

## Assignment 5 – Gradient Descent and Eigenvalues

### I. Introduction

This experiment involves the use of gradient descent for polynomial interpolation and the power method for predicting population behavior. The entire experiment was performed on my personal machine running a second-generation Intel i5 (Sandy Bridge) processor in MATLAB. Some code was reused from the previous assignment, as well as lecture slides.

### II. Gradient Descent – US Population

The first experiment uses gradient descent to calculate coefficients for a polynomial approximation of US population data. Population data is shown in Table 1. I first attempted to compute polynomial solutions with degrees 3 through 10 using US census data. To compute a polynomial solution of degree  $n$ , the  $n + 1$  most recent data were chosen and transformed into a Vandermonde matrix using MATLAB's built in `vander()` function. Without any scaling or normalization, gradient descent failed to converge within 1 million iterations and an early-out tolerance of  $1 \times 10^{-5}$ .

Year	1900	1910	1920	1930	1940	1950	1960	1970	1980	1990	2000
Scaled Year	-1	-0.8	-0.6	-0.4	-0.2	0	0.2	0.4	0.6	0.8	1
Pop. (Millions)	75.995	91.972	105.711	123.203	131.669	150.697	179.323	203.212	226.505	249.633	281.422

Table 1 – US Census data from 1900 to 200 in millions of persons.

After inspecting the condition value for the 10<sup>th</sup> degree Vandermonde matrix (11x11), the condition number,  $\kappa$ , is incredibly high at  $4.05 \times 10^{44}$ . This is an incredibly ill-conditioned and must be transformed. To combat the poor condition, time was scaled according to:

$$s = \frac{t - 1950}{50}$$

resulting in a range of  $[-1,1]$ . After generating the 10<sup>th</sup> degree Vandermonde matrix with the new  $s$  values, the resulting condition number was  $\kappa = 1.40 \times 10^4$ , which is a sizable reduction. The scaled lower degree Vandermonde matrices are conditioned much better. Using the scaled time values, I attempted to compute polynomial approximations of degrees 2 through 5. The least squares residuals and predictions for 2010 and 2019 populations for each degree can be seen in **Table 2**. My best polynomial was the 2<sup>nd</sup> degree approximation since it had to lowest sum of least squares residuals and the closest predictions. This could be based on how I selected my points for interpolation, results could have differed if I spread my data points across the set, as opposed to just taking the most recent data for interpolation. After selecting the second-degree polynomial,  $\alpha$  was scaled by a factor from 1 to .01 to see if it could be made to converge more quickly. A factor of .5 worked best, reducing the number of iterations to converge from 358 to 197, a reduction nearing a factor of 2.

Degree	Sum LSR	2010 Prediction	2019 Prediction
2	7.71E-06	321.87	365.82
3	8.35E-06	330.69	397.29
4	4.74E+153	3.45E+153	9.81E+152
5	5.30E+153	1.41E+153	1.35E+154
Ground Truth	-	308.745	328.239

Table 2 – Results of scaled gradient descent method, degrees 2 through 5. Population estimates in millions of persons.

### III. Eigenvalues & Biological Application

The second experiment uses the power method to find the largest eigenvalues of various matrices then applies properties of eigenvalues to a real-world biology application. The first step of the experiment is to verify my own method, *simplepm()*, versus MATLAB's built-in *eig()* function on matrix:

$$A = \begin{bmatrix} 1 & 2 & 3 \\ 4 & 5 & 6 \\ 7 & 8 & 9 \end{bmatrix}$$

The largest eigenvalue was calculated using a random  $3 \times 1$  starting matrix and with a result of 16.11 which matches MATLAB's function. I attempted to use the power method again to find the largest eigenvalues for matrix  $B$  using starting guess  $B_0$

$$B = \begin{bmatrix} 2 & 3 & 2 \\ 1 & 0 & -2 \\ -1 & -3 & -1 \end{bmatrix} B_0 = \begin{bmatrix} 2 \\ 3 \\ 2 \end{bmatrix}$$

Attempting to compute the largest eigenvalue via the power method fails to converge within  $10k$  iterations likely because two of the eigenvalues for  $B$  have the same magnitude. Adjusting the starting guess to:

$$B_0 = \begin{bmatrix} 1 \\ -1 \\ 1 \end{bmatrix}$$

yields a strange result of 1. This is likely due to the fact the initial guess does not have the components of the largest eigenvalues (3, -3). Applying the power method to the finding the smallest eigenvalue of  $A$  can be done by calculating the largest eigenvalue of  $A$  inverse. Something strange happened here, but my results agree with MATLAB's result of  $-2.70 \times 10^{16}$ . This method can be seen in the attached source code in function *inversepm()*.

Finally, I applied my power method to a biological system given by:

$$P^n = A^n P^0, \quad A = \begin{bmatrix} b_1 & b_2 & b_3 & b_4 \\ 1-d_1 & 0 & 0 & 0 \\ 0 & 1-d_2 & 0 & 0 \\ 0 & 0 & 1-d_3 & 1-d_4 \end{bmatrix}, \quad P^0 = \begin{bmatrix} 100 \\ 200 \\ 150 \\ 75 \end{bmatrix}$$

Where  $P^n$  represents four segments of a population after  $n$  years and  $P^0$  is the starting populations of each segment, with birth rates  $b = [0.3, 0.3, 0.3, 0.1]$  and death rates  $d = [0.1, 0.2, 0.5, 0.9]$ . Using my power method on  $A$  found the largest eigenvalue to be .91 which is less than 1. Meaning the population should eventually die off as time goes by. This stands to reason because there is a 90% death rate in the 4<sup>th</sup> age segment of the population. To confirm this hypothesis, I calculated the population of each age segment after 1000 years. The results were near zero, in the  $1 \times 10^{-38}$  range confirming my hypothesis. I adjusted  $d_4$  to be 0.1 and recomputed to the largest eigenvalue to be 1.08 which means the population should grow unbounded. Calculation the population after a thousand years resulted in population segments in the  $1 \times 10^{35}$  ranges, indicating that the population does grow unbounded.

## IV. Conclusion

While I had some strange results with the inverse matrix eigenvalue calculations and the polynomial approximations for the US census data, most of the results seem to follow my intuition. I personally enjoyed the modeling segments in both experiments especially with the real-world applications. Population modeling has readily apparent uses and is easy to understand intuitively.