

Bayesian Modelling and Analysis of Challenging Data

Kerrie Mengersen
School of Mathematical Sciences
QUT

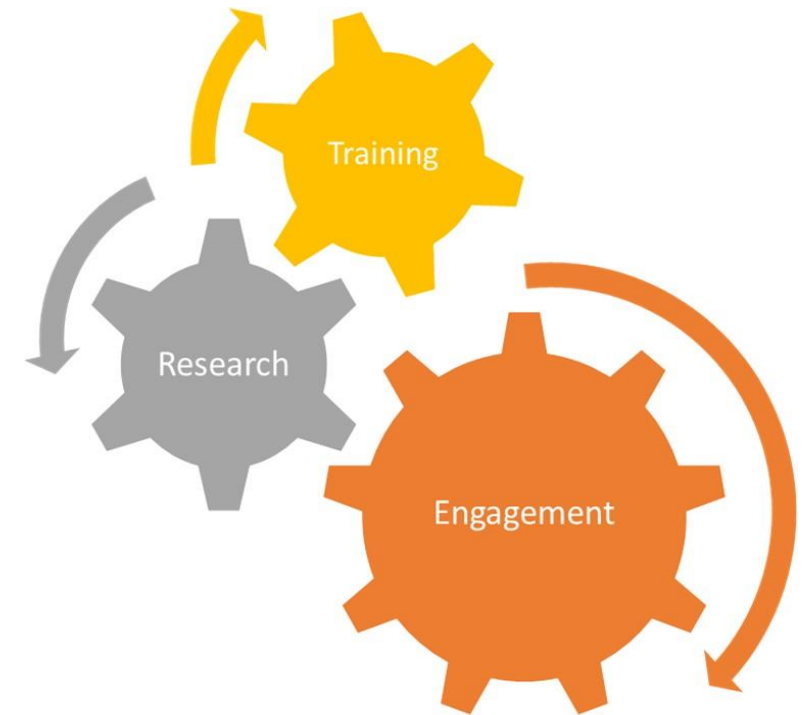
PC Mahalanobis Lecture Series
January 2021



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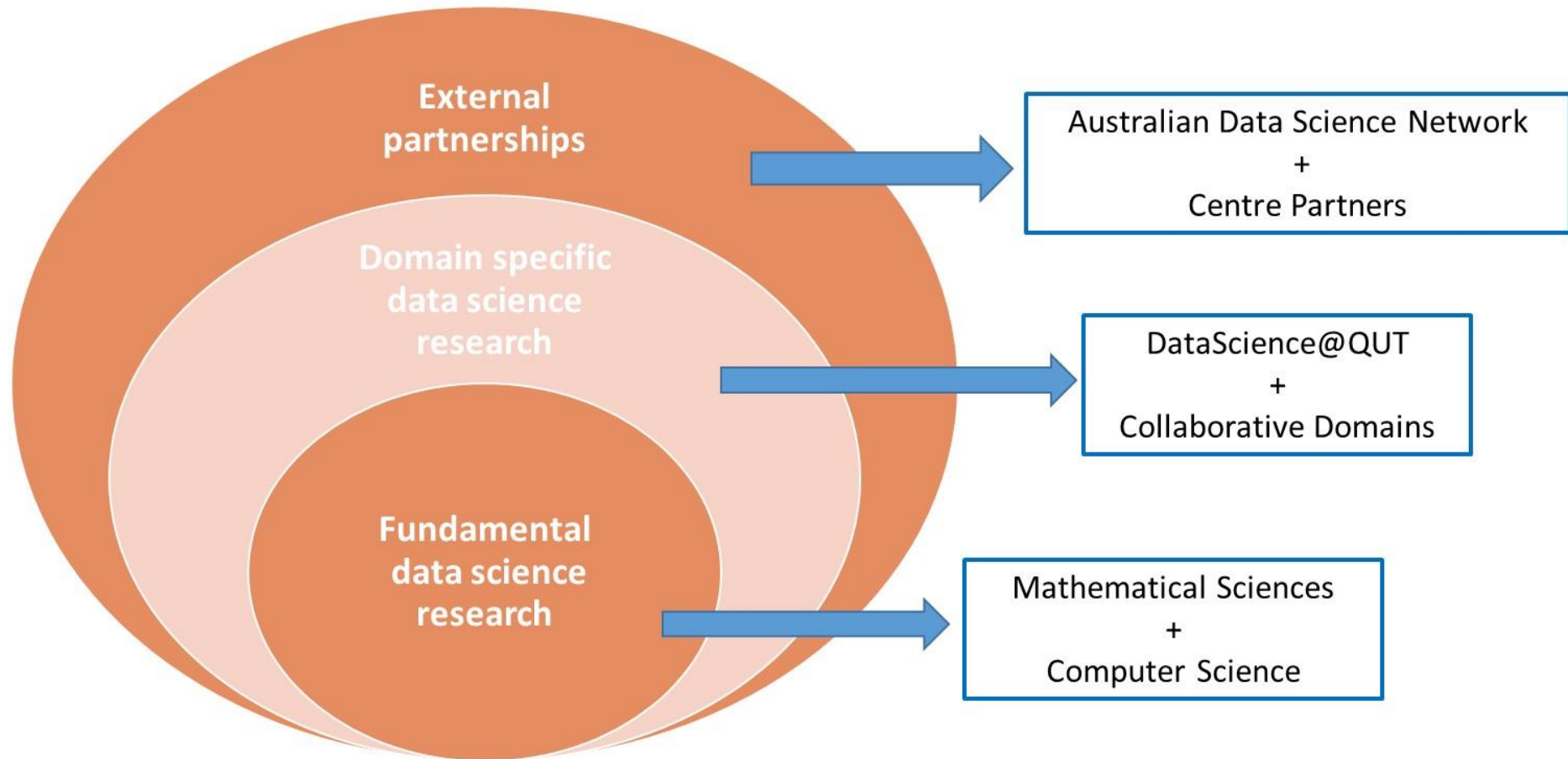


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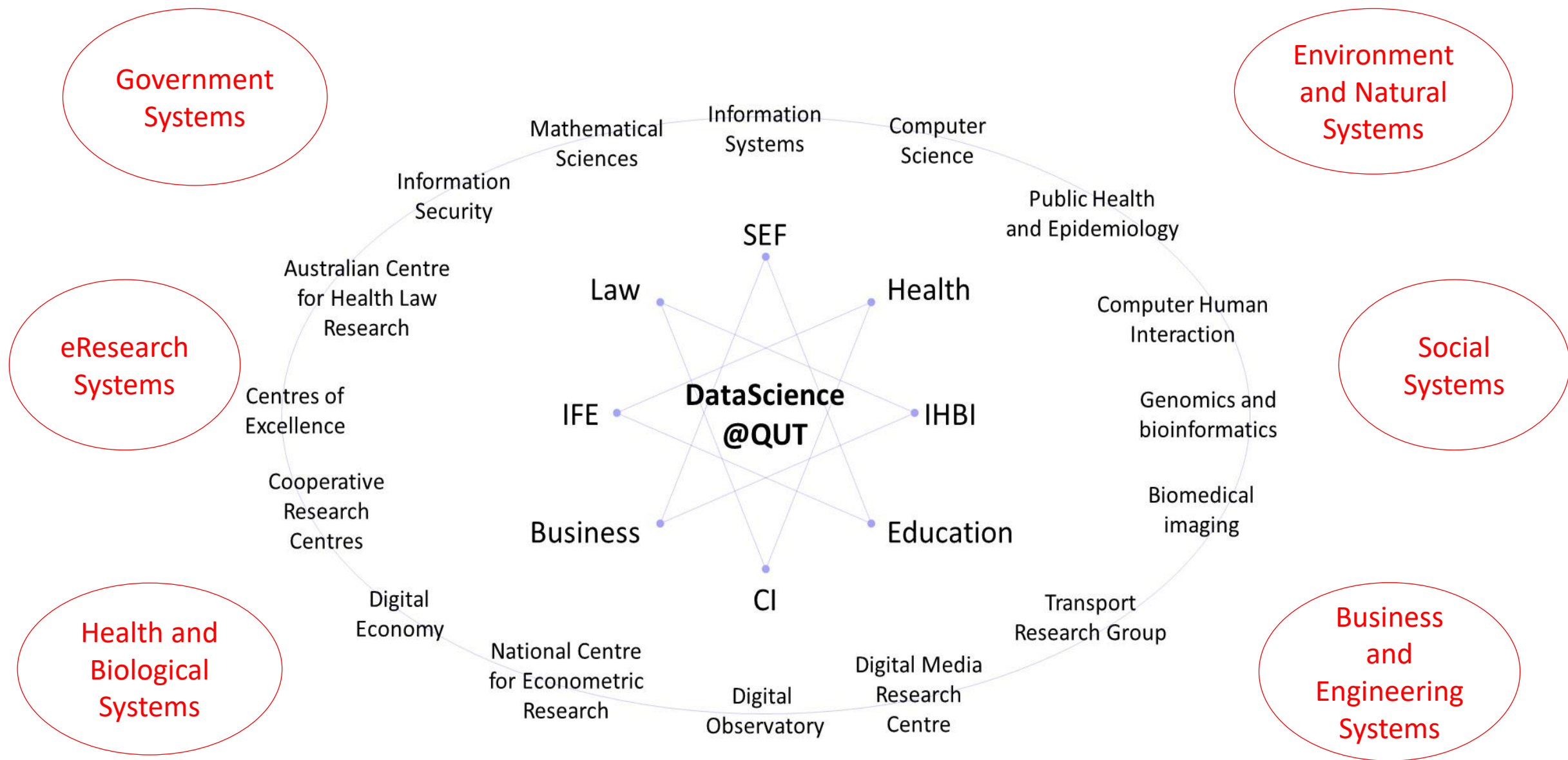
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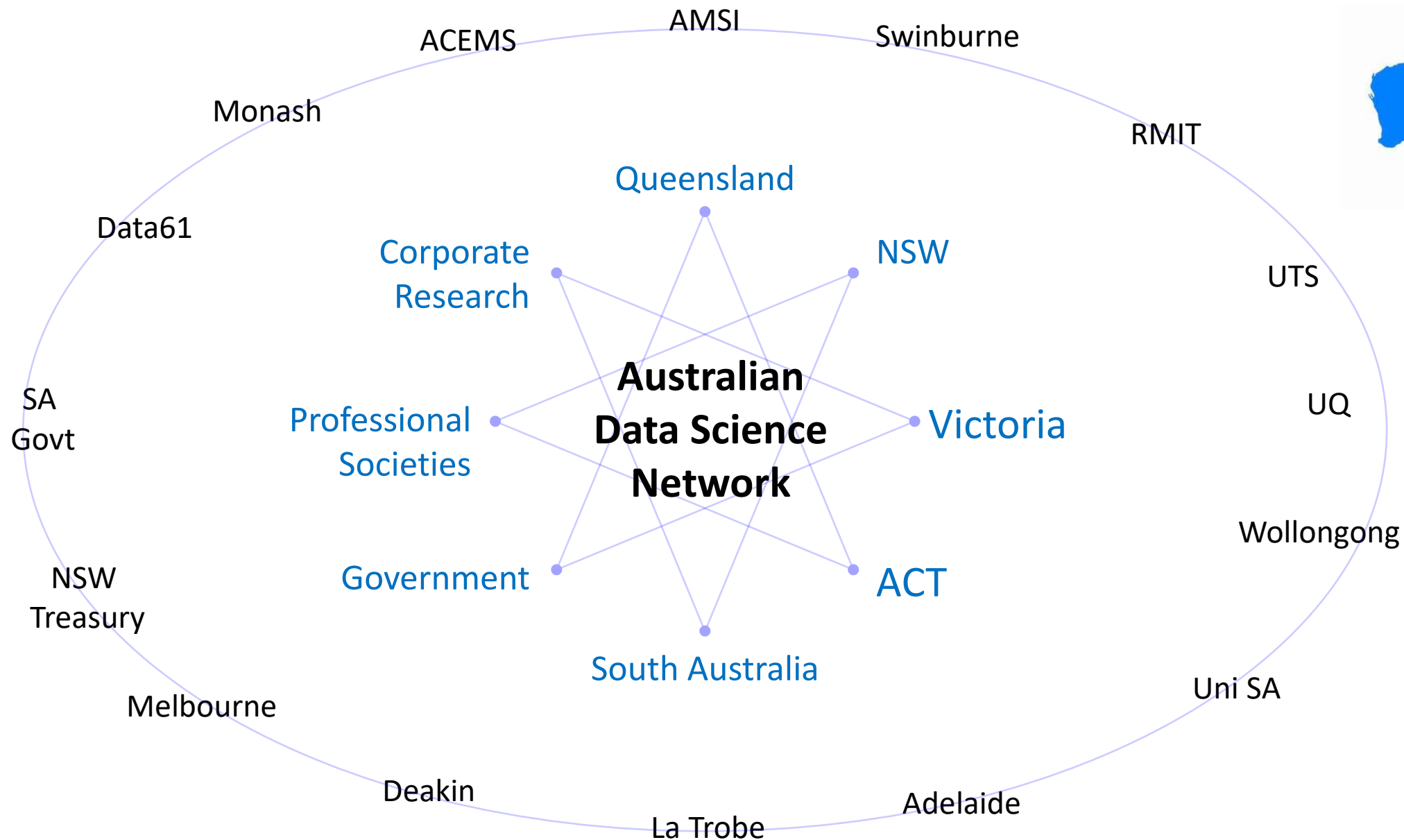


