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Homework 1

- 1) I could use regression to fredict tumor size in radiology from Medical images.
 - a) Some features I would use are fixel intensity Values, Shape features, and texture features.
 - b) For labels, I would use tumor size and tumor value
 - () For data Collection, I would find hospitals' datasets of Godiclesy Medical images and corresponding measurements in Hem.
 - d) Some chalkinges are Medical images are very raisy, the labeled data may have alot of variance, and biological systems are complex to predict.
- I could use classification to classify if a patient has a specific disease.
 - a) Some features I would use are results from medical diagnostic tests, lab tests, and imaging Studies, specifically blood pressure, heat rate, body temp, and respitany rate.
 - b) For labels, I would have either "has disease" or "no disease".
 - C) For data, I would get data sets from hospitals and treatment Centers.
 - 1) The data collected could all be from one place, which cause an imbolance and May not be diverse enough.
- 31) Yes, the histogram for x does look like a gaussian distribution.

Time to run 3d: 1.94 seconds Time to run 3e: 0.00024 seconds keshayshankar@Keshays-Mac

The Second way in Ze is muc efficient, because numpy has a built in override operator to perform such a calculation.

3F)

Elements retrieved in 3f: 375588 (.venv) keshavshankar@Keshavs—MacBoo

Elements retrieved in 3f: 374844

(.venv) keshavshankar@Keshavs-MacBoo

Elements retrieved in 3f: 374233

(.venv) keshavshankar@Keshavs-MacBoo

Yes, Hele is a difference. This is because we are governing Condon numbers for the "Z" vector, thus the # of Values btown,

0 & 1.5 Will always change,

46)

The resultant solution for 4b is:

venv) keshavshankar@Keshavs-MacBoo

$$Y(x) = [-0.5 \ 0 \ 1.5] = 7(-0.5, 0, 1.5)^{2} = (0.25, 0, 2.25)$$

$$= \sqrt{2.5} = 1.58 \text{ norm}$$

 $x_2 = [-1 \quad -1 \quad 0] = 7(-1,-1,0)^2 = (1,1,0)$

= 52 = 1.41 non

Norm of x1: 1.58

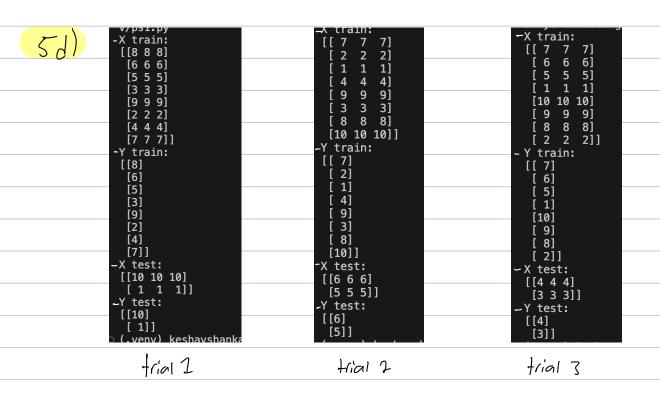
Norm of x2: 1.41

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The pythin Solution Verifies

that the calculations are correct.

5a)



No, you do not get the same submatricies every time because you are using a random seed to shuffle the arrays every time.