

Ex5_student

October 29, 2023

1 Expectation-maximization algorithm

2 Introduction

In this report, we delve into the realm of medical image processing, focusing on the segmentation of three distinct tissue classes within an MR brain image. The primary dataset utilized for this analysis is a 2-dimensional axial slice of a brain scan, accompanied by a mask to isolate the brain tissues from other non-brain elements such as the eyeballs, fat, and skin.

The raw MR data is known to be affected by the bias field artifact, a common issue in MR imaging that can lead to intensity inhomogeneities across the image. To address this, we also work with a corrected version of the image, where the MR bias field artifact has been mitigated using advanced correction techniques as described in section 3.5.

Our approach to tissue segmentation is rooted in generative modeling, and we employ the Expectation-Maximization (EM) algorithm to fit the model parameters to the image data accurately. Through a series of tasks, we iteratively refine our model, ensuring that we capture the underlying distribution of the tissue intensities with precision.

Each task in this report is accompanied by the necessary code implementations, results visualized through informative figures, and comprehensive explanations. These elements together provide a clear insight into the computational processes and the rationale behind each step of our analysis.

2.0.1 Input data and code hints

Import Python libraries:

```
[33]: import numpy as np
import scipy
from scipy.io import loadmat
from scipy import signal
import warnings
warnings.filterwarnings("ignore")
import matplotlib
import matplotlib.pyplot as plt
from scipy.stats import norm
import matplotlib.mlab as mlab
%matplotlib inline
```

2.1 Task 1: Image data

Display the image provided in “correctedData.mat” and plot its histogram.

Hints: - .mat data can be loaded in python as follows

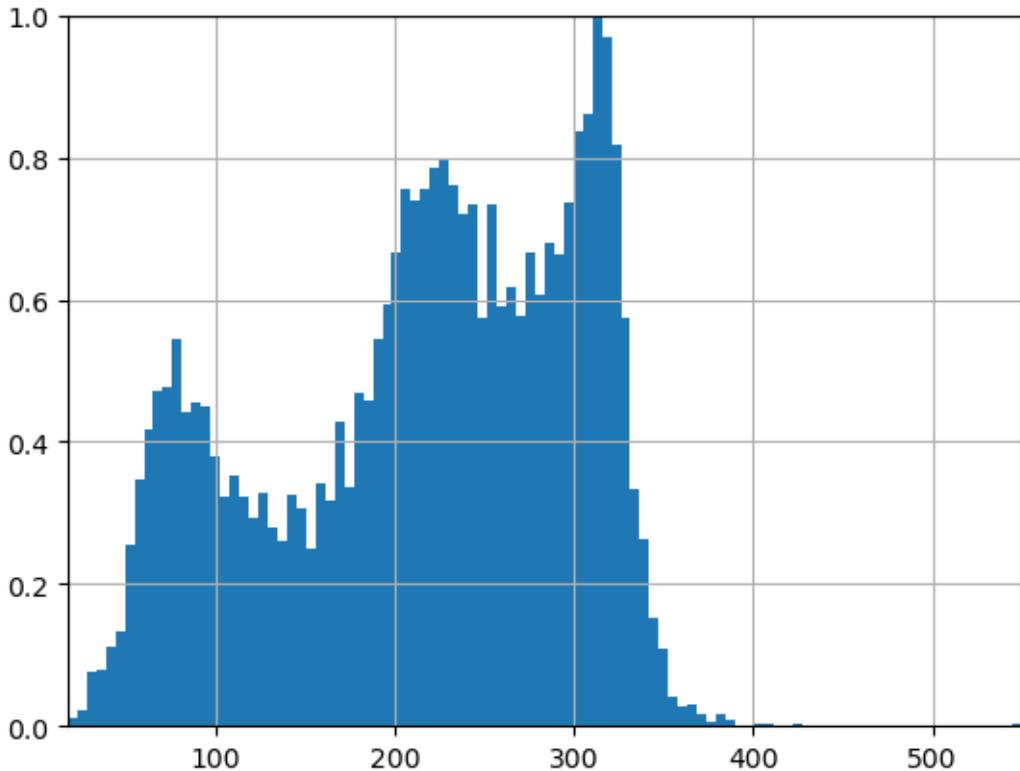
```
mat = loadmat("correctedData.mat")
```

```
data = mat["correctedData"]
```

- Use 100 bins for your histogram
- The mask sets all background pixels to zero. Disregard the background pixels by clipping 0.

```
[34]: mat = loadmat("Ex5_data/correctedData.mat")
data = mat["correctedData"]
data = data[1:,:]
data = data[data != 0]
```

```
[35]: value = np.median( data )
histogram, edges = np.histogram( data.ravel(), bins=100 )
binCenters = ( edges[ 1: ] + edges[ :-1 ] ) / 2
binWidth = edges[ 1 ] - edges[ 0 ]
fig, ax = plt.subplots()
ax.bar( binCenters, histogram/histogram.max(), width=binWidth )
ax.set_ylim( 0,1 )
ax.set_xlim( data.min(), data.max() )
ax.grid()
```



2.2 Task 2: Initialize Gaussian-Mixture Model

Compute the minimum and maximum intensity in the image (non-zero pixels), and divide the intensity range up into three equally wide intervals. Initialize the parameters of a 3-component Gaussian mixture model by setting the means of the Gaussians to the centers of the intensity intervals, the variances to the square of the width of the intervals, and the prior weights to $\frac{1}{3}$ each.

Hint: - In your intensity range, disregard the background pixels by clipping 0

```
[36]: #initialize
pi = 3*[1/3]
k = 3
data_1D=data.ravel()
N = len(data_1D)

max_intensity = data_1D.max()
min_intensity = data_1D.min()

interval=max_intensity-min_intensity
block=interval/k

mean=[min_intensity+block/2,min_intensity+3*block/2,min_intensity+5*block/2]
```

```
variance=3*[pow(block,2)]
```

2.3 Task 3: Display initial Gaussian distributions

Overlay the resulting Gaussian mixture model on the histogram by plotting each Gaussian weighted by its π_k , as well as the total weighted sum of all three Gaussian distributions (as in fig. 3.1(b) in the course notes).

Hint: - A gaussian distribution with the parameters μ , σ^2 , scaled by the weight w and evaluated at positions x can be obtained by the function

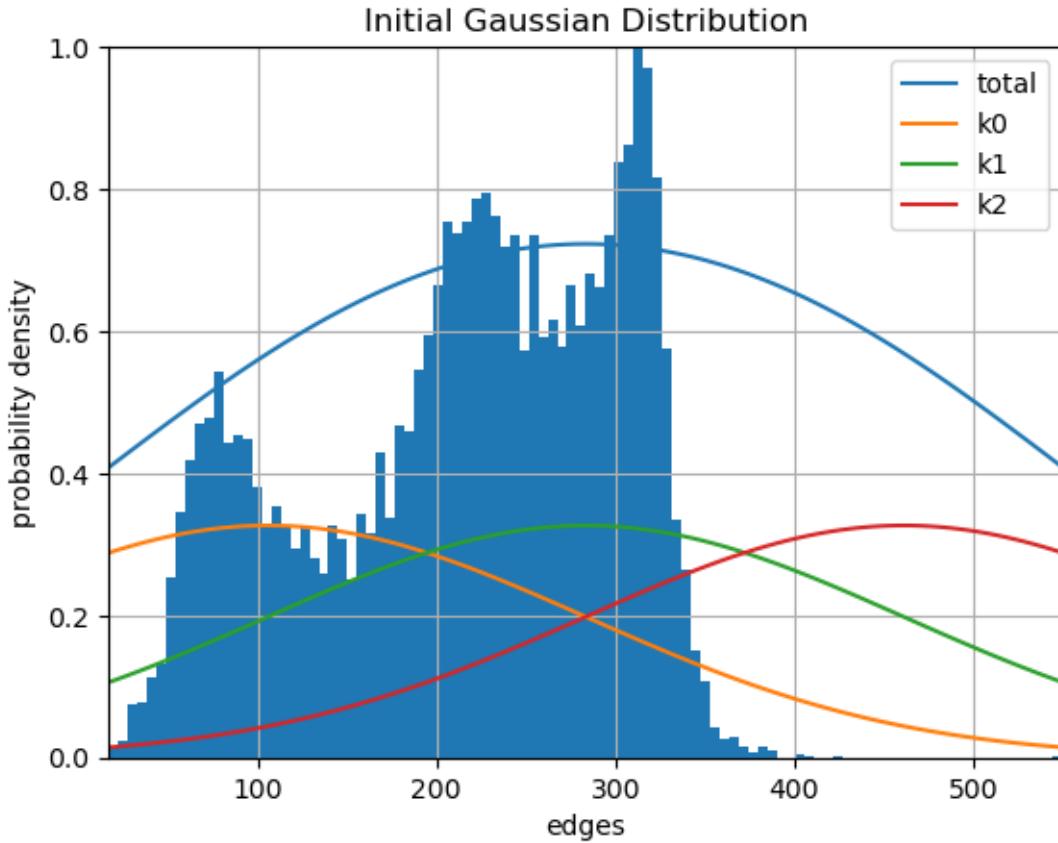
```
w * scipy.stats.norm.pdf( x, mu, sigma^2).
```

- you can use the bin edges of your histogram as x .

```
[37]: from scipy import stats
initial_pdf0= pi[0]*stats.norm.pdf( edges, mean[0], block)
initial_pdf1= pi[1]*stats.norm.pdf( edges, mean[1], block)
initial_pdf2= pi[2]*stats.norm.pdf( edges, mean[2], block)
initial_pdf_total = initial_pdf0+initial_pdf1+initial_pdf2

fig, ax = plt.subplots()
ax.bar( binCenters, histogram/histogram.max(), width=binWidth )
ax.set_ylim( 0,1 )
ax.set_xlim( data_1D.min(), data_1D.max() )
ax.grid()

plt.plot(edges, initial_pdf_total*histogram.max(), label="total")
plt.plot(edges, initial_pdf0*histogram.max(), label="k0")
plt.plot(edges, initial_pdf1*histogram.max(), label="k1")
plt.plot(edges, initial_pdf2*histogram.max(), label="k2")
plt.legend()
plt.title("Initial Gaussian Distribution")
plt.xlabel("edges")
plt.ylabel("probability density")
plt.grid(True)
plt.show()
```



2.4 Task 4: Compute weights

Compute the values of $w_{n,k}$ defined by:

$$\Xi_{n,k} = \frac{\mathcal{N}(d_n | \tilde{\mu}_k, \tilde{\sigma}_k^2) \tilde{\pi}_k}{\sum_{k'=1}^K \mathcal{N}(d_n | \tilde{\mu}'_{k'}, \tilde{\sigma}_{k'}^2) \tilde{\pi}'_{k'}}.$$

Visualize the values of each $w_{n,k}$ in a figure. You should have three plots which each display only the pixels that belong to the respective class, according to the weights.

Hint: - The segmentation of a pixel is determined by assigning the class of the highest probability. - In your visualization, disregard the background pixels by clipping 0

```
[38]: num0 = pi[0]*stats.norm.pdf(edges,mean[0],block)
num1 = pi[1]*stats.norm.pdf(edges,mean[1],block)
num2 = pi[2]*stats.norm.pdf(edges,mean[2],block)
denominator = num0+num1+num2

w0 = num0/denominator
w1 = num1/denominator
```

```

w2 = num2/denominator

#define 3 subsets
pixel0=[]
pixel1=[]
pixel2=[]
N1=len(edges)
#find the points for segmentation
for i in range(N1):
    if w0[i]> w1[i] and w0[i]>w2[i]:
        pixel0.append(edges[i])
    elif w1[i]>w2[i]:
        pixel1.append(edges[i])
    else:
        pixel2.append(edges[i])

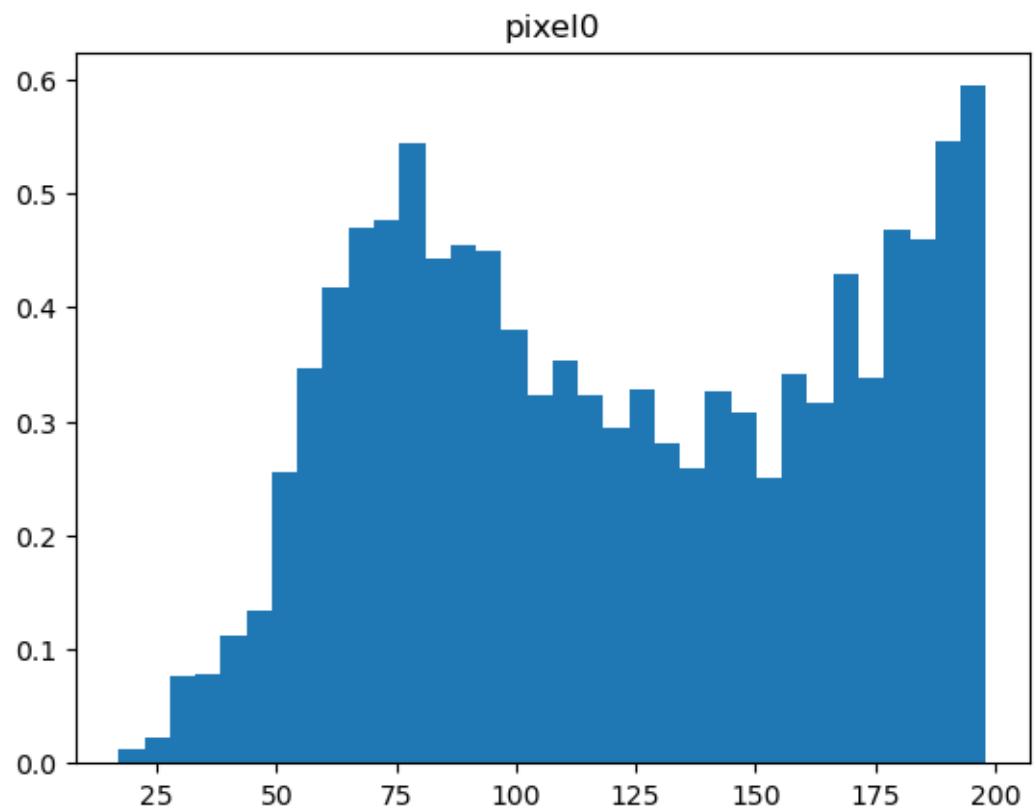
import matplotlib.pyplot as plt

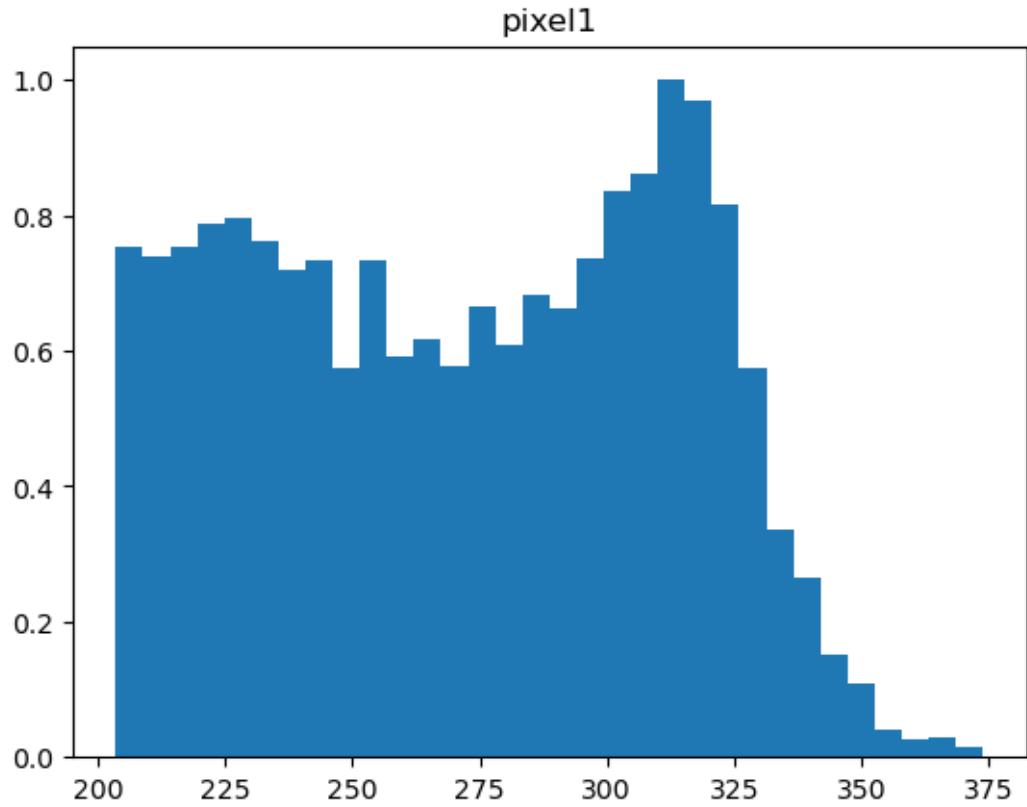
fig, ax = plt.subplots()
ax.bar( binCenters[:len(pixel0)], histogram[:len(pixel0)]/histogram.max() ,width=binWidth )
plt.title("pixel0")

fig, ax = plt.subplots()
ax.bar( binCenters[len(pixel0)+1:len(pixel0)+len(pixel1)], histogram[len(pixel0)+1:len(pixel0)+len(pixel1)]/histogram.max() ,width=binWidth )
plt.title("pixel1")

```

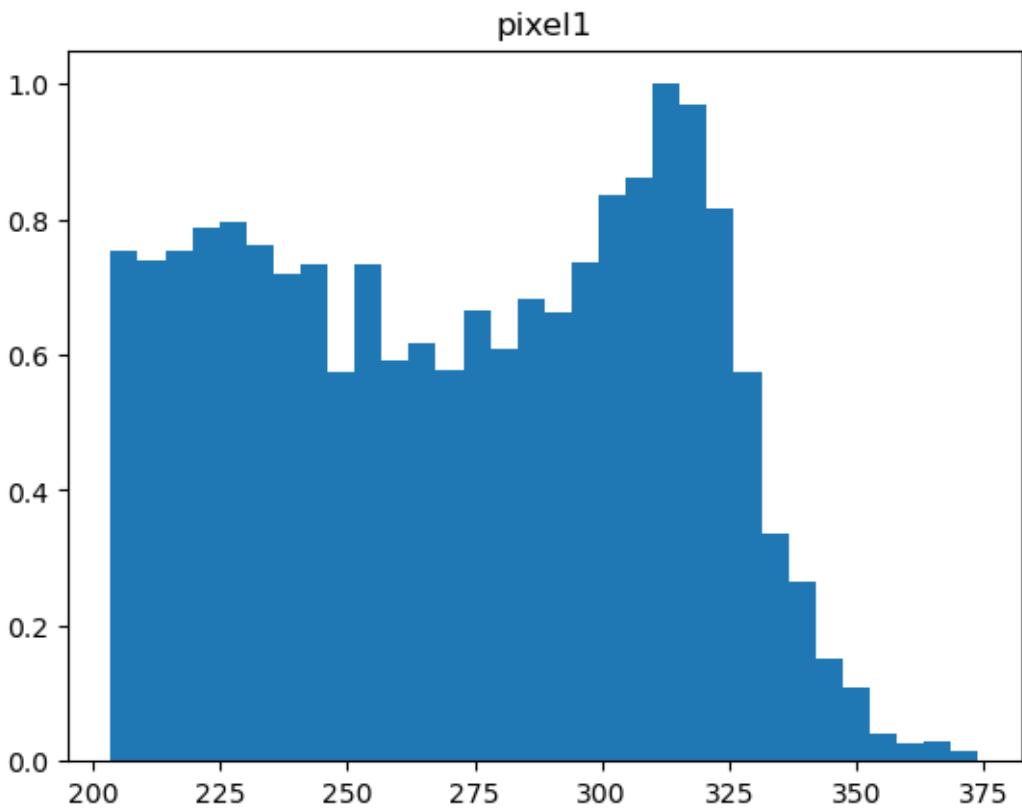
[38]: Text(0.5, 1.0, 'pixel1')





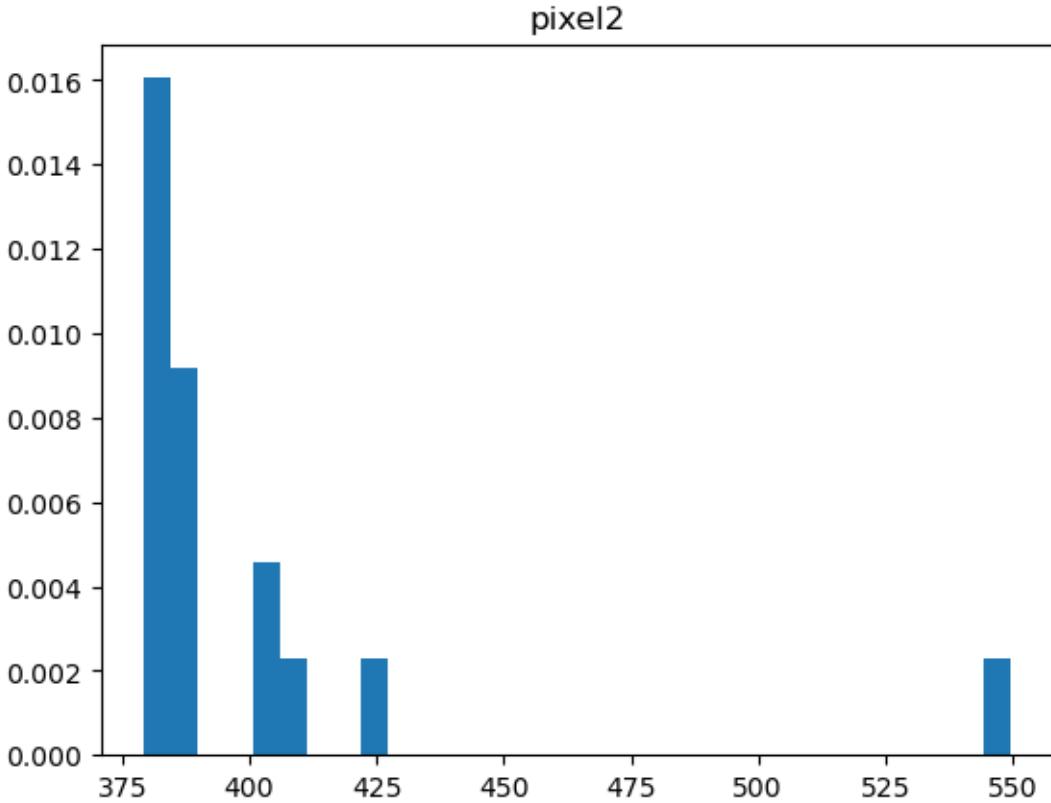
```
[39]: fig, ax = plt.subplots()
ax.bar( binCenters[len(pixel0)+1:len(pixel0)+len(pixel1)], □
        ↪histogram[len(pixel0)+1:len(pixel0)+len(pixel1)]/histogram.max(), □
        ↪width=binWidth )
plt.title("pixel1")
```

```
[39]: Text(0.5, 1.0, 'pixel1')
```



```
[40]: fig, ax = plt.subplots()
ax.bar( binCenters[len(pixel0)+len(pixel1)+1:], ↴
        histogram[len(pixel0)+len(pixel1)+1:]/histogram.max(), width=binWidth )
plt.title("pixel2")
```

```
[40]: Text(0.5, 1.0, 'pixel2')
```



2.5 Task 5: Estimate Maximum Likelihood parameters

Estimate the maximum likelihood parameters by iterating between updating the model parameter estimate according to

$$\tilde{\mu}_k \leftarrow \frac{\sum_{n=1}^N w_{n,k} d_n}{\sum_{n=1}^N w_{n,k}}$$

$$\tilde{\sigma}_k^2 \leftarrow \frac{\sum_{n=1}^N w_{n,k} (d_n - \tilde{\mu}_k)^2}{\sum_{n=1}^N w_{n,k}}$$

$$\tilde{\pi}_k \leftarrow \frac{\sum_{n=1}^N w_{n,k}}{N}$$

and by recomputing $w_{n,k}$ according to eq. 3.33 (see Task 4).

Make sure to perform enough iterations (e.g., 100) for the algorithm to converge. As the iterations progress, plot the evolution of the log likelihood function, and update each time the display of $w_{n,k}$ as well as the Gaussian mixture model plot overlaid on the histogram. Include the evolution of the log likelihood function and the plot of the final $w_{n,k}$ and the final mixture model in your report.