James McGree
Data for Discovery



David Lovell
Data Focused
Decision Making





Programme of Lectures

January 27th:

- Lecture 1: 10-1045am IST (230pm-3:15pm AEST)
Identifying the Intrinsic Dimension of High-Dimensional Data
- Lecture 2: 11-11:45am IST (3:30pm-4:15pm AEST)
Finding Patterns in Highly Structured Spatio-Temporal Data

January 29th:

- Lecture 3: 10-1045am IST (230pm-3:15pm AEST)
Describing Systems of Data
- Lecture 4: 11-11:45am IST (3:30pm-4:15pm AEST)
Making New Sources of Data Trustworthy

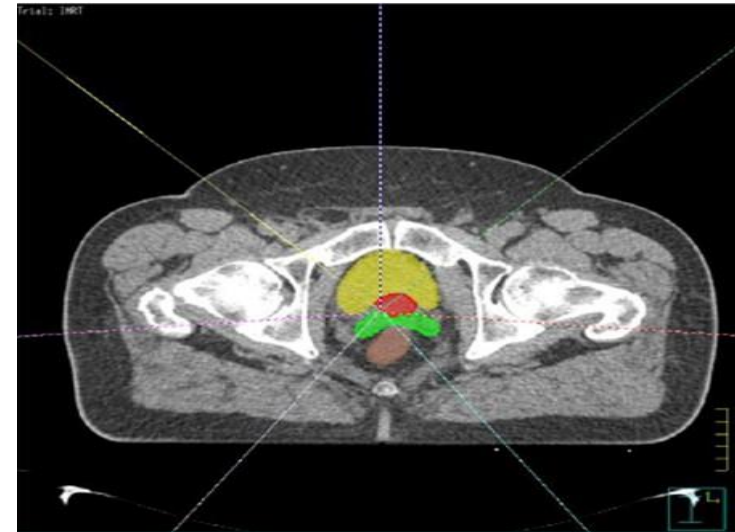
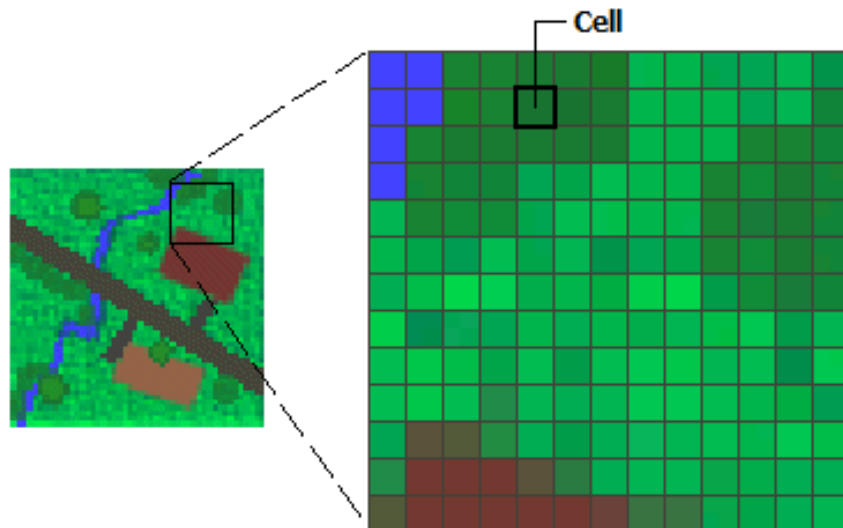
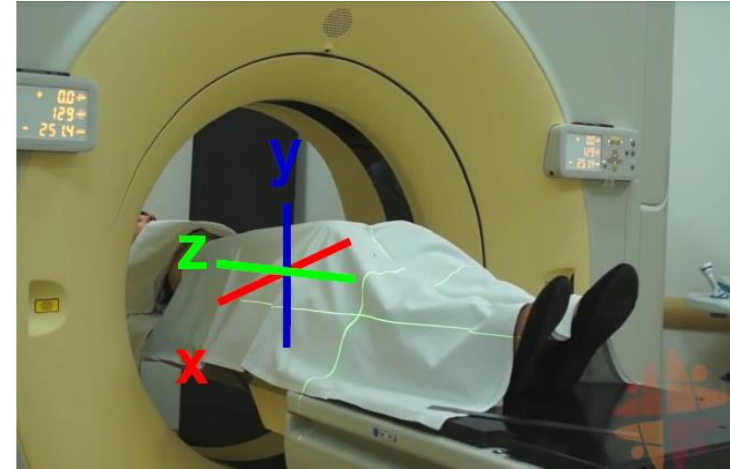


Bayesian Modelling and Analysis of Challenging Data

Lecture 1: Identifying the intrinsic dimension of high-dimensional data

Hongbo Xie, Insha Ullah,
Edgar Santos-Fernandez, Antonietta Mira,
Benoit Liqueet, Matthew Sutton

Case Study 1: Analysis of images

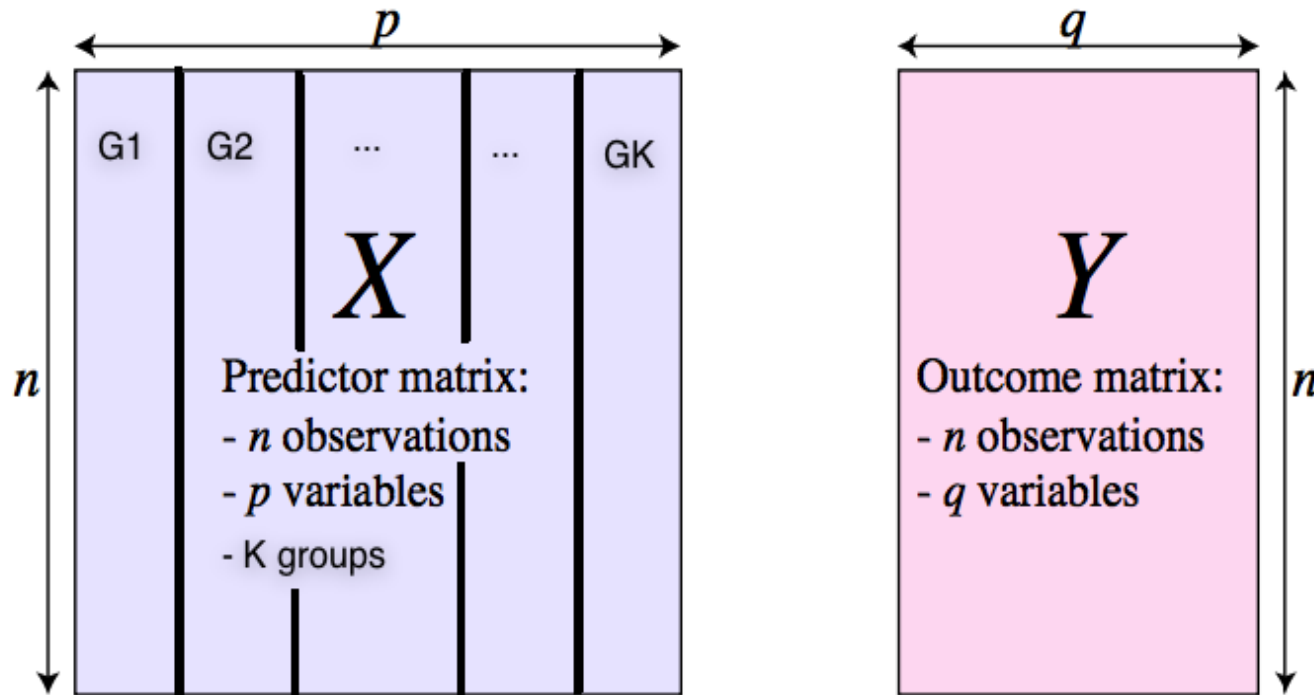


Case study 2: player tracking



- Individual player tracking devices
- What to analyse and compare plays
- Home vs away?
Winning vs losing teams?

