

High-dimensional CCA

Lennie Wells

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Introduction and outline

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Structure of talk

- Population CCA
- CCA as a tool for data analysis
- Our specific motivations and contributions

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In words: Given random variables $X \in \mathbb{R}^p$, $Y \in \mathbb{R}^q$ find linear combinations $u^T X, v^T Y$ with maximal correlation, successively, subject to orthogonality.

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$$\text{subject to } \text{Var}(u^T X) = \text{Var}(v^T Y) = 1,$$

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Notation:

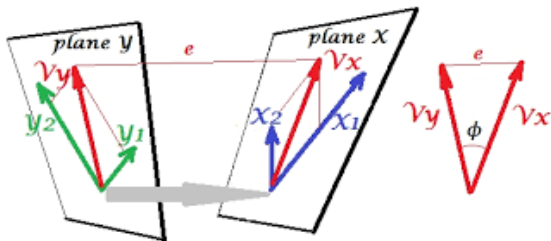
- ρ_k the optimal value called k^{th} *canonical correlation*
- $u_k^T X, v_k^T Y$ called *canonical variates*
- u_k, v_k called *weights*

Visualisation of CCA

$$\text{maximize}_{u \in \mathbb{R}^p, v \in \mathbb{R}^q} \text{Cov}(u^T X, v^T Y)$$

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$$\underset{u \in \mathbb{R}^p, v \in \mathbb{R}^q}{\text{maximize}} u^T \Sigma_{xy} v$$

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Notation: Define *canonical loadings*

$$\Sigma_{xx} u_k = \text{Cov}(X, u_k^T X), \quad \Sigma_{yy} v_k = \text{Cov}(Y, v_k^T Y)$$

Reconstruction

Orthonormality constraints $u_k^T \Sigma_{xx} u_j = v_k^T \Sigma_{yy} v_j = \delta_{jk}$ for $1 \leq j \leq k - 1$.

So $(u_k), (\Sigma_{xx} u_k)$ and $(v_k), (\Sigma_{yy} v_k)$ are each pairs of *dual bases*.

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Hence

$$X = \sum_{k=1}^p \Sigma_{xx} u_k \langle u_k, X \rangle, \quad Y = \sum_{k=1}^q \Sigma_{yy} v_k \langle v_k, Y \rangle$$

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Probabilistic CCA: Consider the model

$$\begin{aligned} Z &\sim \mathcal{N}(0, I_d), & \min(p, q) \geq d \geq 1 \\ X|Z &\sim \mathcal{N}(W_1 Z + \mu_1, \Psi_1), & W_1 \in \mathbb{R}^{p \times d}, \Psi_1 \succcurlyeq 0 \\ Y|Z &\sim \mathcal{N}(W_2 Z + \mu_2, \Psi_2), & W_2 \in \mathbb{R}^{p \times d}, \Psi_2 \succcurlyeq 0 \end{aligned}$$

Then MLEs for W_1, W_2 are essentially matrices of canonical loadings

- **High-level:** two sets of data and want to understand interactions
- **Different perspectives:**
 - stats: estimation
 - bio-informatics: algorithm for data matrices, part of pipeline...
- **Uses:** Dimension reduction, visualisation / interpretation, multi-view / self-supervised learning
- **Motivating Example:** Multi-OMICS for human microbiome measuring $p = 200$ metabolites, and $q = 800$ enzymes for $n = 500$ individuals.

Just stick in sample covariances

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Problem: Arbitrary correlations of 1 in high dimensions ($q \geq n$).

Add regularisation

$$\underset{u \in \mathbb{R}^p, v \in \mathbb{R}^q}{\text{maximize}} \widehat{\text{Cov}}(u^\top \mathbf{X}, v^\top \mathbf{Y}) - \tau_u \|u\|_1 - \tau_v \|v\|_1$$

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Setting the stage

- **Main perspective:** Exploratory Data Analysis (EDA) with an eye on physical interpretation. Loosely frequentist approach.
- **Regularised CCA algorithms:**
 - ridge CCA: l_2 penalty
 - sparse CCA: l_1 penalty
- **Practical considerations:**
 - model / tuning parameter selection
 - number of pairs to consider
 - interpretation
- **Unanswered question:** Are these regularised CCA methods appropriate for real data? Might other structural assumptions be more natural.

