Random projection to dimention reduction of large scale data

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Indroduction

Masive Data

Large Scale Data

- more dimensions than records (D $>$ n)
- unable to compute $A^T A$ and using PCA
- online/stream calculation
- unable to store whole data
- covariance is not finite

Big Data

- Volume
- Velocity
- Variety

Heavy tail data

- Common in real data like market data, rare events are more probable than normal distribution
- Random variable X with right side heavy-tail distribution:

$$P(X > x) \sim cx^{-\alpha}, x \to \infty$$

Dimention Reduction

Random Coordinate Sampling

Pros:

- Simplicity $O(nk)$
- Flexability for estimating various summary statistics

Cons:

- Not accurate for losing rare events
- Not suitable for sparse data

Principal components analysis

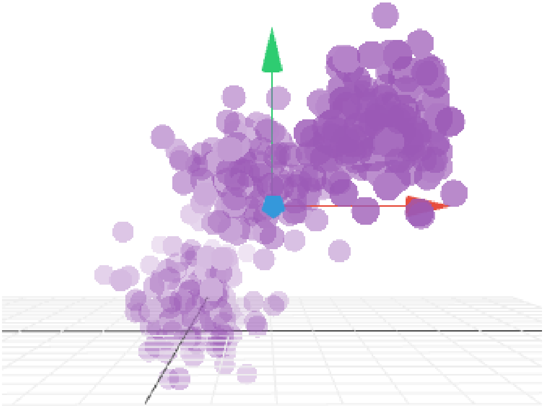


Figure 1:

Principal components analysis

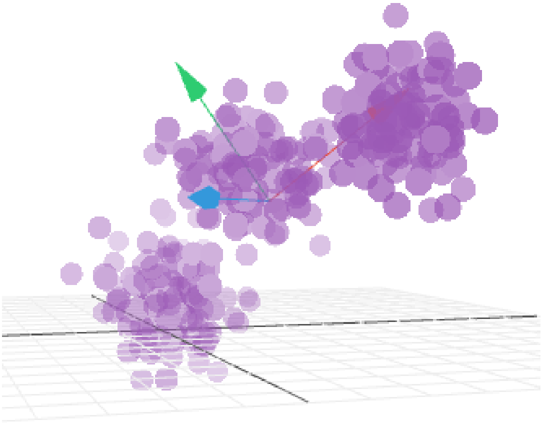


Figure 2:

Clustring

Clustering

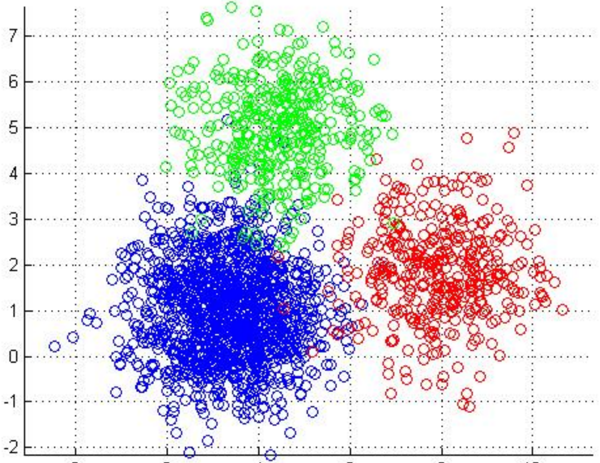


Figure 3: Clustering

k-means

Non-hierarchical clustering method

minimize within-cluster sum of squares

$$\arg\min_{\mathbf{S}} \sum_{i=1}^{k} \sum_{\mathbf{x} \in S_i} \left\| \mathbf{x} - \boldsymbol{\mu}_i \right\|^2 = \arg\min_{\mathbf{S}} \sum_{i=1}^{k} |S_i| \operatorname{Var} S_i$$

Adjusted Rand Index

$$\frac{a+b}{a+b+c+d}$$

Adjusted Rand Index

Class \Cluster	v_1	v_2	$\ldots$	v_C	Sums
u_1	n_{11}	n_{12}	$\ldots$	n_{1C}	$n_{1.}$
u_2	n_{21}	n_{22}	$\ldots$	n_{2C}	$n_{2.}$
$\vdots$	$\vdots$	$\vdots$	$\ddots$	$\vdots$	$\vdots$
u_R	n_{R1}	n_{R2}	$\ldots$	n_{RC}	$n_{R.}$
Sums	$n_{.1}$	$n_{.2}$	$\ldots$	$n_{.C}$	$n_{..} = n$

