses using full-batch PLS were limited to much smaller datasets (Lorenzi2018; Taquet et al., 2021; Le Floch et al., 2012). The only other analysis on the UK Biobank at comparable scale partitions the data into clusters and bootstrapping local PLS solutions on these clusters (Lorenzi et al., 2017; Altmann et al., 2023). We ran PLS-EY with mini-batch size 500 on brain imaging (82 regional volumes) and genetics (582,565 variants) data for 33,333 subjects. See supplement (Section ??) for data pre-processing details. To our knowledge, this is the largest-scale PLS analysis of biomedical data to-date.

Further details: The UK BioBank data consisted of real-valued continuous brain volumes and ordinal, integer genetic variants. We used pre-processed (using FreeSurfer (Fischl, 2012)) grey-matter volumes for 66 cortical (Desikan-Killiany atlas) and 16 subcortical brain regions and 582,565 autosomal genetic variants. The affects of age, age squared, intracranial volume, sex, and the first 20 genetic principal components for population structure were removed from the brain features using linear regression to account for any confounding effects. Each brain ROI was normalized by removing the mean and dividing the standard deviation. We processed the genetics data using PLINK (Purcell et al., 2007) keeping genetic

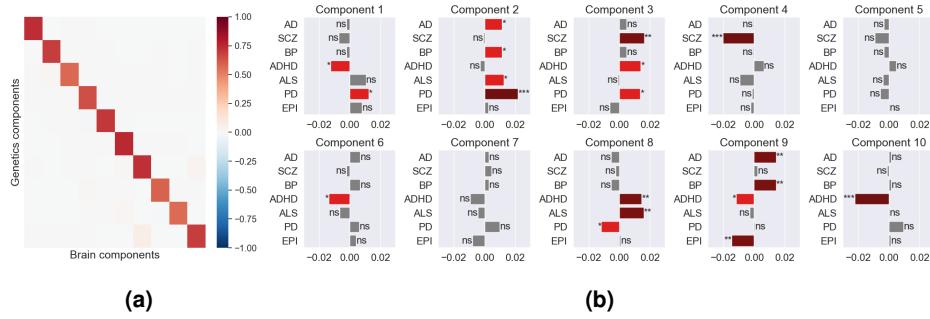


Figure V.3: (a) Correlations between PLS components for UK Biobank. (b) Correlations between PLS brain components and genetic risk scores.

AD=Alzheimer's disease, SCZ=Schizophrenia, BP=Bipolar, ADHD=Attention deficit hyperactivity disorder, ALS=Amyotrophic lateral sclerosis, PD=Parkinson's disease, EPI=Epilepsy.

ns : $0.05 < p \leq 1$, * : $0.01 < p \leq 0.05$, ** : $0.001 < p \leq 0.01$, *** : $0.0001 < p \leq 0.001$.

variants with a minor allele frequency of at least 1% and a maximum missingness rate of 2%. We used mean imputation to fill in missing values and centered each variant.

To generate measures of genetic disease risk, we calculated polygenic risk scores using PRSice (Euesden, Lewis, and O'Reilly, 2014). We calculated scores, with a p-value threshold of 0.05, using GWAS summary statistics for the following diseases; Alzheimer's (Lambert et al., 2013), Schizophrenia (Trubetskoy et al., 2022), Bipolar (Mullins et al., 2021), ADHD (Demontis et al., 2023), ALS (Rheenen et al., 2021), Parkinson's (Nalls et al., 2019), and Epilepsy (International League Against Epilepsy Consortium on Complex Epilepsies, 2018), using the referenced GWAS studies.

The GEP-EY PLS analysis was trained for 100 epochs using a learning rate of 0.0001 with a minibatch size of 500.

Observations: We see strong validation correlation between all 10 corresponding pairs of vectors in the PLS subspace and weak cross correlation, indicating that our model learnt a coherent and orthogonal subspace of covariation (Figure V.3a), a remarkable feat for such high-dimensional data. We found that the PLS brain subspace was associated with genetic risk measures for several disorders (Figure V.3b), suggesting that the PLS subspace encodes relevant information for genetic disease risk, a significant finding for biomedical research.

5 Conclusion

In this chapter, we introduced a class of efficient, scalable algorithms for Canonical Correlation Analysis, and Generalized Eigenvalue Problems more broadly, rooted in a novel unconstrained loss function. These algorithms are computationally lightweight, making them uniquely suited for large-scale problems where traditional methods struggle.

Chapter VI

Deep CCA and CCA for Self-Supervised Learning

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Preface

This chapter is based on work presented in Chapman and Wells (2023) and Chapman, Wells, and Aguila (2023).

1 Introduction

Deep CCA (Andrew et al., 2013) secured a runner-up position for the test-of-time award at ICML 2023 (ICML, 2023). However, its direct application has been limited in large datasets due to biased gradients in the stochastic minibatch setting. There have since been proposals to scale-up Deep CCA in the stochastic case with adaptive whitening W. Wang, Arora, Livescu, and Srebro, 2015 and regularization Chang, Xiang, and T. M. Hospedales, 2018, but these techniques are highly sensitive to hyperparameter tuning.

Self-Supervised Learning (SSL) methods have reached the state of the art in tasks such as image classification (Balestrieri, Ibrahim, et al., 2023). These methods can learn robust data representations without the need for explicit labels or supervision. Recently, a family of SSL methods that are closely aligned with Canonical Correlation Analysis (CCA) has garnered interest. This family notably includes Barlow Twins (Zbontar et al., 2021), VICReg (Bardes, Ponce, and LeCun, 2021), and W-MSE (**ermolov2021whitening**) and they aim to transform a pair of data views into similar representations, similar to the objective of CCA. Similarly, some generative approaches to **SSLsansone2022gedi** bear a striking resemblance to Probabilistic CCABach and Jordan, 2005. These connections have started to be explored in Balestrieri and LeCun, 2022.