Case study 3: genomic data



- Multiple disease outcomes
- Many potential predictors (genes)
- $p \gg n$

Intrinsic dimension

Lower bound of the dimension of a dataset == measure of complexity of dataset or signal

- Pattern recognition: the number of variables needed in a minimal representation of the data.
- Signal processing: how many variables are needed to generate a good approximation of the signal.
- Estimation: a representation in the intrinsic dimension does only need to exist locally, i.e. different intrinsic dimensions in different parts of the data set.
- History:
 - Term coined by Bennet (1965) in information theory
 - 1960's: Estimation of ID in multidimensional scaling
 - 1970's: ID estimation methods based on local eigenvalues, distance functions, etc
 - 1980's: ID of sets and probability measures in dynamical systems (fractal dimension)
 - 2000's: 'curse of dimensionality'

Case Study 1: Matrix Factorization

Aim: to extract low-rank and/or sparse structures (e.g., classes)

Approach: Use matrix factorization techniques

Data: Y ($M \times N$) matrix

Solve: Recover the actual low rank matrix X , i.e.

$$Y = X + E = UV^T + E$$

$$Y \in \mathbb{R}^{M \times N}, U \in \mathbb{R}^{M \times r}, V \in \mathbb{R}^{N \times r}, E \in \mathbb{R}^{M \times N}$$

$r \ll \min(M, N)$ for sparsity

Bayesian model: use priors to induce sparsity

Gaussian priors for columns of U and V:

$$\left. \begin{aligned} p(\mathbf{U}|\gamma) &= \prod_{j=1}^r N(\mathbf{u}_{\cdot j} | 0, \gamma_j^{-1} \mathbf{I}_M) \\ p(\mathbf{V}|\gamma) &= \prod_{j=1}^r N(\mathbf{v}_{\cdot j} | 0, \gamma_j^{-1} \mathbf{I}_M) \end{aligned} \right\} \text{Same } \gamma_j$$

$$p(\gamma_j) = \text{Gamma}(a, \frac{1}{b}) \quad \text{Small } a, b$$

Couple U with a kernel matrix K_U to give a latent matrix G with prior

$$p(\mathbf{G}|\mathbf{U}, K_U, \sigma_g) = \prod_{j=1}^r N(\mathbf{g}_{\cdot j} | K_U^T \cdot \mathbf{u}_{\cdot j}, \sigma_g^{-1} \mathbf{I}_M) \quad \text{Jeffreys prior: } p(\sigma_g) = \sigma_g^{-1}$$

Similarly,

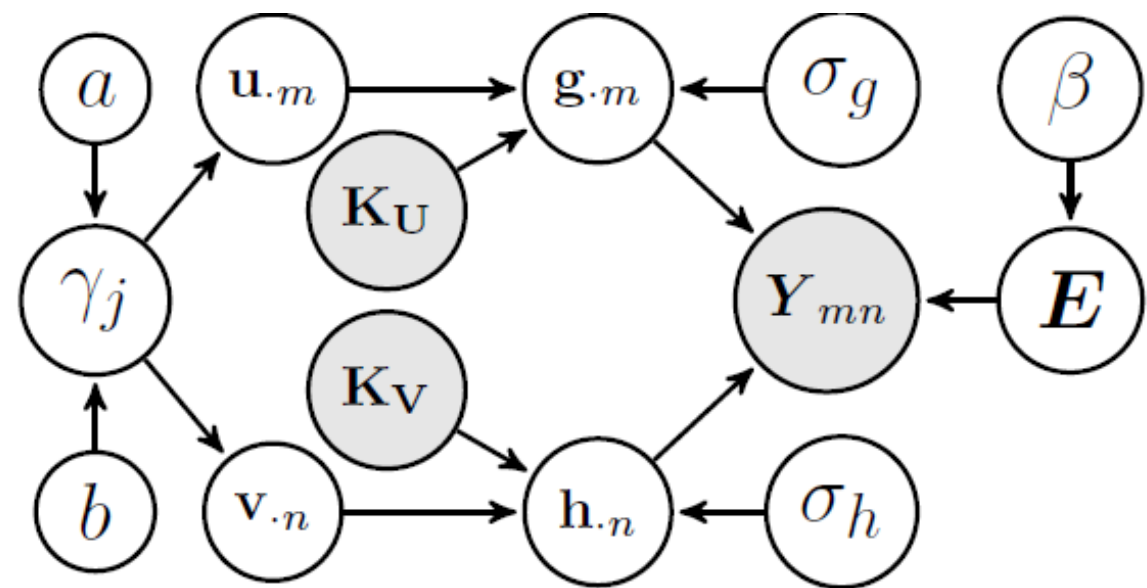
$$p(\mathbf{H}|\mathbf{V}, K_V, \sigma_h) = \prod_{j=1}^r N(\mathbf{h}_{\cdot j} | K_V^T \cdot \mathbf{v}_{\cdot j}, \sigma_h^{-1} \mathbf{I}_N) \quad p(\sigma_h) = \sigma_h^{-1}$$

Residual term

$$p(\mathbf{E}) = \prod_{i=1}^M \prod_{j=1}^N N(\varepsilon_{mn} | 0, \beta^{-1})$$

$$p(\beta) = \beta^{-1}$$

Graphical model



Conditional and joint distributions

Conditional distribution for observation model:

$$p(Y|G, H, \beta) = N(Y|GH^T, \beta^{-1}I_{MN})$$

Joint distribution:

$$p(Y, U, V, G, H, \sigma_g, \sigma_h, \gamma, \beta) = \\ p(Y|G, H, \beta)p(G|U, \sigma_g)p(H|V, \sigma_h)p(U|\gamma)p(V|\gamma)p(\sigma_g)p(\sigma_h)p(\gamma)p(\beta)$$

Computation: Variational Bayes

Choice of kernel

Many different types of kernels. For images, we want one that incorporates similarity information between patches into patch group matrix factorisation.

Let $d_E^{i,j}$ be the Euclidean distance between a pair of patches (i,j) .

Define the similarity between them, i.e., an entry of K_u or K_v as

$$k_{ij} = \sqrt[4]{\frac{1}{1 + d_E^{i,j}/M}}$$

M is the total number of pixels in the patch

- A pixel and its nearest neighbours in a $\sqrt{M} \times \sqrt{M}$ window are modelled as a column vector.
- Construct the $M \times N$ patch group matrix Y by grouping other $N - 1$ patches with similar local spatial structures to the underlying one in the local window.
- Since each column shares similar underlying image structures, the noise-free patch group matrix Y has the low-rank property.

Overall algorithm

1. Cluster patches with similar spatial structure to form a patch matrix.
2. Apply KSBMF in succession on each patch matrix.
3. Aggregate the patches to reconstruct the whole image.

Case study: image restoration

12 test images:



First 10 images 256×256 ; last 2 images 512×512 .

Add $N(0, \sigma^2)$ noise, $\sigma = 20, 50, 70, 100$.

Patch sizes set to 6×6 , ..., 9×9 ; 70, 90, 120, 140.

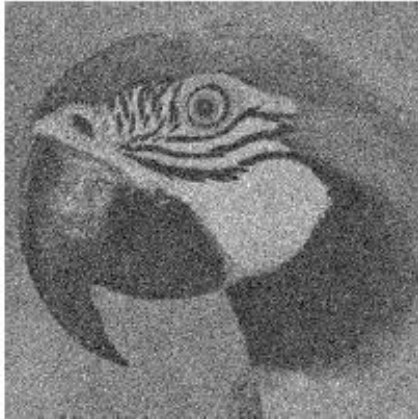
No side information about similarity between patches, so set K_U to be the Identity matrix.

Case study: results

Original

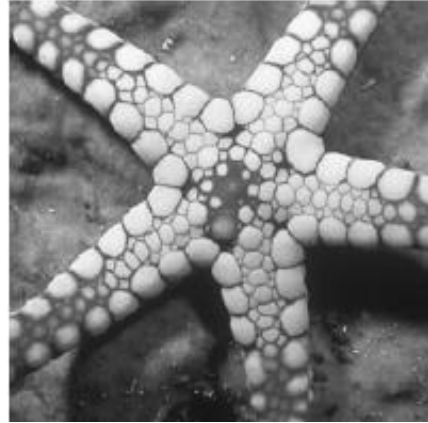


Noisy

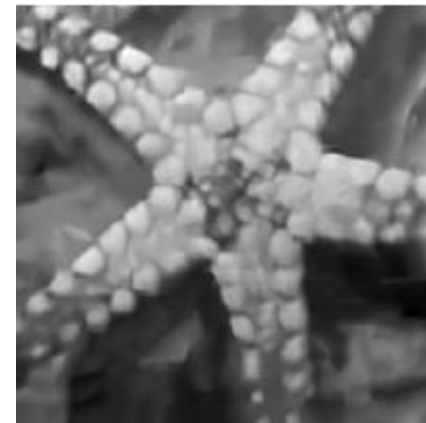
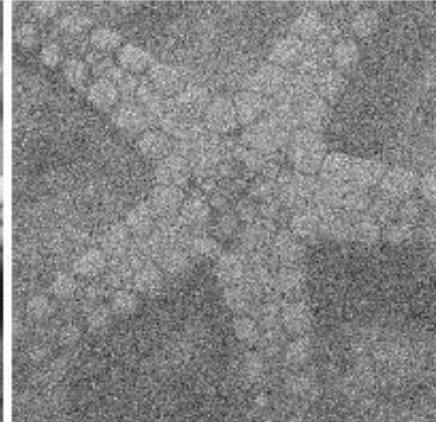


Reconstructed

Original



Noisy



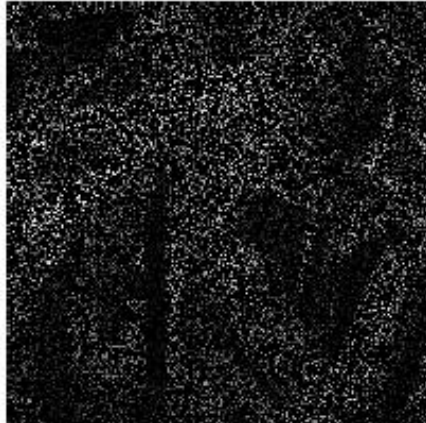
Reconstructed

Case study: results

Original

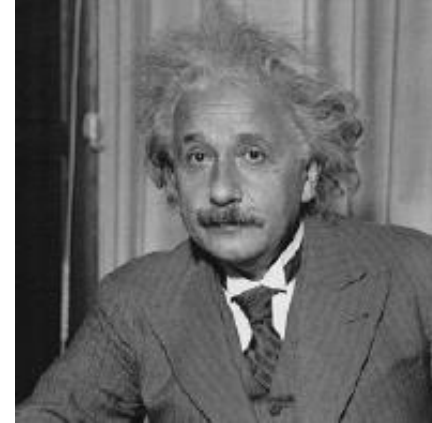


Noisy

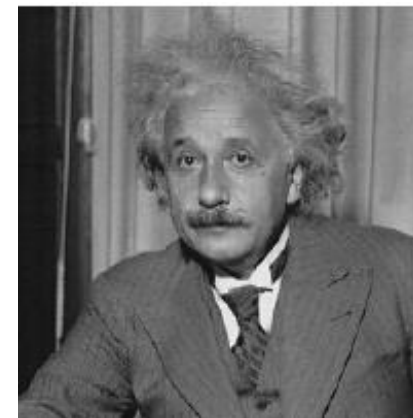


Reconstructed

Original



Noisy



Reconstructed

Summary

- New (KSBMF) model allows integration of side information.
- KSBMF automatically infers the parameters and latent variables including the reduced rank using variational Bayesian inference.
- The model simultaneously achieves low rank through sparsity induced by an enforced constraint on latent factor matrices.
- Experimental results demonstrate that KSBMF outperforms state-of-the-art approaches for image restoration tasks under various types and levels of corruption.

Case Study 2. Dimension reduction of tracking data via ID

- A small number of dimensions/variables is often sufficient to effectively describe high-dimensional data – “intrinsic dimension” (ID)
- ID can vary within the same dataset.

Examples:

- folded vs unfolded configurations in a protein molecular dynamics trajectory
 - active vs inactive regions in brain imaging data
 - organisations with different service delivery profiles
 - sports teams with different strategies for attack/defence, home/away
-
- Aim is to cluster regions with the same local ID in a given data landscape.