Adjusted Rand Index

$$\frac{\sum_{i,j}\binom{n_{ij}}{2} - \left[\sum_i \binom{n_{i.}}{2} \sum_j \binom{n_{.j}}{2}\right] / \binom{n}{2}}{\frac{1}{2}\left[\sum_i \binom{n_{i.}}{2} + \sum_j \binom{n_{.j}}{2}\right] - \left[\sum_i \binom{n_{i.}}{2} \sum_j \binom{n_{.j}}{2}\right] / \binom{n}{2}} \tag{1}$$

C_e

$$C_e = 100(\mathrm{ARI}_d - \mathrm{ARI}_p)$$

$$(d < p)$$

Applications

Distances

$$a = u_1^T u_2 = \sum_{i=1}^{D} u_{1,i} u_{2,i} \tag{2}$$

$$d_{(\alpha)} = \sum_{i=1}^{D} |u_1 - u_2|^{\alpha} \tag{3}$$

Distances

$$A^T A : O(n^2 D)$$

$$O(n^2 \hat{f})$$

Database Query Optimization

joins and execution plan

Sub-linear Nearest Neighbor Searching

$$O(nD) \to O(nk)$$

$$(\alpha > 1) l_\alpha \to O(n^\gamma)(\gamma < 1)$$

Stable Random Projection

Stable Distribution

Stable Distribution

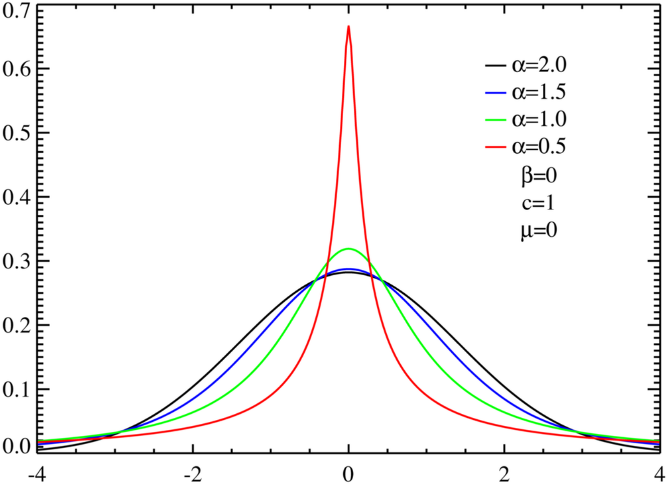


Figure 4: Stable distribution

Stable Distribution

$$X_1 + X_2 + \cdots + X_n =^d c_n X + d_n$$

Gaussian/normal:

$$f(x) = (2\pi)^{1/2} \exp(-x^2/2)$$

Cauchy:

$$f(x) = 1/(\pi(1 + x^2))$$

Stable Normal N(0,1)