In this chapter, we propose a novel formulation of Deep CCA that is unbiased in the stochastic setting and scales to large datasets. We also propose a novel SSL method, SSL-EY, that is competitive with existing methods on CIFAR-10 and CIFAR-100. We highlight the connections between our work and existing SSL methods, and show that our method is more robust to hyperparameter tuning.

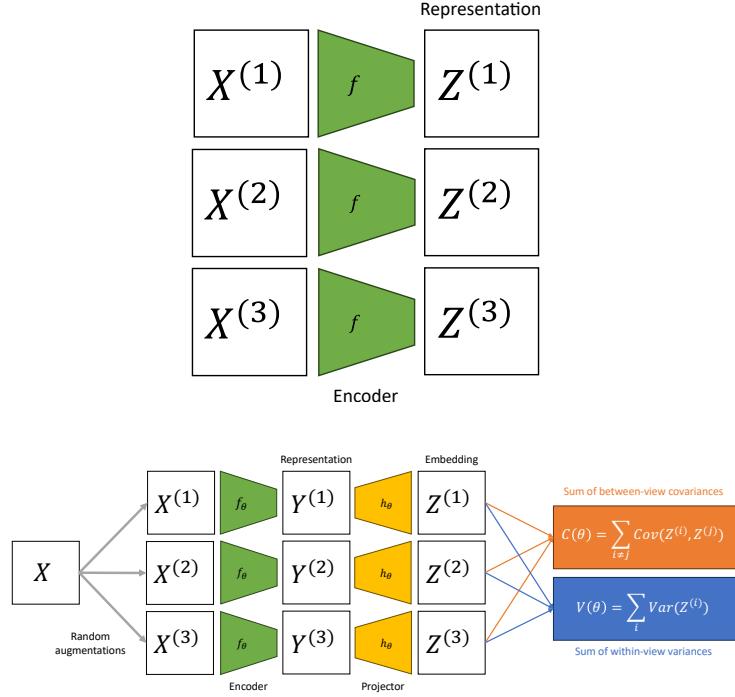
2 Background

2.1 DCCA and Deep Multiview CCA

The goal of DCCA and DMCCA can be defined using our MCCA notation as maximizing

$$\|\text{MCCA}_K(Z^{(1)}, \dots Z^{(I)})\|_2 \quad (\text{VI.1})$$

over parameters θ of neural networks defining the representations $Z^{(i)} = f^{(i)}(X^{(i)}; \theta^{(i)})$ for $i \in [I]$.



The deep canonical correlation analysis (DCCA) landscape comprises three principal approaches with inherent limitations. The first, known as the full-batch approach, uses analytic gradient derivations based on the full sample covariance matrix (Andrew et al., 2013). The second involves applying the full batch objective to large mini-batches, an approach referred to as **DCCA-STOL** (W. Wang, Arora, Livescu, and Bilmes, 2015). However, this approach gives biased gradients and therefore requires batch sizes much larger than the representation size in practice. This is the approach taken by both **DMCCA** (Somandepalli et al., 2019) and **DGCCA** (Benton et al., 2017). The final set of approaches use an adaptive whitening matrix (W. Wang, Arora, Livescu, and Srebro, 2015; Chang, Xiang, and T. M. Hospedales, 2018) to mitigate the bias of the Deep CCA objective. However, the authors of **DCCA-NOI** highlight that the associated time constant complicates analysis and requires extensive tuning. These limitations make existing DCCA methods less practical and resource-efficient.

2.2 Self-Supervised Learning

Barlow Twins and **VICReg** have come to be known as part of the canonical correlation family of algorithms (Balestrieri, Ibrahim, et al., 2023). Barlow Twins employs a redundancy reduction objective to make the representations of two augmented views both similar and decorrelated (Zbontar et al., 2021). Similarly, VICReg uses variance-invariance-covariance regularization, which draws upon canonical correlation principles, to achieve robust performance in diverse tasks (Bardes, Ponce, and LeCun, 2021). These methods serve as vital baselines for our experiments, owing to their foundational use of canonical correlation ideas.

3 Methods: Novel Objectives and Algorithms

3.1 Applications to (multi-view) stochastic CCA and PLS, and Deep CCA

Lemma 3.1 (Objective recovers GEP formulation of linear (multi-view) CCA). *When the $f^{(i)}$ are linear, as in ??, the population loss from Equation (V.5) recovers MCCA as defined in ??.*

Proof. By construction, for linear MCCA we have $C = U^T A U$, $V_\alpha = U^T B_\alpha U$, where (A, B_α) define the GEP for MCCA introduced in Equation (II.29). So $\mathcal{L}_{EY}(U) = \mathcal{L}_{EY-GEP}(U)$ and by Proposition 3.1 the optimal set of weights define a top- K subspace of the GEP, and so is a MCCA solution. \square

Moreover, by following through the chain of back-propagation, we obtain gradient estimates in $\mathcal{O}(MKD)$ time. Indeed, we can obtain gradients for the transformed variables in $\mathcal{O}(MK^2)$ time so the dominant cost is then updating U ; we flesh this out with full details in ??.

Lemma 3.2. [Objective recovers Deep Multi-view CCA] *Assume that there is a final linear layer in each neural network $f^{(i)}$. Then at any local optimum, $\hat{\theta}$, of the population problem, we have*

$$\mathcal{L}_{EY}(\hat{\theta}) = -\|\text{MCCA}_K(\hat{Z})\|_2^2$$

where $\hat{Z} = f_{\hat{\theta}}(X)$. Therefore, $\hat{\theta}$ is also a local optimum of objectives from Andrew et al., 2013; Somandepalli et al., 2019 as defined in Equation (VI.1).