Hint: - The log likelihood can be simply computed by $\log(\sum_k w_k x_k)$

```
[41]: import math
iteration=100
u=[0,0,0]
sig=[0,0,0]
for j in range (iteration):
    demoninator_k0 = w0.sum()
    demoninator_k1 = w1.sum()
    demoninator_k2 = w2.sum()
    #mean
    for i in range(N1):
        u[0] += w0[i]*edges[i]/demoninator_k0
        u[1] += w1[i]*edges[i]/demoninator_k1
        u[2] += w2[i]*edges[i]/demoninator_k2
    #variance
    for i in range(N1):
        sig[0] += w0[i]*pow((edges[i]-u[0]),2)/demoninator_k0
        sig[1] += w1[i]*pow((edges[i]-u[1]),2)/demoninator_k1
        sig[2] += w2[i]*pow((edges[i]-u[2]),2)/demoninator_k2
    #pi
    pi[0] = demoninator_k0/N1
    pi[1] = demoninator_k1/N1
    pi[2] = demoninator_k2/N1
    #calculate weight
    #numerator
    num0 = pi[0]*stats.norm.pdf( edges,u[0] ,math.sqrt(sig[0]))
    num1 = pi[1]*stats.norm.pdf( edges,u[1] ,math.sqrt(sig[1]))
    num2 = pi[2]*stats.norm.pdf( edges,u[2] ,math.sqrt(sig[2]))
    denominator1 = num0+num1+num2
    w0 = num0/denominator1
    w1 = num1/denominator1
    w2 = num2/denominator1

    #plot histogram
    iternate_pdf0=[]
    iternate_pdf1=[]
    iternate_pdf2=[]
    iternate_pdf_total=[]

    for i in range(N1):
        iternate_pdf0.append(w0[i]*(math.log(num0[i]/w0[i])))
        iternate_pdf1.append(w1[i]*(math.log(num1[i]/w1[i])))
        iternate_pdf2.append(w2[i]*(math.log(num2[i]/w2[i])))
        iternate_pdf_total.append(w0[i]*(math.log(num0[i]/w0[i]))+w1[i]*(math.
        ↪log(num1[i]/w1[i]))+w2[i]*(math.log(num2[i]/w2[i])))

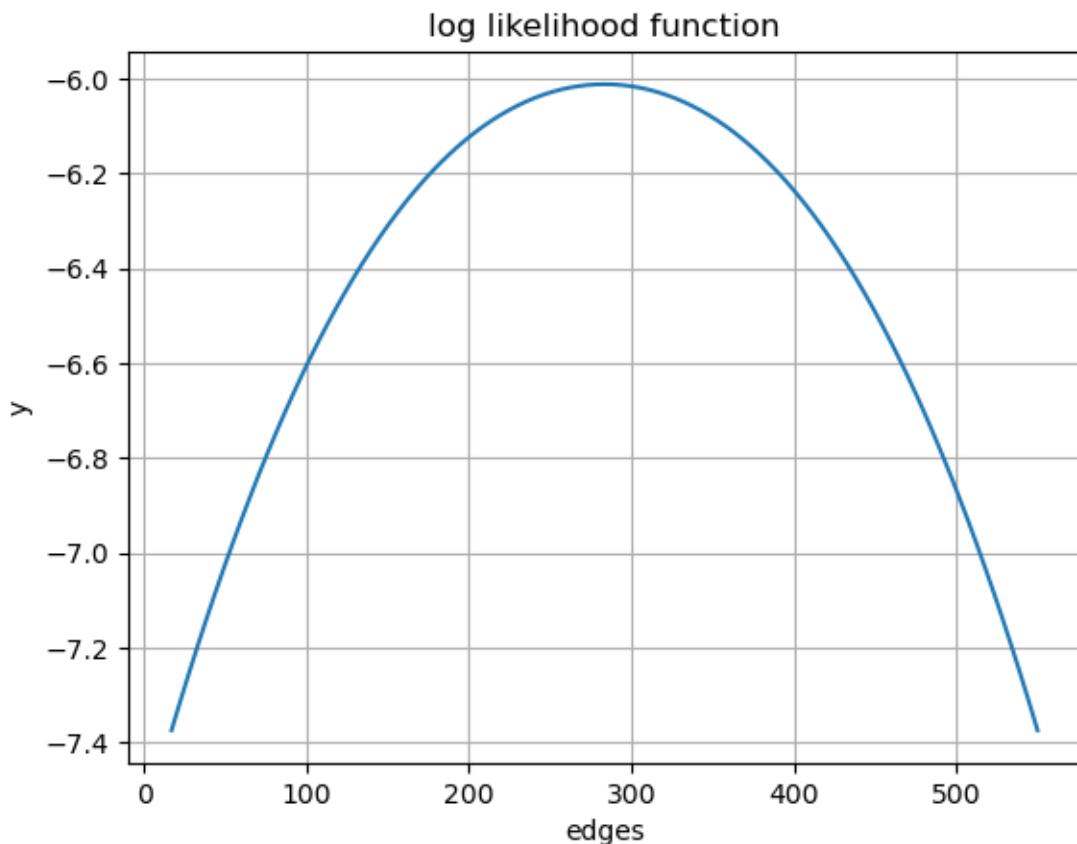
    #plot
    plt.figure()
```

```

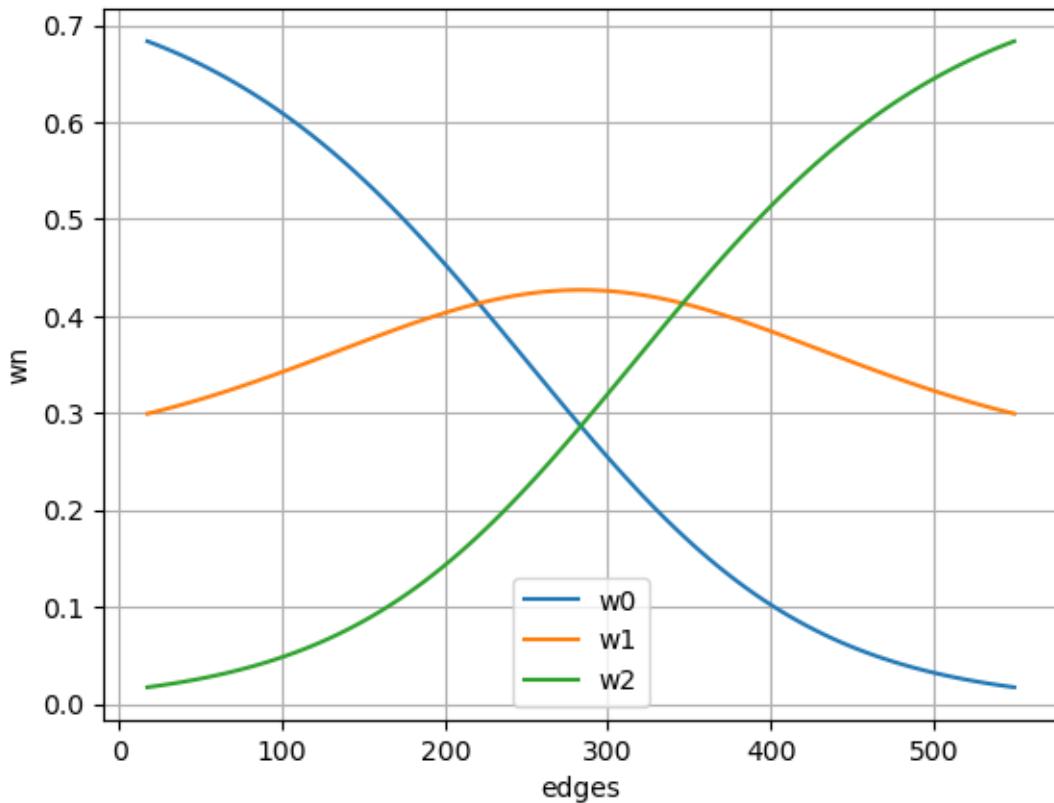
plt.plot(edges, iternate_pdf_total)
plt.title("log likelihood function")
plt.xlabel("edges")
plt.ylabel("y")
plt.grid(True)
plt.show()

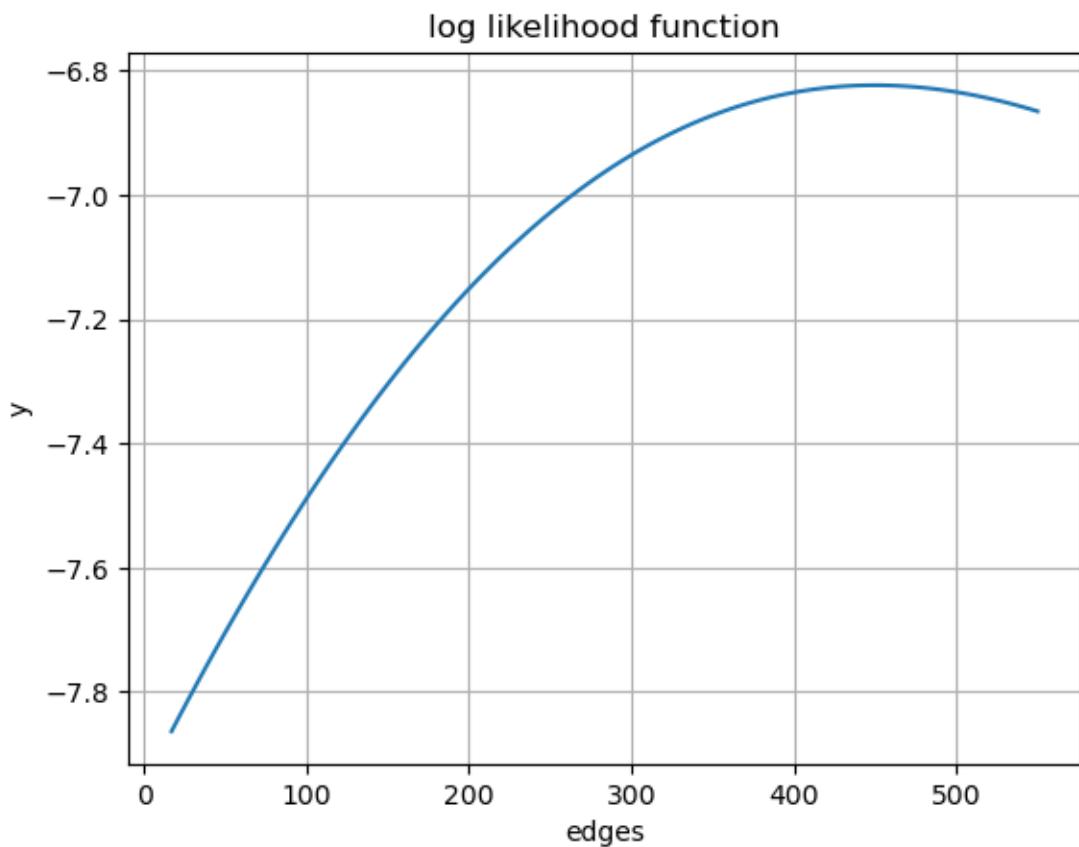
plt.figure()
plt.plot(edges, w0, label="w0")
plt.plot(edges, w1, label="w1")
plt.plot(edges, w2, label="w2")
plt.legend()
plt.title("visualize w")
plt.xlabel("edges")
plt.ylabel("wn")
plt.grid(True)
plt.show()

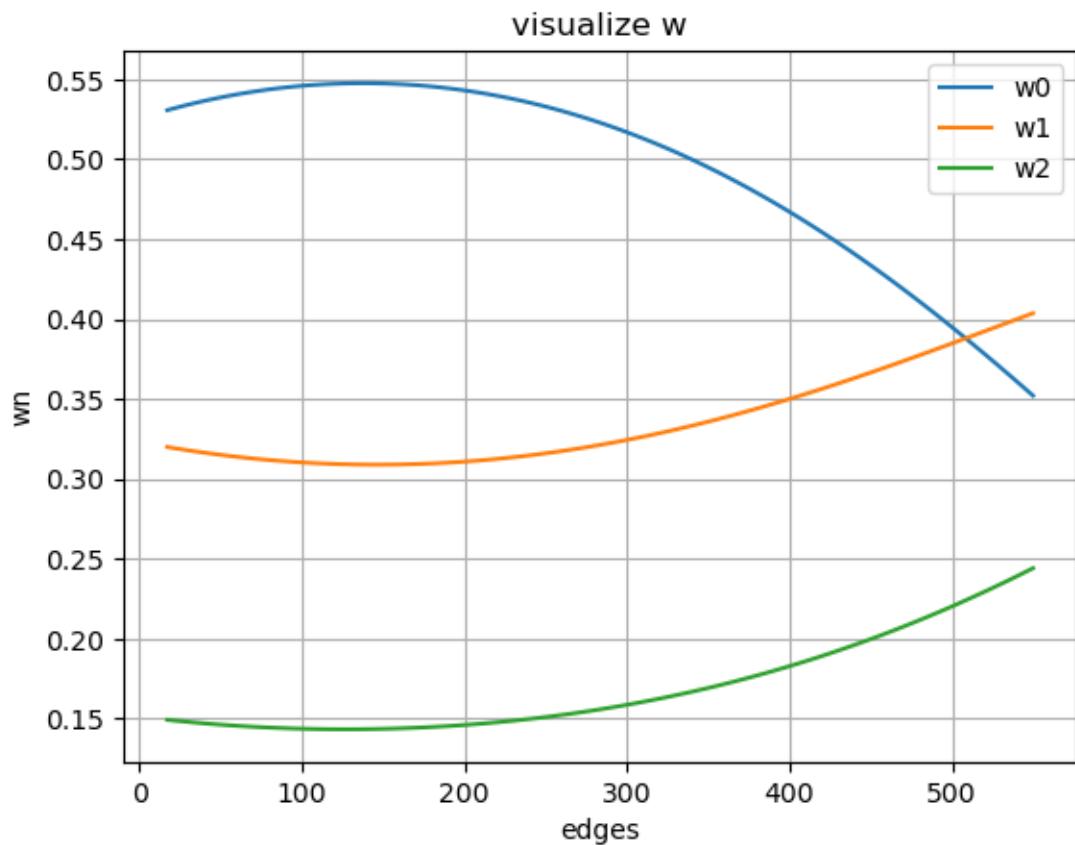
```