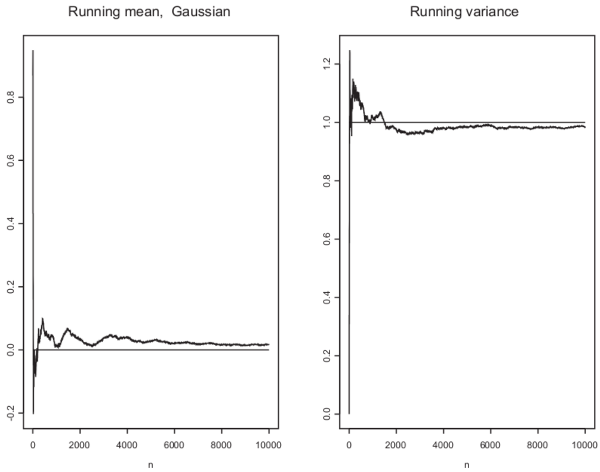


Figure 5: Normal $\alpha = 2$

Stable $\alpha = 1.5$

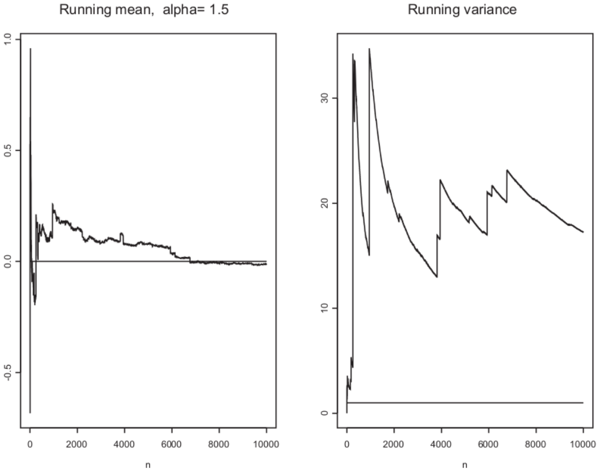


Figure 6: $\alpha = 1.5$

Stable $\alpha = 0.75$

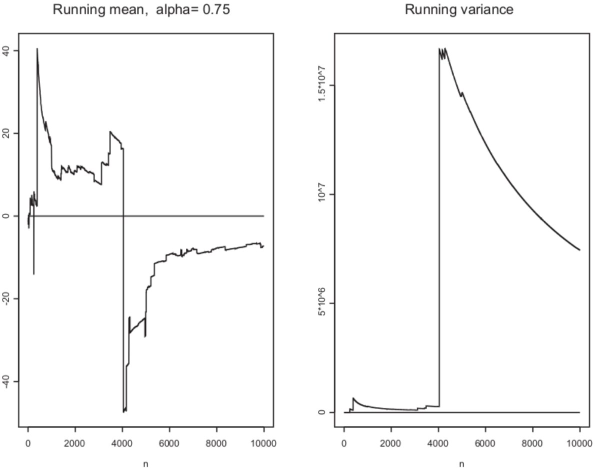


Figure 7: $\alpha = 0.75$

Stable Random Projection

Stable Random Projection

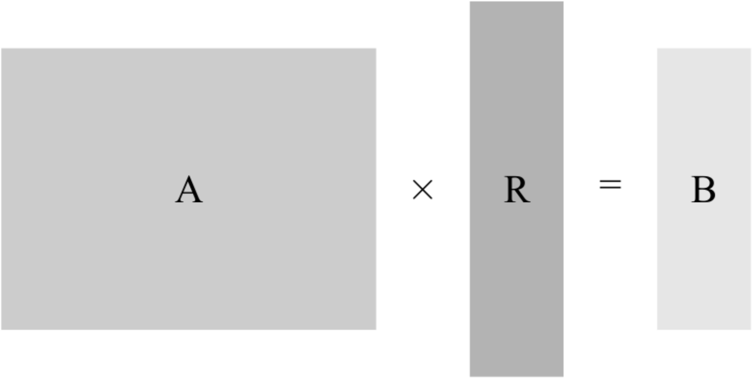


Figure 8:

Stable Random Projection

Johnson-Lindenstrauss Lemma:

$$k = O\left(\frac{\log n}{\epsilon^2}\right)$$

$$l_2 : 1 \pm \epsilon$$

Statistical estimation problem

$$v_{1,j} \sim S\left(\alpha, \sum_{i=1}^{D} |u_{1,i}|^{\alpha}\right), \quad v_{2,j} \sim S\left(\alpha, \sum_{i=1}^{D} |u_{2,i}|^{\alpha}\right), \tag{4}$$

$$x_j = v_{1,j} - v_{2,j} \sim S\left(\alpha, d_{(\alpha)} = \sum_{i=1}^{D} |u_{1,i} - u_{2,i}|^{\alpha}\right). \tag{5}$$

Couchy Random Projection

$$d = \sum_{i=1}^{D} |u_{1,i} - u_{2,i}|$$

Very Sparse Random Projection

$$\{-1, 0, 1\}$$

$$\left\{ \frac{1}{2s}, 1 - \frac{1}{s}, \frac{1}{2s} \right\}$$

$$O(Dk) \rightarrow O(Dk/s)$$

l_α Random Projection

$$d_{(\alpha)} = \sum_{i=1}^{D} |u_{1,i} - u_{2,i}|^\alpha$$

Data & Implementation

Data summary

Dataset	n	D	N_{class}
Thyroid	215	5	3
Iris	150	4	3
Diabetes	145	3	3
Swiss Banknotes	200	6	2
Seeds	210	7	3
Mice Protein Expression	1080	77	8
Crabs	200	6	2