Proof sketch: see ?? for full details. Consider treating the penultimate-layer representations as fixed, and optimising over the weights in the final layer. This is precisely equivalent to optimising the Eckhart-Young loss for linear CCA where the input variables are the penultimate-layer representations. So by Proposition 3.2, a local optimum is also a global optimum, and by Proposition 3.1 the optimal value is the negative sum of squared generalised eigenvalues. \square

3.2 Application to SSL

We can directly apply Algorithm 1 to SSL. If we wish to have the same neural network transforming each view, we can simply tie the weights $\theta^{(1)} = \theta^{(2)}$. When the paired data are generated from applying independent, identically distributed (i.i.d.) augmentations to the same original datum, it is intuitive that tying the weights is a sensible procedure, and perhaps acts as a regulariser. We make certain notions of this intuition precise for CCA and Deep CCA in ??.

To provide context for this proposal, we also explored in detail how VICReg and Barlow twins are related to CCA. For now we focus on VICReg, whose loss can be written as

$$\mathcal{L}_{\text{VR}}(Z^{(1)}, Z^{(2)}) = \gamma \mathbb{E} \|Z^{(1)} - Z^{(2)}\|^2 + \sum_{i \in \{1, 2\}} \left[\alpha \sum_{k=1}^K \left(1 - \sqrt{\text{Var}(Z_i^{(k)})} \right)_+ + \beta \sum_{\substack{k, l=1 \\ k \neq l}}^K \text{Cov}(Z_k^{(i)}, Z_l^{(i)})^2 \right]$$

where $\alpha, \beta, \gamma > 0$ are tuning parameters and, as in the framework of Section 2, the $Z^{(1)}, Z^{(2)}$ are K -dimensional representations, parameterised by neural networks in Equation (II.1). Our main conclusions regarding optima of the population loss are:

- Consider the linear setting with untied weights. Then global optimisers of the VICReg loss define CCA subspaces, but may not be of full rank.
- Consider the linear setting with tied weights and additionally assume that the data are generated by i.i.d. augmentations. Then the same conclusion holds.
- In either of these settings, the optimal VICReg loss is a component-wise decreasing function of $\text{CCA}_K(X^{(1)}, X^{(2)})$ the vector of population canonical correlations.
- VICReg can therefore be interpreted as a formulation of Deep CCA, but one that will not in general recover full rank representations.

We give full mathematical details and further discussion in ?? . The analysis for Barlow twins is more difficult, but we present a combination of mathematical and

empirical arguments which suggest all the same conclusions hold, again see ??.

4 Experiments

4.1 Deep CCA

Second, we compare DCCA-EY against the DCCA methods described in ?? . The experimental setup is identical to that of W. Wang, Arora, Livescu, and Srebro, 2015. We learn $K = 50$ dimensional representations, using mini-batch sizes ranging from 20 to 100 and train for 50 epochs. Because there is no longer a ground truth we have to use Total Correlation Captured (TCC), given by $TCC = \sum_{i=k}^K \rho_k$ where ρ_k are now the empirical correlations between the representations on a validation set.

Further details: As in W. Wang, Arora, Livescu, and Srebro (2015), we used multilayer perceptrons with two hidden layers with size 800 and an output layer of 50 with ReLU activations. We train for 20 epochs.

Parameters: For each method, we searched over a hyperparameter grid using Biewald (2020).

Parameter	Values
minibatch size	100, 50, 20
lr	1e-3, 1e-4, 1e-5
ρ^1	0.6, 0.8, 0.9
epochs	50

Observations: Figure VI.1 compares the methods on the splitMNIST dataset. DCCA-STOL captures significantly less correlation than the other methods, and breaks down when the mini-batch size is less than the dimension $K = 50$ due to low rank empirical covariances. DCCA-NOI performs similarly to DCCA-EY but requires careful tuning of an additional hyperparameter, and shows significantly slower speed to convergence (Figure VI.1b).

Figure VI.2 compares the methods on the XRMB dataset. DCCA-STOL captures significantly less correlation than the other methods, and breaks down when the mini-batch size is less than the dimension $K = 50$ due to low rank empirical covariances. DCCA-NOI performs similarly to DCCA-EY but requires careful tuning of an additional hyperparameter, and shows significantly slower speed to convergence (Figure VI.1b).

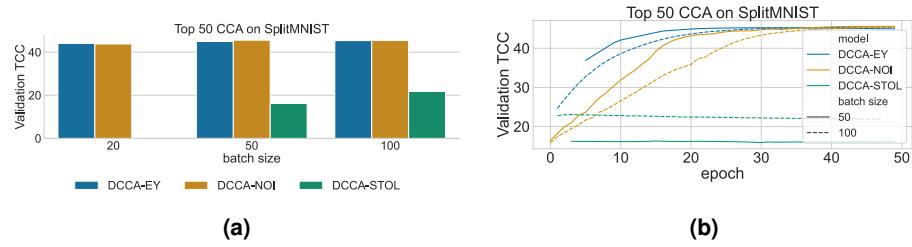


Figure VI.1: Deep CCA on SplitMNIST using the Validation TCC metric: (a) after training each model for 50 epochs with varying batch sizes; (b) learning progress over 50 epochs.

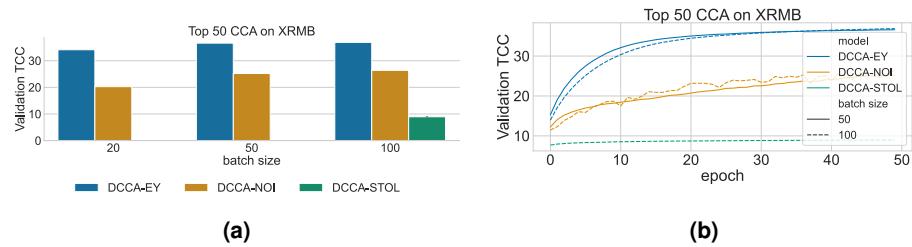


Figure VI.2: Deep CCA on XRMB using the Validation TCC metric: (a) after training each model for 50 epochs with varying batch sizes; (b) learning progress over 50 epochs.