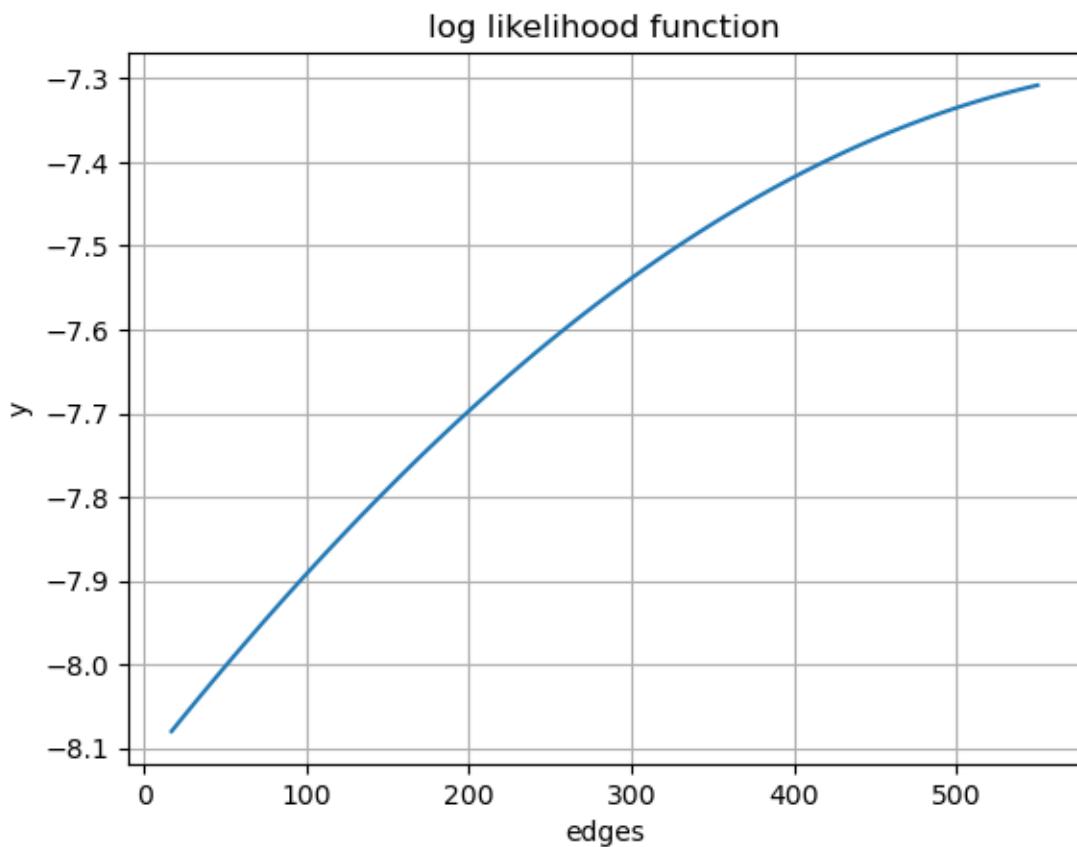


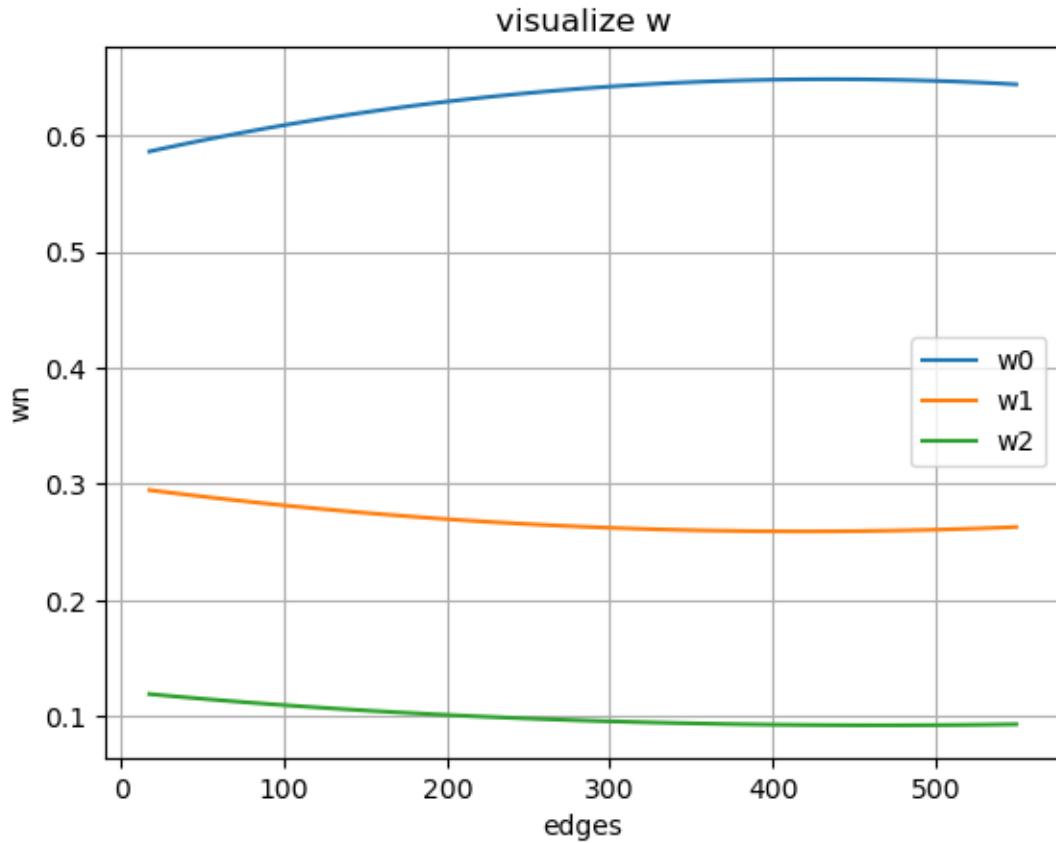
visualize w



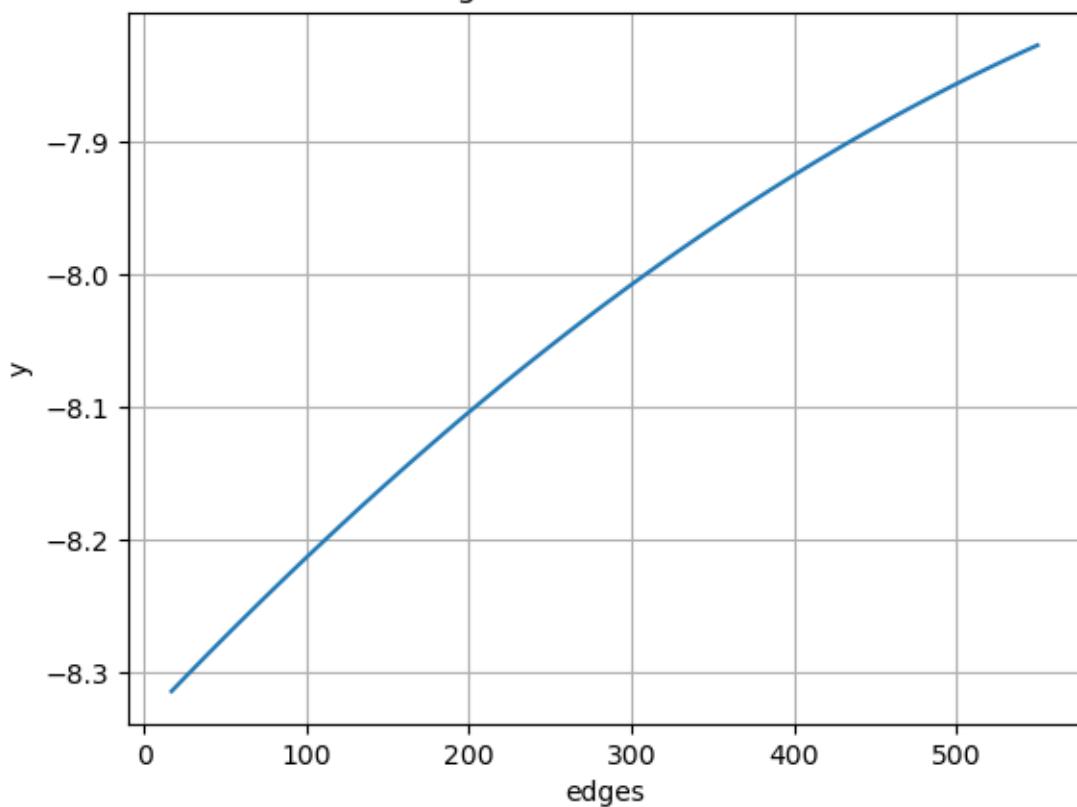


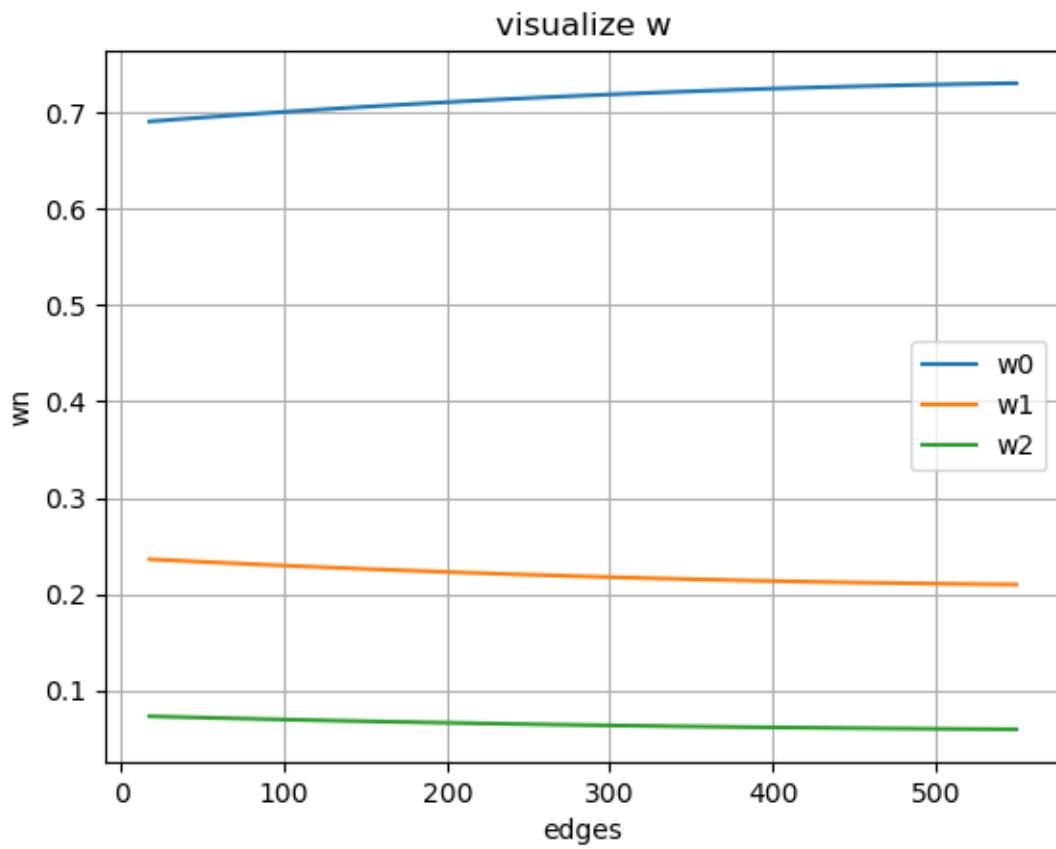




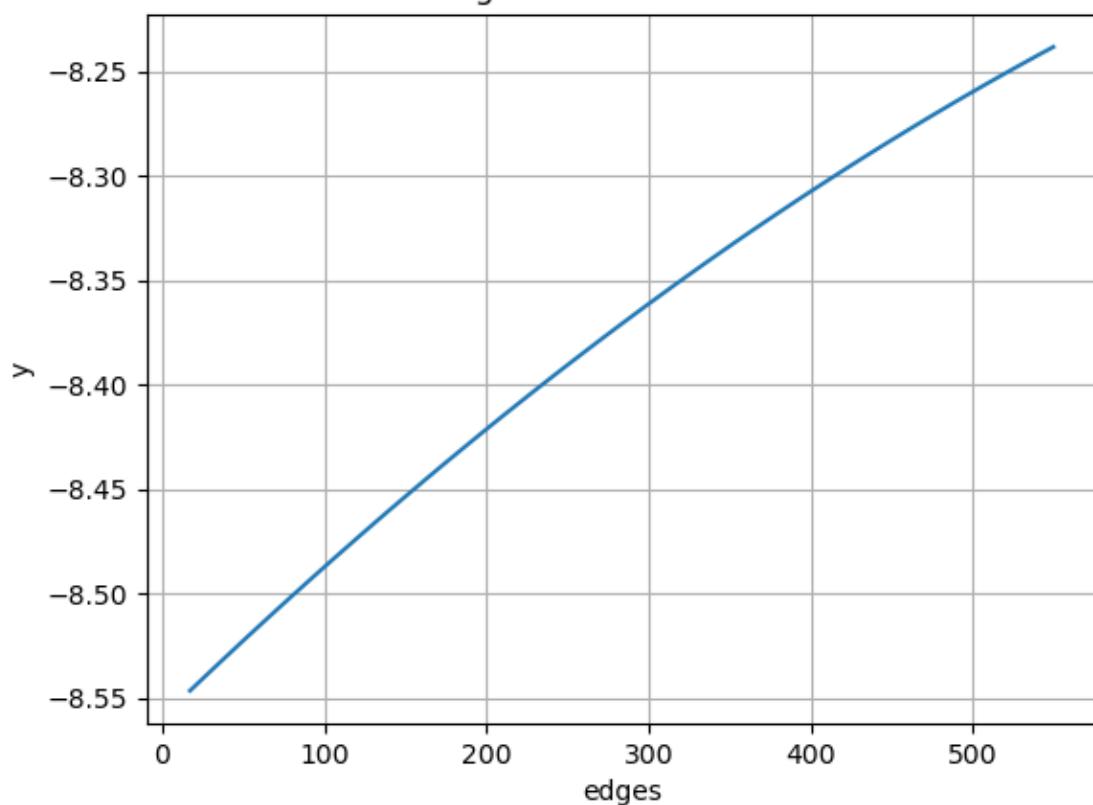


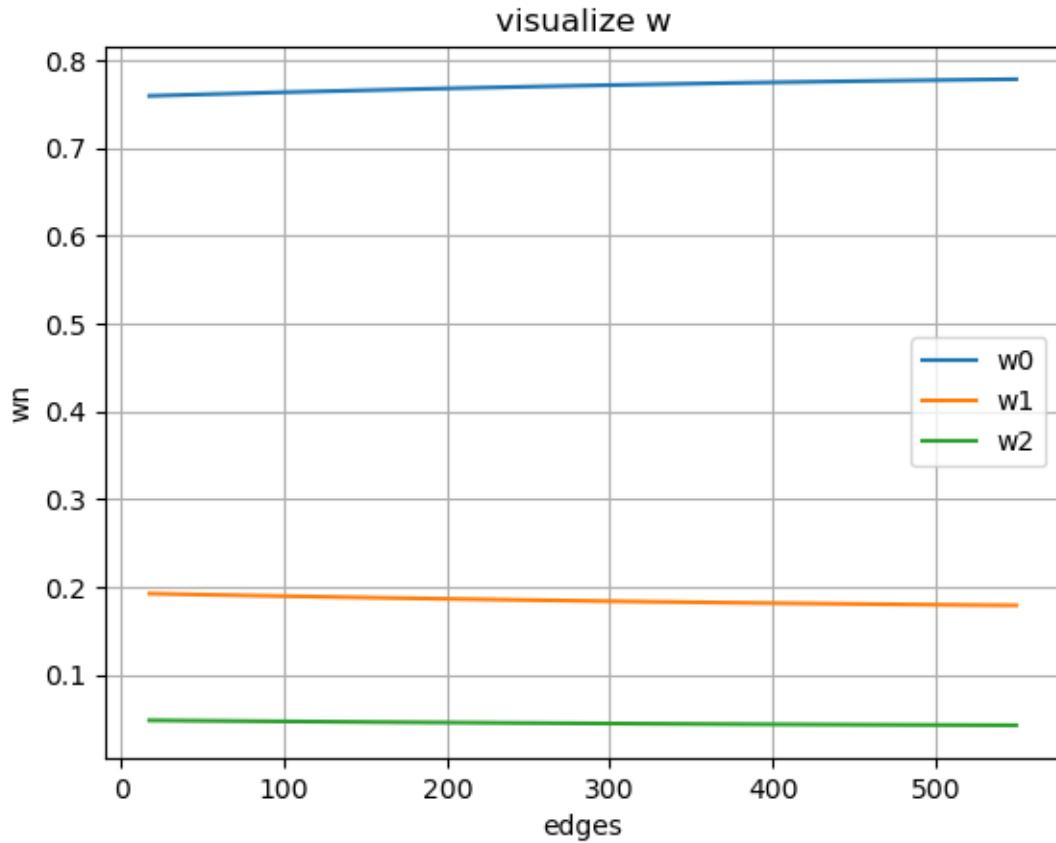
log likelihood function

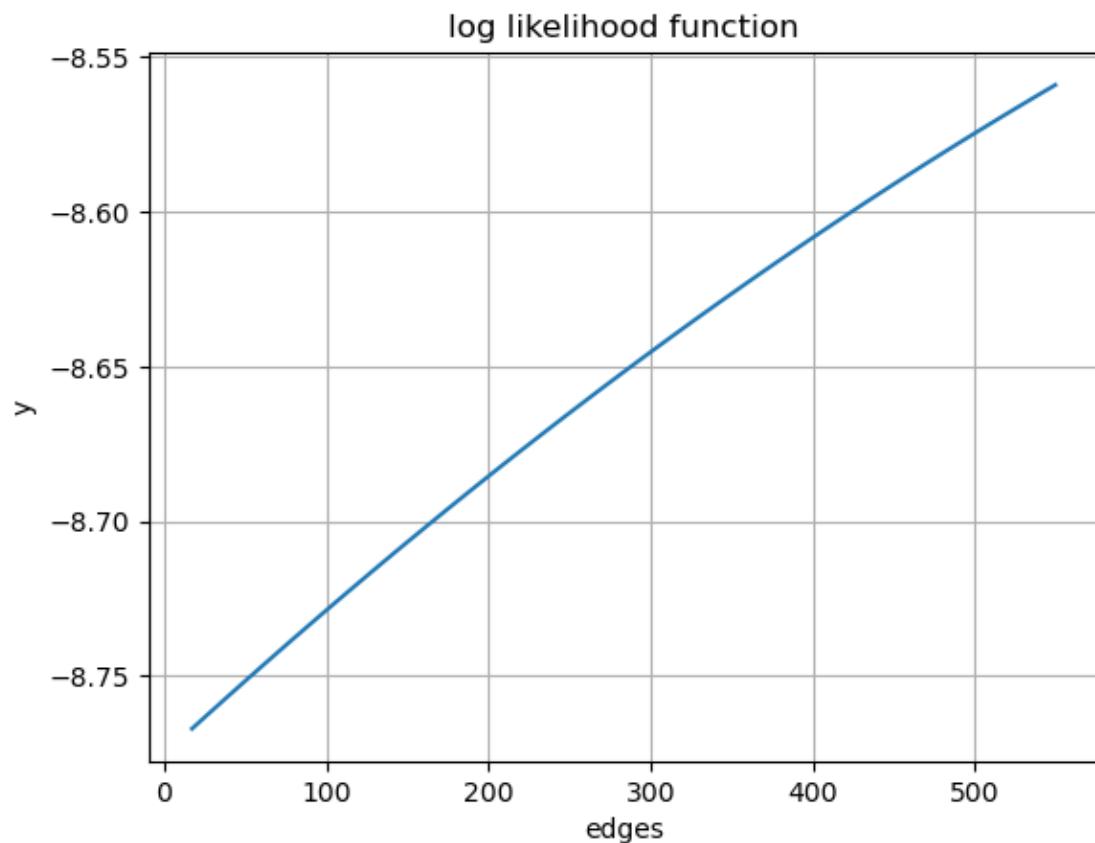


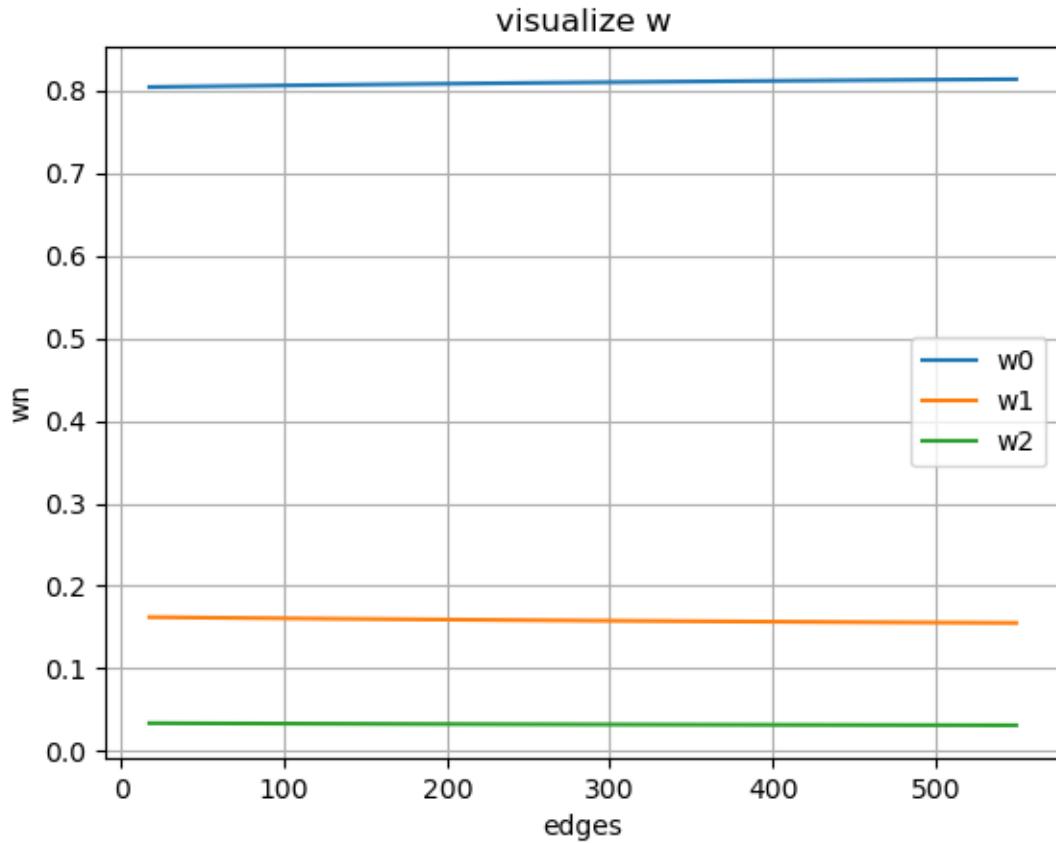


log likelihood function

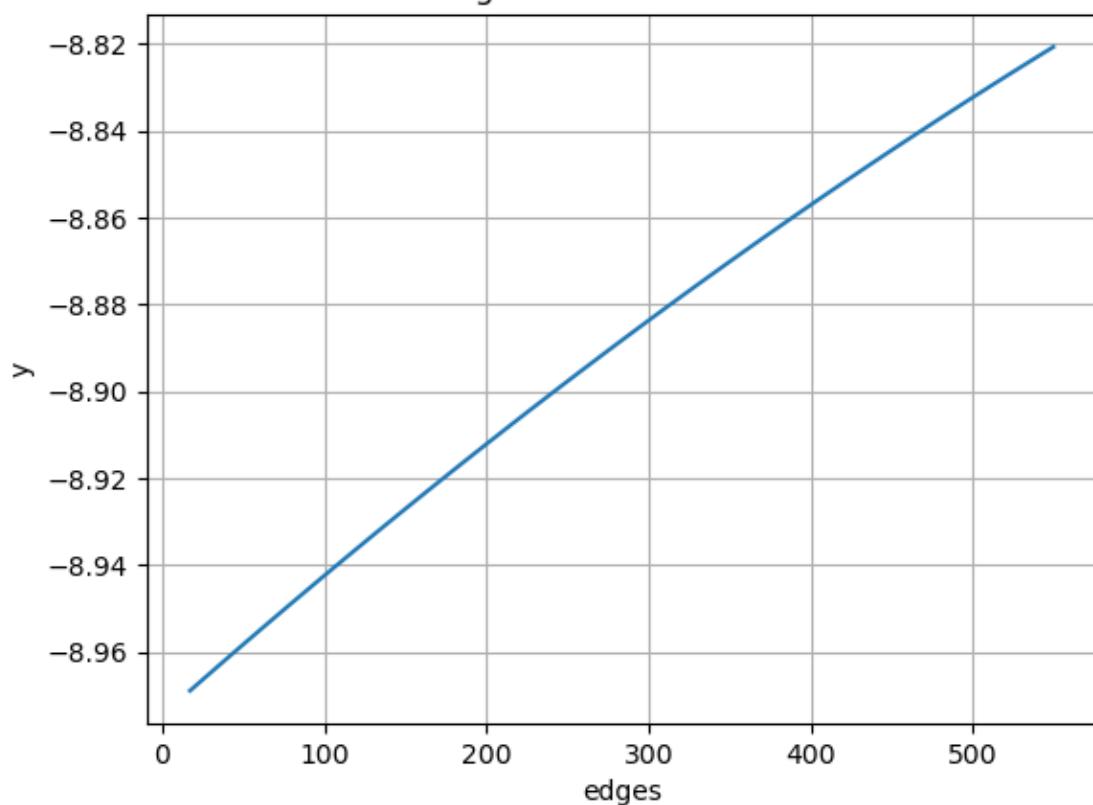


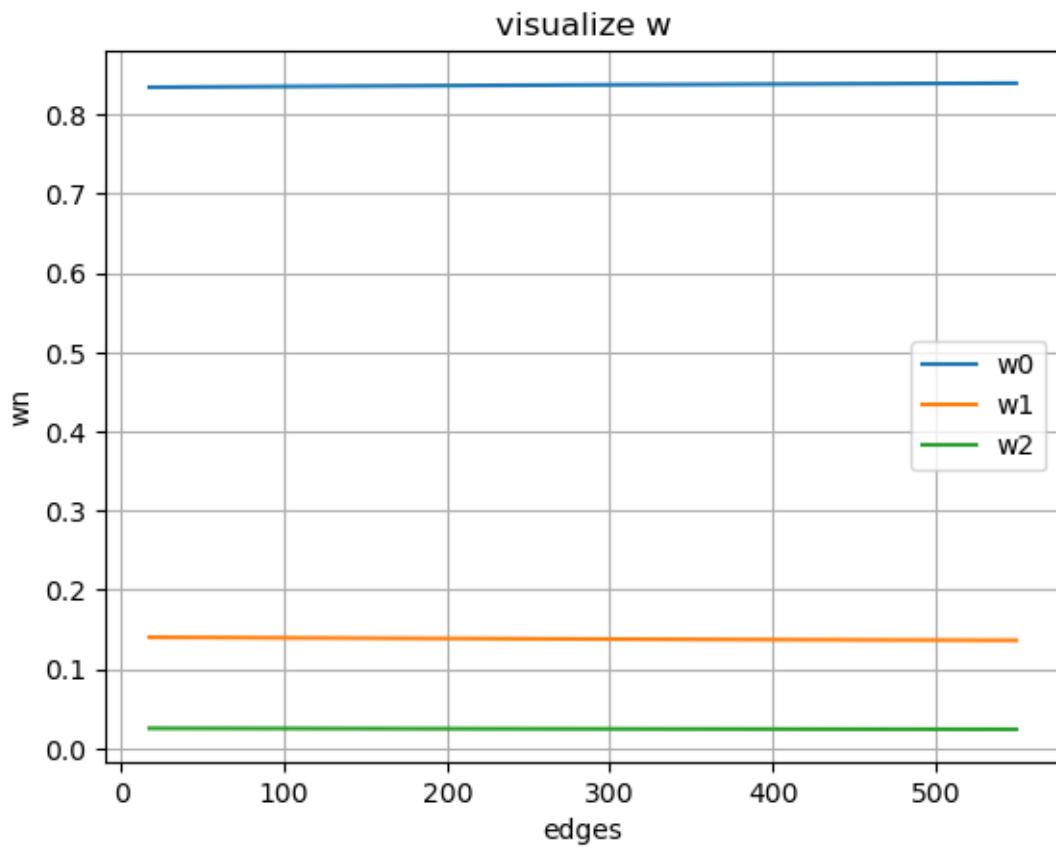


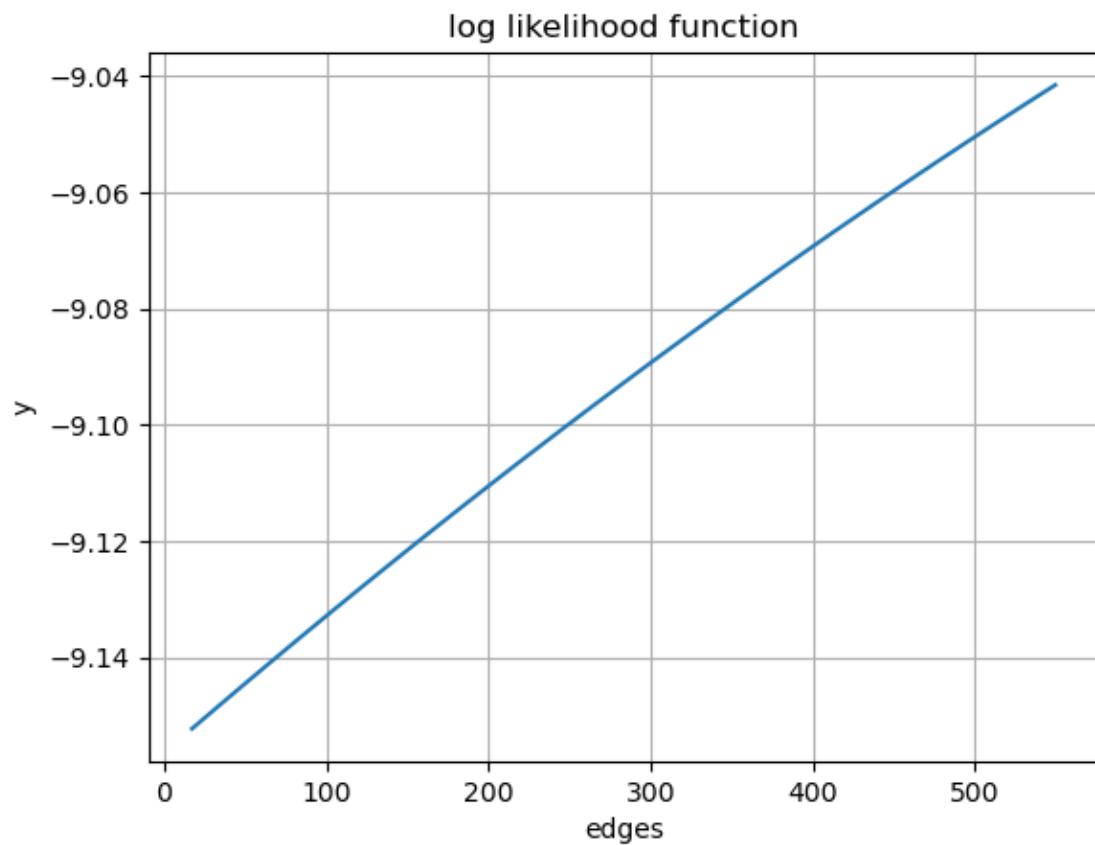