Results

C_e

$$C_e = 100(\mathrm{ARI}_d - \mathrm{ARI}_p)$$

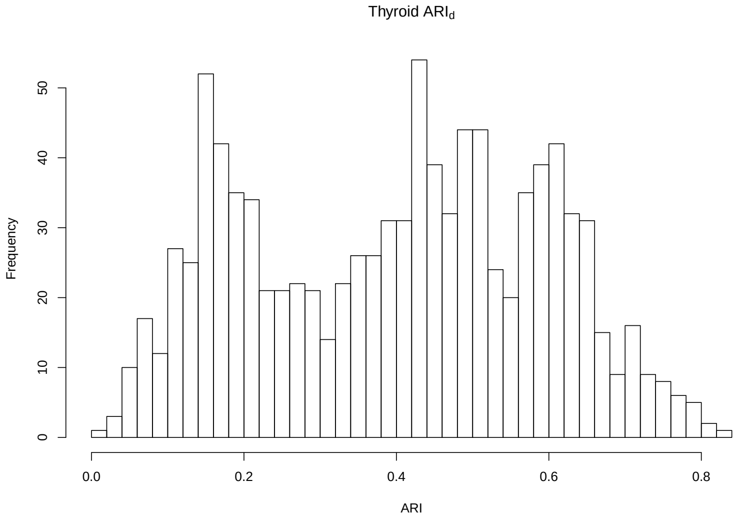
$$(d < p)$$

Normal $\alpha = 2, d = 2$

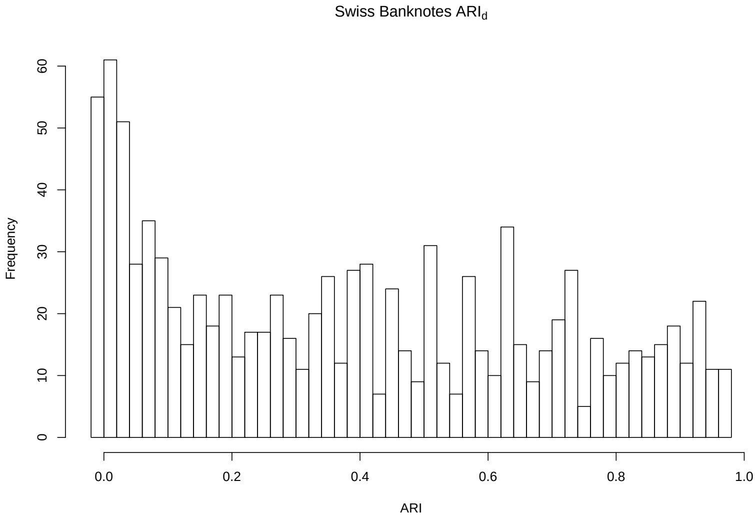
Tabel $\alpha = 2, d = 2$

Dataset	ARI_p	ARI_d	C_e
Thyroid	0.58	0.40	-18
Iris	0.62	0.47	-15
Diabetes	0.38	0.36	-2
Swiss Banknotes	0.85	0.39	-46
Seeds	0.77	0.45	-33
Mice Protein Expression	0.13	0.07	-7
Crabs	0.05	0.04	0