Proposed approach: homogeneous model

- Data $x = (x_1, x_2, \dots, x_N)$ sampled from a density $\rho(x)$ defined on a manifold with unknown ID, d , s.t. ρ is approximately constant in the region defined by the second neighbour of each point.
- Let r_{i1} and r_{i2} be the distances of the first and second neighbour of x_i .
- Then $\mu_i = r_{i2}/r_{i1}$ follows the Pareto distribution $f(\mu_i|d) = d\mu_i^{-(d+1)}$.
- Assuming $\mu = (\mu_1, \mu_2, \dots, \mu_N)$ are independent, then

$$P(\mu|d) = d^N \prod_{i=1}^N \mu_i^{-(d+1)} = d^N e^{-(d+1)V}$$

where $V = \sum_{i=1}^N \log(\mu_i)$

➡ Place a suitable prior on d and estimate d .

Proposed approach: heterogeneous model

- Let x be sampled from a density $\rho(x)$ with support on the union of K manifolds with varying dimensions. Then

$$\rho(x) = \sum_{k=1}^K \rho_k(x)$$

- each $\rho_k(x)$ has support on a manifold of dimension d_k
- $p=(p_1, p_2, \dots, p_K)$ are the *a priori* probabilities that a point belongs to the manifolds $1, \dots, K$.
- Now the distribution of μ_i is a mixture of Pareto distributions:

$$P(\mu|d) = \sum_{k=1}^K p_k d_k \mu_i^{-(d+1)V}$$

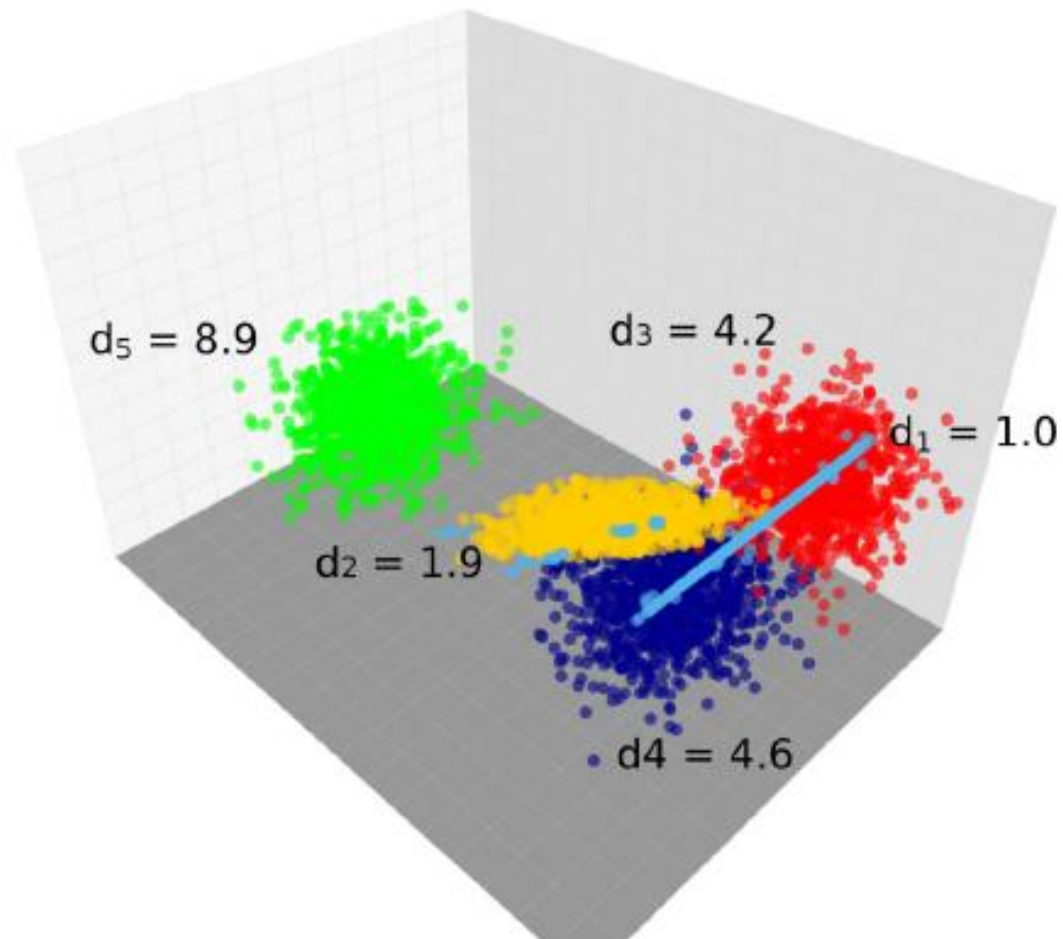
- Introduce latent variables $z = (z_1, z_2, \dots, z_K)$ where $z_1 = k$ indicates that point i belongs to manifold k . Hence

$$P_{post}(z, d, p|\mu) \propto P(\mu|z, d)P(z|p)P(d)P(p)$$

- Priors $d_k \sim \text{Gamma}(a_k, b_k)$, $p \sim \text{Dir}(c_1, \dots, c_K)$; $a_k, b_k, c_k = 1$

Simulation study

$N=1000$ points drawn from five Gaussians in dimensions
 $d_1 = 1, d_2 = 2, d_3 = 4, d_4 = 5, d_5 = 9$



Case Study: ID in basketball

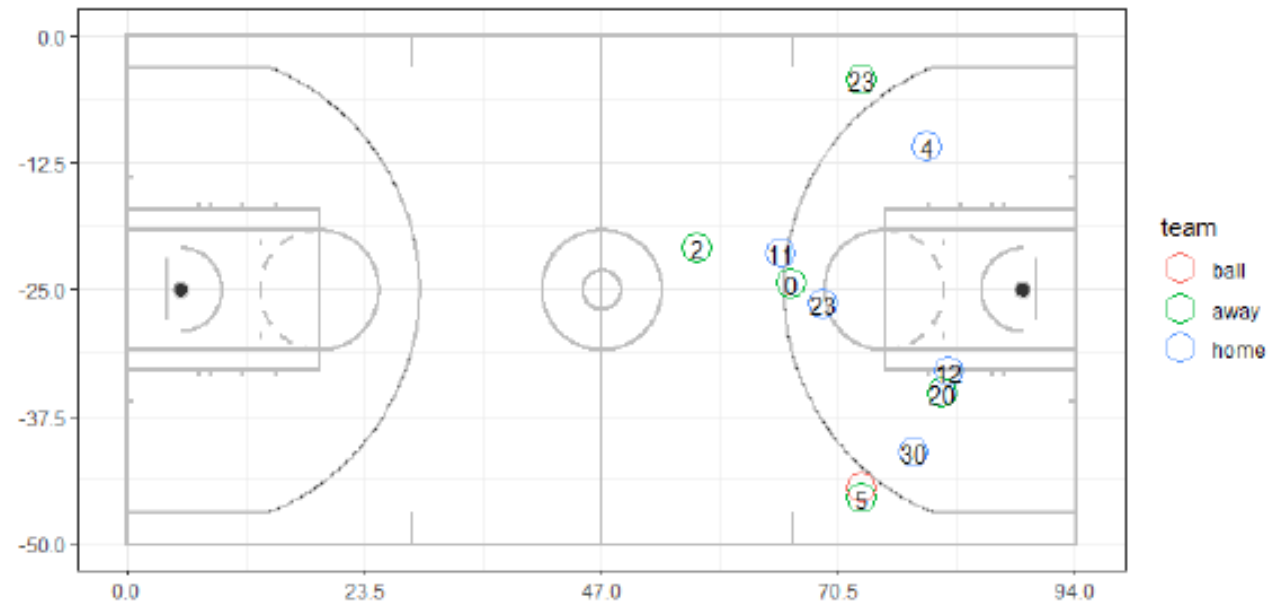
- SportVU NBA player tracking technology: player movement measurement 25 frames/sec.
- How is the placement of the players in attack and defence related to the success of a play?
- Do teams that have greater offensive ability produce successful shots from more unique locations in the court and do they create more shoot opportunities by passing the ball more effectively?
- What could ID tell us about the plays and teams?



Example

- High-resolution player tracking raw data from the NBA season 2015-16.
- Play-by-play events description and other statistics (<https://stats.nba.com/>).
- Verified via manual video annotation of the game (<https://www.youtube.com/>).
- From each play, we inferred the locations of the players at the moment of the shoot, and selected the events = {ShotMissed, ShotMade}.
- 15 games were included in the analysis.

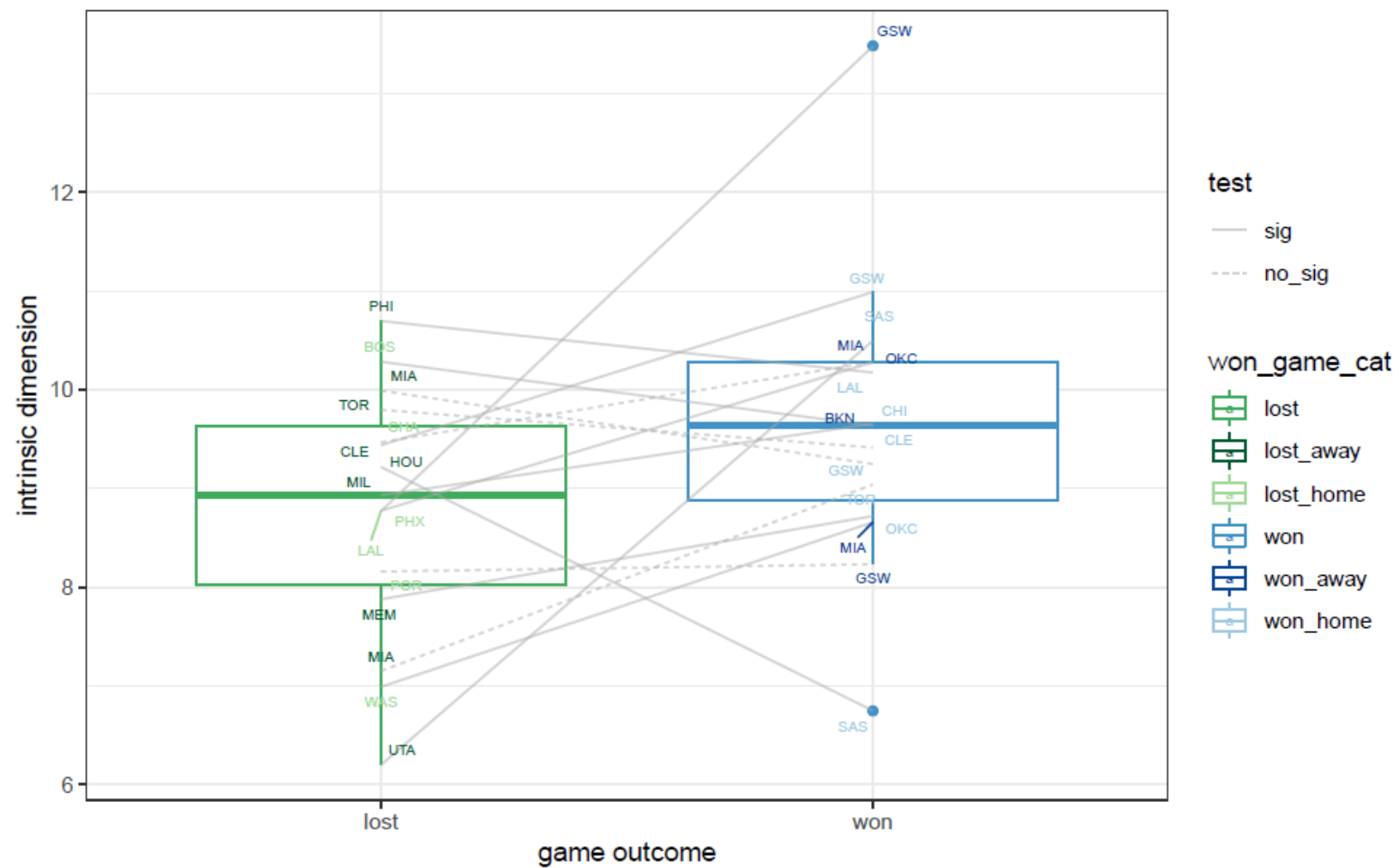
Consider the game Cleveland Cavaliers (CLE) and the Golden State Warriors (GSW) from the 25th of December 2015.