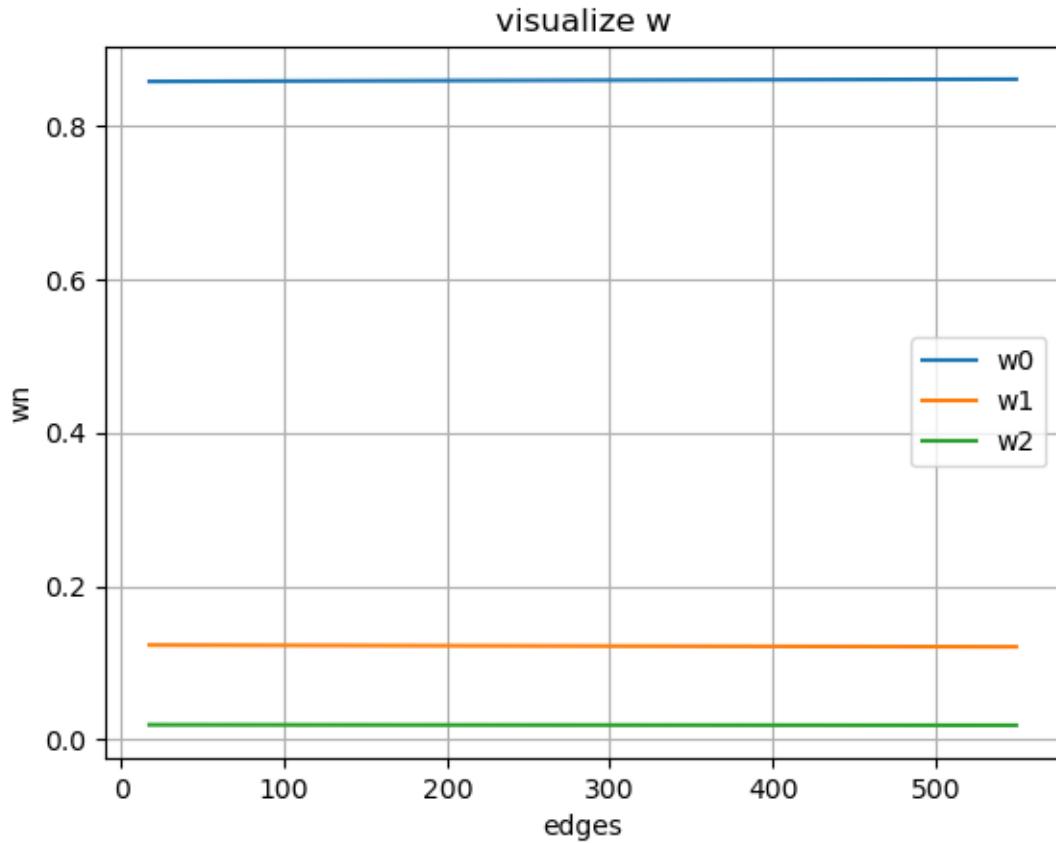


log likelihood function

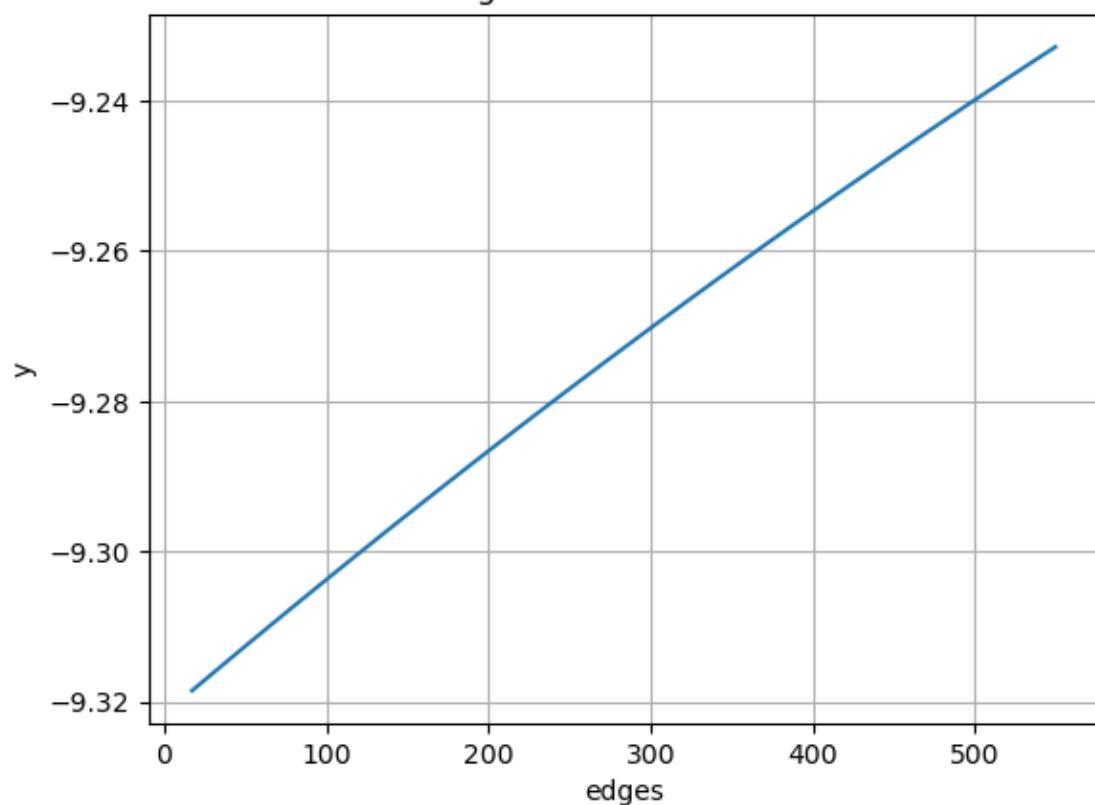


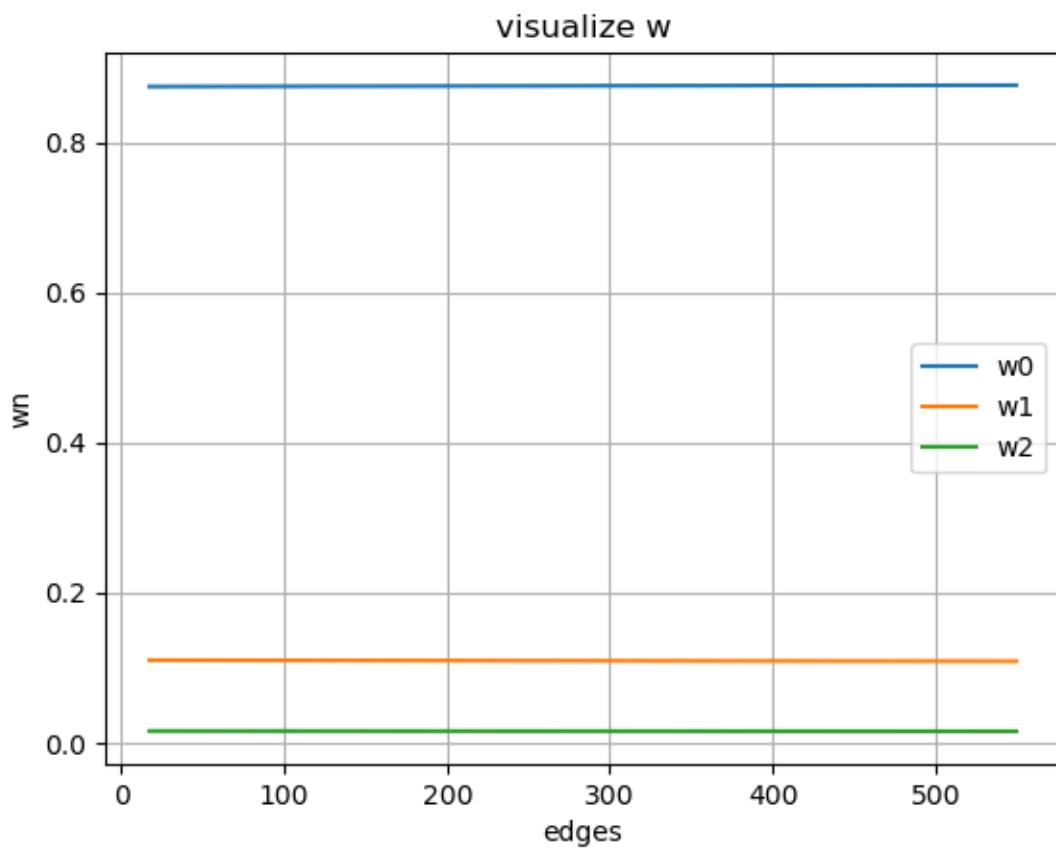




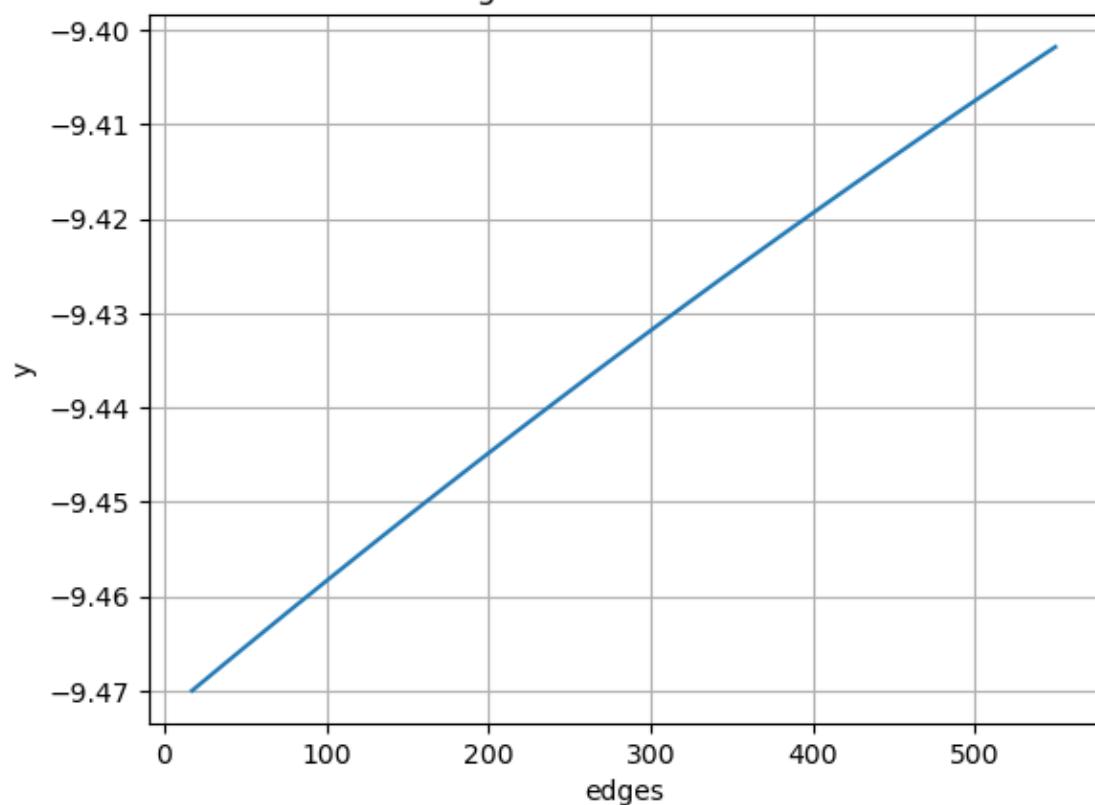


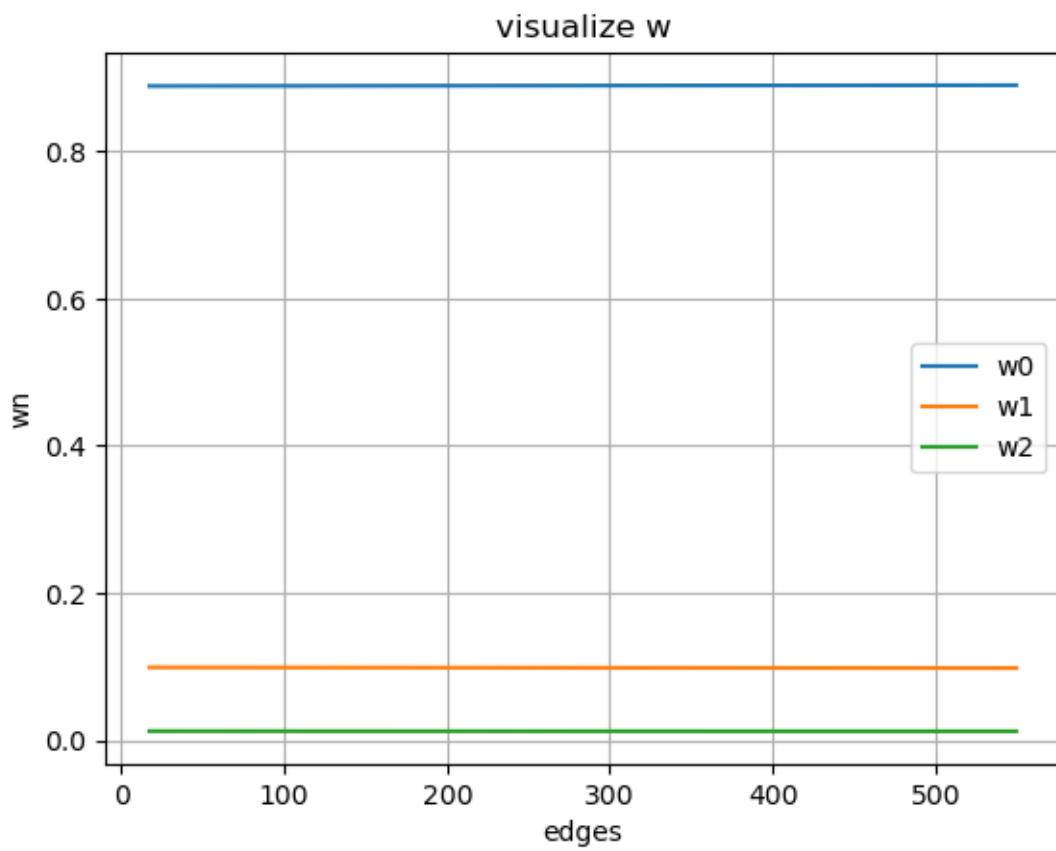
log likelihood function



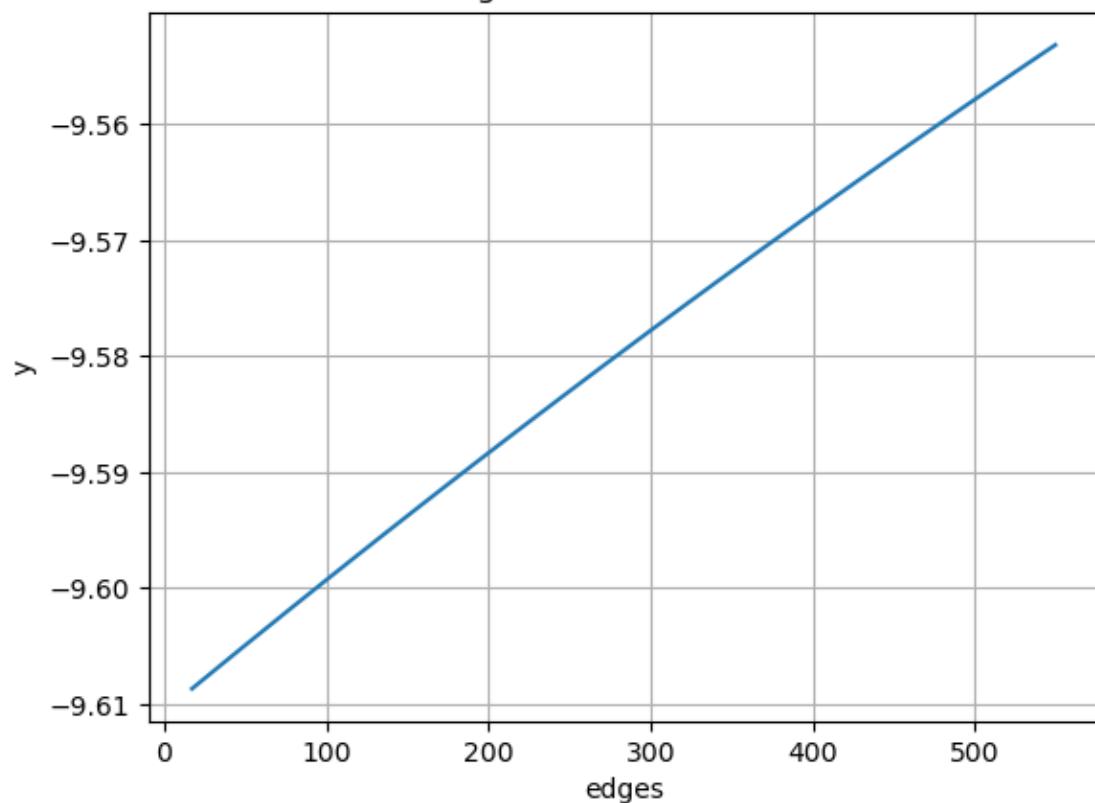


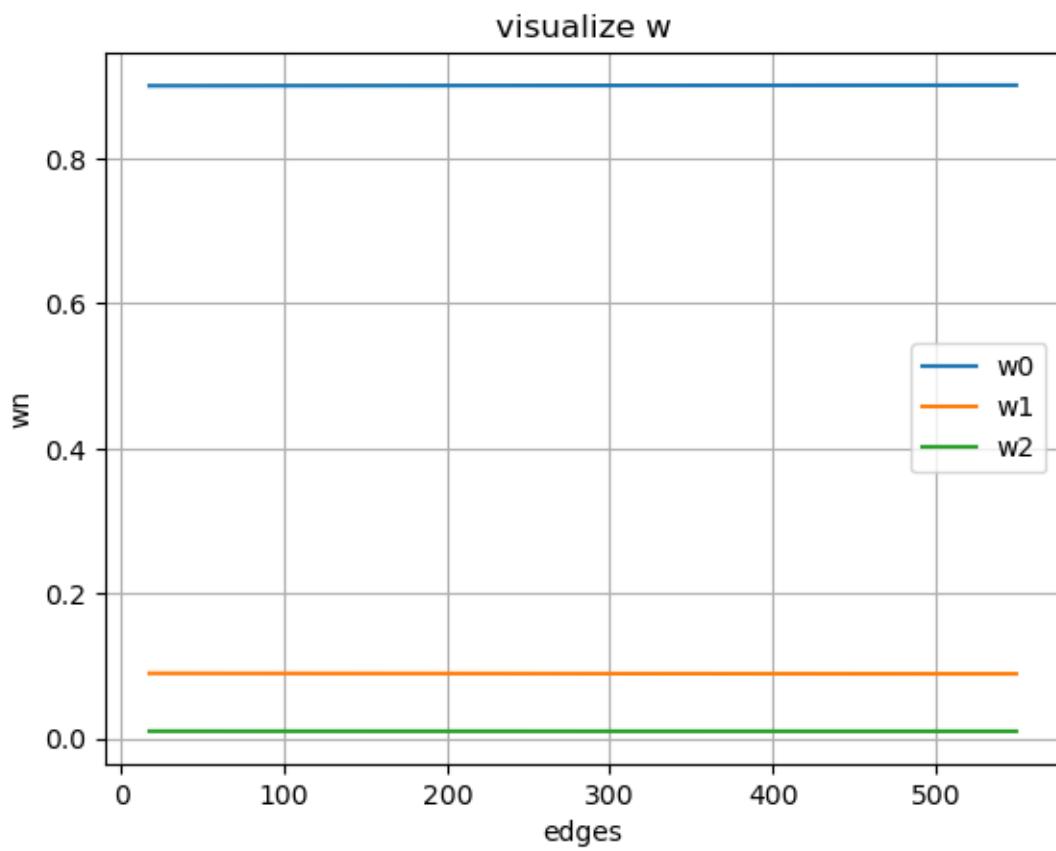
log likelihood function



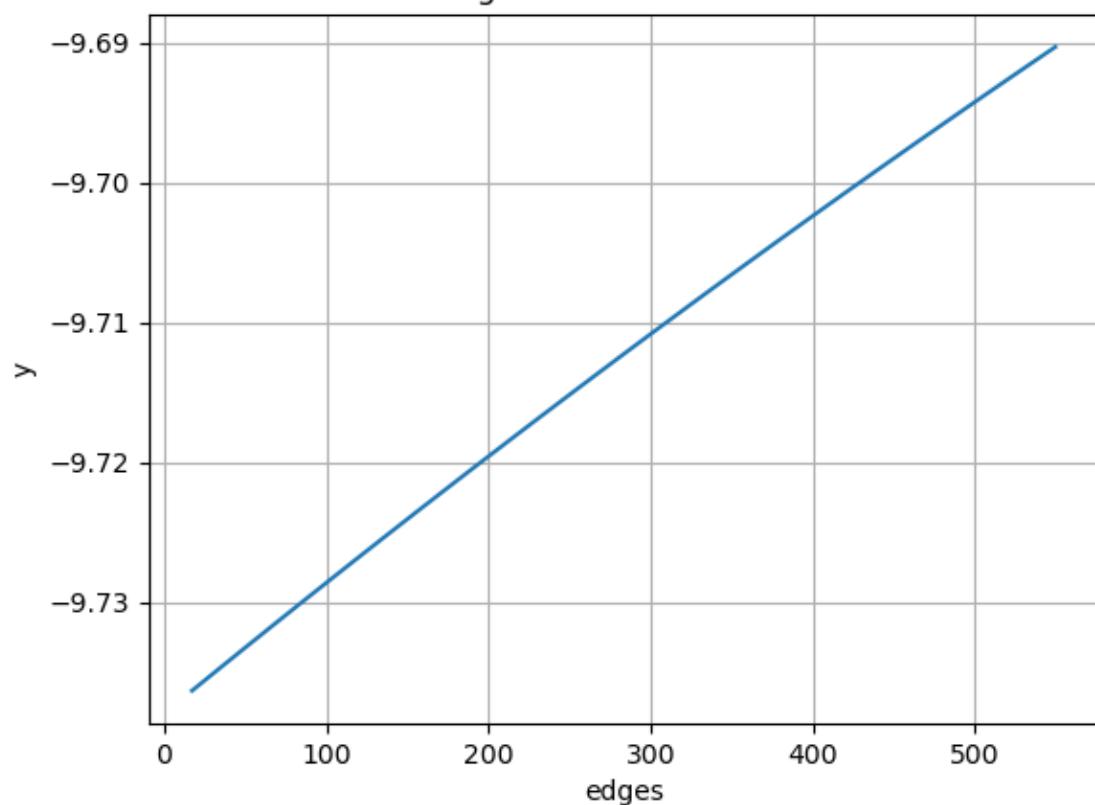


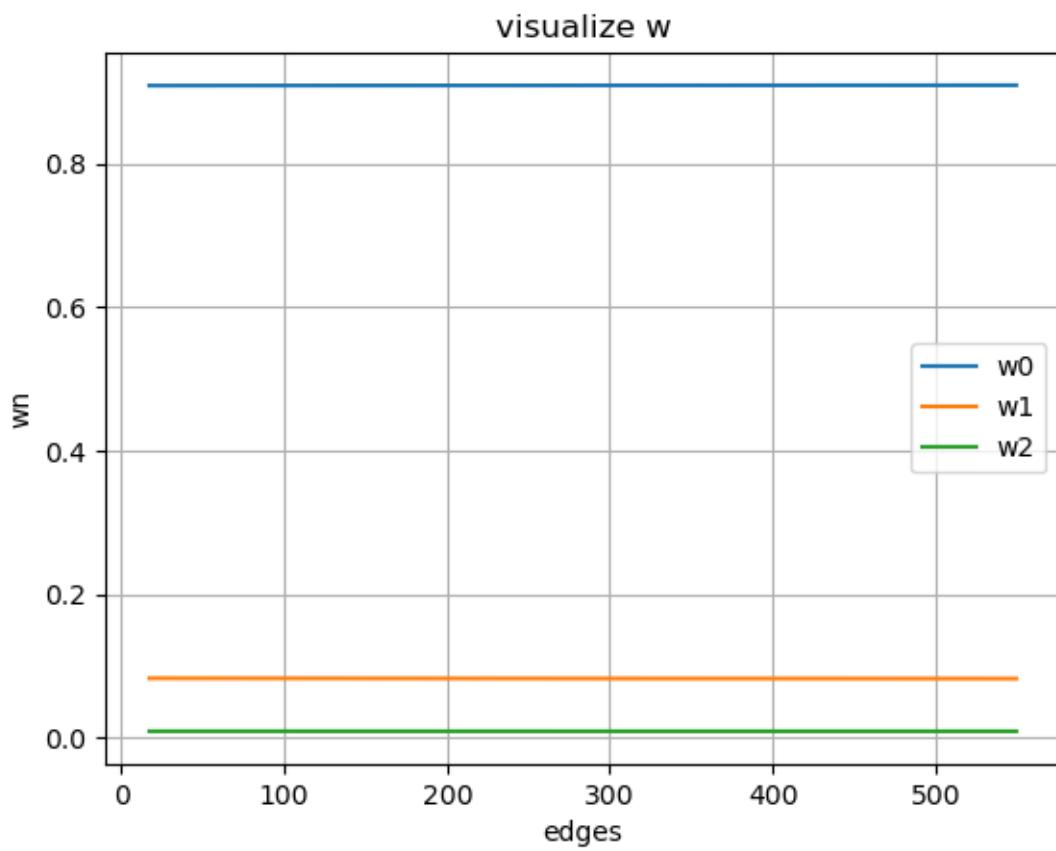
log likelihood function

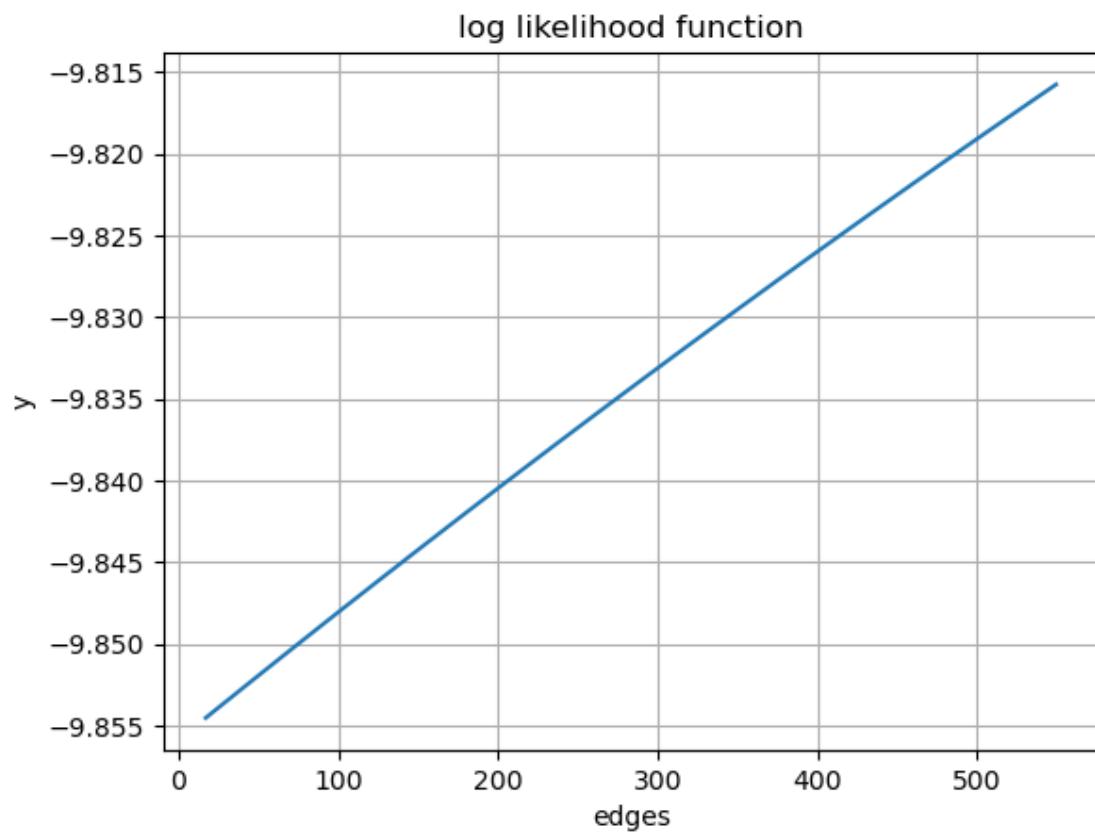