Our contributions

- **New algorithm:** using **graphical lasso**; motivated by graphical models and conditional independence.
- **Practical advice:** for model comparison and interpretation motivated by the fundamental geometry of population CCA.

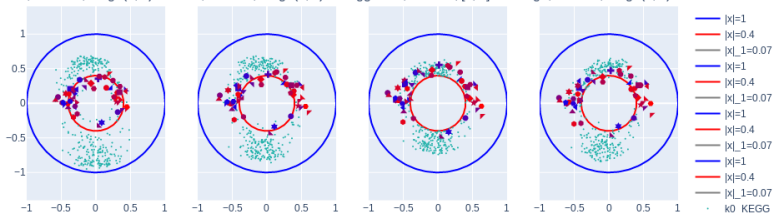
- **New algorithm:** using **graphical lasso**; motivated by graphical models and conditional independence.
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 - CCA is fundamentally a subspace problem
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 - Powerful visualisation via biplots
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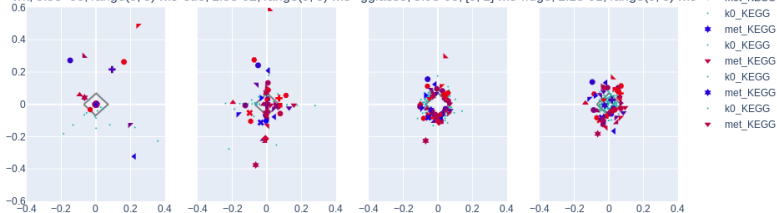
These may seem natural, but are far from the accepted wisdom, and should be a welcome contribution to the field.

Questions?

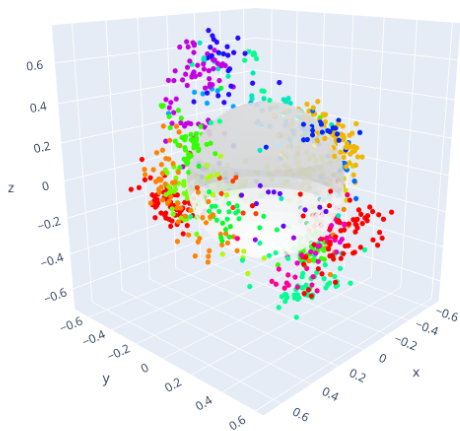
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Pretty picture



Links with matrix analysis

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- **Singular Value Decomposition**

$(\rho_k, \Sigma_x^{1/2} u_k, \Sigma_y^{1/2} v_k)$ give SVD of $M := \Sigma_{xx}^{-1/2} \Sigma_{xy} \Sigma_{yy}^{-1/2}$

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- **Canonical Angles**

$\mathcal{X} := \text{span}(\{X_j : j = 1, \dots, p\})$, $\mathcal{Y} := \text{span}(\{Y_j : j = 1, \dots, q\})$ then CCA is

$$\text{maximize}_{W_k \in \mathcal{X}, Z_k \in \mathcal{Y}} \langle W_k, Z_k \rangle$$

$$\text{subject to } \|W_k\|_2 \leq 1, \|Z_k\|_2 \leq 1,$$

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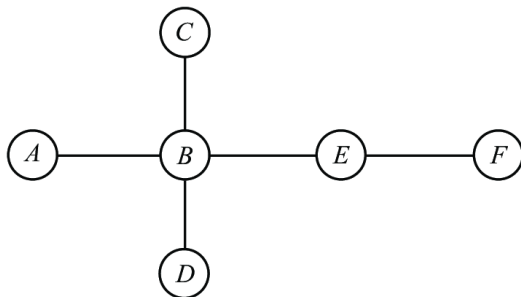
Then the MLEs of the parameters $W_1, W_2, \Psi_1, \Psi_2, \mu_1, \mu_2$ are

$$\begin{aligned} \hat{W}_1 &= \hat{\Sigma}_{xx} U_d M_1 \\ \hat{W}_2 &= \hat{\Sigma}_{yy} V_d M_2 \\ \hat{\Psi}_1 &= \hat{\Sigma}_{xx} - \hat{W}_1 \hat{W}_1^T \\ \hat{\Psi}_2 &= \hat{\Sigma}_{yy} - \hat{W}_2 \hat{W}_2^T \end{aligned}$$

and $\hat{\mu}_1 = \bar{X}$, $\hat{\mu}_2 = \bar{Y}$ where $M_1, M_2 \in \mathbb{R}^{d \times d}$ are arbitrary matrices with $M_1 M_2^T = R$, $\|M_1\| \leq 1$, $\|M_2\| \leq 1$