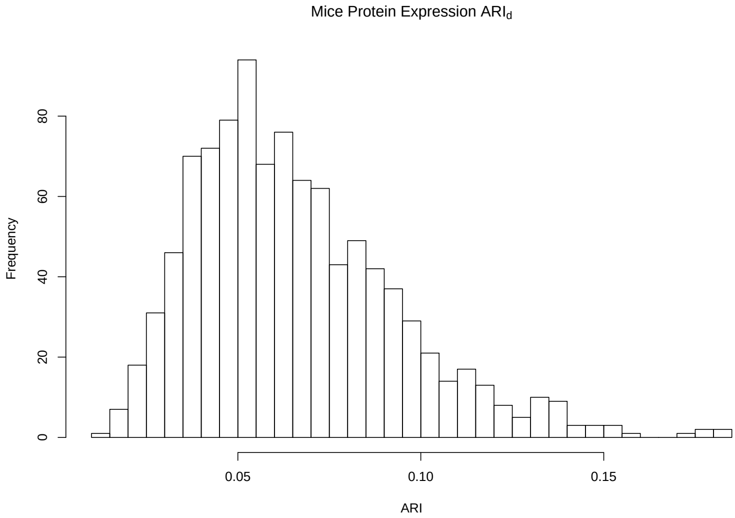
Histogram 2 peak



Hisogram undefined



Hisogram efficient



Normal $\alpha = 2, d = 3$

Tabel $\alpha = 2, d = 3$

Dataset	ARI_p	ARI_d	C_e
Thyroid	0.58	0.43	-15
Iris	0.62	0.54	-8
Diabetes	0.38	0.38	0
Swiss Banknotes	0.85	0.47	-37
Seeds	0.77	0.53	-24
Mice Protein Expression	0.13	0.08	-5
Crabs	0.05	0.05	0

Cauchy $\alpha = 1, d = 2$

Tabel $\alpha = 1, d = 2$

Dataset	ARI_p	ARI_d	C_e
Thyroid	0.58	0.36	-23
Iris	0.62	0.51	-11
Diabetes	0.38	0.33	-5
Swiss Banknotes	0.85	0.40	-44
Seeds	0.77	0.45	-32
Mice Protein Expression	0.13	0.06	-7
Crabs	0.05	0.05	0

Cauchy $\alpha = 1, d = 3$

Tabel $\alpha = 1, d = 3$

Dataset	ARI_p	ARI_d	C_e
Thyroid	0.58	0.37	-22
Iris	0.62	0.54	-8
Diabetes	0.38	0.35	-3
Swiss Banknotes	0.85	0.43	-41
Seeds	0.77	0.47	-30
Mice Protein Expression	0.13	0.07	-7
Crabs	0.05	0.05	0

Sparse $s = 2, d = 2$

Tabel $s = 2, d = 2$

Dataset	ARI_p	ARI_d	C_e
Thyroid	0.58	0.40	-18
Iris	0.62	0.49	-13
Diabetes	0.38	0.35	-3
Swiss Banknotes	0.85	0.40	-44
Seeds	0.77	0.45	-33
Mice Protein Expression	0.13	0.06	-7
Crabs	0.05	0.05	0

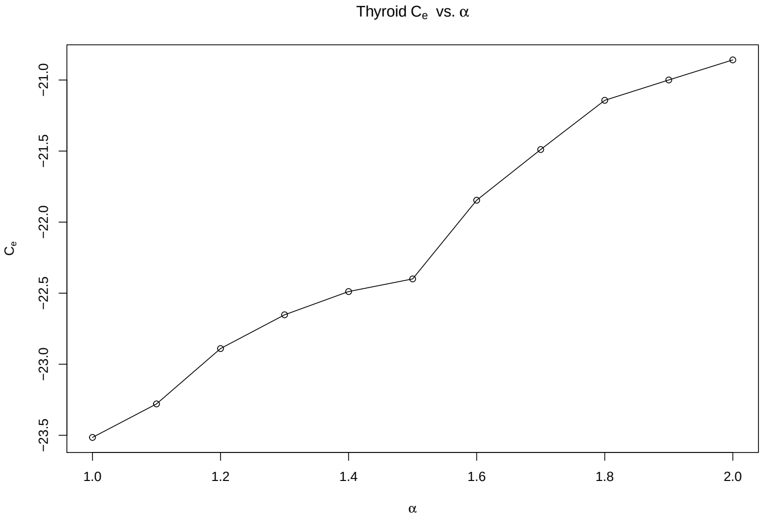
Sparse $s = 2, d = 3$

Tabel $s = 2, d = 3$

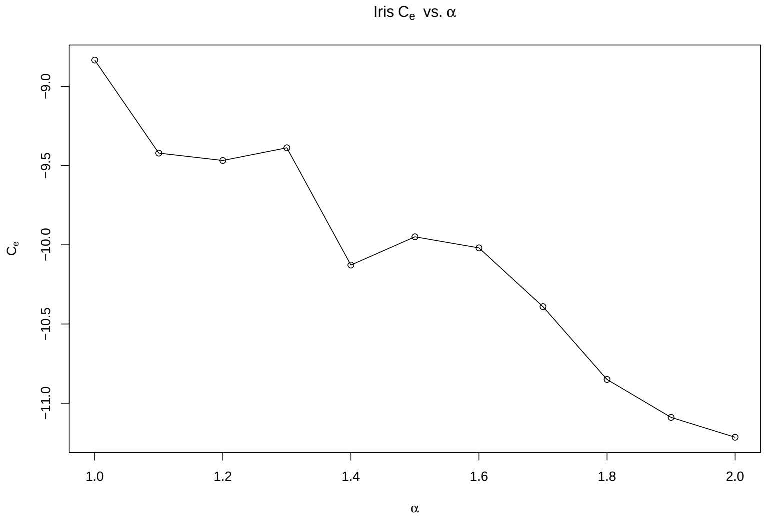
Dataset	ARI_p	ARI_d	C_e
Thyroid	0.58	0.44	-14
Iris	0.62	0.54	-8
Diabetes	0.38	0.37	-1
Swiss Banknotes	0.85	0.49	-36
Seeds	0.77	0.53	-24
Mice Protein Expression	0.13	0.08	-5
Crabs	0.05	0.05	0