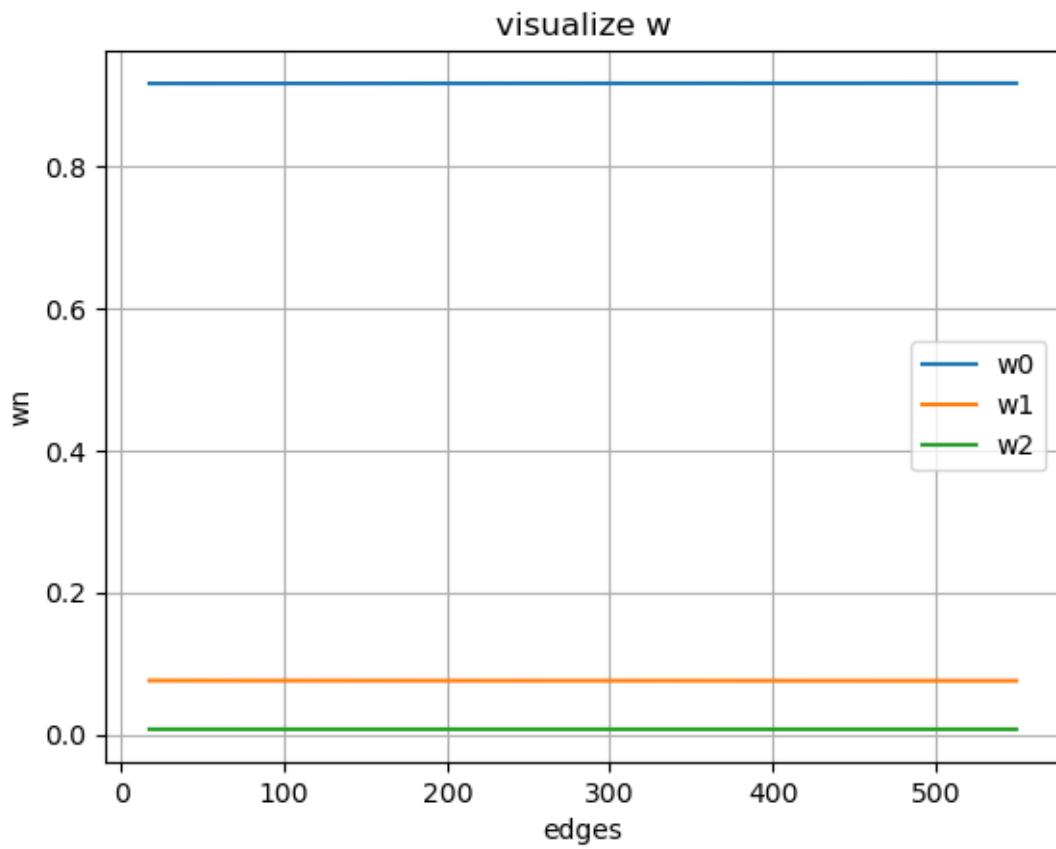


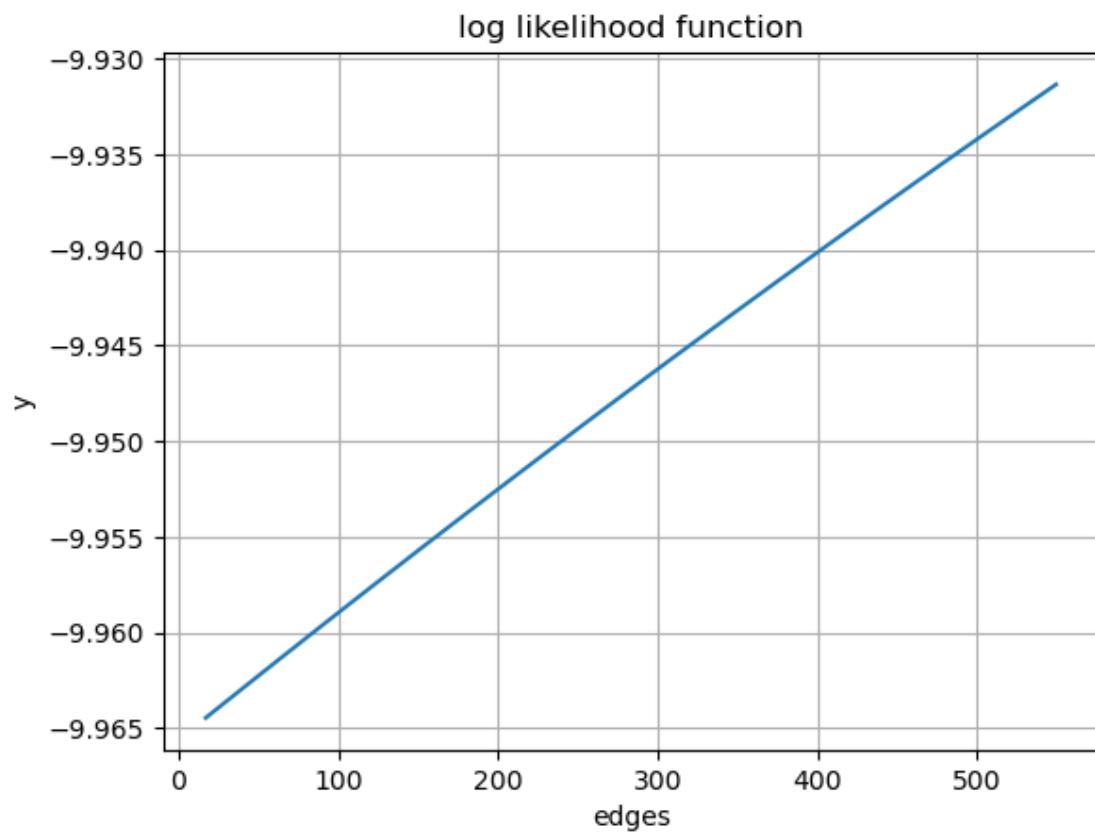
log likelihood function

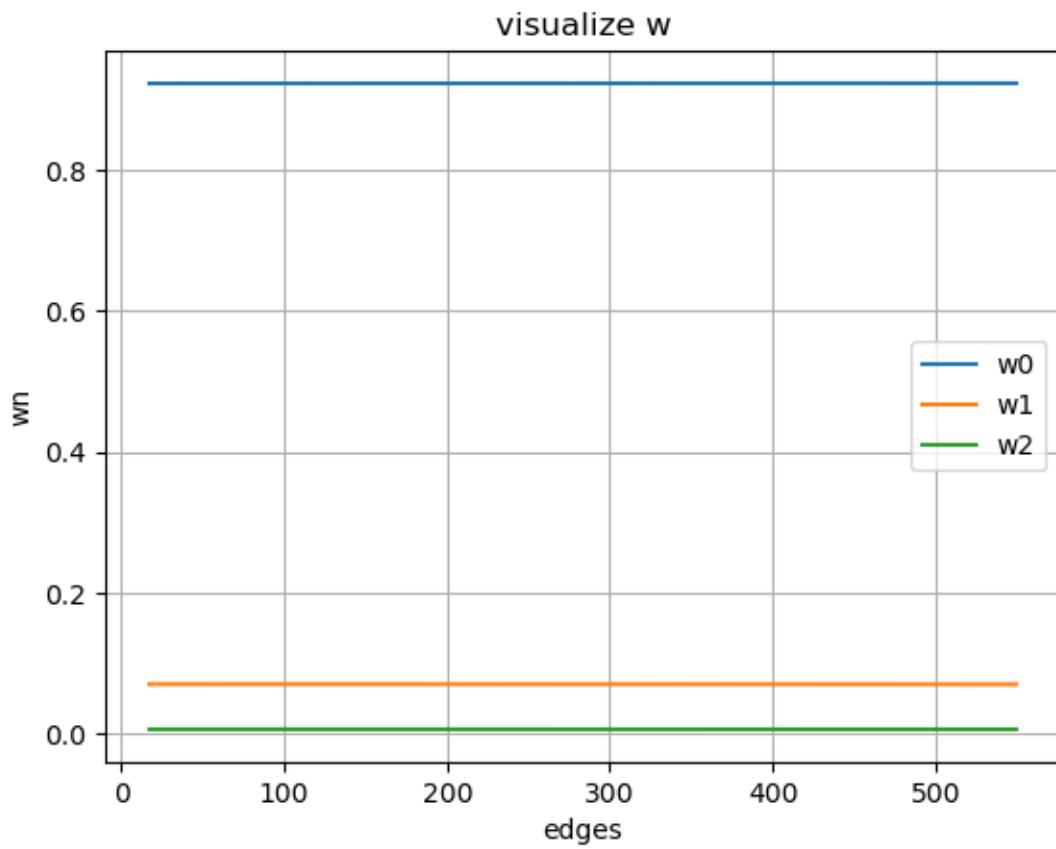




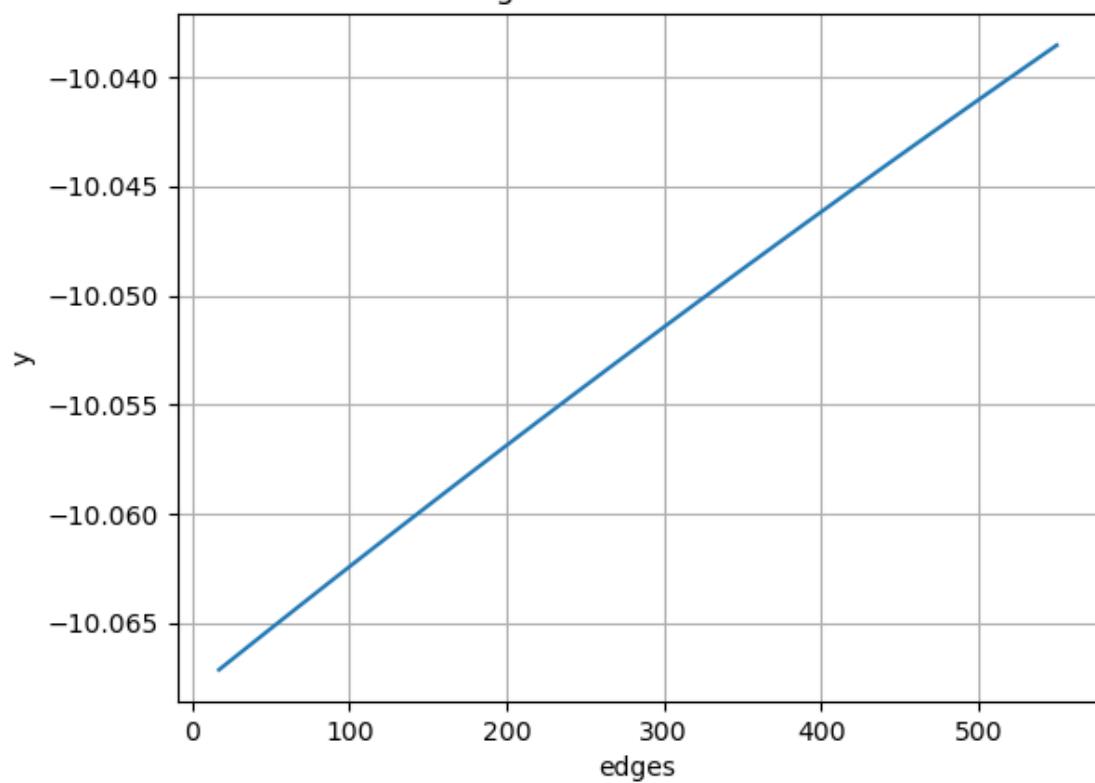


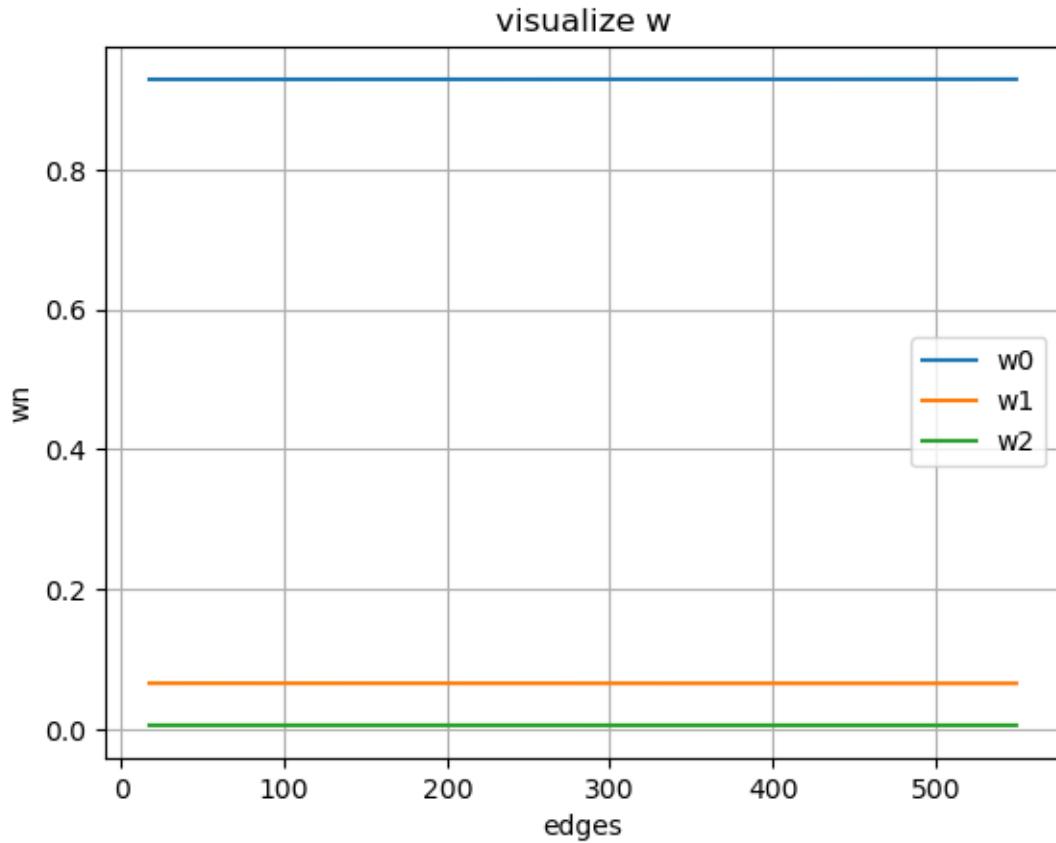




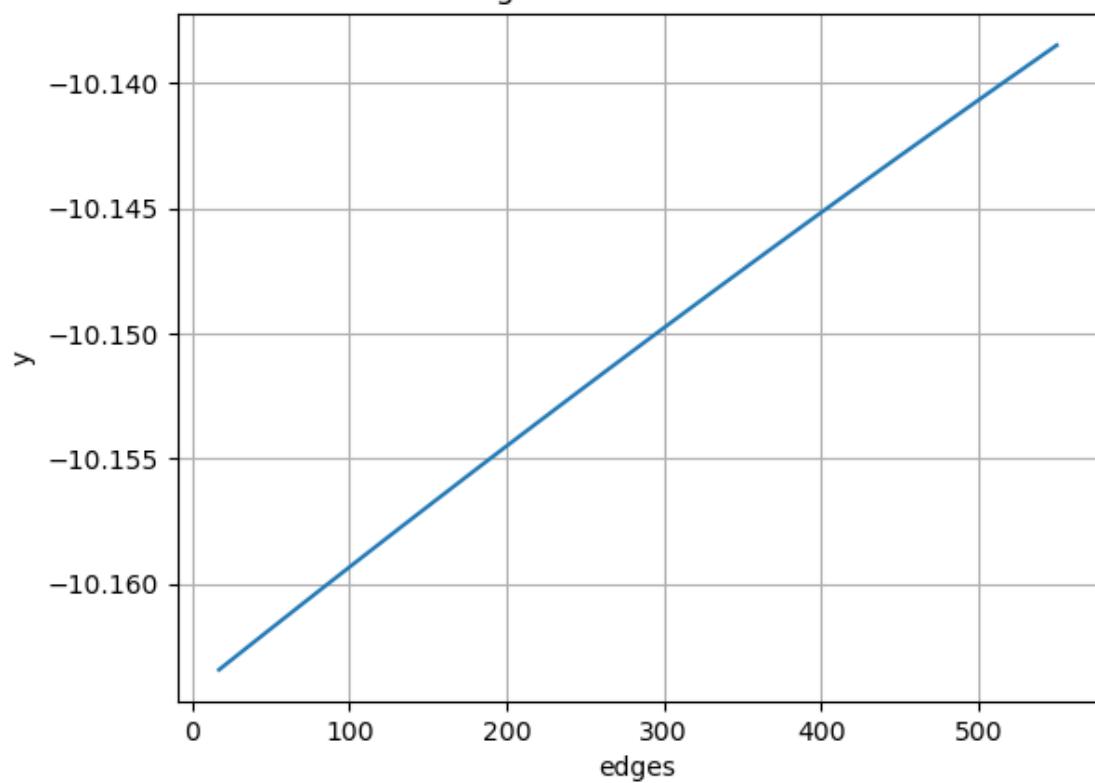


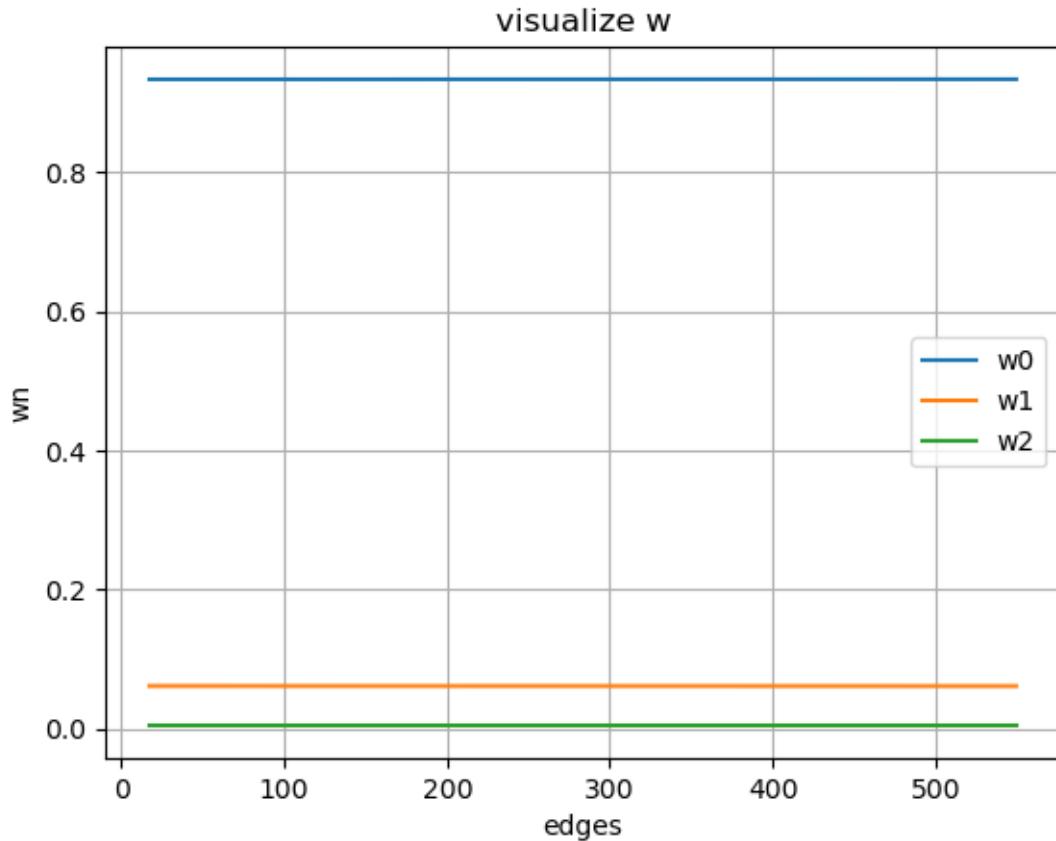
log likelihood function



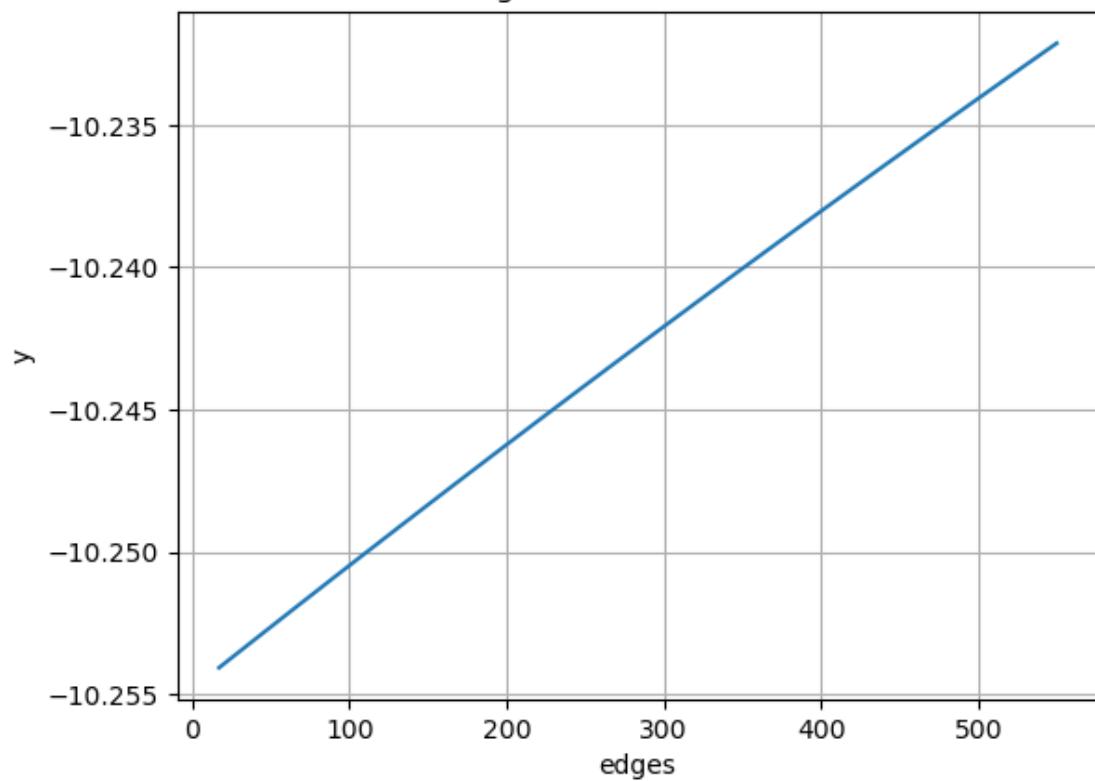


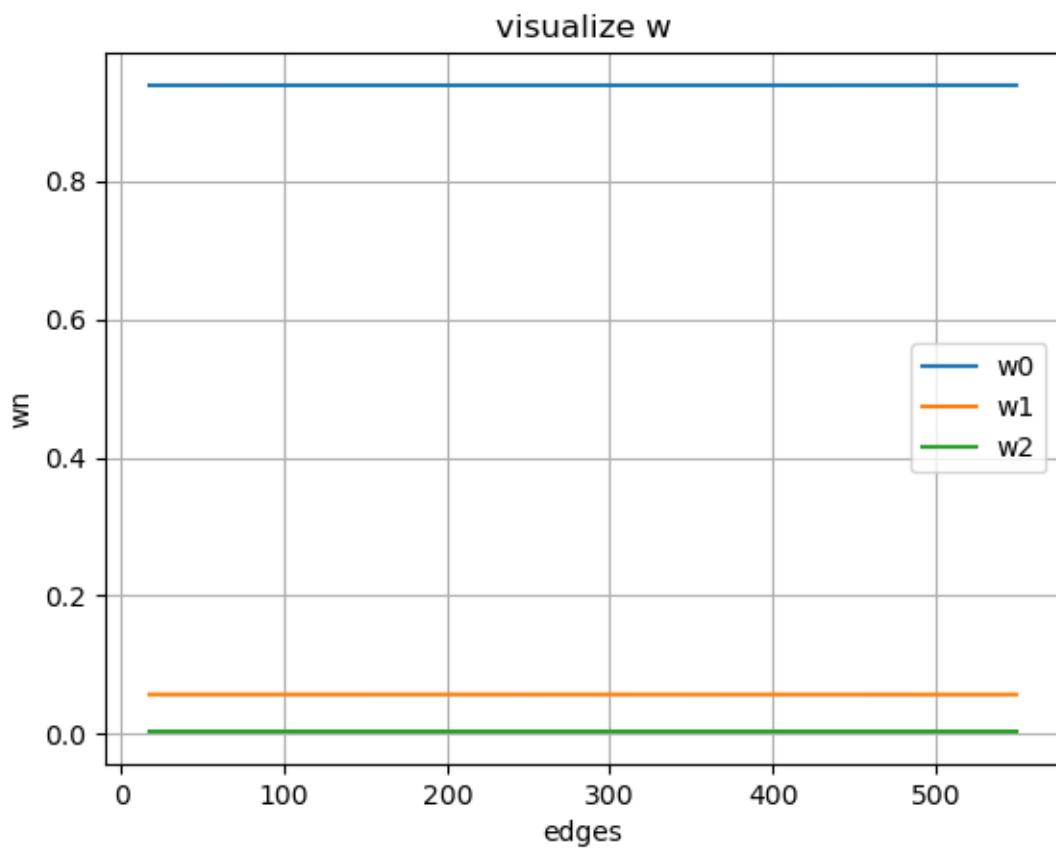
log likelihood function

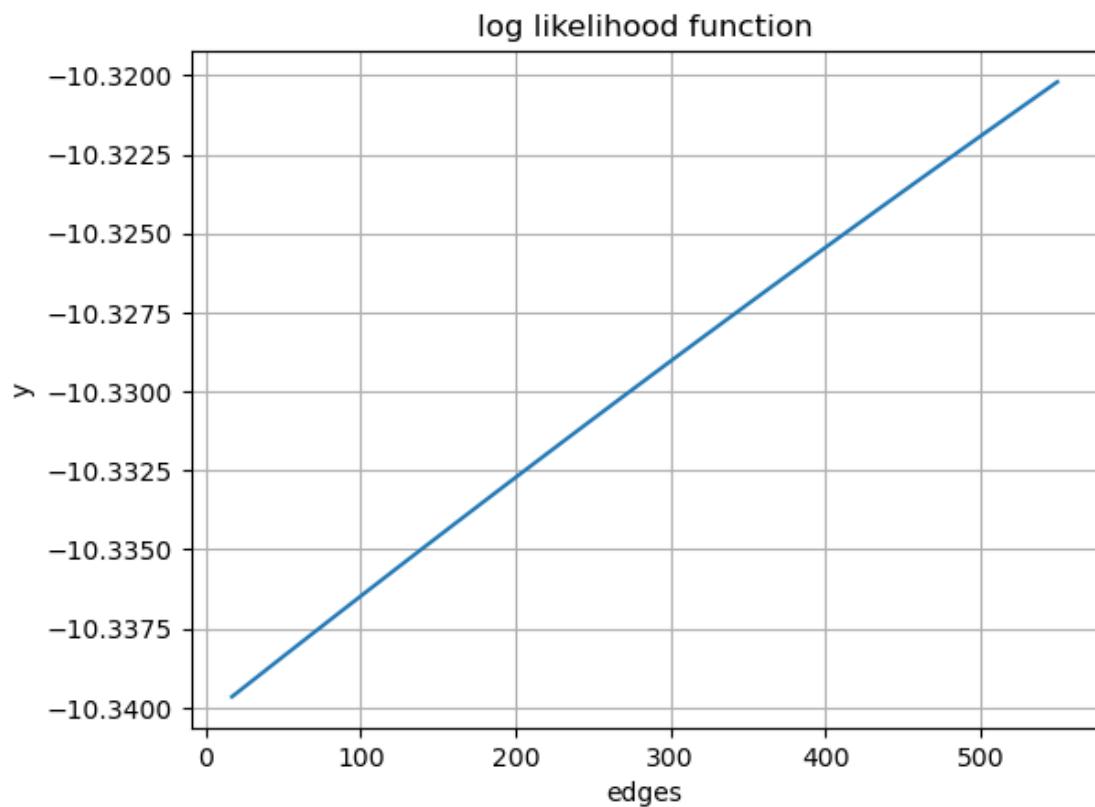


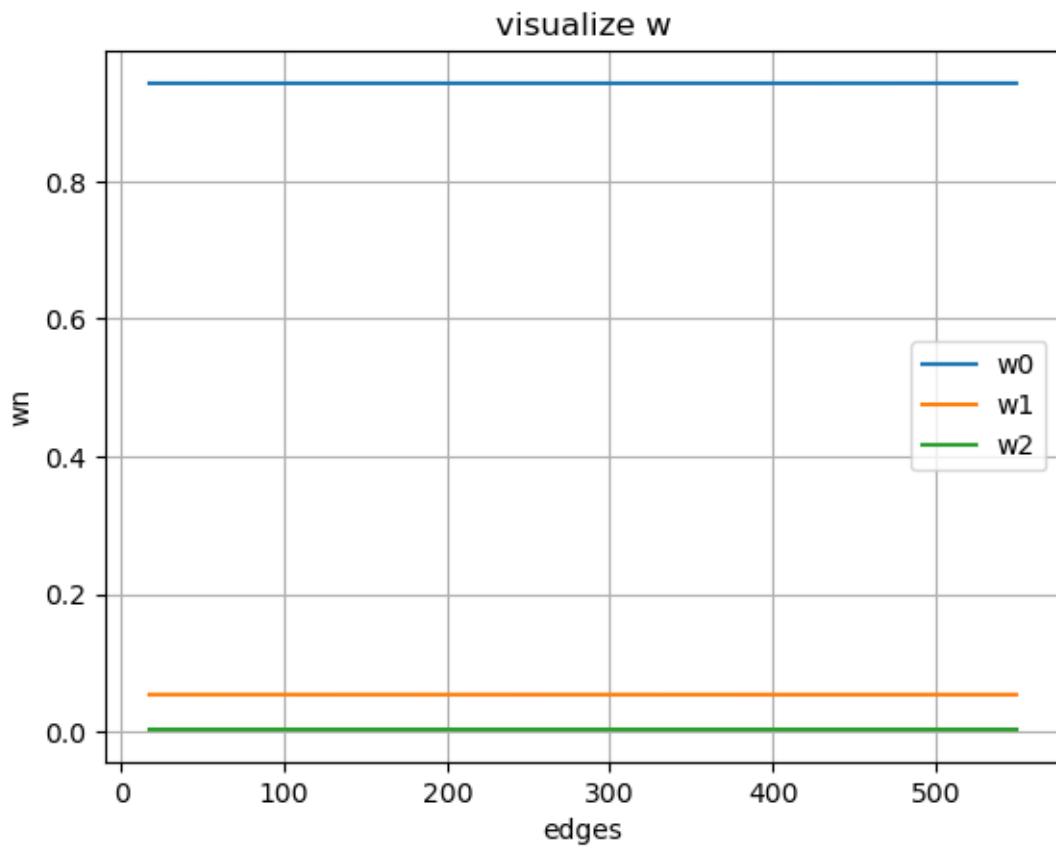


