High-Dimensional Probability and Statistics

MATH/STAT/ECE 888: Topics in Mathematical Data Science Sebastien Roch (Math+Stat) UW-Madison Fall 2021

Lecture 1 (09/08/21)

Classical statistics (we'll review some):

- small number p of parameters
- large number n of observations
- investigate performance of estimators as $n \rightarrow \infty$ (CLT...)

Today's slides based on Chap 1 (read it!) of Giraud

https://www.imo.universite-paris-saclay.fr/~giraud/Orsay/slides/slidesC1.pdf

High-dimensional data

Chapter 1

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High-dimension data

- biotech data (sense thousands of features)
- \bullet images (millions of pixels / voxels)
- marketing, business data
- **o** crowdsourcing data
- e etc

Blessing?

 \Diamond we can sense thousands of variables on each "individual" : potentially we will be able to scan every variables that may influence the phenomenon under study.

 \Diamond the curse of dimensionality : separating the signal from the noise is in general almost impossible in high-dimensional data and computations can rapidly exceed the available resources.

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Curse of dimensionality

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Curse 1 : fluctuations cumulate

Example : $X^{(1)}, \ldots, X^{(n)} \in \mathbb{R}^p$ i.i.d. with $\text{cov}(X) = \sigma^2 I_p$. We want to estimate $E[X]$ with the sample mean

$$
\bar{X}_n = \frac{1}{n} \sum_{i=1}^n X^{(i)}.
$$

Then

$$
\mathbb{E}\left[\|\bar{X}_n - \mathbb{E}[X]\|^2\right] = \sum_{j=1}^p \mathbb{E}\left[\left([\bar{X}_n]_j - \mathbb{E}[X_j]\right)^2\right] \\
= \sum_{j=1}^p \text{var}\left([\bar{X}_n]_j\right) = \frac{p}{n}\sigma^2.
$$

 \odot It can be huge when $p \gg n...$

Curse 2 : locality is lost

Observations $(Y_i, X^{(i)}) \in \mathbb{R} \times [0,1]^p$ for $i = 1, \ldots, n$.

Model: $Y_i = f(X^{(i)}) + \varepsilon_i$ with f smooth. assume that $(Y_i, X^{(i)})_{i=1,...,n}$ i.i.d. and that $X^{(i)} \sim \mathcal{U}\left([0,1]^p\right)$

Local averaging: $\widehat{f}(x) = \text{average of } \{Y_i : X^{(i)} \text{ close to } x\}$

 $A \equiv A$ \equiv $A \cap B$

Curse 2 : locality is lost

Figure: Histograms of the pairwise-distances between $n = 100$ points sampled uniformly in the hypercube $[0,1]^p$, for $p = 2, 10, 100$ and 1000.

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Why?

Square distances.

$$
\mathbb{E}\left[\|X^{(i)}-X^{(j)}\|^2\right]=\sum_{k=1}^p\mathbb{E}\left[\left(X_k^{(i)}-X_k^{(j)}\right)^2\right]=\rho\,\mathbb{E}\left[(U-U')^2\right]=\rho/6,
$$

with U, U' two independent random variables with $\mathcal{U}[0,1]$ distribution.

Standard deviation of the square distances

$$
\begin{aligned} \text{sdev}\left[\|X^{(i)} - X^{(j)}\|^2\right] &= \sqrt{\sum_{k=1}^p \text{var}\left[\left(X_k^{(i)} - X_k^{(j)}\right)^2\right]} \\ &= \sqrt{p \text{var}\left[(U' - U)^2\right]} \approx 0.2\sqrt{p} \,. \end{aligned}
$$

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Curse 3 : lost in high-dimensional spaces

High-dimensional balls have a vanishing volume!

 $V_p(r)$ = volume of a ball of radius r in dimension p $= r^p V_p(1)$

with

$$
V_p(1) \stackrel{p\to\infty}{\sim} \left(\frac{2\pi e}{p}\right)^{p/2} (p\pi)^{-1/2}.
$$

Curse 3 : lost in high-dimensional space

Which sample size to avoid the lost of locality?

Number *n* of points x_1, \ldots, x_n required for covering $[0, 1]^p$ by the balls $B(x_i, 1)$:

$$
n \geq \frac{1}{V_p(1)} \stackrel{p \to \infty}{\sim} \left(\frac{p}{2\pi e}\right)^{p/2} \sqrt{p\pi}
$$

Curse 4: Thin tails concentrate the mass!

Figure: Mass of the standard Gaussian distribution $g_p(x) dx$ in the "bell" $B_{p,0.001} = \{x \in \mathbb{R}^p : g_p(x) \ge 0.001 g_p(0)\}\)$ for increasing dimensions p.

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Why?

Volume of a ball: $V_p(r) = r^p V_p(1)$

The volume of a high-dimensional ball is concentrated in its crust!

Ball: $B_p(0,r)$ **Crust:** $C_p(r) = B_p(0, r) \setminus B_p(0, 0.99r)$

The fraction of the volume in the crust

$$
\frac{\mathrm{volume}(C_p(r))}{\mathrm{volume}(B_p(0,r))} = 1 - 0.99^p
$$

goes exponentially fast to 1!

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Forget your low-dimensional intuitions!

Curse 4: Thin tails concentrate the mass!

Where is the Gaussian mass located?

For $X \sim \mathcal{N}(0, I_p)$ and $\varepsilon > 0$ small

$$
\frac{1}{\varepsilon} \mathbb{P} \left[R \le ||X|| \le R + \varepsilon \right] = \frac{1}{\varepsilon} \int_{R \le ||x|| \le R + \varepsilon} e^{-||x||^2/2} \frac{dx}{(2\pi)^{p/2}}
$$

$$
= \frac{1}{\varepsilon} \int_{R}^{R + \varepsilon} e^{-r^2/2} r^{p-1} \frac{pV_p(1) dr}{(2\pi)^{p/2}}
$$

$$
\approx \frac{p}{2^{p/2} \Gamma(1 + p/2)} R^{p-1} \times e^{-R^2/2}.
$$

This mass is concentrated around $R=\,$ √ $p-1!$

$Gaussian = \text{uniform}$?

The Gaussian $\mathcal{N}(0, I_p)$ distribution looks like a uniform distribution on the The Gaussian *J* v (0, I_p) dis
sphere of radius $\sqrt{p-1}$!

Curse 5: weak signals are lost

Finding active genes: we observe *n* repetitions for p genes

$$
Z_j^{(i)} = \theta_j + \varepsilon_j^{(i)}, \quad j = 1, \ldots, p, \quad i = 1, \ldots, n,
$$

with the $\varepsilon_i^{(i)}$ $j^{(\prime)}_j$ i.i.d. with $\mathcal{N}(0,\sigma^2)$ Gaussian distribution. **Our goal:** find which genes have $\theta_i \neq 0$

For a single gene

Set

$$
X_j = n^{-1/2} (Z_j^{(1)} + \ldots + Z_j^{(n)}) \sim \mathcal{N}(\sqrt{n}\theta_j, \sigma^2)
$$

Since $\mathbb{P}\left[|\mathcal{N}(0, \sigma^2)| \geq 2\sigma\right] \leq 0.05$, we can detect the active gene with X_j when

$$
|\theta_j|\geq \frac{2\sigma}{\sqrt{n}}
$$

Curse 5: weak signals are lost

Maximum of Gaussian For $\mathcal{W}_1,\ldots,\mathcal{W}_p$ i.i.d. with $\mathcal{N}(0,\sigma^2)$ distribution, we have (see later) $\max_{j=1,\dots,p} W_j \approx \sigma \sqrt{2 \log(p)}.$

Consequence: When we consider the p genes together, we need a signal of order

$$
|\theta_j| \ge \sigma \sqrt{\frac{2\log(p)}{n}}
$$

in order to dominate the noise \odot

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- Curse 6 : an accumulation of rare events may not be rare (false discoveries, etc)
- Curse 7 : algorithmic complexity must remain low

 e etc

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Low-dimensional structures in high-dimensional data Hopeless?

Low dimensional structures : high-dimensional data are usually concentrated around low-dimensional structures reflecting the (relatively) small complexity of the systems producing the data

- **•** geometrical structures in an image,
- regulation network of a "biological system",
- social structures in marketing data,
- **•** human technologies have limited complexity, etc.

Dimension reduction :

- "unsupervised" (PCA)
- "supervised"

Principal Component Analysis

For any data points $X^{(1)},\ldots,X^{(n)}\in\mathbb{R}^p$ and any dimension $d \leq p$, the PCA computes the linear span in \mathbb{R}^p

$$
V_d \in \operatornamewithlimits{argmin}_{\dim(V) \le d} \quad \sum_{i=1}^n \|X^{(i)} - \operatorname{Proj}_V X^{(i)}\|^2,
$$

where $Proj_V$ is the orthogonal projection matrix onto V.

 V_2 in dimension $p = 3$.

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Recap on PCA Exercise 1.6.4

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"Supervised" dimension reduction

PCA

LDA

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Summary

Statistical difficulty

- high-dimensional data
- **o** small sample size

Good feature

Data generated by a large stochastic system

- existence of low dimensional structures
- (sometimes: expert models)

The way to success

Finding, from the data, the hidden structure in order to exploit them.

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Mathematics of high-dimensional statistics

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Paradigm shift

Classical statistics:

- \bullet small number p of parameters
- \bullet large number *n* of observations
- we investigate the performances of the estimators when $n \to \infty$ (central limit theorem...)

Actual data:

- \bullet inflation of the number p of parameters
- small sample size: $n \approx p$ ou $n \ll p$

 \Longrightarrow Change our point of view on statistics! (the $n \to \infty$ asymptotic does not fit anymore)

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Statistical settings

- double asymptotic: both $n, p \rightarrow \infty$ with $p \sim g(n)$
- non asymptotic: treat n and p as they are

Double asymptotic

- more easy to analyse, sharp results \mathbb{C}
- but sensitive to the choice of $g \odot$

ex: if $n=33$ and $p=1000$, do we have $g(n)=n^2$ or $g(n)=e^{n/5}$?

Non-asymptotic

- no ambiguity \odot
- \bullet but the analysis is more involved \odot

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