C_e versus α for $d = 2$

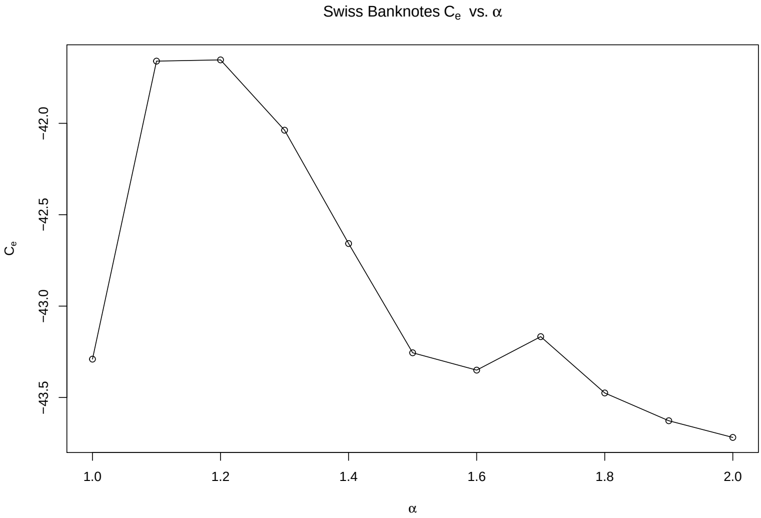
Normal is better



Cauchy is better

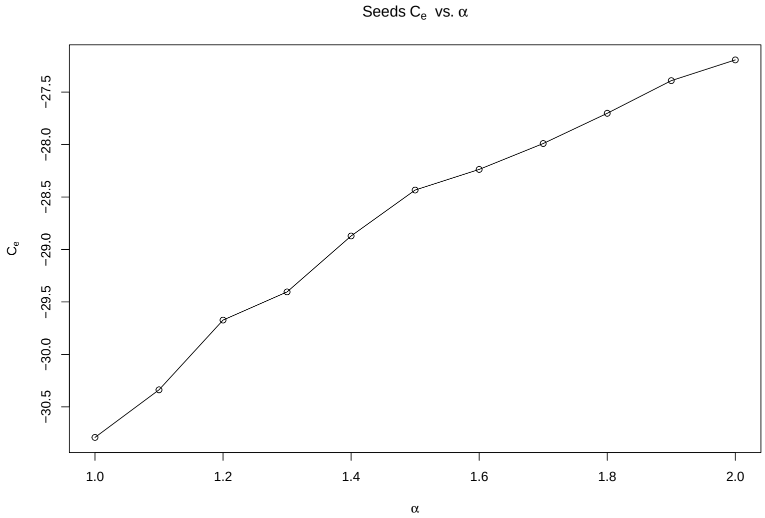


$0 < \alpha < 1$ is better

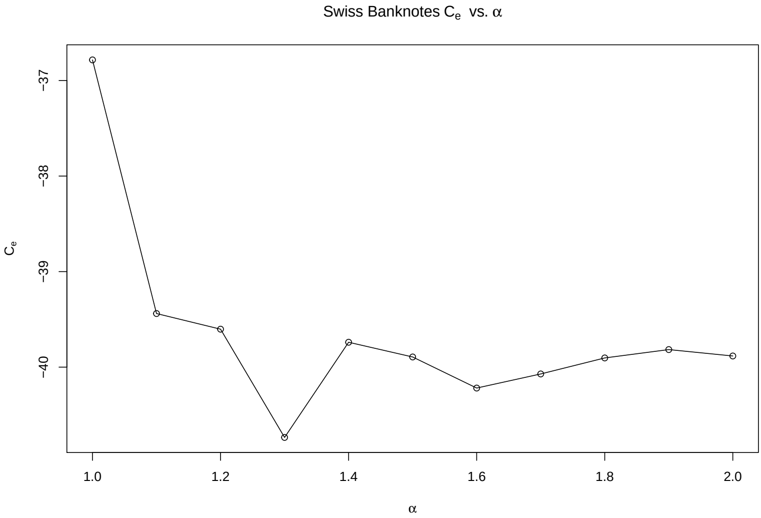


C_e versus α for $d = 3$

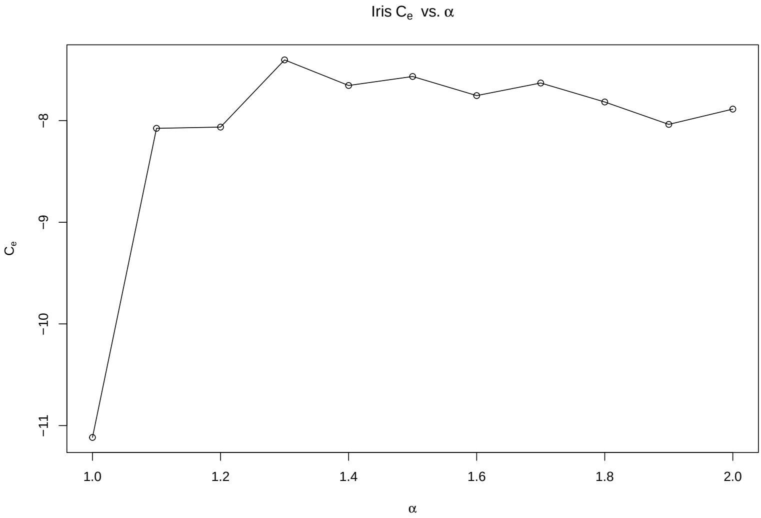
Normal is better



Cauchy is better

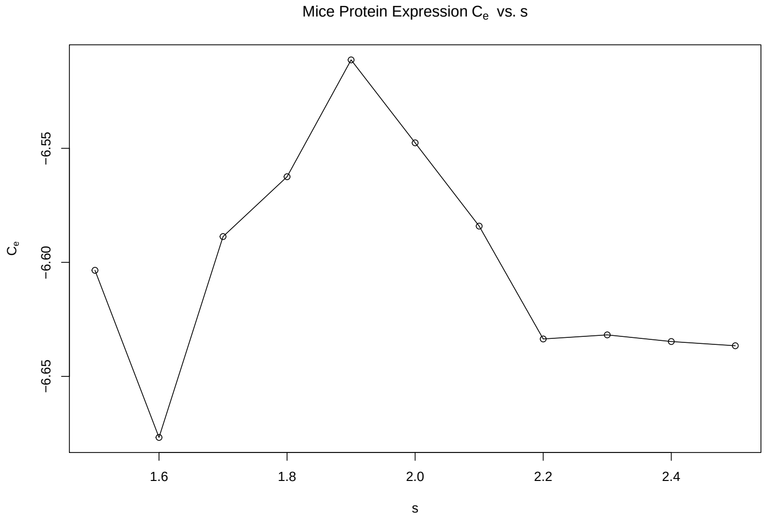


$0 < \alpha < 1$ is better



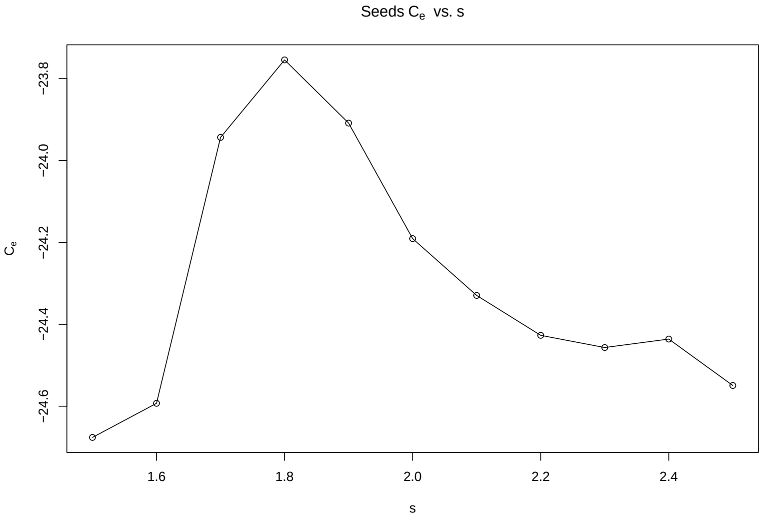
C_e versus s in Sparse for $d = 2$

MPE



C_e versus s in Sparse for $d = 3$

Seeds



Comparision $d = 2$

Comparision $d = 2$

Dataset	$\text{RP}_{\alpha=2}$	$\text{RP}_{\alpha=1}$	$\text{RP}_{s=2}$	Cov.	ρ_s	ρ'	η_p	SCV_2	FSCV_1	SCV_1
Thyroid	-18	-23	-18	-10	35	30	-6	36	37	37
Iris	-15	-11	-13	1	3	3	0	0	0	0
Diabetes	-2	-5	-3	0	22	33	8	4	38	4
Banknotes	-46	-44	-44	0	0	-97	-71	-93	0	-15
Seeds	-33	-32	-33	-14	0	-14	2	2	0	2