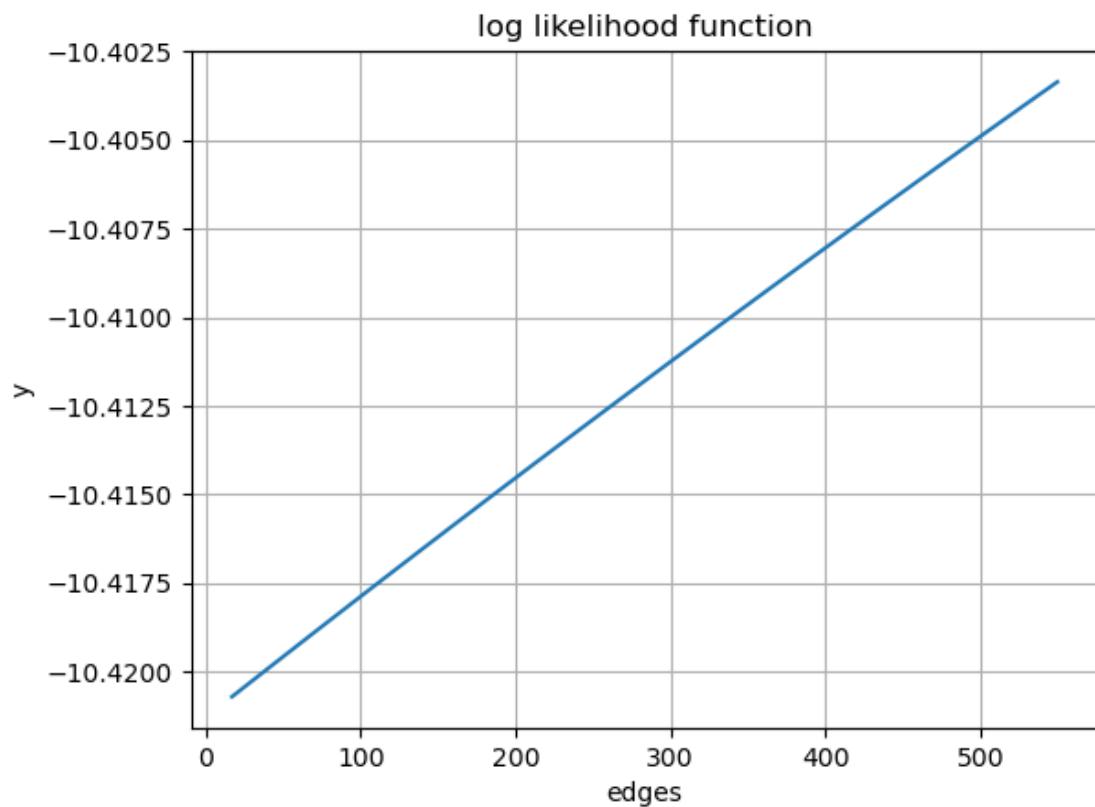
log likelihood function

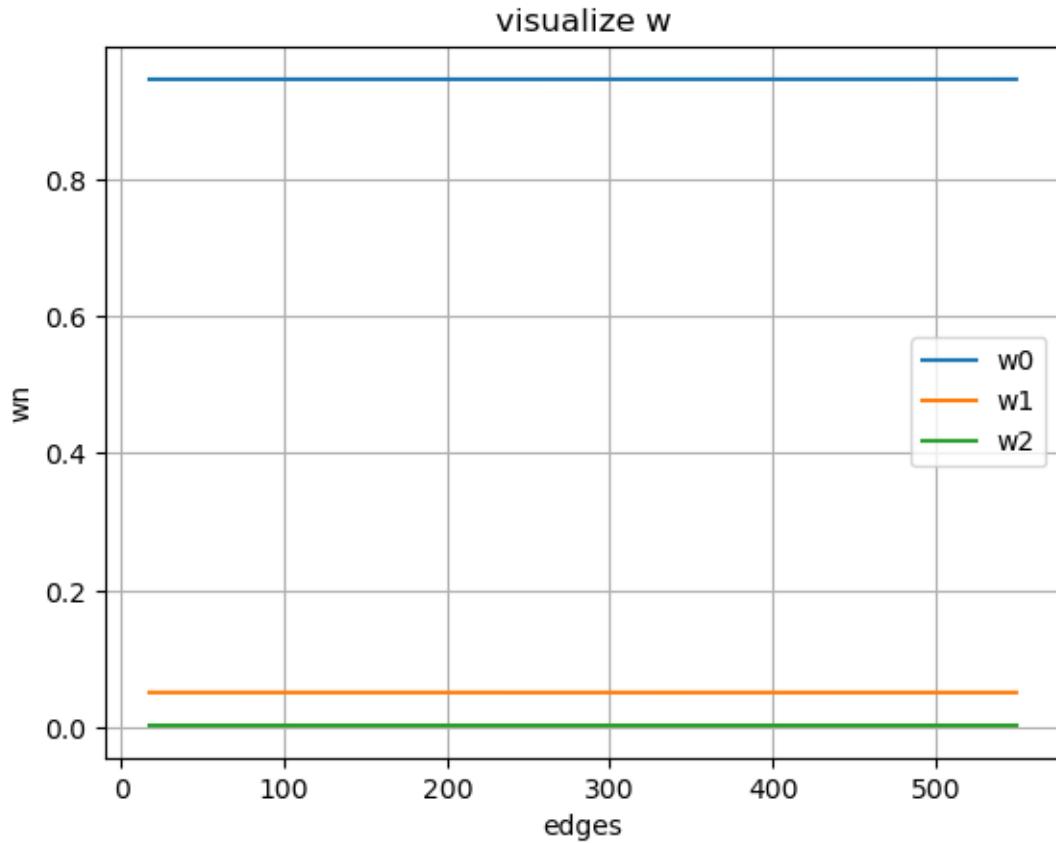


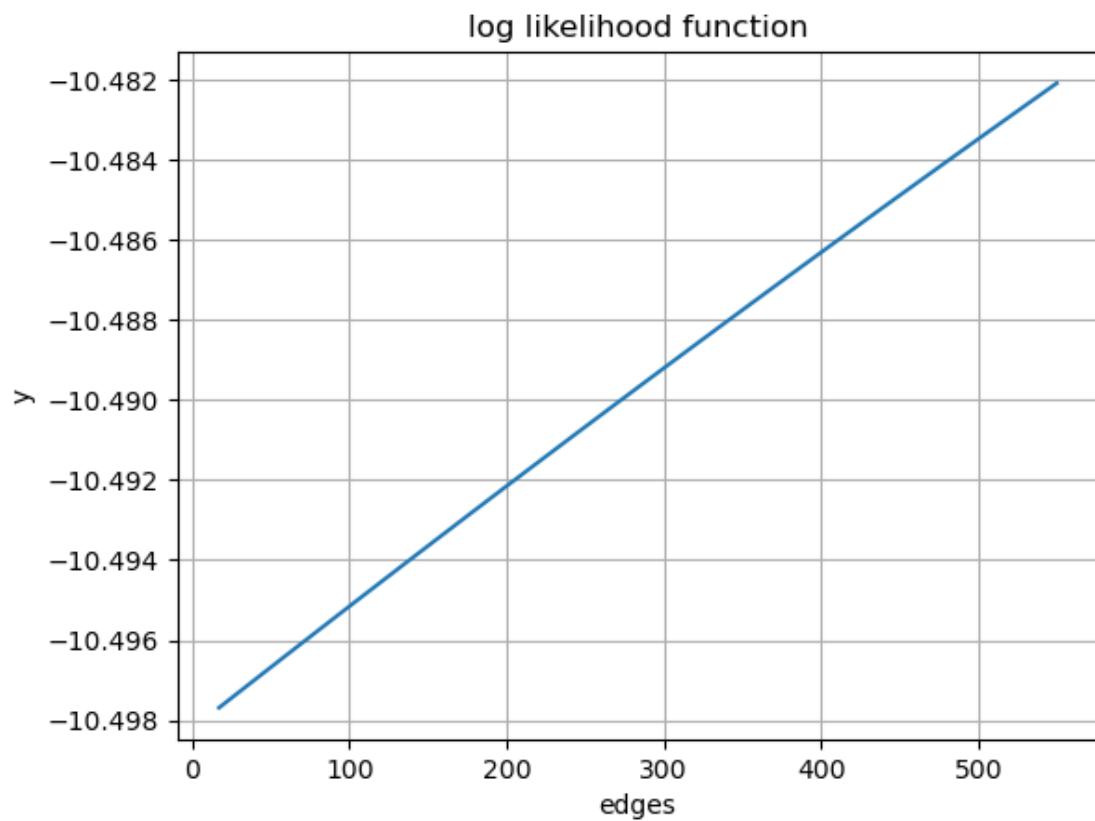


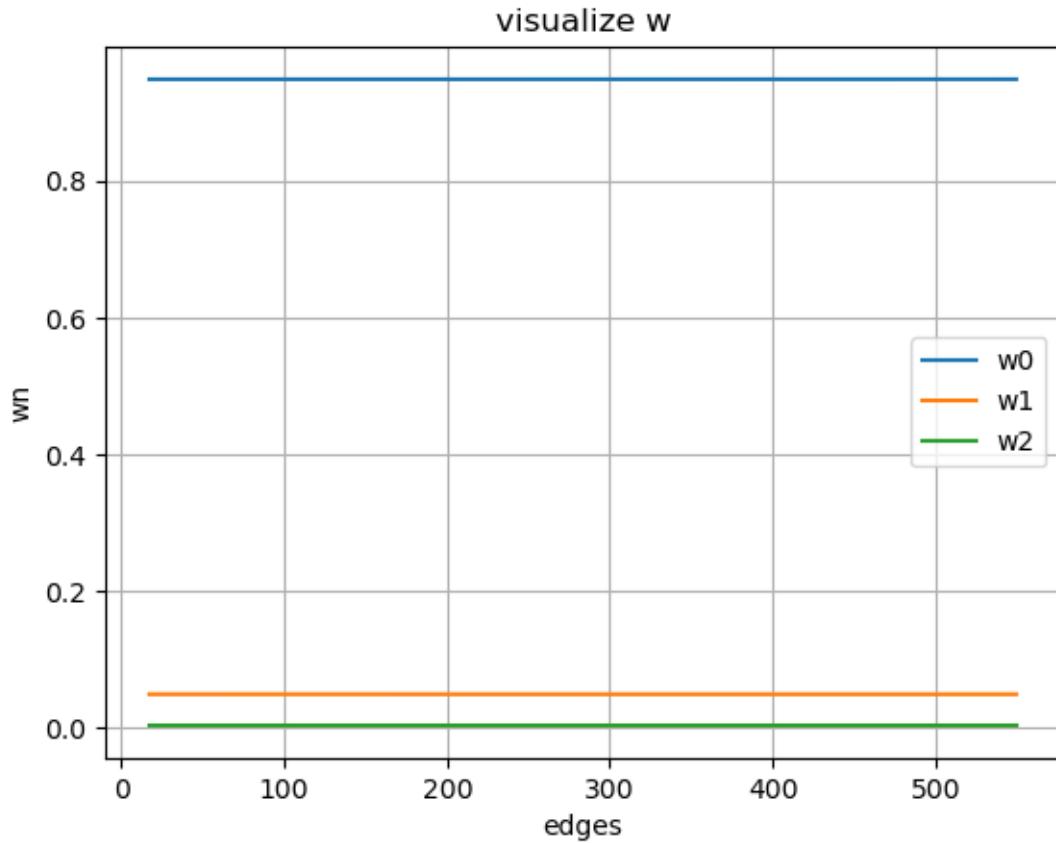


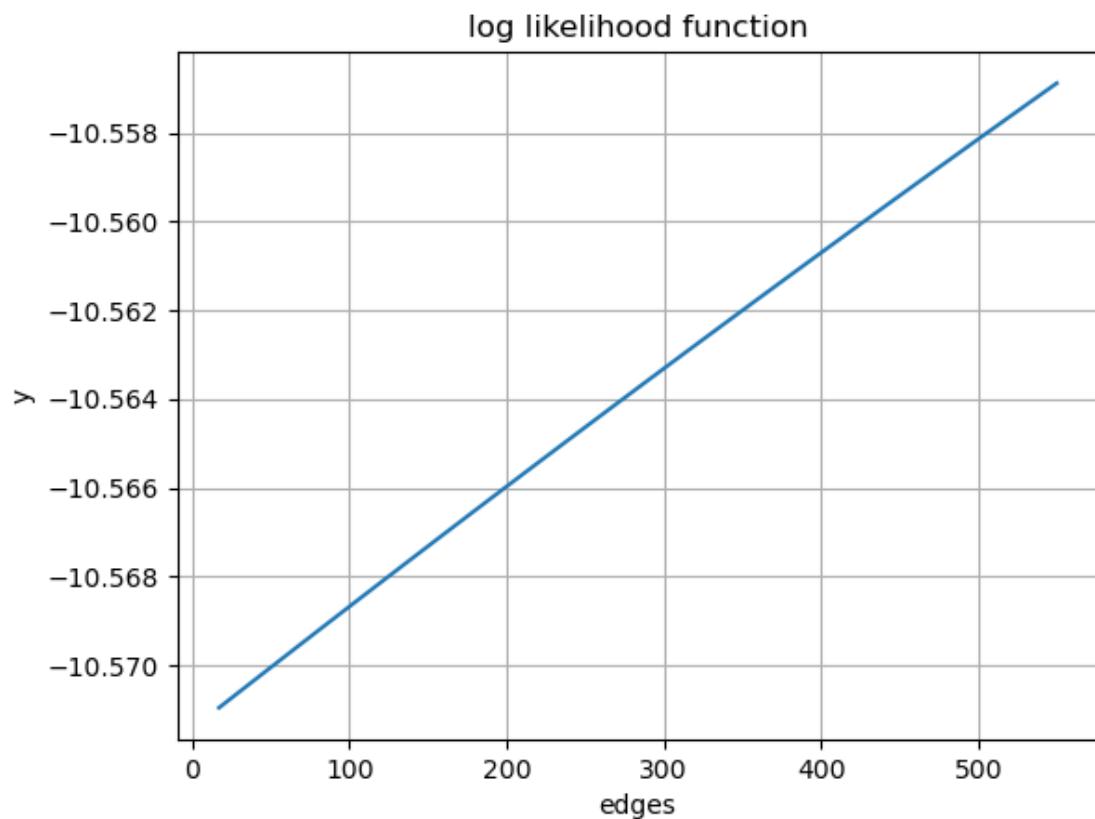


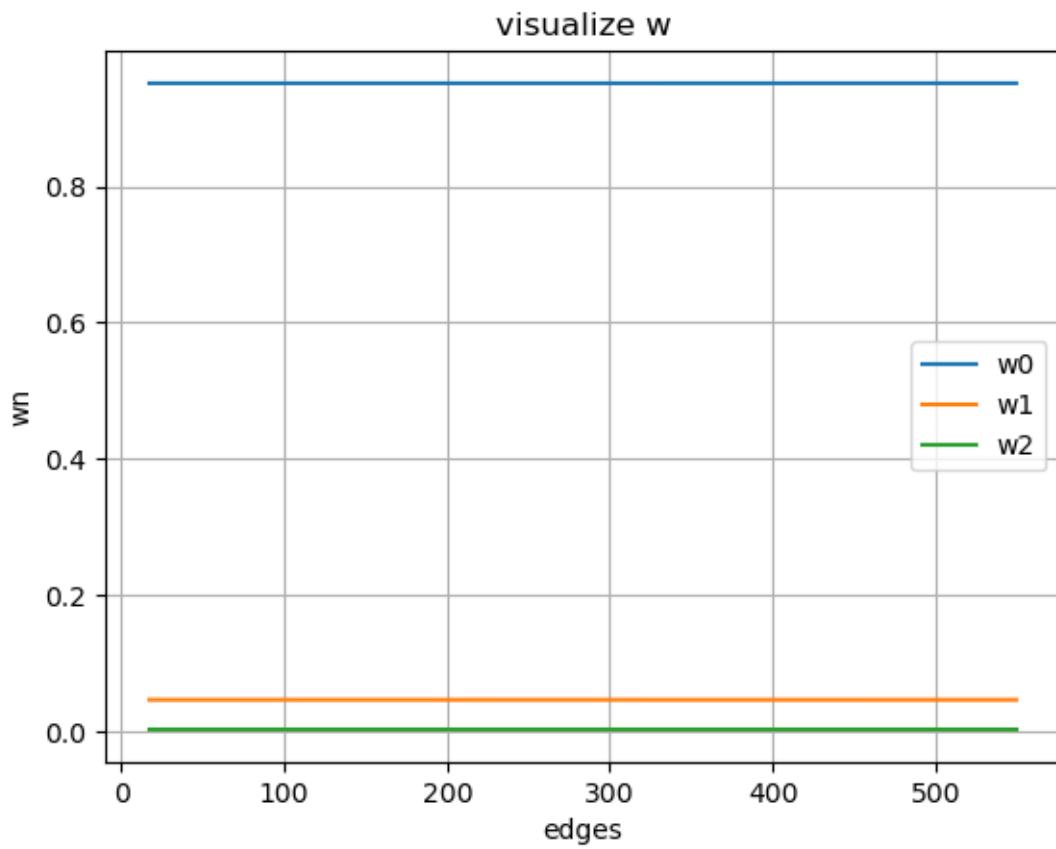




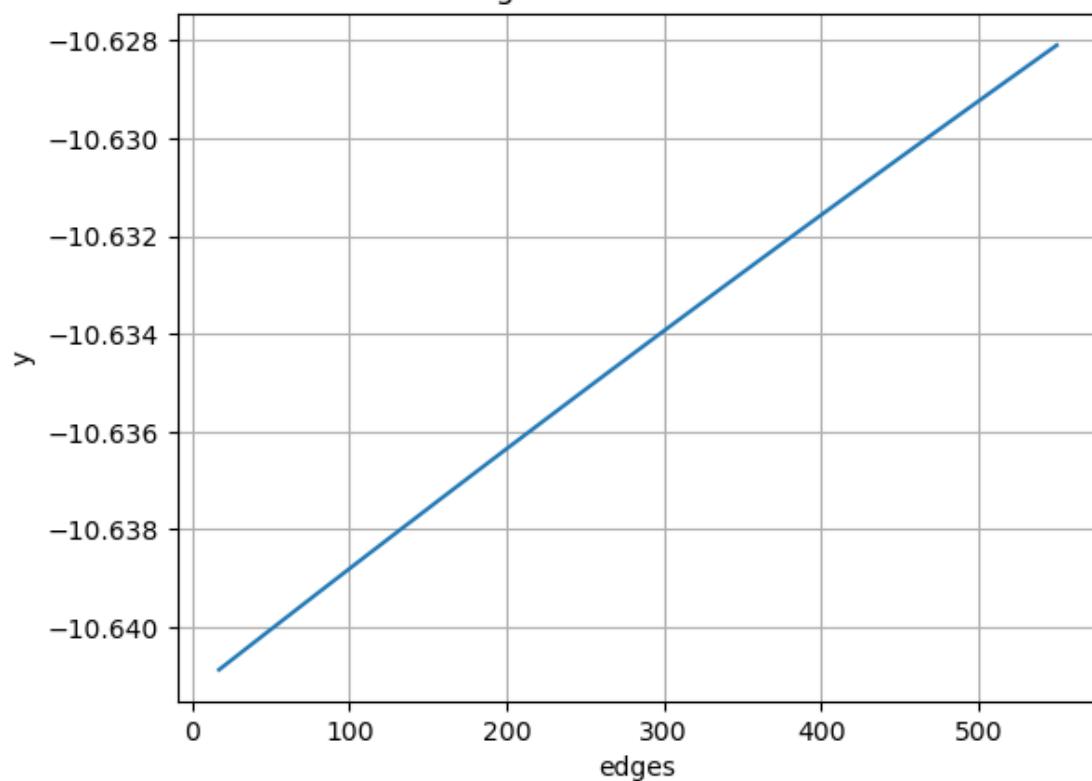


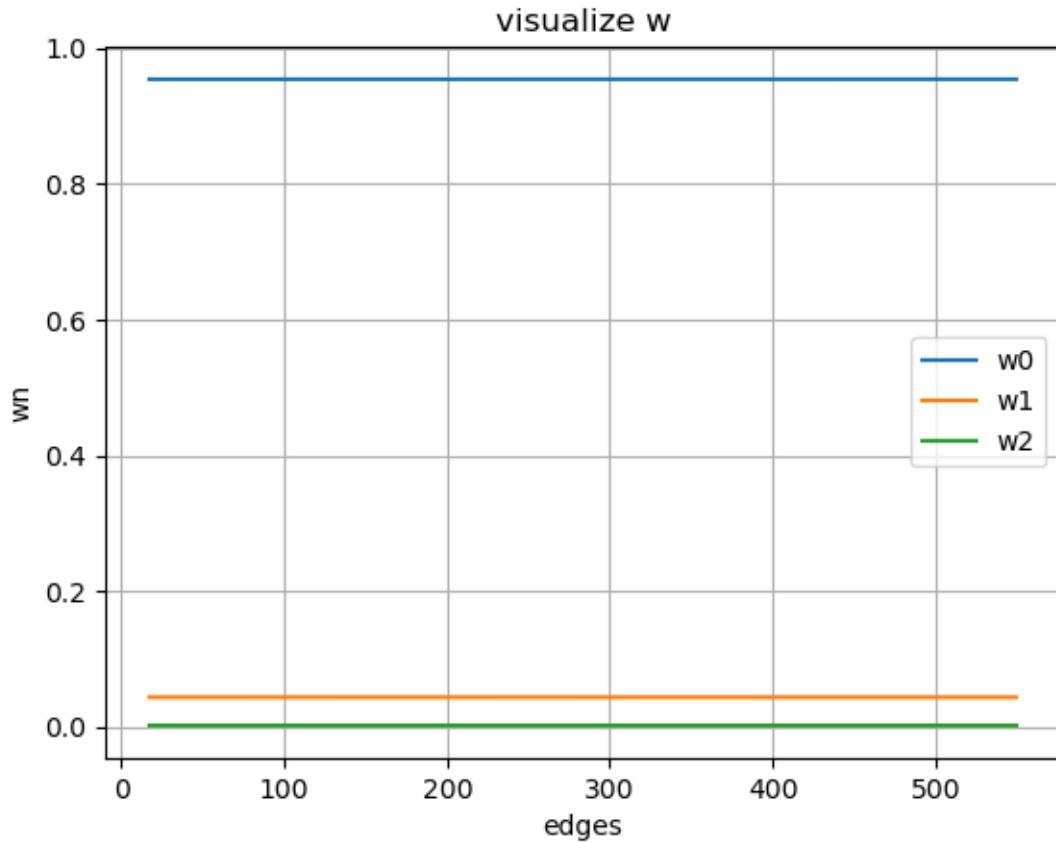


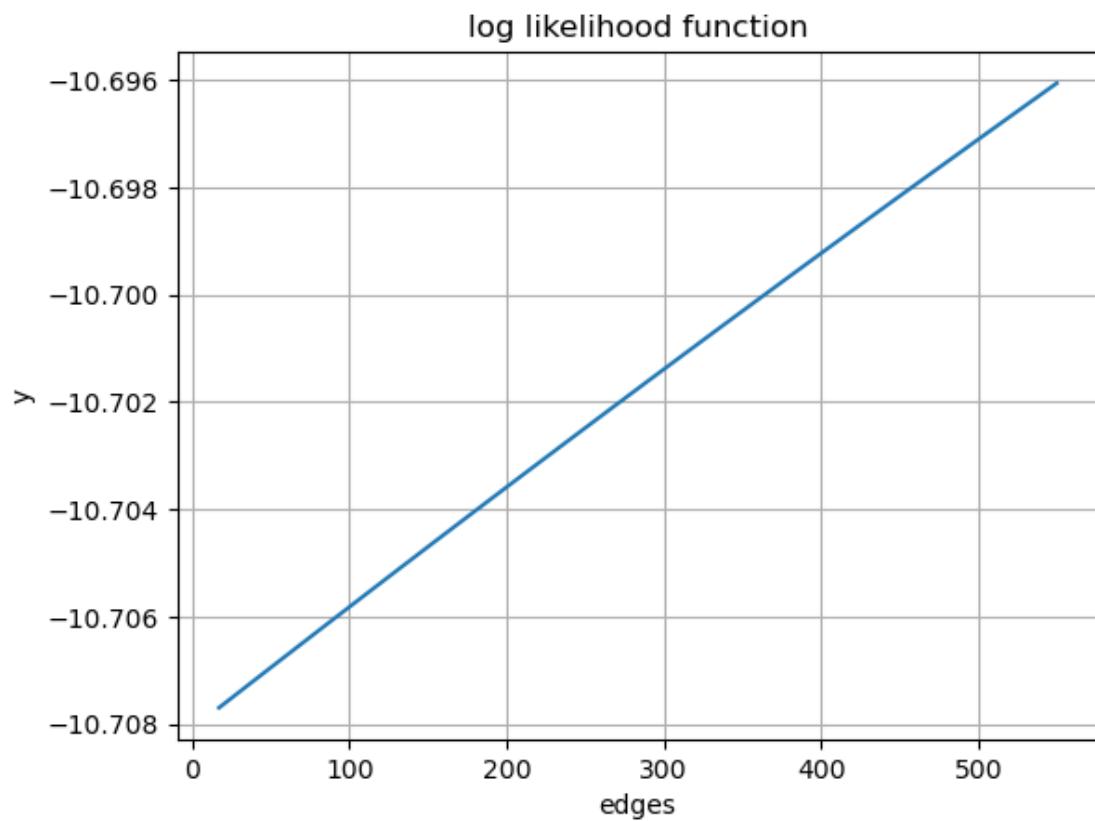


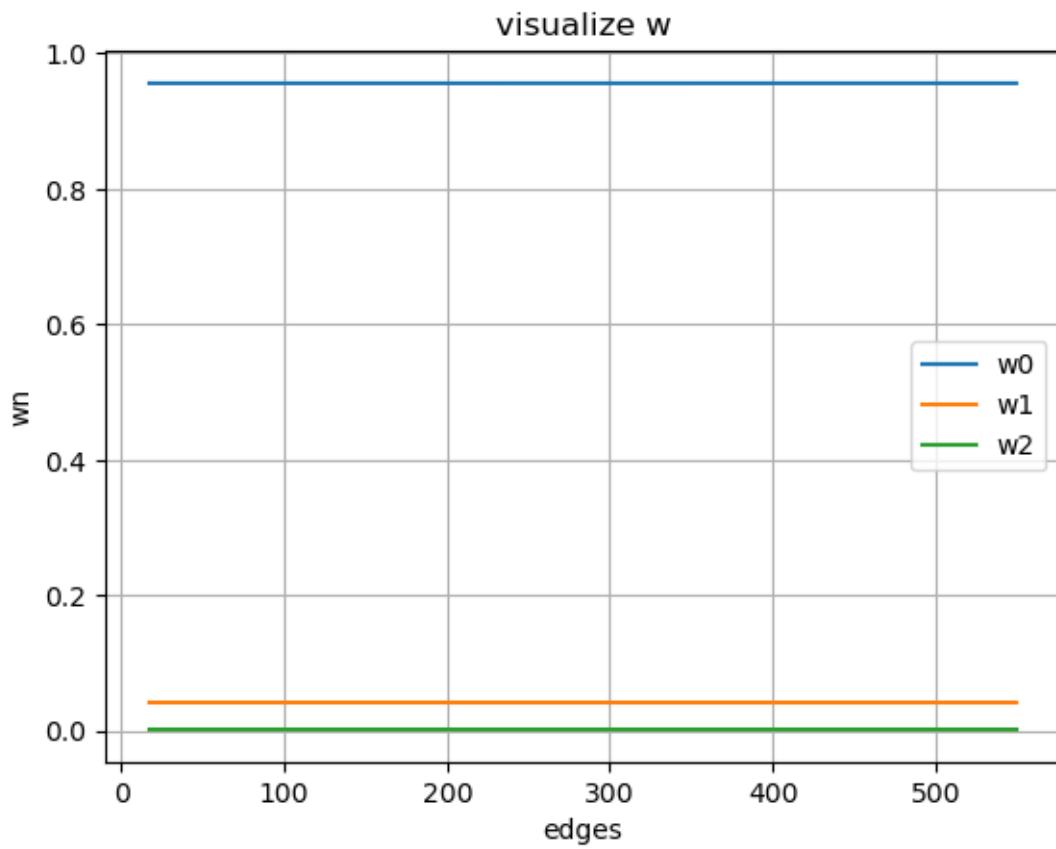


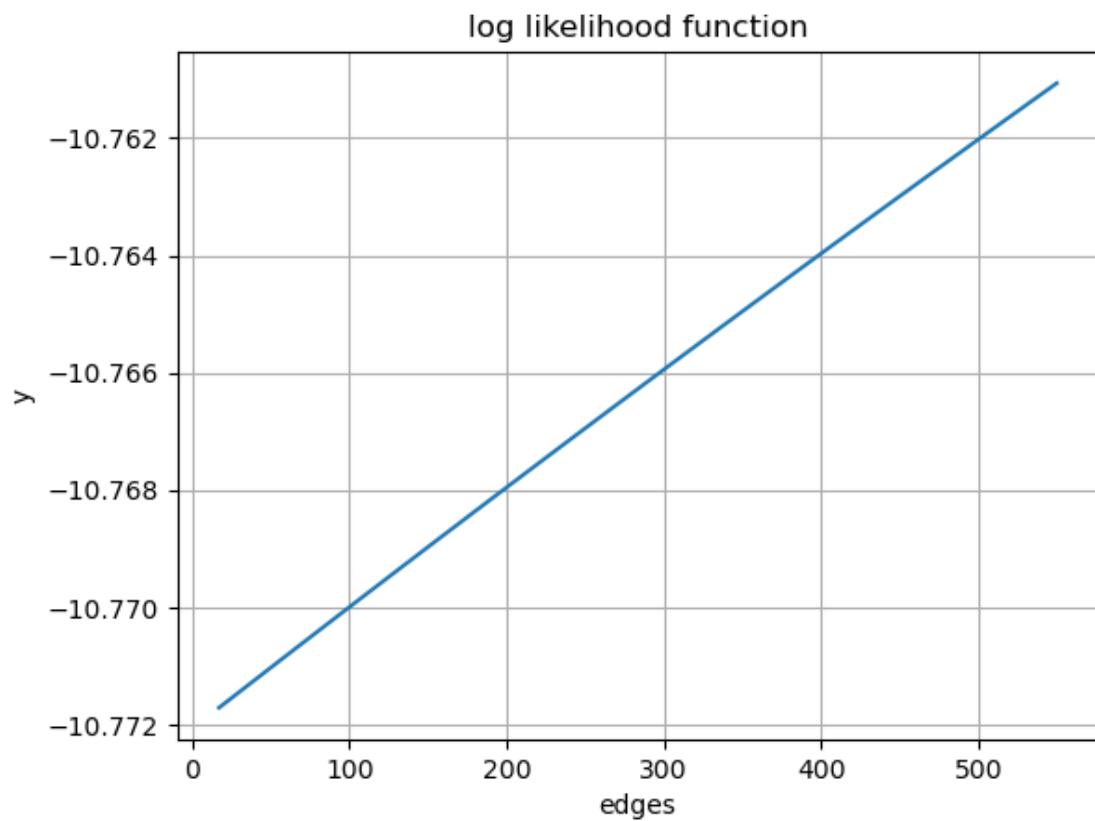
log likelihood function