4.2 Deep Multiview CCA: Robustness Across Different Batch Sizes

Third, we compare DCCA-EY to the existing DMCCA and DGCCA methods on the mfeat dataset; this contains 2,000 handwritten numeral patterns across six distinct feature sets, including Fourier coefficients, profile correlations, Karhunen-Love coefficients, pixel averages in 2×3 windows, Zernike moments, and morphological features. We again learn $K = 50$ dimensional representations, but now train for 100 epochs. We use a multiview extension of the TCC metric, which averages correlation across views; we call this Total Multiview Correlation Captured (TMCC), defined as $\text{TMCC} = \sum_{k=1}^K \frac{1}{I(I-1)} \sum_{i,j \leq I, i \neq j} \text{corr}(Z_k^{(i)}, Z_k^{(j)})$, using the notation of Section 2.

Parameters: For each method, we searched over a hyperparameter grid using Biewald (2020).

Parameter	Values
minibatch size	5, 10, 20, 50, 100, 200
components	50
epochs	100
lr	0.01, 0.001, 0.0001, 0.00001

Observations: Figure VI.3a shows that DCCA-EY consistently outperforms both DGCCA and DMCCA across various mini-batch sizes in capturing validation TMCC. Just like DCCA-NOI, DMCCA breaks down when the batch size is smaller than K . This is due to singular empirical covariances; DGCCA does not break down, but does significantly underperform with smaller batch sizes. This limits their practical applicability to large-scale data. Figure VI.3b shows learning curves for batch sizes 50 and 100. DMCCA and DGCCA both quickly learn significant correlations but then plateau out; our method consistently improves, and significantly outperforms them by the end of training.

4.3 Self-Supervised Learning with SSL-EY

Finally, we benchmark our self-supervised learning algorithm, SSL-EY, with Barlow Twins and VICReg on CIFAR-10 and CIFAR-100. Each dataset contains 60,000 labelled images, but these are over 10 classes for CIFAR-10 and 100 classes for CIFAR-100.

We follow a standard experimental design (Tong et al., 2023). Indeed, we use the sololearn library (Da Costa et al., 2022), which offers optimized setups particularly tailored for VICReg and Barlow Twins. All methods utilize a ResNet-18 encoder

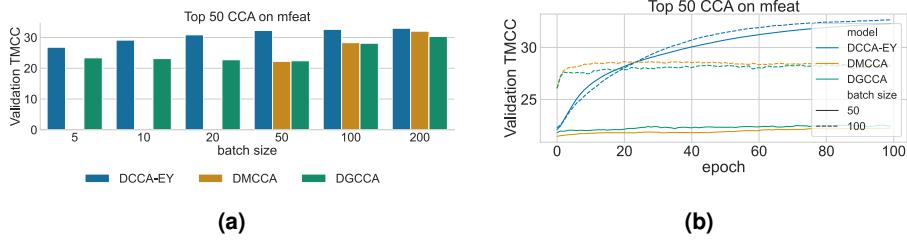


Figure VI.3: Deep Multi-view CCA on mfeat using the Validation TMCC metric: (a) after training each model for 100 epochs with varying batch sizes; (b) learning progress over 100 epochs.

Method	CIFAR-10 Top-1	CIFAR-10 Top-5	CIFAR-100 Top-1	CIFAR-100 Top-5
Barlow Twins	92.1	99.73	71.38	92.32
VICReg	91.68	99.66	68.56	90.76
SSL-EY	91.43	99.75	67.52	90.17

Table 4.1: Performance comparison of SSL methods on CIFAR-10 and CIFAR-100.

coupled with a bi-layer projector network. Training spans 1,000 epochs with batches of 256 images. For SSL-EY, we use the hyperparameters optimized for Barlow Twins, aiming not to outperform but to showcase the robustness of our method. We predict labels via a linear probe on the learnt representations and evaluate performance with Top-1 and Top-5 accuracies on the validation set. For more details, refer to the supplementary material ??.

Observations: Table 4.2 shows that SSL-EY is competitive with Barlow Twins and VICReg. This is remarkable because we used out-of-the-box hyperparameters for SSL-EY but used hyperparameters for Barlow Twins and VICReg that had been heavily optimized in previous studies.

Model Convergence: The Learning curves in Figure VI.4 indicate that the performance variation at 1,000 epochs in table 4.2 mainly results from optimization noise and speed of convergence is similar.

Smaller Projector or None at All: One key motivation for projectors is to prevent excessive collapse of meaningful information. Because SSL-EY learns does not suffer from collapse, we had a prior that it may be more robust to projector size, and perhaps even to removing the projector altogether. For this reason, in another set of experiments, we explored varying the projector’s output dimensions from 2048 to 64 and removing the projector completely while holding the encoder output size constant. Figure VI.5a demonstrates that SSL-EY maintains good performance

even with a smaller projector, making the representations more efficient than Barlow Twins and VICReg (they contain the same amount of useful information for the classification task in much fewer dimensions). While Figure VI.5a shows the strong performance of Barlow Twins and VICReg at larger projector sizes for this task, we would argue that our objective is more robust to this design choice, potentially offering a more reliable choice for practitioners employing SSL to unfamiliar datasets. At the bottom of Table 4.2, we further highlight the efficiency of SSL-EY by showing that our model performs similarly when we have no projector (just using the a 2048 dimensional representation), suggesting that SSL-EY is less reliant on this architecture². In contrast, we show in appendix ?? that Barlow Twins and VICReg's performance drops substantially without the use of a projector.

\mathcal{L}_{EY} is an informative metric: Figure VI.5b offers two key insights. First, it shows that the EY loss, which provides an unbiased estimate of the canonical correlations of the embeddings, is closely related to classification accuracy. This suggests that maximizing canonical correlation is a promising pretext task for self-supervised learning. Second, the figure reveals that even a reduced-dimensionality projector output (64 dimensions) has not reached its full capacity by 1,000 epochs. Specifically, the sum of squared canonical correlations reaches 46, out of a maximum possible value of 64. This indicates that there is still room for further optimization, implying that SSL-EY's representations have not yet saturated their capacity for capturing meaningful information. Lastly, the evolution of the correlation, as measured by \mathcal{L}_{EY} , offers a novel way of monitoring model training even without the need for a separate validation task like classification, and could potentially eliminate the requirement for a validation set altogether. This is a particularly interesting direction given recent work on the stepwise eigenvalue behavior of the representations in SSL models [simon2023stepwise](#).

Method	CIFAR-10 Top-1	CIFAR-10 Top-5	CIFAR-100 Top-1	CIFAR-100 Top-5
Barlow Twins	92.1	99.73	71.38	92.32
VICReg	91.68	99.66	68.56	90.76
SSL-EY	91.43	99.75	67.52	90.17
SSL-EY No Proj.	90.98	99.69	65.21	88.09

Table 4.2: Performance comparison of SSL methods on CIFAR-10 and CIFAR-100.

²We note that W-MSE, a close relative of our work, also didn't use a projector despite its use being seemingly ubiquitous

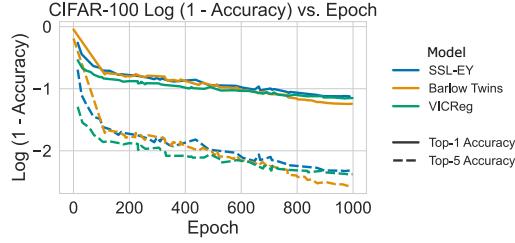


Figure VI.4: CIFAR 100: Learning curves for SSL-EY, Barlow Twins, and VICReg, showing performance across 1,000 epochs.

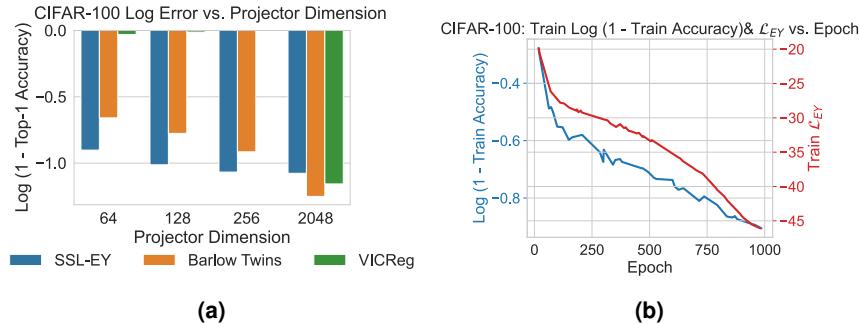


Figure VI.5: CIFAR 100: (a) Performance of SSL-EY with reduced projector size compared to Barlow Twins and VICReg. (b) SSL-EY's learned embeddings indicate untapped representation capacity.

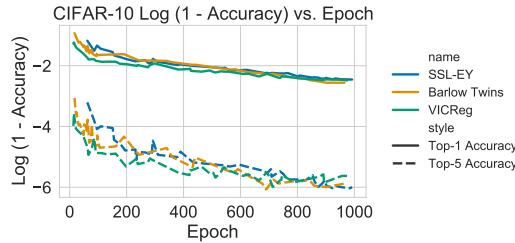


Figure VI.6: CIFAR 100: Learning curves for SSL-EY, Barlow Twins, and VICReg, showing performance across 1,000 epochs.

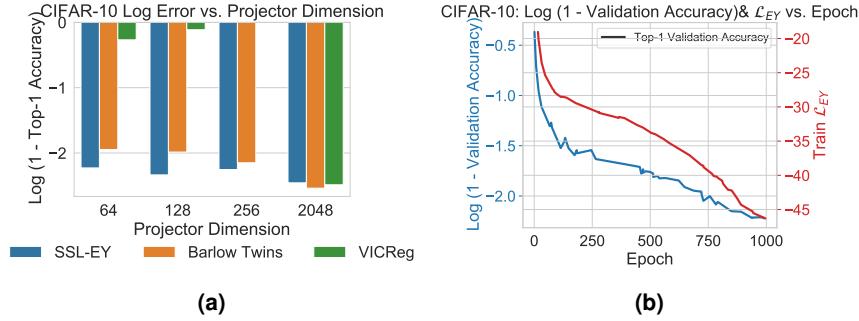


Figure VI.7: CIFAR 10: (a) Performance of SSL-EY with reduced projector size compared to Barlow Twins and VICReg. (b) SSL-EY's learned embeddings indicate untapped representation capacity.

5 Conclusion

In this chapter, we extended our work on CCA to the deep learning setting. We illustrated state-of-the-art performance on the DCCA and DMCCA tasks. By highlighting links between modern Self-Supervised Learning methods and CCA, we were able to propose a novel self-supervised learning method, SSL-EY, which is competitive with existing methods on CIFAR-10 and CIFAR-100.

Chapter VII

CCA-Zoo: A collection of Regularized, Deep Learning-based, Kernel, and Probabilistic methods in a scikit-learn style framework

Preface

This work was published in the Journal of Open Source Software (Chapman and H.-T. Wang, 2021). I have been the lead developer of the CCA-Zoo package since its inception in 2020. Almost all of the methods we have described in this thesis are implemented in CCA-Zoo.