MPE	-7	-7	-7	-11	-11	-19	-6	-13	-19	-10
Crabs	0	0	0	2	1	-1	0	-1	1	-2

Figure 9: d = 2

Comparision $d = 3$

Comparision $d = 3$

Dataset	$RP_{\alpha=2}$	$RP_{\alpha=1}$	$RP_{s=2}$	Cov.	ρ_s	ρ'	η_p	SCV_2	$FSCV_1$	SCV_1
Thyroid	-15	-22	-14	-12	3	-6	5	4	2	4
Iris	-8	-8	-8	0	2	1	0	3	-1	3
Banknotes	-37	-41	-36	0	-5	0	-88	0	-24	0
Seeds	-24	-30	-24	1	0	-1	0	-26	-15	-15
MPE	-5	-7	-5	-9	-8	-12	-4	-8	-7	-8
Crabs	0	0	0	-1	0	1	0	1	-1	2

Figure 10: d = 3

???

Similarity measures

تعریف ۷

X بردار تصادفی پایدار با پارامترهای α و اندازه‌ی طیفی Γ،
معیار وابستگی η_p برای $i, j = ۱, \ldots, d \quad (X_i, X_j)$:

$$\eta_p = \eta_p\left(X_i, X_j\right) = \| \gamma^{\alpha}\left(u_i, u_j\right) - \gamma_{\perp}^{\alpha}\left(u_i, u_j\right) \|_{L_p, du} \qquad (۳)$$

$\gamma_{\perp}$ تابع مقیاس تصویر توزیع پایدار دو متغیره با مولفه‌های مستقل