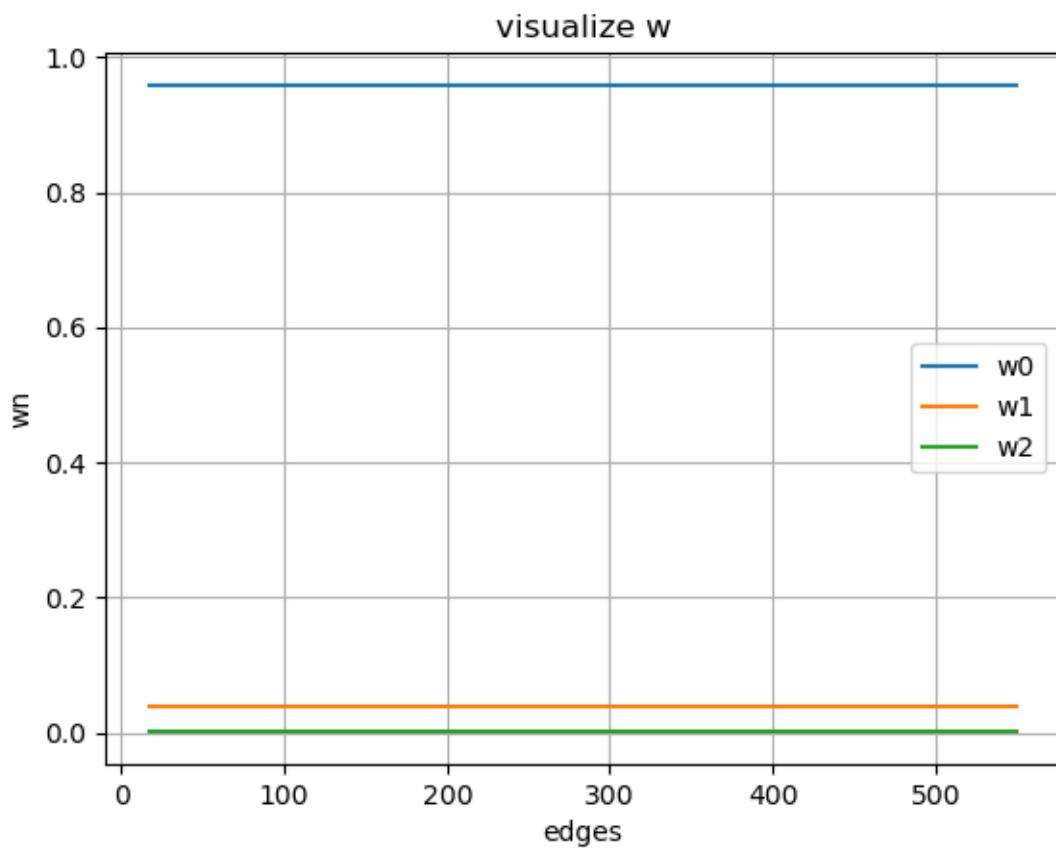


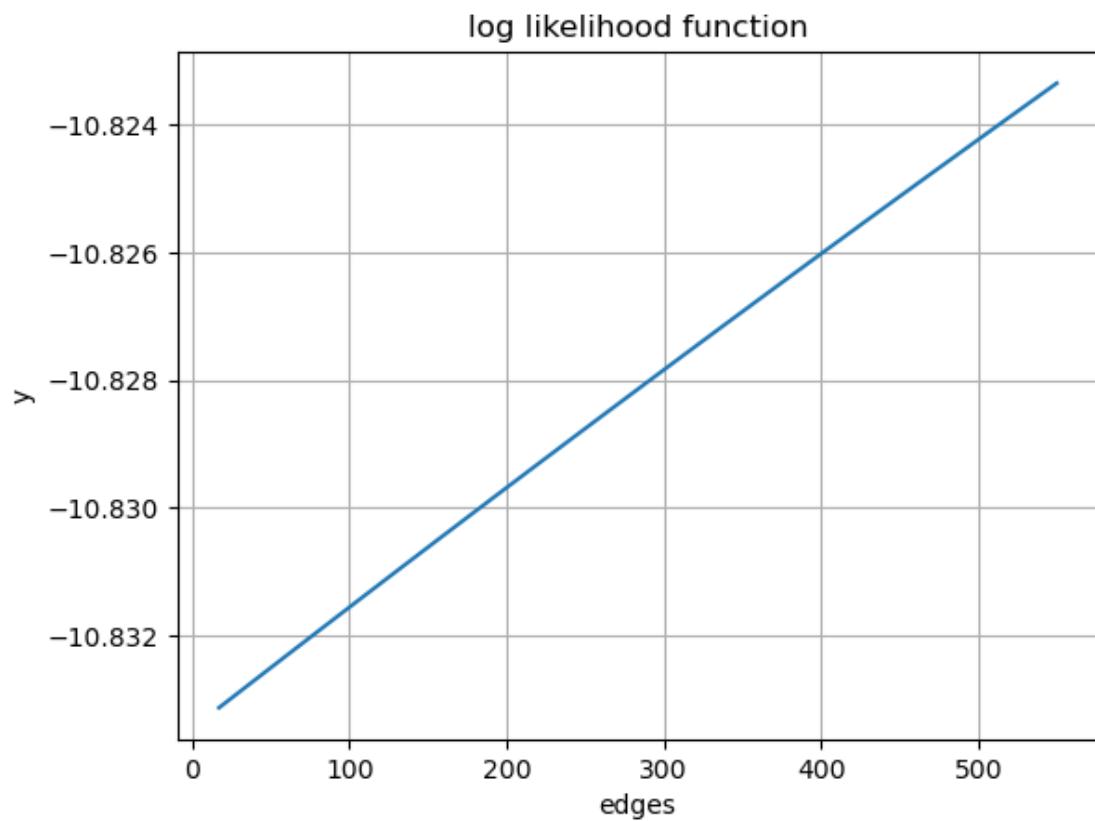


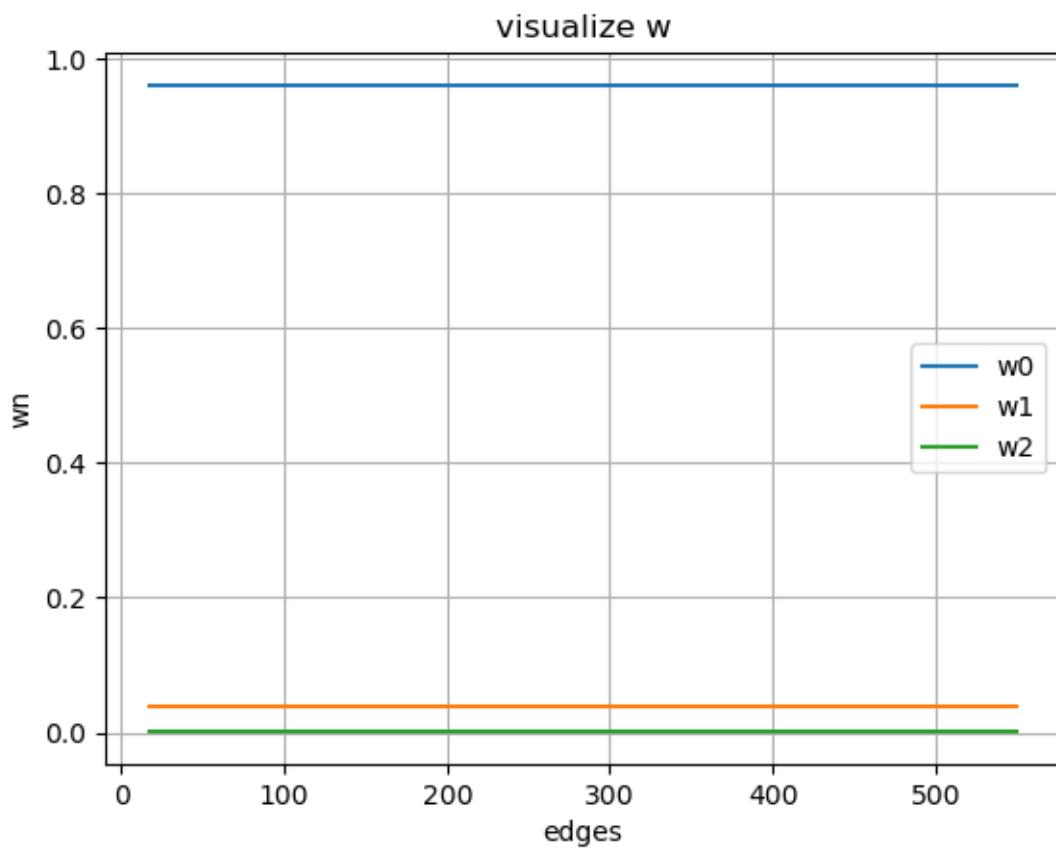




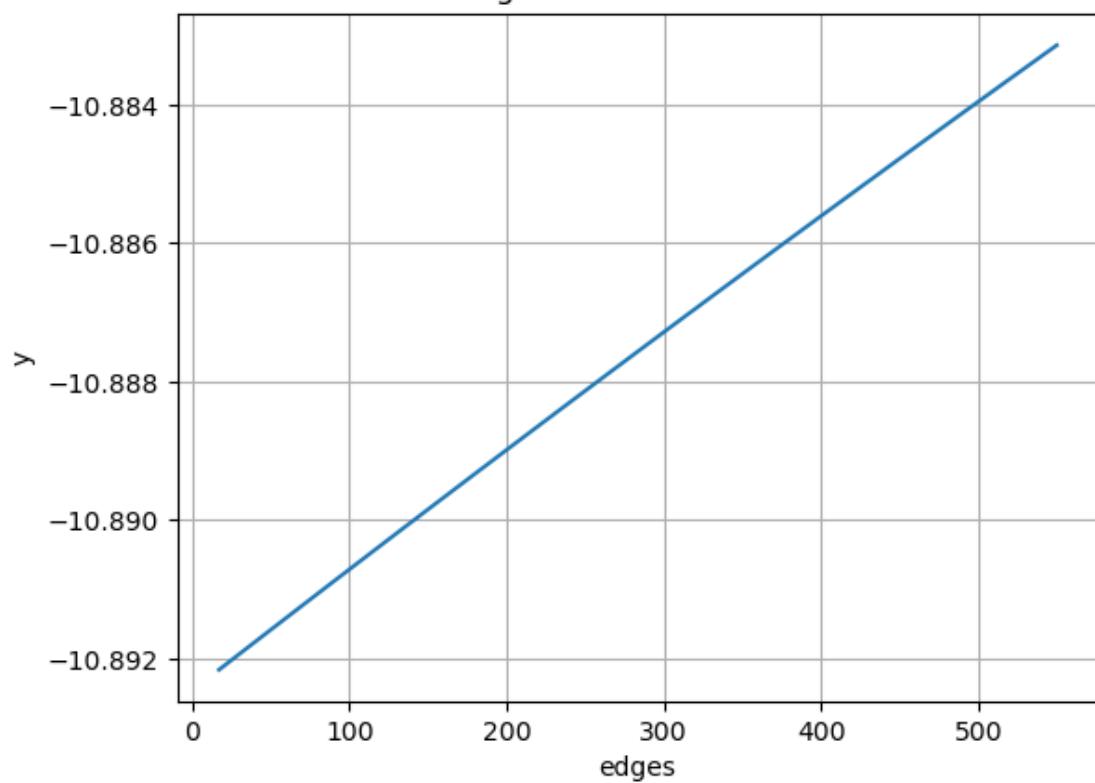


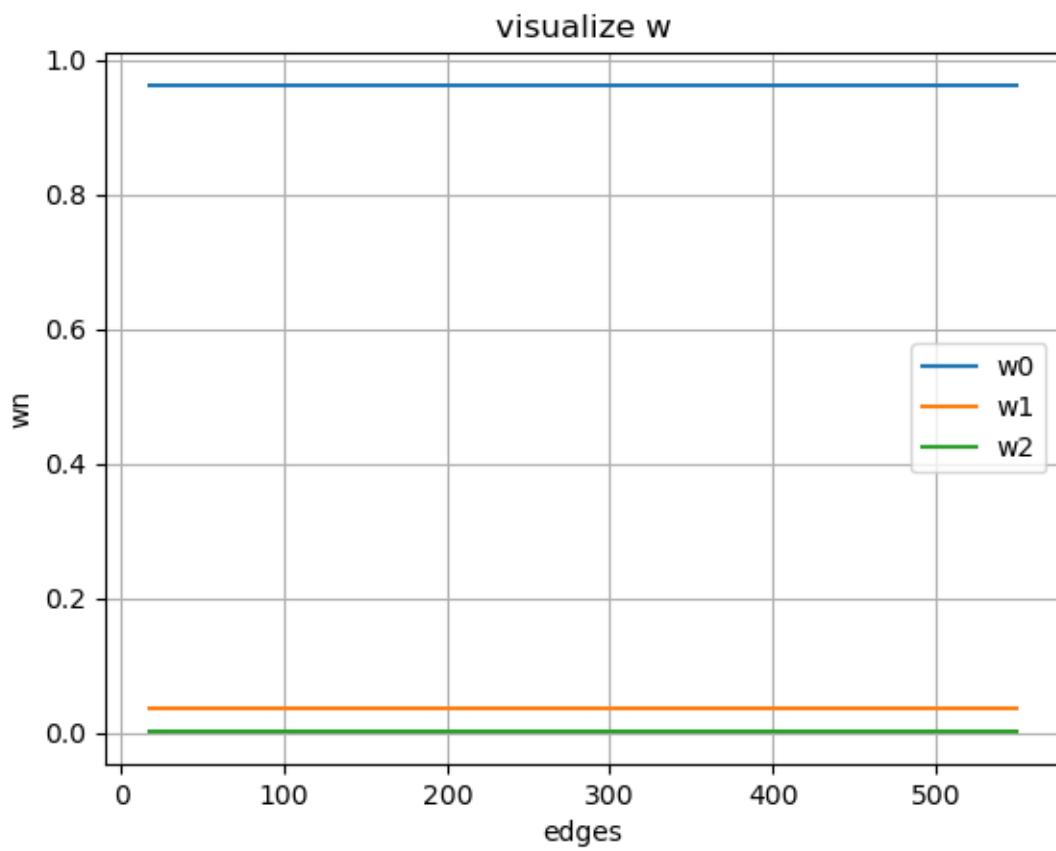


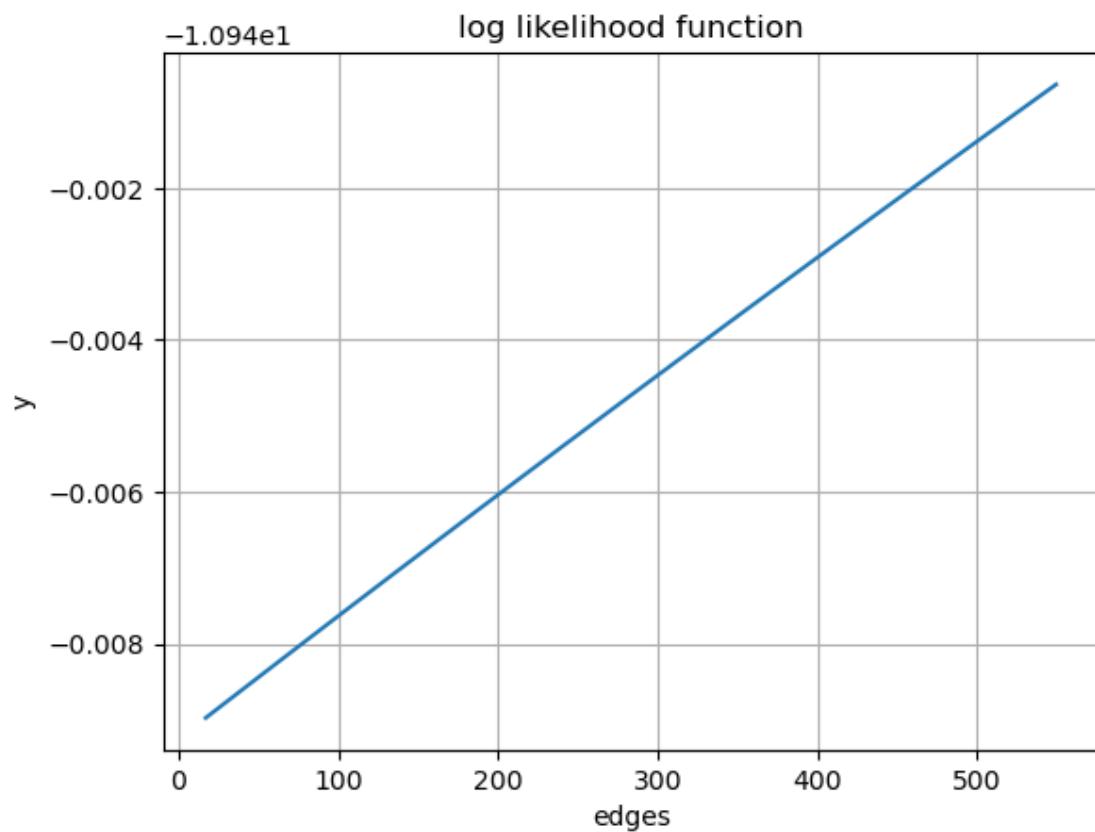


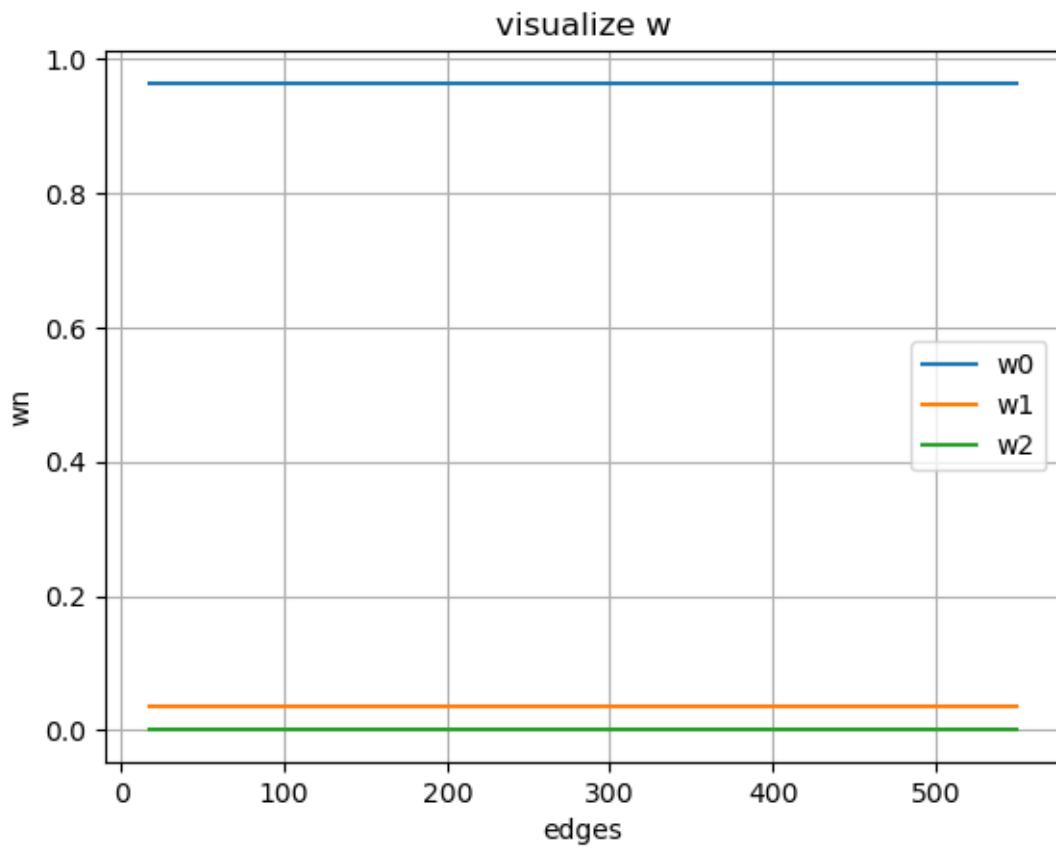


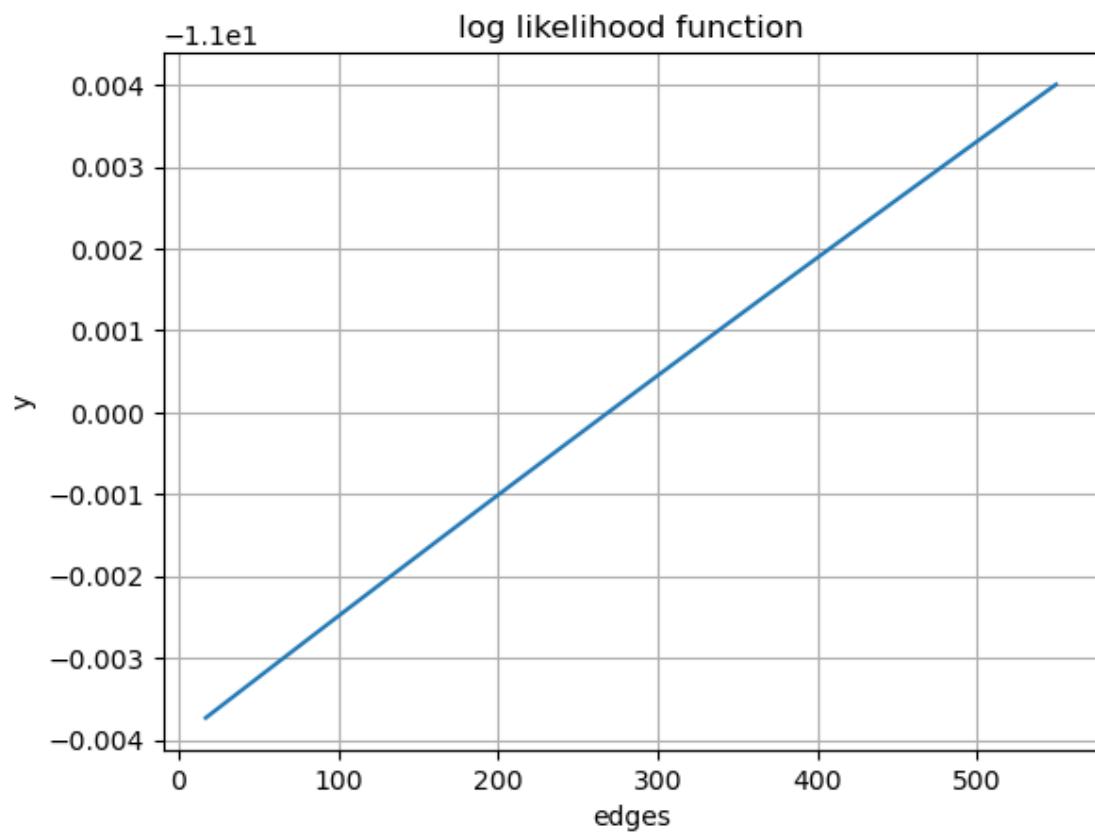
log likelihood function

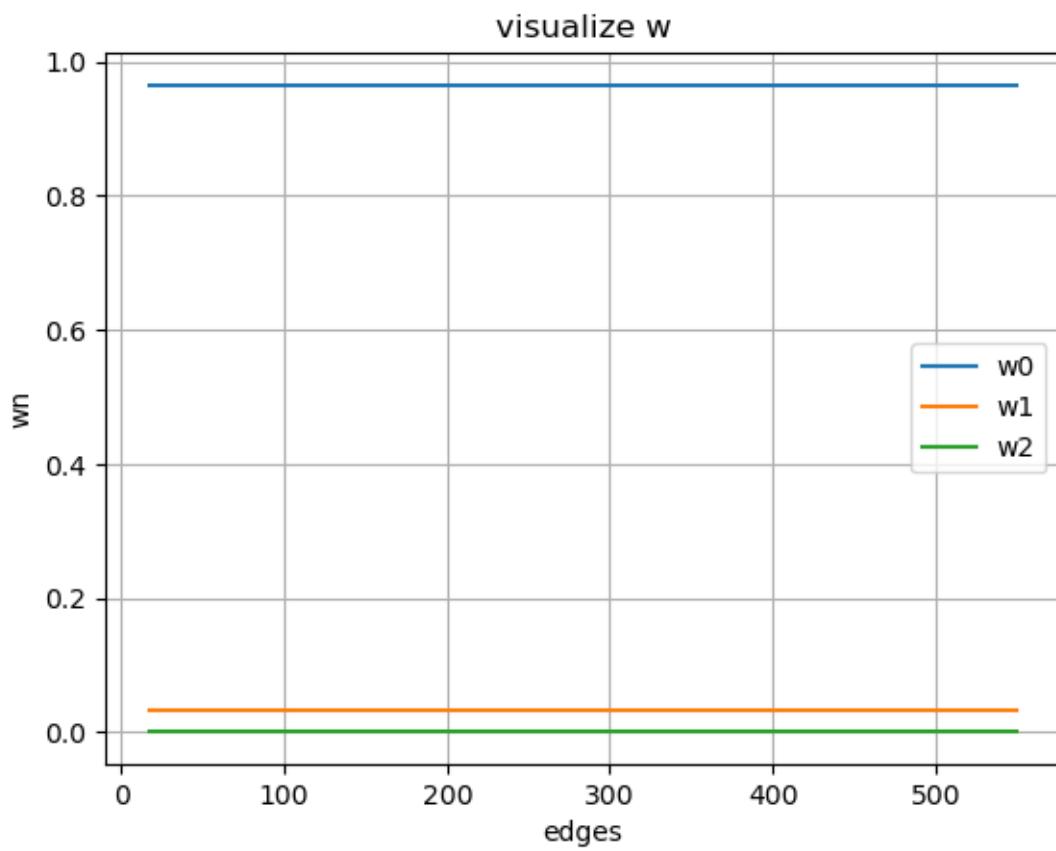


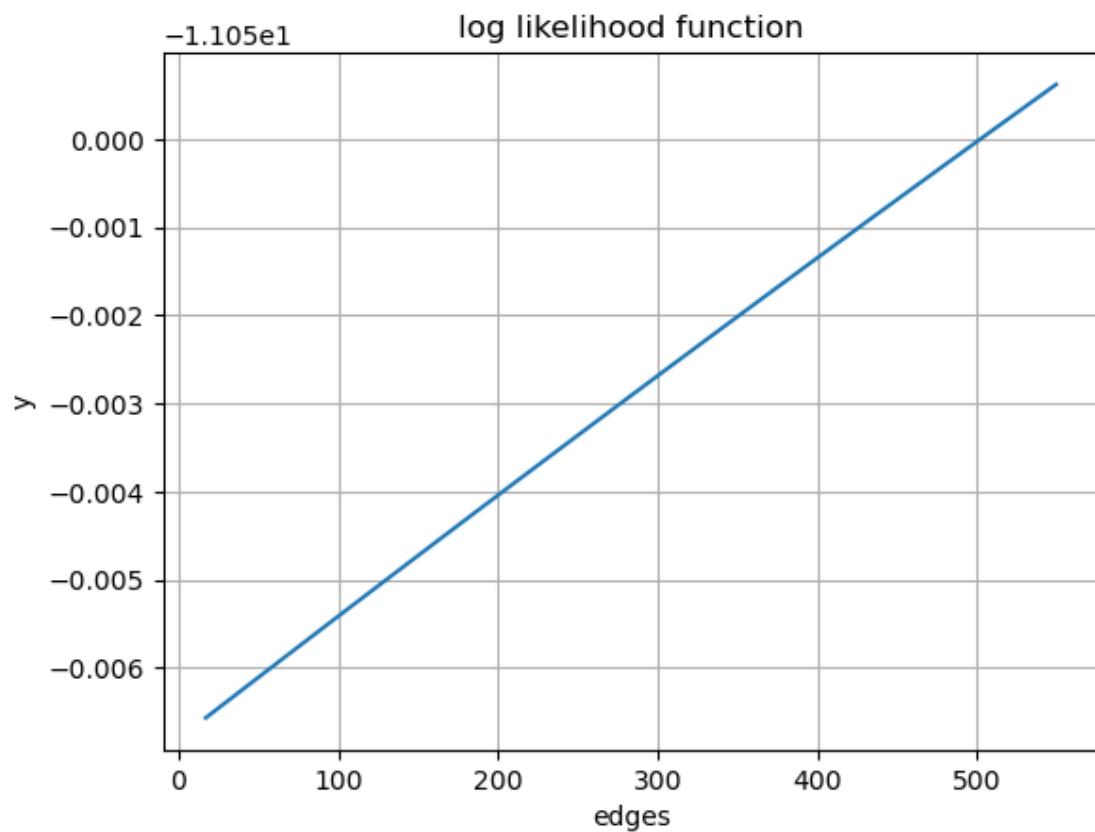


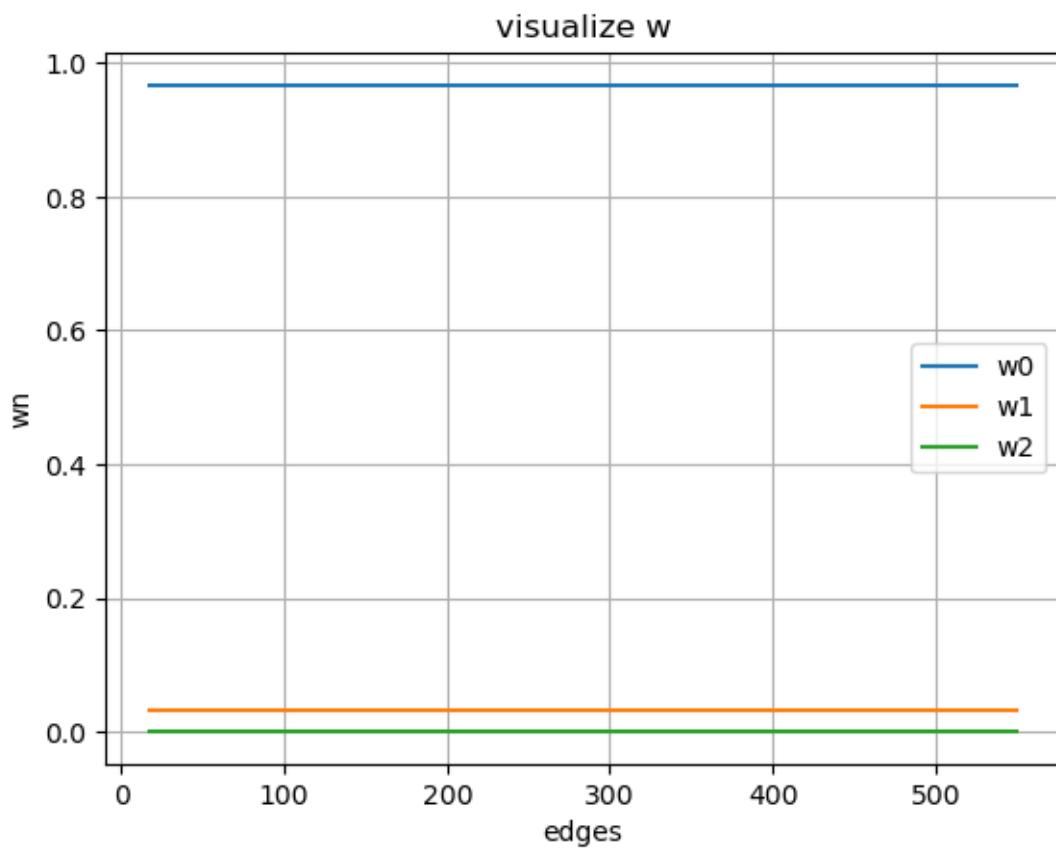


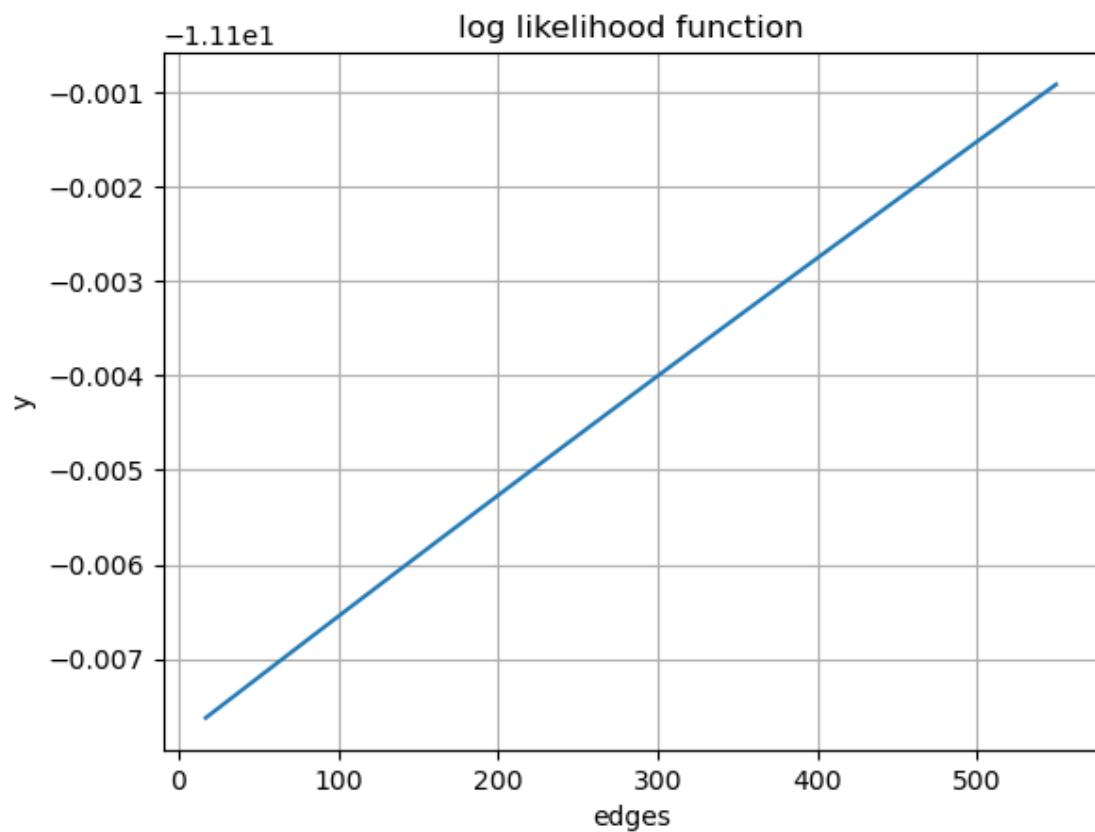