Example

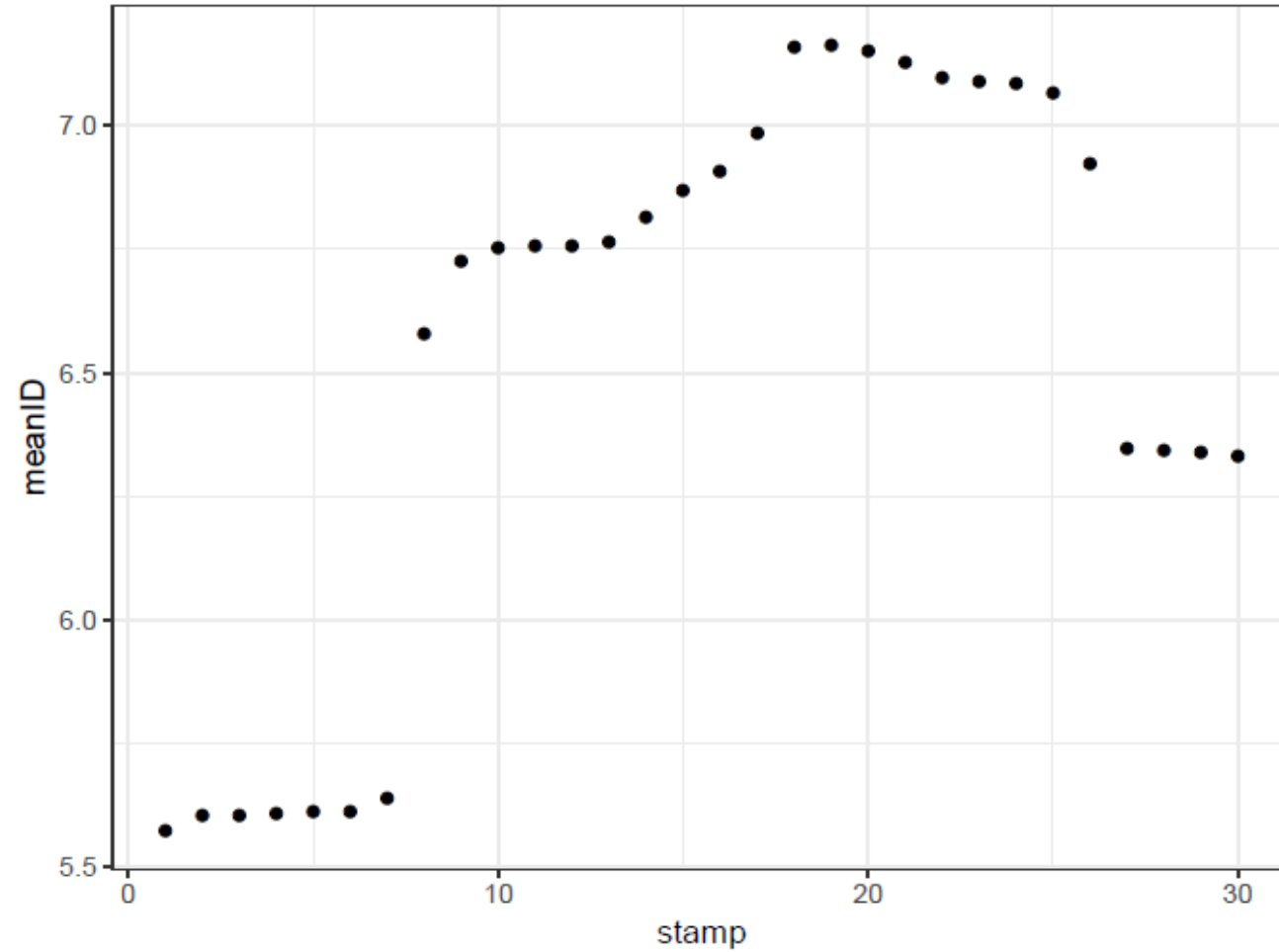
- Aim: compute the intrinsic dimension using the shot chart data from the home and away teams.
- Split the data into two sets: (1) field goals shots taken when the home team (GSW) is attacking, and (2) ... when CLE is attacking.
- No. rows on each dataset = no. attempted field shots.
No. columns = $D = 20$ (2 players' coordinates (x and y) 5 players 2 teams).
- The intrinsic dimension for the set of players (5 vs 5) corresponds to the number of independent directions in which the 20-dimensional points are embedded.

Results



Results

Posterior means of
The ID over the course
of play for the first
3-point field goal.



Case Study 3: High-dimensional variable selection

Challenge 1: wide, high-dimensional data



We have too many variables, prone to overfitting. Need to remove variable, or regularize, or both

- ▶ **Main constraint:** situation with $p > n$
- ▶ **Strong colinearity** among the variables.

Challenge 2: grouped data

- **Genomics**: genes within the same pathway have similar functions and act together in regulating a biological system.

↪ These genes can add up to have a larger effect

↪ can be detected as a group (i.e., at a pathway or gene set/module level).

We consider variables are divided into groups:

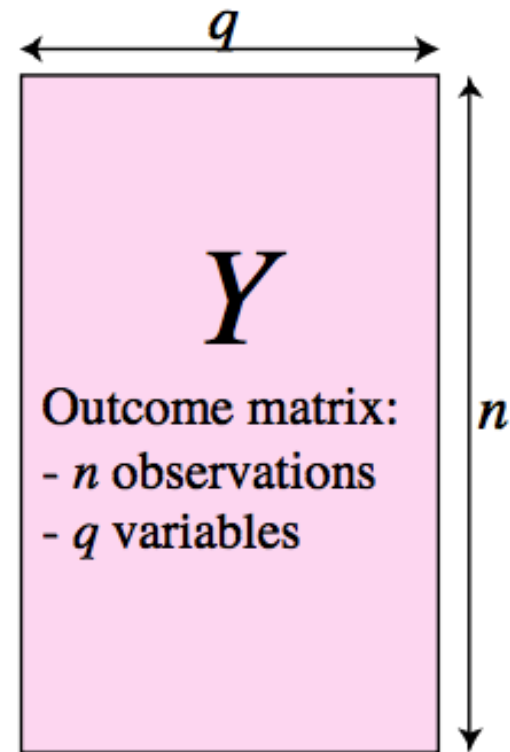
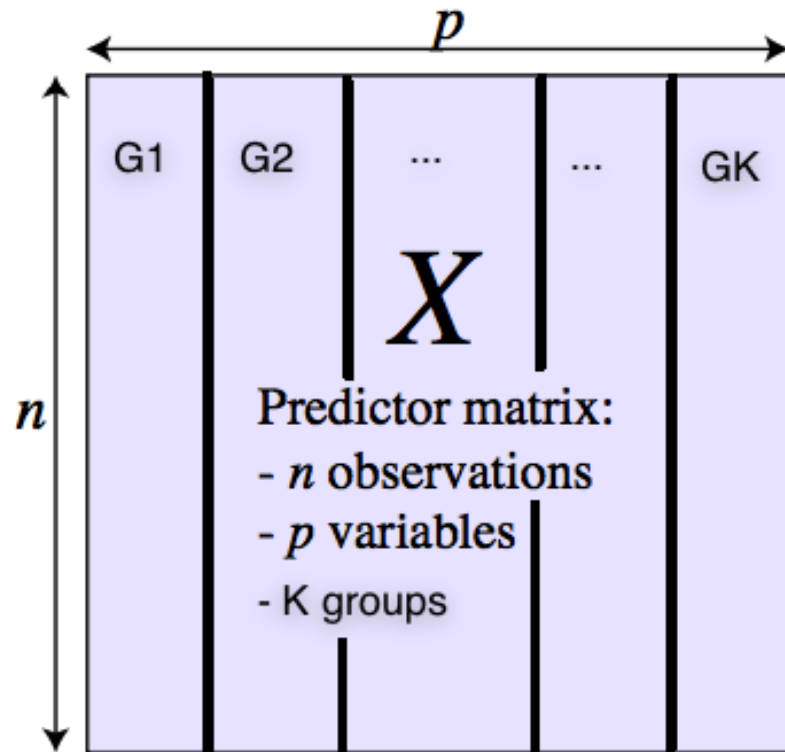
- **Example p : SNPs grouped into K genes**

$$\mathbf{X} = [\underbrace{SNP_1, \dots, SNP_k}_{gene_1} \mid \underbrace{SNP_{k+1}, SNP_{k+2}, \dots, SNP_h}_{gene_2} \mid \dots \mid \underbrace{SNP_{l+1}, \dots, SNP_p}_{gene_K}]$$

- **Example p : genes grouped into K pathways/modules**
($X_j = gene_j$)

$$\mathbf{X} = [\underbrace{X_1, X_2, \dots, X_k}_{M_1} \mid \underbrace{X_{k+1}, X_{k+2}, \dots, X_h}_{M_2} \mid \dots \mid \underbrace{X_{l+1}, X_{l+2}, \dots, X_p}_{M_K}]$$

Challenge 3: multivariate data



Solution?

Fully Bayesian sparse regression analysis for:

- Number of predictors (p) $\gg$ number observations (n)
 - Multivariate response
 - Covariates grouped by blocks
 - Sparsity for blocks and within blocks
-
- Select group variables taking into account the data structures; all the variables within a group are selected, otherwise none of them are selected
 - Combine both sparsity of groups and within each group; only relevant variables within a group are selected

Frequentist approaches: Partial Least Squares (PLS)

- ▶ Sparse Group PLS : $\text{SNP} \subset \text{Gene}$ or $\text{Gene} \subset \text{Pathways}$

Liquet B., Lafaye de Micheaux P., Hejblum B. and Thiebaut R., (2016) *Group and Sparse Group Partial Least Square Approaches Applied in Genomics Context*. **Bioinformatics**, 32(1), 35–42.

- ▶ Sparse Group subgroup PLS : $\text{SNP} \subset \text{Gene} \subset \text{Pathways}$

M. Sutton, R. Thiebaut, and B. Liquet. (2018) *Sparse group subgroup Partial Least Squares with application to genomics data*. Statistics in Medicine.

- ▶ combining L_1 and L_2 penalties into the optimization function
- ▶ **Sparse Group Penalties:**

$$\lambda_1 \sum_{g=1}^G \sqrt{p_g} \|\beta_g\|_2 + \lambda_2 \|\beta\|_1$$

Multivariate Bayesian solution

Bayesian group lasso model with spike and slab priors

Liquet, Mengersen, Pettitt, Sutton (2017) Bayesian Analysis.

- ▶ **spike and slab** priors providing variable selection at the **group level**.
- ▶ **hierarchical** spike and slab prior structure to select variables both at the **group level** and **within each group**.

Model formulation

$$\mathbf{Y}|\mathbf{X}, \mathbb{B}, \Sigma \sim MN_{n \times q}(\mathbf{X}\mathbb{B}, \Sigma, \mathbf{I}_n),$$

$$\text{Vec}(\mathbb{B}_g^T | \Sigma, \tau_g, \pi_0) \stackrel{\text{ind}}{\sim} (1 - \pi_0) N_{m_g q}(0, \mathbf{I}_{m_g} \otimes \tau_g^2 \Sigma) + \pi_0 \delta_0(\text{Vec}(\mathbb{B}_g^T))$$

$$\tau_g^2 \sim \text{Gamma}\left(\frac{m_g + 1}{2}, \frac{\lambda_g^2}{2}\right), g = 1, \dots, G$$

$$\Sigma \sim \text{IW}(d, Q)$$

$$\pi_0 \sim \text{Beta}(a, b)$$

$\lambda_g = \sqrt{m_g} \lambda$: shrinkage for g th group

λ : global shrinkage parameter, estimated using Empirical Bayes

m_g : size of the group

λ_g is 'adaptive shrinkage', estimated using Monte Carlo EM

$\delta_0(\text{Vec}(\mathbb{B}_g^T))$: point mass at $\mathbf{0} \in \mathbb{R}^{m_g q}$

$\mathbb{B}_g$: $m_g \times q$ regression coefficient matrix for group g

d : d.f.

$Q = k \mathbf{I}_q$: positive finite scale matrix

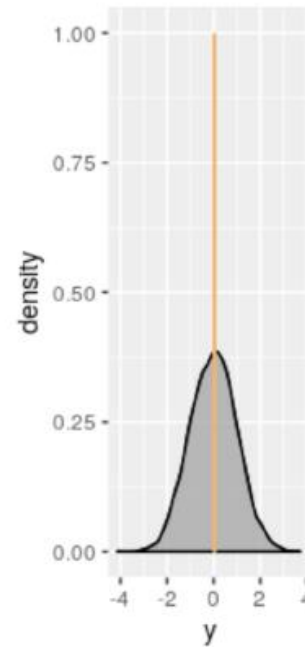
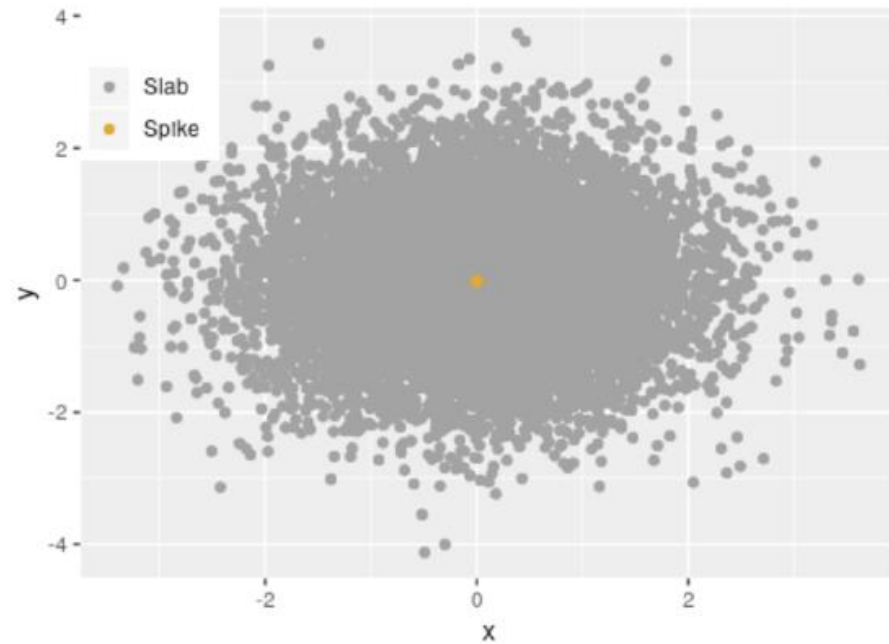
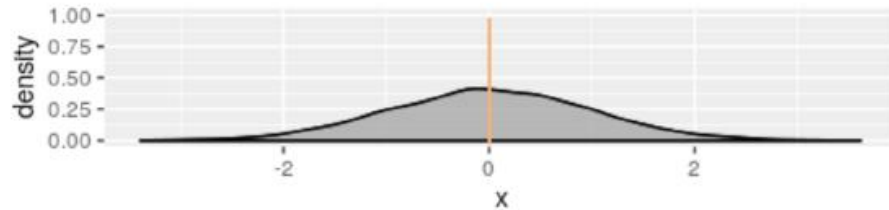
$k \approx \text{Var}(\mathbf{Y}|\mathbf{X})$

$E(\Sigma) = Q/(d - 2)$

$d = 3$: smallest integer ensuring existence of $E(\Sigma)$

a, b : prior information

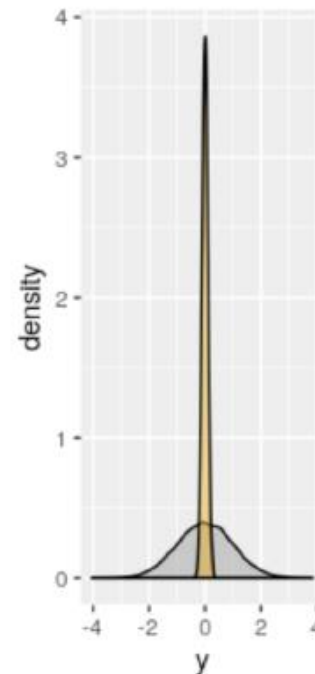
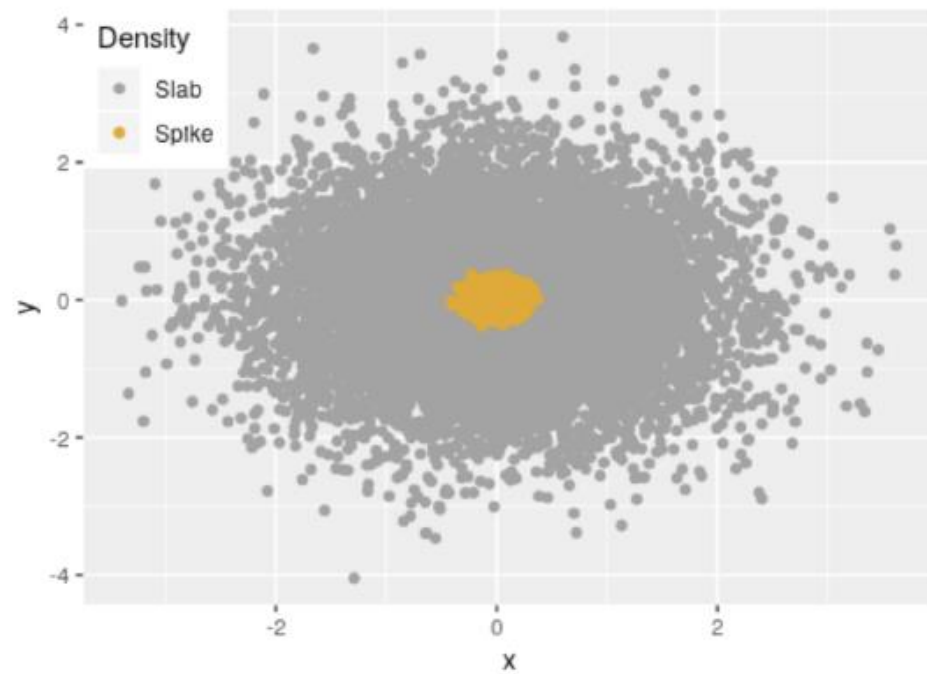
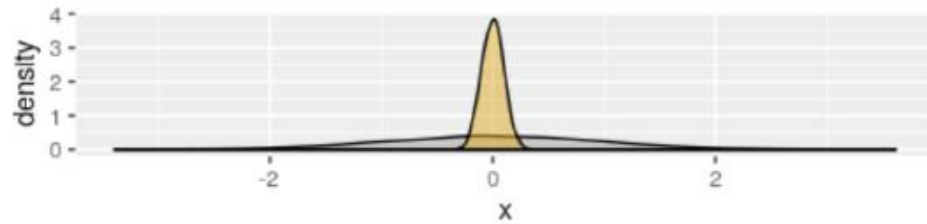
Spike and slab prior



Bivariate Dirac spike prior:

5000 samples at zero (spike)
and
5000 $N(0,1)$ samples (slab)

Spike and slab prior



Bivariate Dirac spike prior:

5000 $N(0,10^{-2})$ samples (spike)
and
5000 $N(0,1)$ samples (slab)

Posterior median estimator

Use the posterior median estimator for both selection and estimation at the same time.

Benefits:

- Enables group variable selection by obtaining a zero coefficient for some groups
- Can be expressed as a soft thresholding estimator
- Consistent in model selection and has optimal asymptotic estimation rate.

Analysis via Gibbs sampler

$$p(\mathbb{B}, \boldsymbol{\tau}^2, \Sigma, \pi_0 | \mathbb{Y}, \mathbb{X}) \propto p(\mathbb{Y} | \mathbb{B}, \boldsymbol{\tau}^2, \Sigma, \pi_0) \times p(\mathbb{B} | \boldsymbol{\tau}^2, \Sigma, \pi_0) \times p(\boldsymbol{\tau}^2) \times p(\Sigma) \times p(\pi_0)$$

$$Vec(\mathbb{B}_g^T) | \text{rest} \sim (1 - l_g) N_{m_g q} (Vec(\mathbb{M}_g^T), \Sigma_g \otimes \Sigma) + l_g \delta_0 (Vec(\mathbb{B}_g^T)), \quad g = 1, \dots, G.$$

$$\alpha_g^2 | \text{rest} \sim \begin{cases} \text{Inverse Gamma} \left(\text{shape} = \frac{m_g q + 1}{2}, \text{scale} = \frac{\lambda_g^2}{2} \right), & \text{if } \mathbb{B}_g = 0 \\ \text{Inverse Gaussian} \left(\frac{\lambda_g}{(Tr[\mathbb{B}_g \Sigma^{-1} \mathbb{B}_g^T])^{-1/2}}, \lambda_g^2 \right), & \text{if } \mathbb{B}_g \neq 0 \end{cases} \quad \alpha_g^2 = 1/\tau_g^2$$

$$\Sigma | \text{rest} \sim \text{IW} \left(d + n + \sum_{g=1}^G m_g Z_g, (\mathbb{Y} - \mathbb{X}\mathbb{B})^T (\mathbb{Y} - \mathbb{X}\mathbb{B}) + \mathbb{B}^T \mathbb{D}_{\boldsymbol{\tau}} \mathbb{B} + Q \right) \quad Z_g = \begin{cases} 1 & \text{if } \mathbb{B}_g \neq 0, \\ 0 & \text{if } \mathbb{B}_g = 0 \end{cases}$$

$$\pi_0 | \text{rest} \sim \text{Beta} \left(a + G - \sum_{g=1}^G Z_g, b + \sum_{g=1}^G Z_g \right)$$

Sparsity of groups and within each group

1. Reparametrise the coefficient matrices to tackle the two kinds of sparsity separately
2. Assume a multivariate spike and slab prior:
 - for each group-specific vector $\mathbb{B}_g$ to choose groups
 - for each τ_{gj} to choose variables within a group

Case study

Expression Quantitative Trait Loci (eQTL):

- Discover the genetic causes of variation in the expression (i.e. transcription) of genes
- gene expression data are treated as a quantitative phenotype
- genotype data (SNPs) are used as predictors

Example:

- Hopx genes, part of a larger study (Heinig et al., 2010; Liquet et al., 2016)
- Identify a parsimonious set of predictors that explains the joint variability of gene expression in four tissues (adrenal gland, fat, heart, and kidney).

Case study - data

- Predictor matrix: 770 SNPs in 29 inbred rats ($n = 29, p = 770$)
- Outcome: the 29 measured expression levels in the 4 tissues ($q = 4$)

	Correlation				Summary statistics	
	ADR	Fat	Heart	Kidney	Mean	Variance
ADR	1.00	0.46	0.44	0.70	4.72	0.07
Fat		1.00	0.24	0.42	8.23	0.09
Heart			1.00	0.44	8.79	1.61
Kidney				1.00	6.65	0.07

Chromosome	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
Group size	74	67	63	60	39	45	52	43	31	51	21	26	33	22	15	27	18	30	34	19

Repartition of the SNPs along the chromosomes, defines the group structure

Results

- 32 SNPs which belong to 6 groups/chromosomes
- Empirical estimates of the probability of inclusion of each chromosome

Chromosome	1	2	3	4	5	6	7	8	9	10
EPI	0.00	1.00	1.00	1.00	0.72	0.00	1.00	0.00	0.00	1.00
Chromosome	11	12	13	14	15	16	17	18	19	20
EPI	0.83	0.12	0.46	1.00	0.93	0.88	0.79	0.59	0.89	0.40

- Posterior median estimates

Chromosome	SNP Name	ADR	Fat	Heart	Kidney
2	D2Rat147	0.00553	0.00238	-	0.00329
2	D2Rat222	0.00442	0.00116	-	0.00305
2	D2CebrP476s2	0.00123	-	-	-
2	D2Rat69	0.00715	0.01748	0.00730	0.00620
2	D4Ucsf2	0.00054	-	-	-
2	D7Cebr205s3	0.00246	-	0.00950	0.00461
3	D7Cebr14C16s2	0.00209	0.00326	-	0.00049
4	D7Rat112	0.00035	0.00001	-	-
4	D7Rat19	0.01113	0.01800	0.03680	0.01828
4	Cyp11b2	0.00075	0.00374	-	0.00394
7	D10Ntr32	0.00123	-	0.01112	0.00143
7	D10Rat31	0.00031	0.00573	0.00442	0.00316
7	D10Cebr39s2	0.00280	0.00490	0.00821	0.00586
7	Es13	0.00539	-	0.00924	0.00419
7	D10Rat226	0.00415	0.00006	0.00987	0.00372
7	D14Rat36	0.00036	-	0.03076	-
7	D14Cebrp312s2	0.00004	-	0.05427	-
10	D14Mit3	0.04963	0.05415	0.33434	0.07491
10	D15Rat21	0.00937	0.00569	0.03140	0.01704
10	D19Utr1	0.00149	0.00297	0.00251	0.00487
10	Ednra	0.00026	-	-	-
10	D2Mit16	-	0.00077	-	-
10	D2Rat70	-	0.00190	-	-
10	D3Cebr204s4	-	0.00042	-	-
14	D4Rat49	-	0.00102	0.00092	0.00401
14	D7Mit6	-	0.00002	-	-
14	D10Rat102	-	0.00112	-	-
14	D4Rat252	-	-	-0.00184	-
14	Myc	-	-	0.00669	-
15	D10Mit3	-	-	0.00104	-
19	D14Rat8	-	-	0.00058	-
19	D14Rat52	-	-	0.00361	-

Overall:

New Bayesian methods for group-sparse modelling of a multivariate correlated response variable.

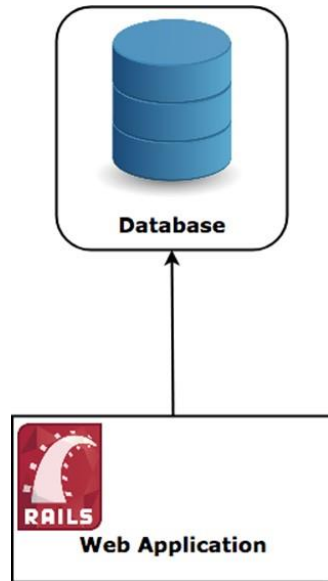
Highlights:

- Spike and slab type priors can facilitate both group and variable selection
- Posterior median estimator can both select and estimate the regression coefficients, and produce sparsity
- Simulation results showed excellent performance of the model and superior performance compared to other approaches
- Computation time is quite reasonable (minutes for case study)

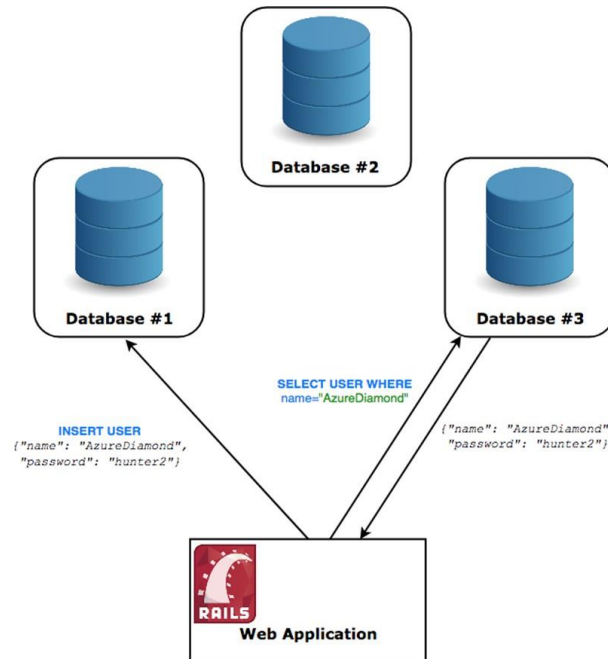
Concern: (Not) Aggregating Data



Options



Single Database



Distributed Computing

Distributed Computing:

Horizontal scaling

Fault tolerance

Low latency

Sharding

MapReduce, Apache Spark,
Hadoop, etc

[A Thorough Introduction
to Distributed Systems
\(freecodecamp.org\)](https://www.freecodecamp.org)

Options



Decentralised Computing

- Information processed in the cloud
- Not owned by one actor
- Dapps
- Edge Computing

Edge Computing

- Information not processed on the cloud filtered through remote data centres; instead, the cloud comes to the centres
- Federated learning, Federated analysis

Federated Learning: Overview

Li et al. (2020)

- Groups:

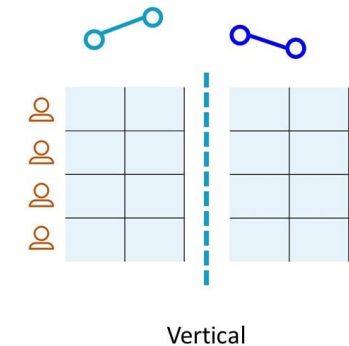
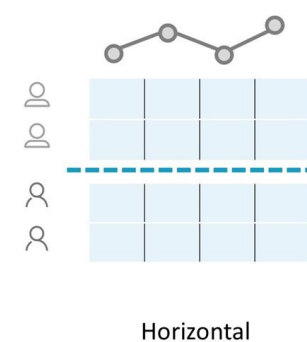
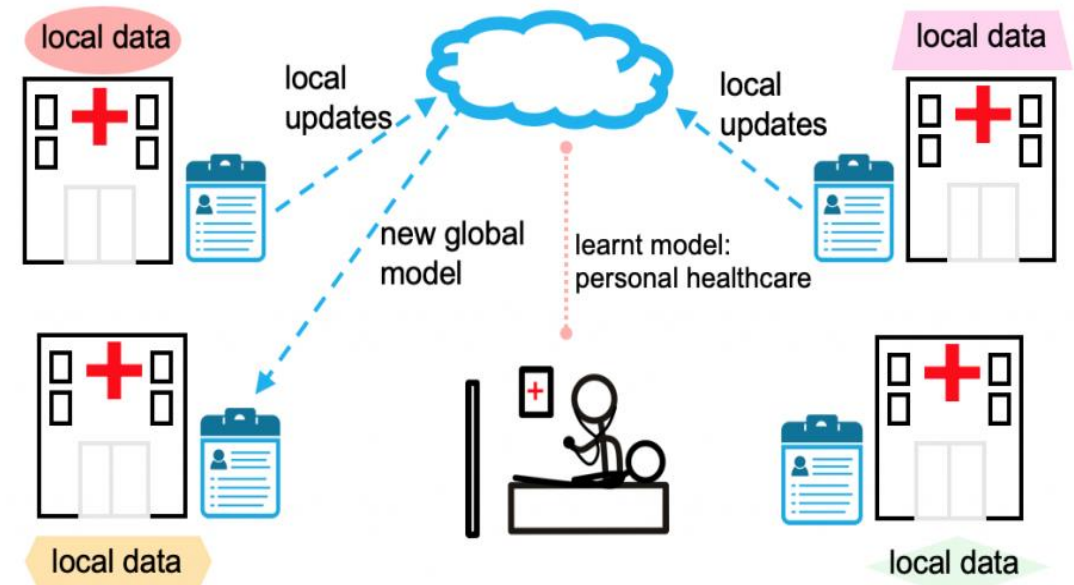
- the parties (e.g., clients)
- the manager (e.g., server)
- the communication-computation framework

- Components:

- Data partitioning
- Model
- Privacy mechanism
- Communication architecture

- Modelling approaches:

- deep neural networks, gradient boosted decision trees, linear and logistic regression, support vector machines.



Cmu ML blog

Vantage6

Federated Learning Approaches

- **Commentary:**
 - Kairous *et al.* (2019) Advances and open problems in Federated Learning. *Arxiv*.
 - Li *et al.* (2020) A survey on federated learning systems: vision, hope and reality for data privacy and protection. *Arxiv*
- **Repository with data-sharing agreements:**
 - Canakoglu, A., *et al.* (2020) Federated sharing and processing of genomic datasets for tertiary data analysis. *Briefings in Bioinformatics*
- **Bayesian Networks:**
 - Jochems (2017) Survival prediction model through distributed learning across 3 countries. *Radiotherapy and Oncology*.
- **Neural Networks:**
 - Yurochkin (2019) Bayesian nonparametric federated learning of neural networks. *ICML*.
- **Sequential and Hierarchical Bayesian models for time series data:**
 - Fang *et al.* (2020) Bayesian Inference Federated Learning for Heart Rate Prediction. *International Conference on Intelligent Computing*.
- **Communication-efficient surrogate likelihood (CSL):**
 - Jordan, Lee, Yang (2018) Communication-efficient distributed statistical inference. *JASA*.

Case Study 1: Federated Matrix Factorisation

- Observation matrix $\mathbf{Y} \in R^{i \times j}$
- MF: decompose into two latent matrices $\mathbf{U} \in R^{i \times r}$ and $\mathbf{V} \in R^{j \times r}$
- Solve $\mathbf{Y} = \mathbf{UV}^T + \mathbf{E}$
- SGD algorithm:
 - Formulate the regularised sum error (RSE) between $\hat{\mathbf{Y}}$ and $\mathbf{Y}$ as

$$RSE = \sum_{i,j} [(y_{i,j} - u_i v_j^T)^2 + \lambda (\|u_i\|^2 + \|v_j\|^2)] \quad \lambda : \text{regularisation coefficient}$$

- Update parameters by moving in the opposite direction of the gradient for each entry.
- Represent error at step $t-1$ as

$$e_{i,j}^{t-1} = y_{i,j} - u_i^{t-1} (v_j^{t-1})^T$$

- Obtain the gradient of the RSE over u_i^{t-1} and v_j^{t-1}
- Update rule:

$$u_i^t = u_i^{t-1} + \beta g_i^{t-1}$$

$$v_j^t = v_j^{t-1} + \beta g_j^{t-1}$$

β : learning rate

Xie et al. (2021)

Adaptive learning rate

- Use the cosine of the angle between the learning directions of two consecutive epochs as an index to adaptively adjust the learning rate.
- For u_i (similarly for v_j):

$$g_{i(y_{i,j})}^t = -\frac{1}{2} \nabla_{u_i} = e_{i,j}^t v_j^{t-1} - \lambda u_i^{t-1},$$

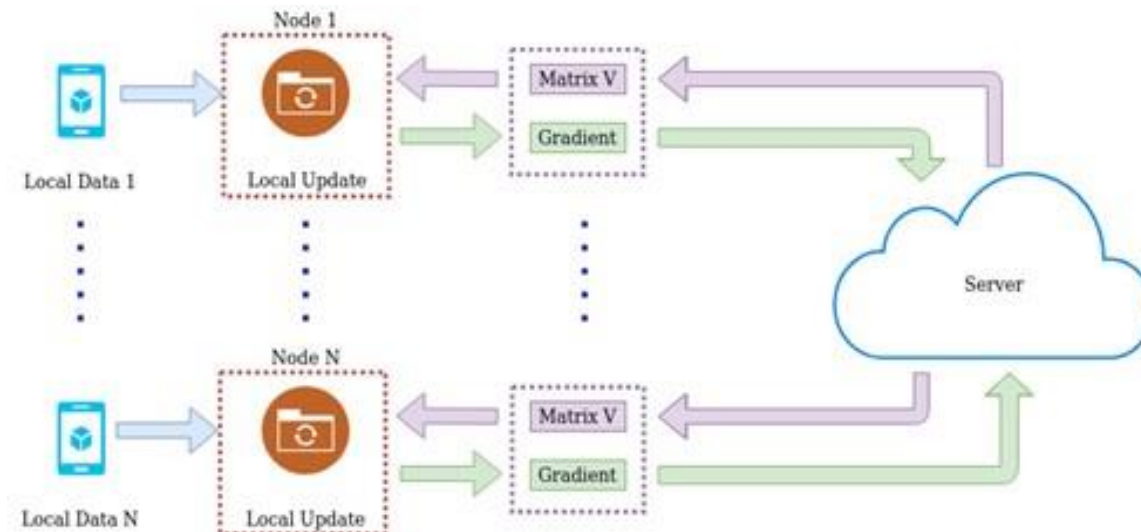
$$\cos \omega_{i(y_{i,j})}^t = (g_{i(y_{i,j})}^t \lrcorner g_{i(y_{i,j})}^{t-1}) / (\|g_{i(y_{i,j})}^t\| \lrcorner \|g_{i(y_{i,j})}^{t-1}\|),$$

$$\beta_{i(y_{i,j})}^t = \beta_{i(y_{i,j})}^{t-1} (1 + \rho \lrcorner \cos \omega_{i(y_{i,j})}^t), \quad \rho : \text{adjusts the fluctuation of the learning rate}$$

$$u_i^t = u_i^{t-1} + \beta_{i(y_{i,j})}^t \lrcorner g_{i(y_{i,j})}^{t-1},$$

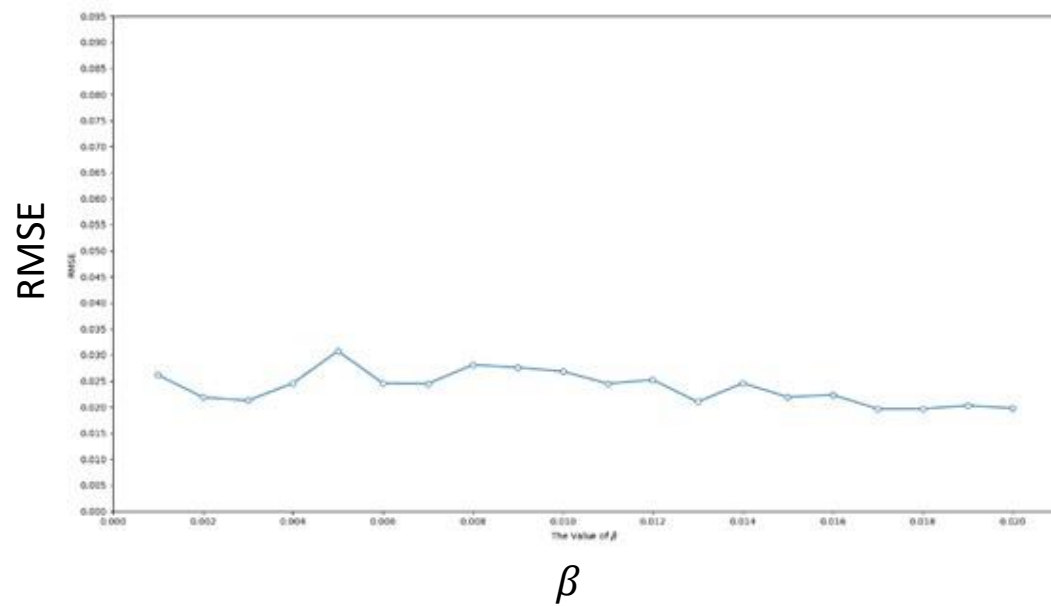
Federated Matrix Factorization

1. Node update: update u_i and gradient $g'_{j(y_{ij})}$ on each node i .
2. Upload information: upload encrypted $g'_{j(y_{ij})}$ to update v_j (two steps).
3. Server update: update $\mathbf{V}$ (encrypted).
4. Download information: each node downloads encrypted $\mathbf{V}$ from server and decrypts it to perform a new node update.
5. Stop when converged (small RSE).

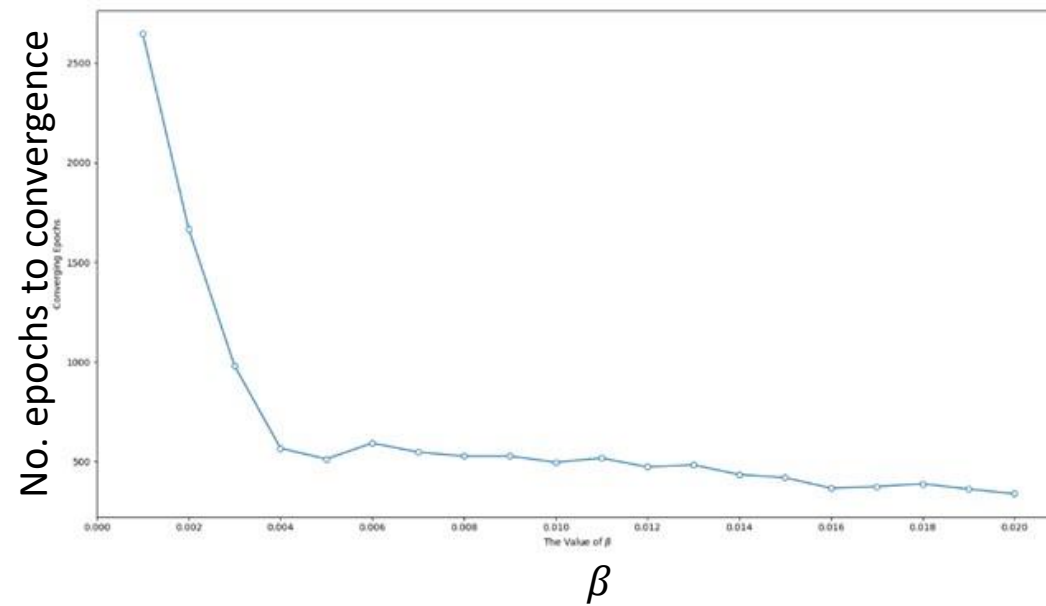


Results

RMSE vs learning rate

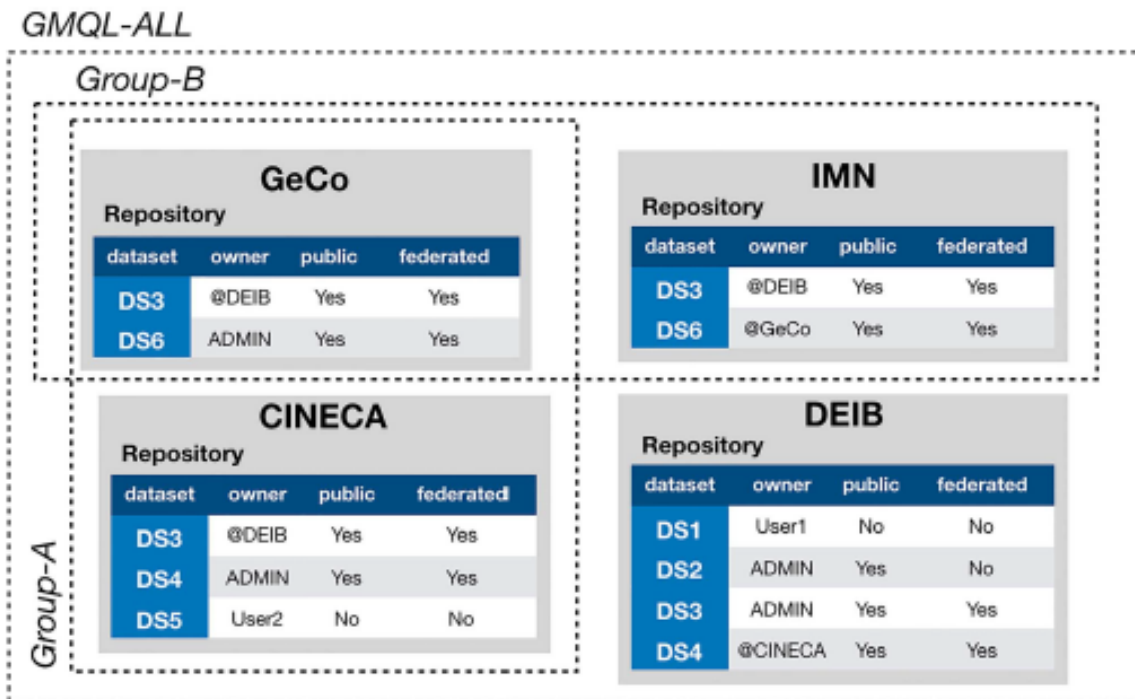


Convergence epochs vs learning rate



Case Study 3: Federated sharing of genomic datasets

- Huge growth of genomics data over last decade
- Many independent consortia and institutes
- Federated GMQL: web-based system for querying distributed genomics datasets across many instances connected through the Web.
- Automatically distribute the computation while preserving privacy constraints.
- Data sharing agreements across the Repository
- Facilitated by GMQL groups, each controlled by an administrator, who can dynamically add (or drop) GMQL instances to (from) the group and make agreements about the group



Summary

- Data are changing! Size, privacy, provenance, quality, diversity, ...
- Federated analysis / federated learning offers some solutions.
- Current interest is in federated estimation of intrinsic dimension
- Statistical methods *and their implementation* are required!

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