1 Introduction

The Python programming language has seen a surge in popularity in the machine learning community due to its versatility and extensive libraries. However, when it comes to the domain of multiview learning, there is a noticeable void in the Python ecosystem. Existing libraries, such as `scikit-learn` Pedregosa et al., 2011, offer

basic implementations for CCA and PLS, yet fall short of providing a comprehensive toolkit for multiview learning techniques. This is particularly striking given the widespread recognition that the availability of quality software implementations often acts as a catalyst for the adoption of novel methodologies in the statistical learning community.

One glaring example of this trend is Sparse PLS. Despite its known limitations, Sparse PLS has effectively become the go-to method for sparse CCA applications, primarily due to its robust implementation in the R programming language. The discrepancy between the availability of multiview learning tools in R and Python has not only hindered the diversification of methodologies but also impeded the community from leveraging the more recent advances in the field.

2 Background

The research community continues to show a heightened interest in multiview learning. Traditionally, this field has been dominated by contributions from statistical learning researchers who predominantly utilized R and MATLAB for their work. These platforms have been the birthplace of many state-of-the-art algorithms and methodologies, including Sparse PLS.

However, this posed a challenge for Python-oriented researchers and practitioners, leaving them with two less-than-ideal options: either port existing R or MATLAB code into Python, often a non-trivial task requiring domain expertise, or resort to using the limited set of methods available in native Python libraries like `scikit-learn`. This fragmentation has, in effect, created barriers to entry and possibly slowed down the progress in applying multiview learning techniques in Python-based projects.

The CCA-Zoo package aims to bridge this divide by offering a broad range of multiview learning algorithms, creating a unified platform that fosters both academic research and practical applications in Python.

3 Methods

In this section, we describe the implementation of CCA-Zoo as depicted in Figure VII.1 and the design decisions that were made during its development. We highlight the package's optimization for use with high-dimensional biomedical data and elaborate on its compatibility with standard machine learning packages.

3.1 API

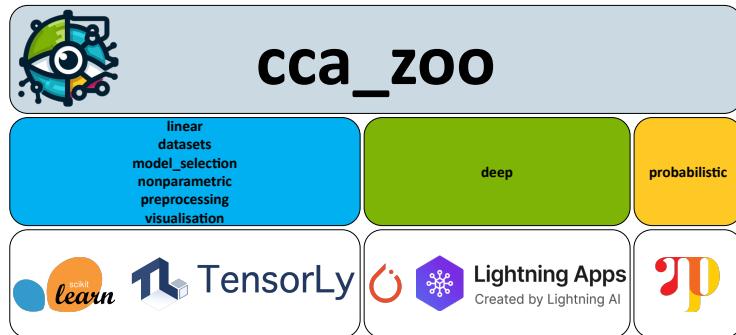


Figure VII.1: The CCA-Zoo compatibility map showcases integration with various machine learning packages. The deep learning module is built upon PyTorch and Lightning, reflecting their status as industry standards for neural network implementations. The probabilistic module employs NumPyro for its Bayesian inference capabilities, enhancing the application of probabilistic approaches in CCA.

The `scikit-learn` API is familiar to many machine learning practitioners and researchers, and is the de facto standard for machine learning in Python. CCA-Zoo has been designed to be consistent with the `scikit-learn` API, inheriting its user-friendly characteristics and ensuring compatibility with the `scikit-learn` ecosystem. Furthermore, the deep module within CCA-Zoo integrates PyTorch and Lightning, harnessing their powerful features for deep learning research and applications. The probabilistic module takes advantage of NumPyro, which offers advanced features for probabilistic programming and Bayesian methods, further extending the versatility and functionality of CCA-Zoo.

3.2 Usage

Use of the CCA-Zoo package is straightforward and intuitive, as demonstrated in the following example, which implements a regularized CCA model with a ridge penalty.

```
# Import required libraries
import numpy as np
from cca_zoo.datasets import LatentVariableData
from cca_zoo.linear import rCCA
from cca_zoo.model_selection import GridSearchCV
```

```

# Generate synthetic multiview data
data = LatentVariableData(view_features=[10,10],latent_dims: int = 2)
(X,Y) = data.sample(n_samples=100)

# Define grid of potential regularization parameters
c1 = [0.1, 0.3, 0.7, 0.9]
c2 = [0.1, 0.3, 0.7, 0.9]
param_grid = {'c': [c1, c2]}

cv = 5 # Number of folds in cross-validation

# Conduct grid search
ridge = GridSearchCV(rCCA(latent_dimensions=2), param_grid=param_grid,
                     cv=cv, verbose=True, scoring=scorer).fit((train_view_1, train_view_2))

```

3.3 Deep

3.4 Code Availability

The code for CCA-Zoo is available at.

CCA-Zoo has received 155 stars and 30 forks on GitHub, and has nearly 500 downloads per month on PyPI¹.

Documentation for CCA-Zoo is available at². The documentation includes a user guide, API reference, and examples.

The package can be installed using `pip install cca-zoo` or `poetry add cca-zoo`.

4 Benchmarking

In this section, we compare the performance of CCA-Zoo against scikit-learn, focusing on the efficiency of the basic CCA and PLS methods. We conducted experiments on synthetic datasets with varying dimensions to evaluate their average execution time. The datasets consisted of random matrices with a varying number of dimensions: 50, 100, 200, 400, and 800. Each matrix had 100 samples. We set the

¹<https://pypistats.org/packages/cca-zoo>

²<https://cca-zoo.readthedocs.io/en/latest/>

latent dimensions for both CCA and PLS to 10. For each dimension, the experiment was repeated 10 times to obtain reliable performance metrics.