Figure 11:

Similarity measures

تعریف ۸

(X,Y) بردار تصادفی پایدار با پارامتر اندازه‌ی طیفی Γ_{XY}،

$$\rho_s(X,Y) = \left(\int_{\mathbb{S}^{2}} \left(\Gamma_{XY}(u) - \Gamma_{\perp}(u)\right)^{2} \mathrm{d}u\right)^{1/2} \qquad (6)$$

که در آن $\Gamma_{\perp}$ اندازه طیفی بردار پایدار با متغیرهای مستقل

Figure 12:

Similarity measures

معیار وابستگی هم‌پراکنشی متقارن

$$SCV_{۱} = \frac{[X_{۱}, X_{۲}]_{\alpha} + [X_{۲}, X_{۱}]_{\alpha}}{۲}.$$

Figure 13:

Similarity measures

معیار وابستگی هم‌پراکنشی متقارن

$$SCV_{۲}(X_i, X_j) = \kappa_\alpha(X_i, X_j)\left|[X_i, X_j]\,[X_j, X_i]\right|^{\frac{۱}{۲}} \quad i, j = ۱, \ldots, p,$$

که درآن

$$\kappa_\alpha(X_i, X_j) = \begin{cases} sign([X_i, X_j]_\alpha), & sign([X_i, X_j]_\alpha) = sign([X_j, X_i]_\alpha), \\ -۱, & sign([X_i, X_j]_\alpha) = -sign([X_j, X_i]_\alpha). \end{cases}$$

Figure 14: