## Lecture 4. High dimensionality & Random Projection

Recall data  $X = [X_1, ..., X_n]^{p \times n}$ Centered data  $X_c = XH$ ,  $H = I - \frac{1}{h}11^T$ ,  $1 = \int_{-\infty}^{\infty} \int_{-\infty}^{\infty} e^{-x} dx$ k = SVD  $X_c = \hat{U}_k \hat{S}_k \hat{V}_k^T$  as best rank-k approximation  $\hat{U}_k \in \mathbb{R}^{p \times k}$  of  $X_c$   $\hat{V}_k \in \mathbb{R}^{n \times k}$  orthogonal column mat.  $\hat{S}_{K} = \text{diag}(\hat{\sigma}_{i}, ... \hat{\sigma}_{k}), \hat{\sigma}_{i} \geq \hat{\sigma}_{i} \geq ... \geq \hat{\sigma}_{k}$ k-PCA is given by  $(\hat{U}_K, \hat{S}_K)$  with projection B=[Bi,...,Bn]= UKXc = SKVK each column gives new coordinates (=) Eigenvalue Decomposition et Covariance Mat.  $\hat{\Sigma}_{n} = \frac{1}{n} \times_{e} \times_{c}^{T} = \hat{U}_{k} \hat{\Lambda}_{k} \hat{U}_{k}^{T}, \hat{\Lambda}_{k} = \hat{S}_{k}^{2}$  $\frac{1}{1000}$  is given by  $(\hat{S}_{K}, \hat{V}_{K})$  with data representation  $\hat{S}_{K}, \hat{V}_{K} \in \mathbb{R}^{K \times N}$ SKVKT ERKEN Esgenvalue Decomp. of Kernel Mat.

Eigenvalue Vecomp, of Kernet Mat  $\hat{K} = \frac{1}{n} X_C X_C \cong V_K \hat{\Lambda}_K V_K$ 

" kernel-PCA/MDS"  $B = HKH = \hat{V}_{K} \hat{\Lambda}_{K} \hat{V}_{K}$ 

Problem: What about big data & high dimensionality?

1>>1

\$>>1 vig data  $n \gg 1$ ,  $\sum_{k=1}^{n} \sum_{i} (x_i - \hat{\mu})(x_i - \hat{\mu})^T$ down sample  $n' \Rightarrow good approximation of <math>\sum_{n} k \cdot \hat{U}_{k} \cdot \hat{S}_{k}$   $\hat{V}_{k} \text{ restricted on subsample}$ high dimensionality P>>1, In & R PxP too big to compute  $K = X_c X_c$ ? easy to approximate? Random Projection! e.g. R= fa A dxp where Aij ~N(0,1).  $X_c^{p*n} \mapsto (RX_c)^{d\times n}, d \ll p.$  $K_R = X_C^T R^T R X_C$  a good approximation of K.1 $\rho_{z}\frac{1}{2}$ · A ij = { (-g- 1/2 sparse with many zeros!  $\bullet \text{ Aij} = \begin{cases} 1 \\ 0 \end{cases}$  $p = \frac{1}{6}$   $1-2p = \frac{2}{3}$ P = 1/6

Examp (Hunan Genome Piversity Project/HGDP) hatp://www.cephb.fr/en/hgdp-panel.php n=1064 persons p=644,258 SNPs X pxn : Xij = D: "AA", 1: "AC"; 2: "CC"; 9: "Missing" Removenz 21 persons with missing values. X 644,258 x 1043 R dxp randomly select d rows/SNPs of X.  $\begin{array}{lll}
X & d \times N \\
X & = RX_C = RXH \cong \hat{U}_R \hat{S}_R \hat{V}_R \\
d = p = 600K & d = 5k & d = 100K.
\end{array}$ FIGURE 1. (Left) Projection of 1043 individuals on the top 2 MDS principal components. (Middle) MDS computed from 5,000 random projections. (Right) MDS computed from 100,000 random projections. Pictures are due to Qing Wang.

In all cases, ( $\hat{S}_{k,d}$ ,  $\hat{V}_{k,d}$ ) are good results! Here: pcA coordinates:  $\hat{S}_{k,d}$   $\hat{V}_{k,d}$   $\in [R^{k\times N}, k=2.$ Why sore it work?

## Johnson-Lindenstrauss Lemma

ldea:  $x_i \in \mathbb{R}^p$ ,  $dij = ||x_i - x_j||$ , i=1, ..., nLook for a transform  $f: X_i \mapsto Y_i \in \mathbb{R}^d$ , d=O(cologn)5.t. 1-E < 11/1 - Yj11 < 1+2. with probability Uniform E-Isometry! = 1-10 aso relative metric-distortion is uniformly bounded by 2! f is a random projection! 1980s Johnson-Lindensfrauss Lipschitz Extension Dimitris Achlioptas.

Computer Science, data compression

newsest reighbor search Then Given  $\mathcal{E} \in (0, 1)$ ,  $n, \alpha > 0$ .  $k = c(\alpha, 2) log n = (4+2\alpha)(\frac{\mathcal{E}}{2} - \frac{\mathcal{E}^3}{3})^7 log n$ Then for any 1 points  $\chi_i \in \mathbb{R}^D$  (i=1,...,n), there exists a map  $f: \mathbb{R}^D \to \mathbb{R}^k$  st.  $\forall x_i: \forall x_j: |f(x_i) - f(x_j)|^2 \le |f(x_i) - f(x_j)|^2$  with prob  $\ge |f(x_i) - f(x_j)|^2$   $\le |f(x_i) - f(x_j)|^2$ (X)

• cx) holds with probability at least  $1-n^{\alpha}$ ,

• f can be found in randomized polynomial time

(random project'cons)

e.g. f(x) = Rx,  $R = (r_1, ..., r_K)^T \in R^{k \times D}$ ,  $x \in R^D$   $r_i \in S^{D-1}$  sphere of D-1 dim.

e.g.  $r_i = \frac{(a_i - a_b)}{\|a_i\|}$ ,  $a_j \sim N(o, 0)$