Graphical Models

- Setup: $X = (X^1, \dots, X^p)$ a random vector; $G = (V, E)$ graph with $V = \{1, \dots, p\}$
- Key idea: graph structure constrains distribution of X
- Gaussian graphical models: $X^i \perp X^j | (X^k)_{k \neq i, j}$ whenever $(i, j) \notin E$



- Aim: Solve structure estimation problem
- Setup: samples x_1, \dots, x_n from some zero-mean Gaussian with precision matrix $\in \mathbb{R}^{p \times p}$
- Write: $\mathbf{S} = \frac{1}{n} \sum_{i=1}^n x_i x_i^T \in \mathbb{R}^{p \times p}$
- Log-likelihood:

$$l(\Omega; \mathbf{X}) = \log \det - \text{trace}(\mathbf{S})$$

- Penalised Objective:

$$\hat{\cdot} \in \operatorname{argmax}_{\succeq \mathbf{0}} \{ \log \det - \text{trace}(\mathbf{S}) - \alpha \rho_1(\cdot) \}$$

where: $\alpha \in (0, \infty)$ is a penalty parameter, $\rho_1(\cdot) = \sum_{i \neq j} |\Omega_{ij}|$

Our Approach

Observations:

- $\Sigma = \Omega^{-1}$ is differentiable function of Ω .
- M is a differentiable function of Σ
- So $M = f(\Omega)$ where f is differentiable

Algorithm: Estimate Ω with graphical lasso, plug-in $\hat{M} = f(\hat{\Omega})$, then apply SVD

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Theorem: can combine results in the literature to see convergence rate

$$\sin \Theta(\hat{B}, B) \lesssim s_0(p) \left(\frac{\log p}{n} \right)^{1/2}$$

Penalised Matrix Decomposition

A natural but difficult objective:

$$\begin{aligned} & \underset{u \in \mathbb{R}^p, v \in \mathbb{R}^q}{\text{maximize}} \quad \frac{1}{n} u^T \mathbf{X}^T \mathbf{Y} v \\ & \text{subject to} \quad \frac{1}{n} \|\mathbf{X}u\|_2^2 \leq 1, \quad \frac{1}{n} \|\mathbf{Y}v\|_2^2 \leq 1, \quad \|u\|_1 \leq c_1, \quad \|v\|_1 \leq c_2 \end{aligned}$$

Make constraints tractable:

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Later pairs: Apply with $\frac{1}{n} \mathbf{X}^T \mathbf{Y} - \sum_{j=1}^{k-1} d_j u_j v_j^T$

Existing Methods: AMA [SMN⁺17]

Alternating Minimisation Algorithm

Use Lagrange multiplier penalty rather than explicit constraints:

$$\begin{aligned} \underset{u,v}{\text{minimize}} \quad & -\frac{1}{n} u^T \mathbf{X}^T \mathbf{Y} v + \tau_1 \|u\|_1 + \tau_2 \|v\|_1 \\ & + \mathbb{1} \left\{ u : \frac{1}{n} \|\mathbf{X}u\|_2^2 \leq 1 \right\} + \mathbb{1} \left\{ v : \frac{1}{n} \|\mathbf{Y}v\|_2^2 \leq 1 \right\} \end{aligned}$$

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subject to $\mathbf{X}u = z$

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Tool: Linearized ADMM

Later pairs: Add constraint $U^T \mathbf{X}^T \mathbf{X}u = 0; V^T \mathbf{Y}^T \mathbf{Y}v = 0$



Xiaotong Suo, Victor Minden, Bradley Nelson, Robert Tibshirani, and Michael Saunders.

Sparse canonical correlation analysis.

arXiv:1705.10865 [stat], June 2017.

arXiv: 1705.10865.



Daniela M. Witten, Robert Tibshirani, and Trevor Hastie.

A penalized matrix decomposition, with applications to sparse principal components and canonical correlation analysis.

Biostatistics, 10(3):515–534, July 2009.