Libraries Used:

- CCA-Zoo (version: 2.4.0)
- Scikit-learn (version: 1.3.0)

4.1 Canonical Correlation Analysis:

Figure VII.2 presents the comparison between CCA-Zoo and scikit-learn for Canonical Correlation Analysis. We observe that CCA-Zoo exhibits a competitive runtime profile when compared to scikit-learn across all dimensions.

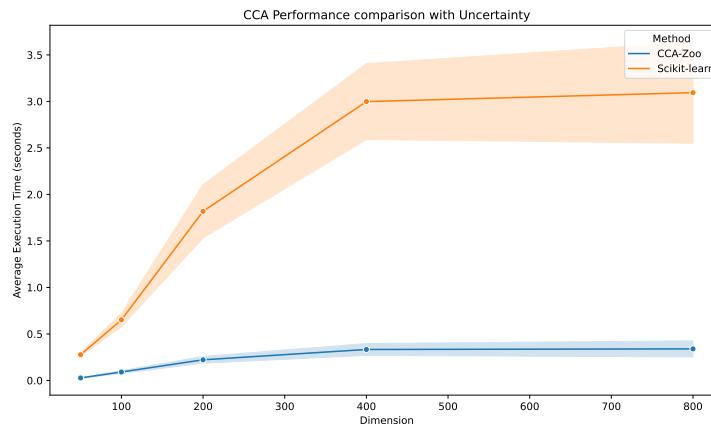


Figure VII.2: Performance comparison for CCA methods

4.2 Partial Least Squares:

The comparison for Partial Least Squares is shown in Figure VII.3. Like the CCA experiment, CCA-Zoo maintains a robust performance profile that is competitive with scikit-learn.

The results indicate that CCA-Zoo is an efficient Python package for both CCA and PLS methods, holding its own against the widely-used scikit-learn library. These experiments underscore the capability of CCA-Zoo to handle high-dimensional data efficiently, making it a suitable choice for applications in bioinformatics, natural language processing, and other high-dimensional data domains.

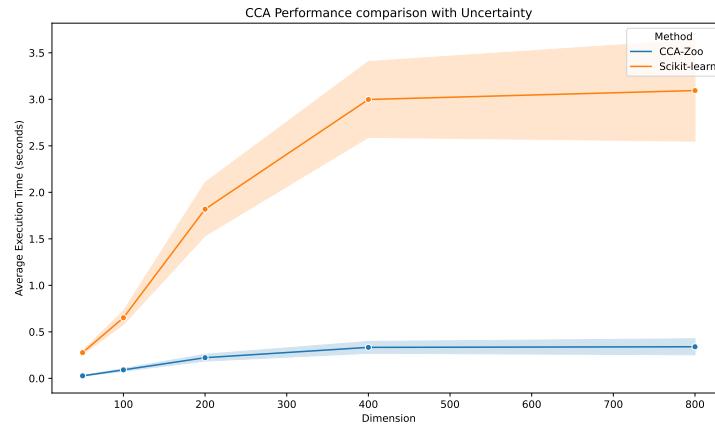


Figure VII.3: Performance comparison for PLS methods

4.3 Conclusion

CCA-Zoo has not only served as a tool for my research but aims to be a community resource that can accelerate research and application in multiview learning. Its design decisions, such as API compatibility and focus on both linear and deep models, reflect a comprehensive understanding of the challenges and opportunities in this field.

Thoughts and Implications

Summary of findings

Implications

Limitations

Future work

Conclusion

1 HCP and ADNI Loadings

1.1 Human Connectome Project (HCP) Data

1.1.1 Brain Connectivity Weights and Loadings

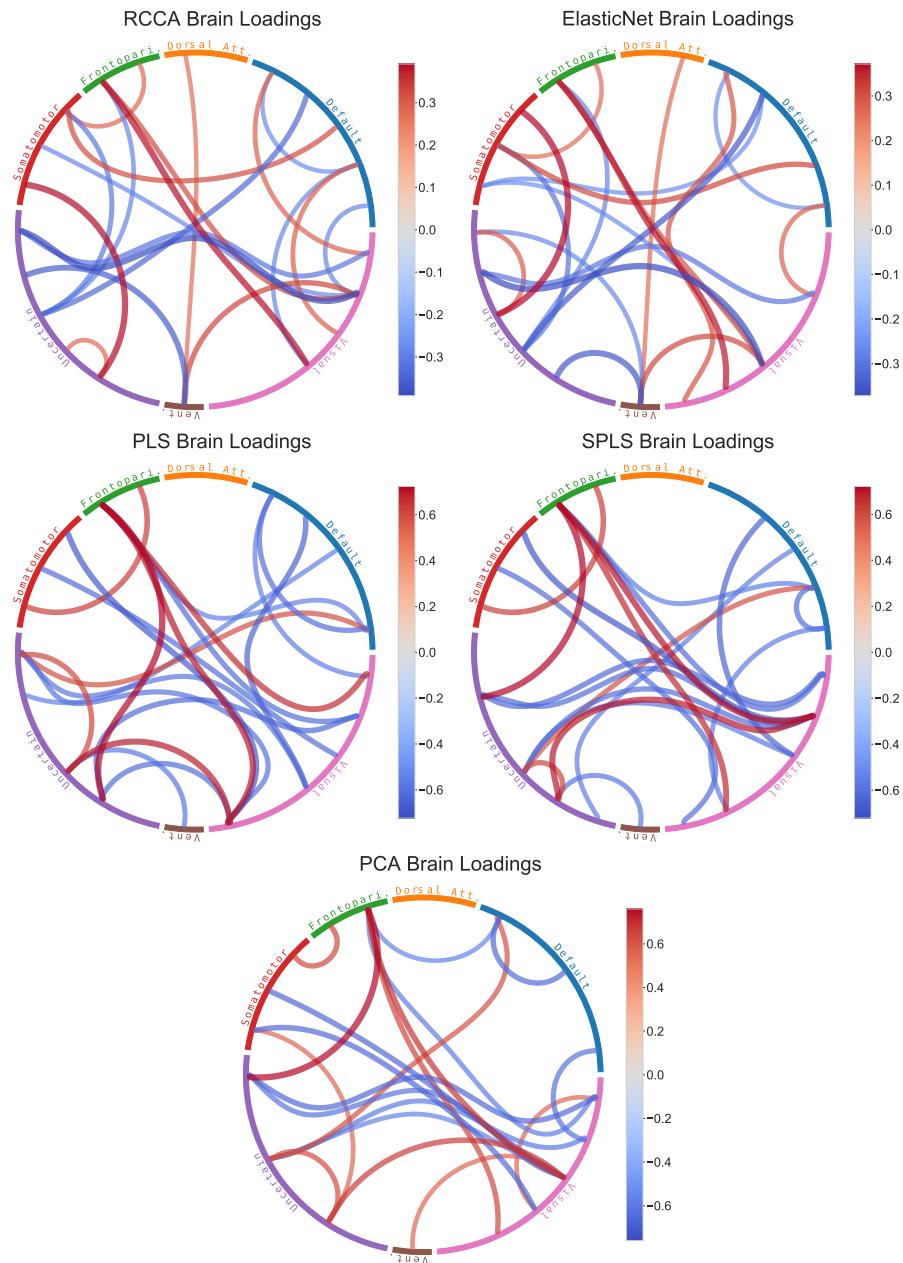
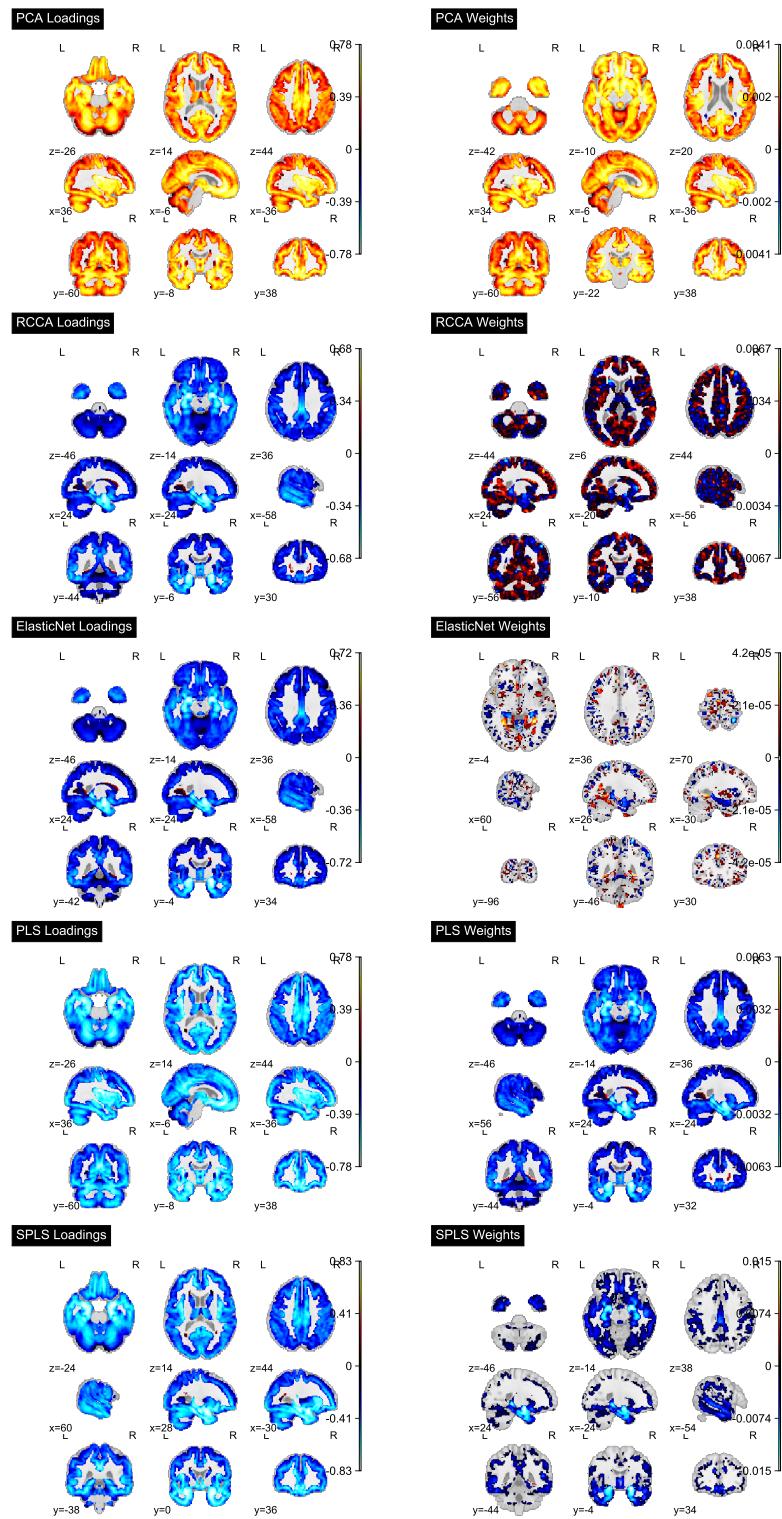


Figure .4: Chord diagrams of the top 8 positive and negative brain loadings for each model.

1.2 Alzheimer's Disease Neuroimaging Initiative (ADNI) Data

1.2.1 Brain Structure Weights and Loadings

**Figure .5:** Statistical maps of brain structure loadings and weights for each model.

2 Tractable Optimization - no spurious local minima

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