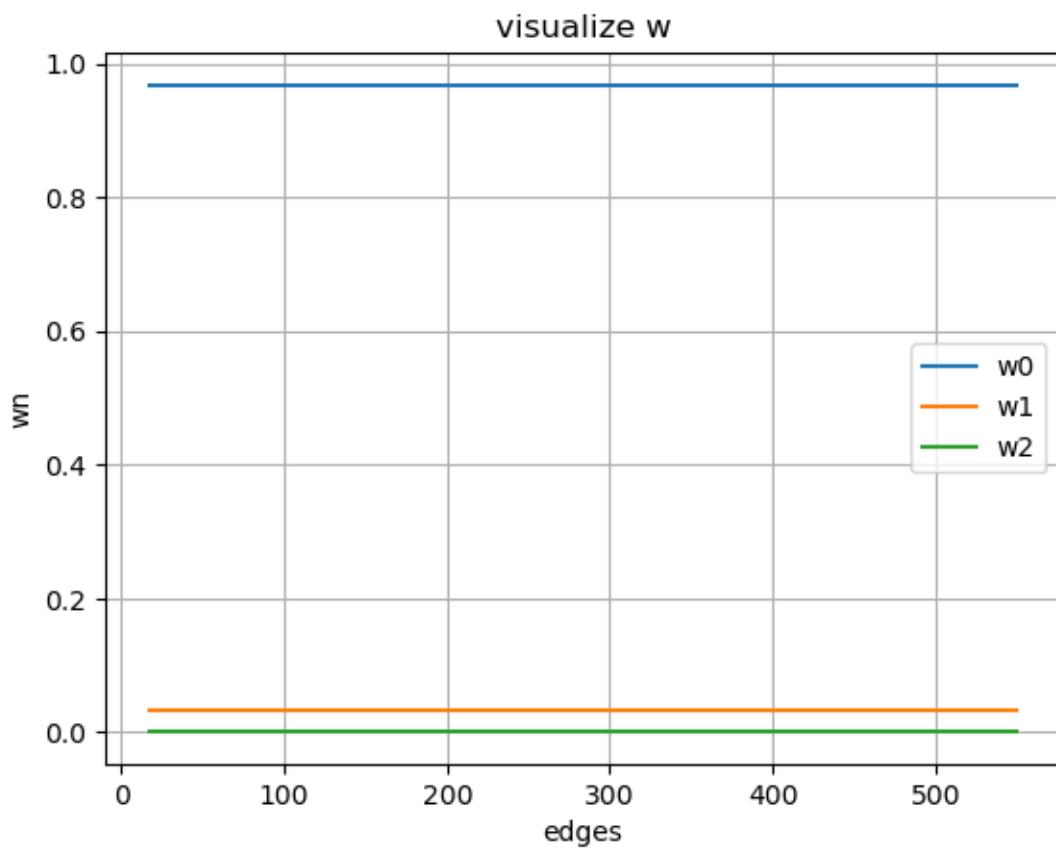


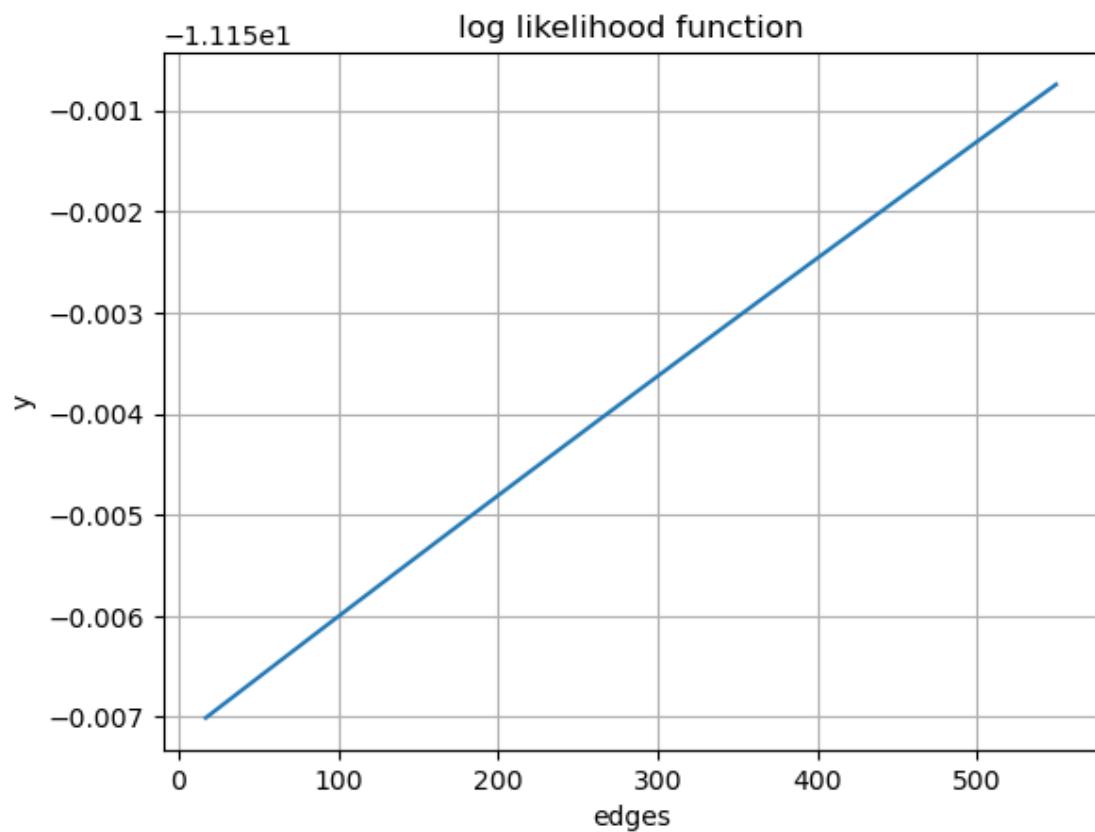


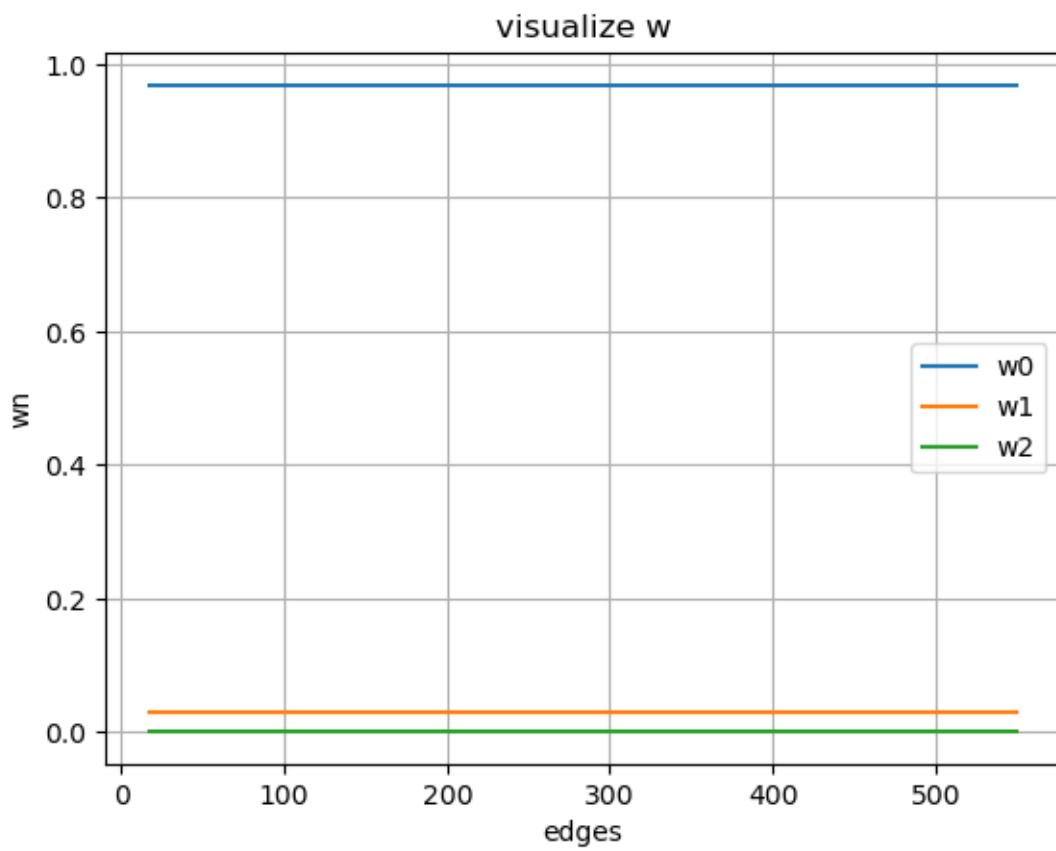


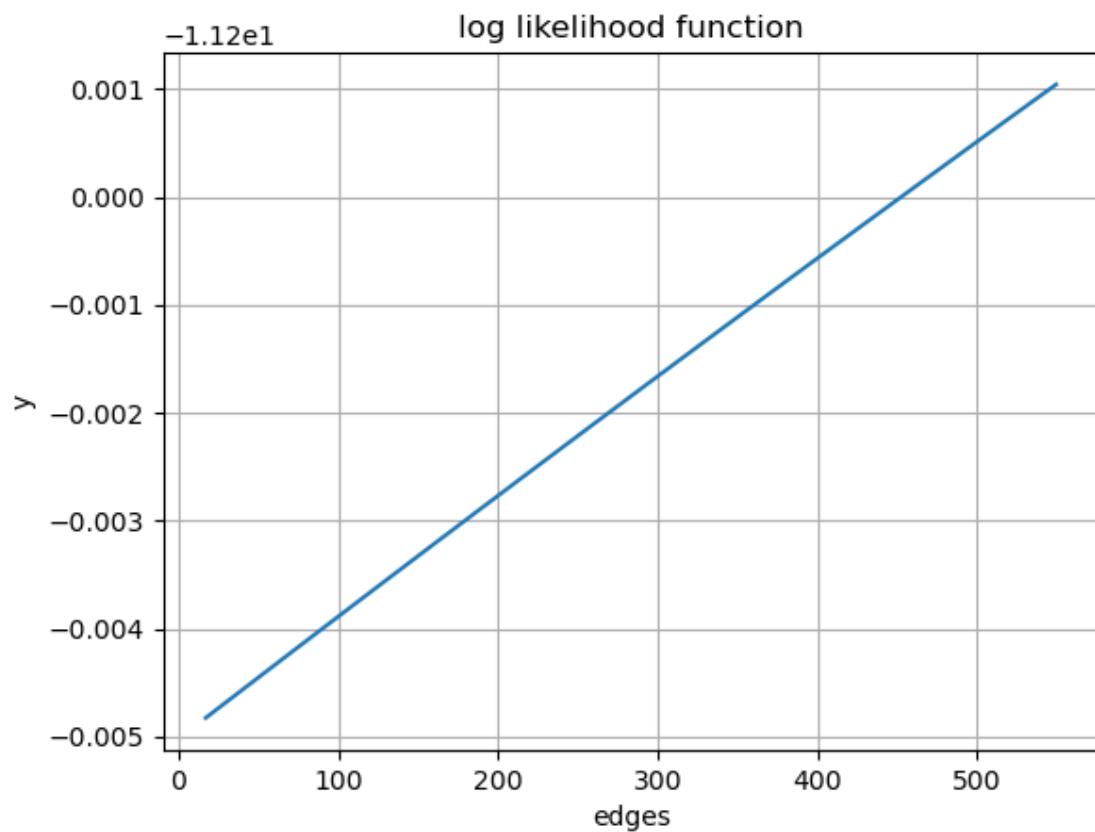


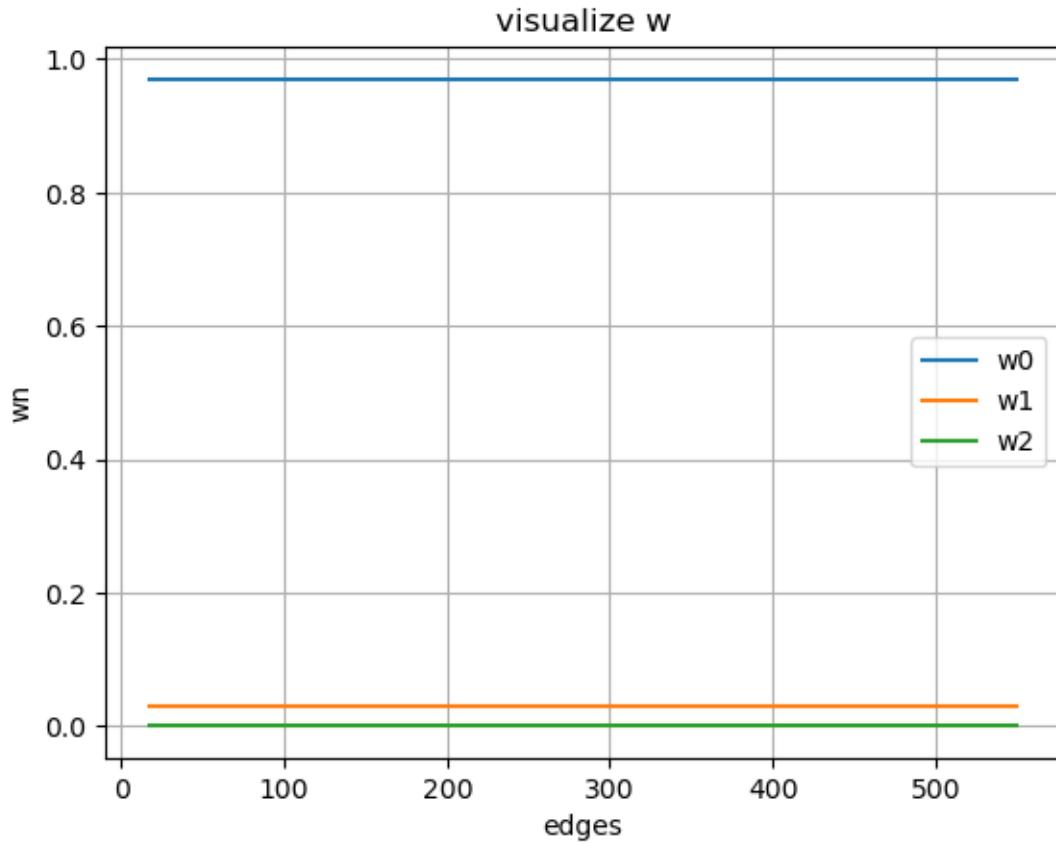


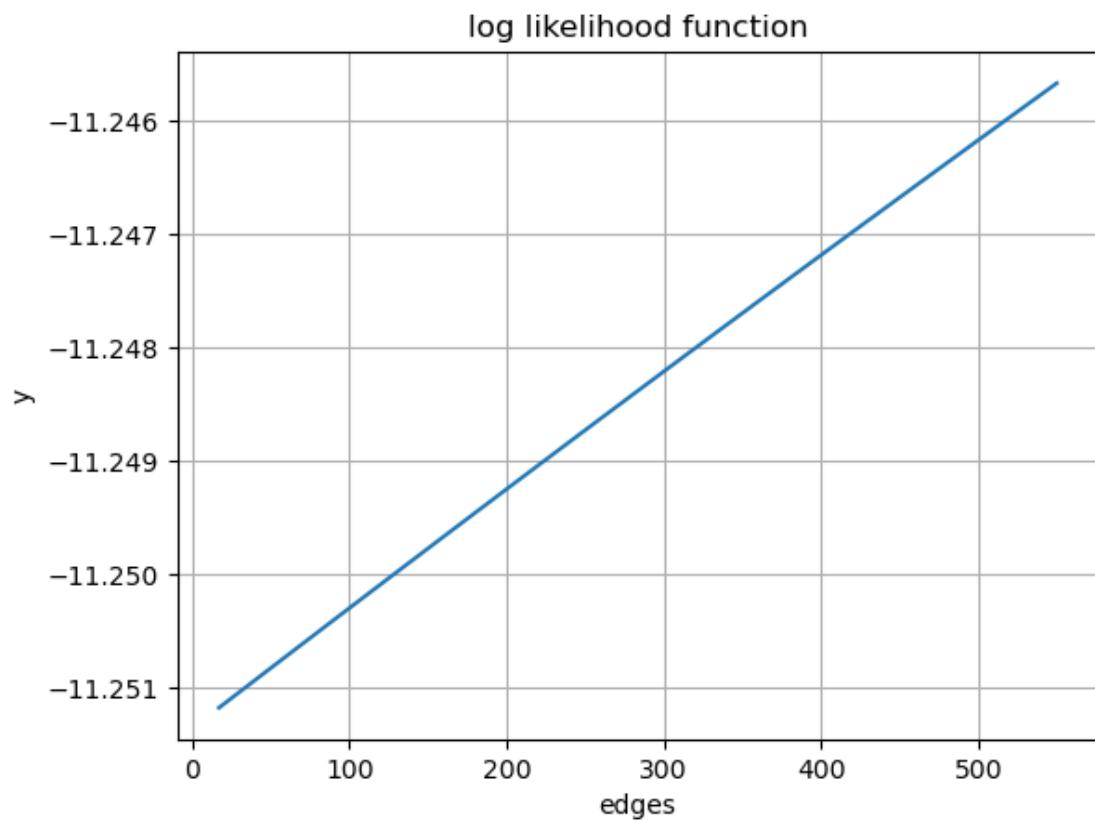


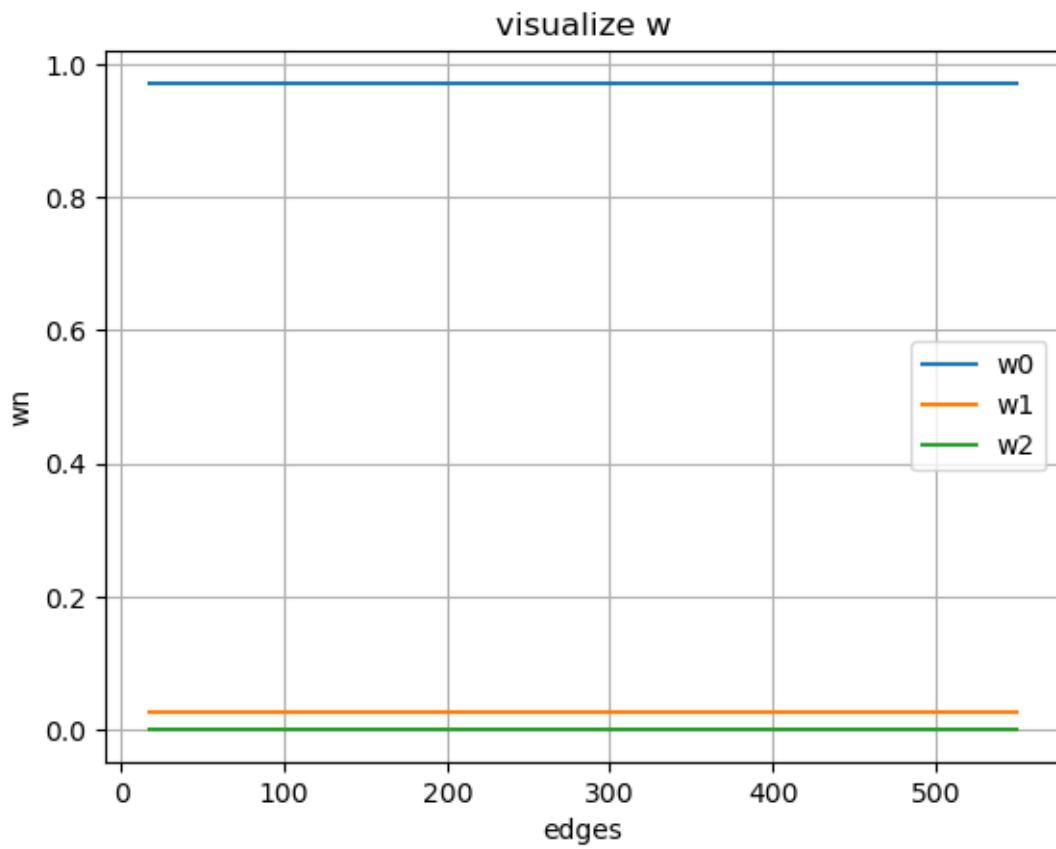


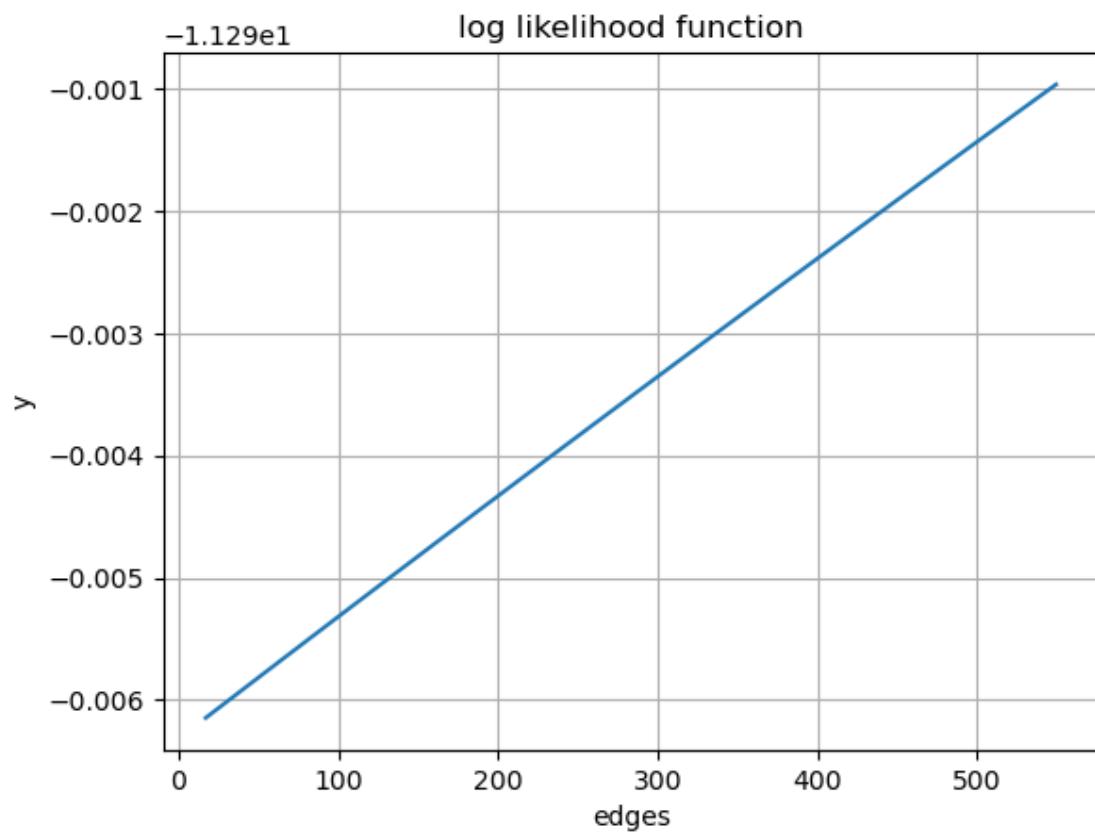


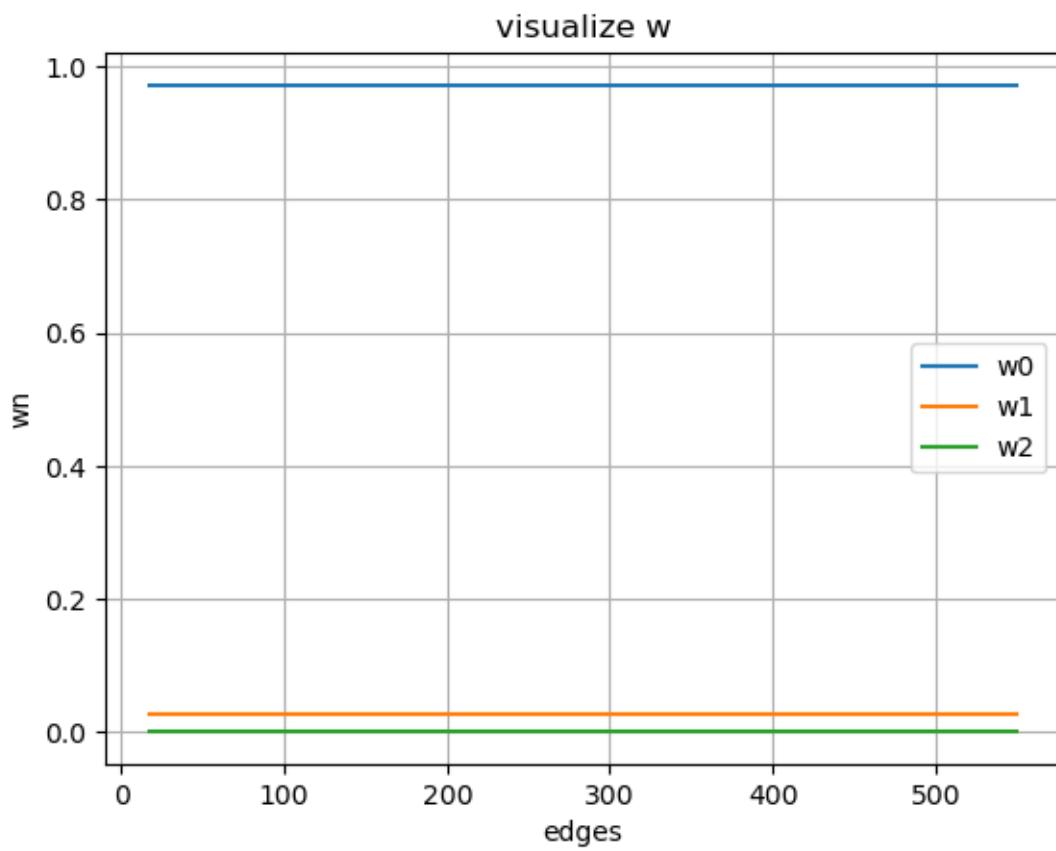


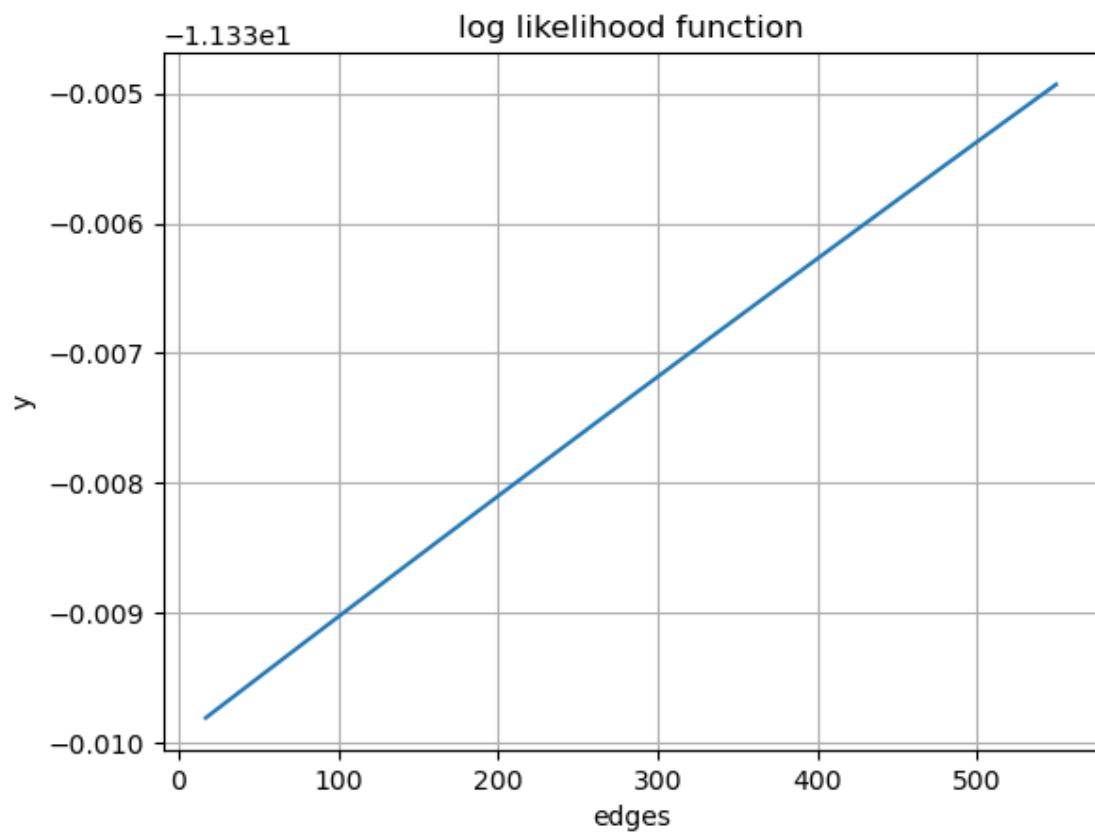


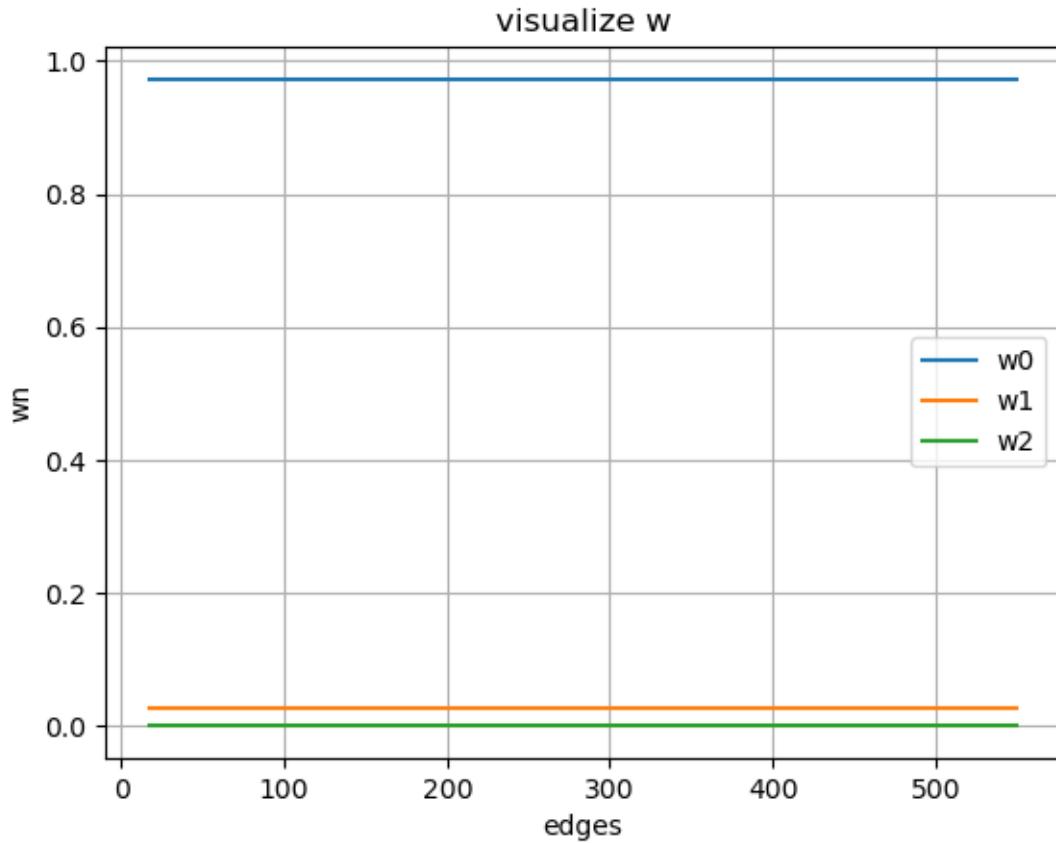


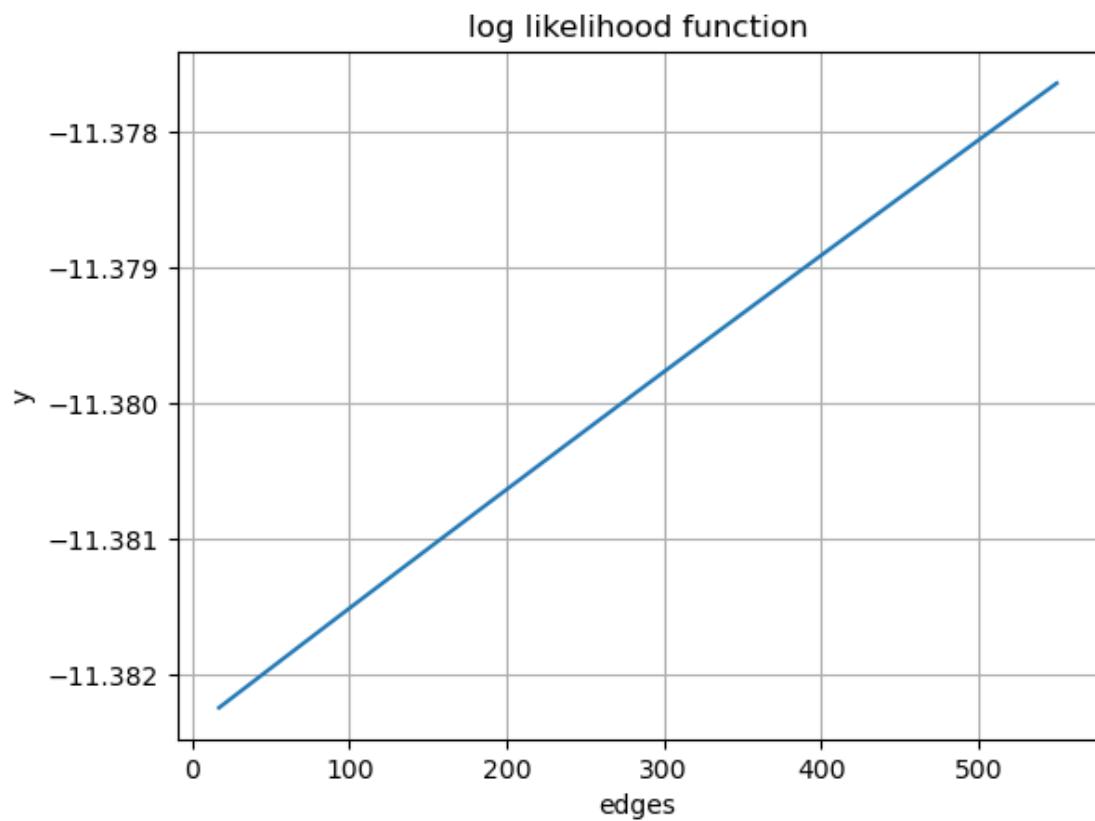


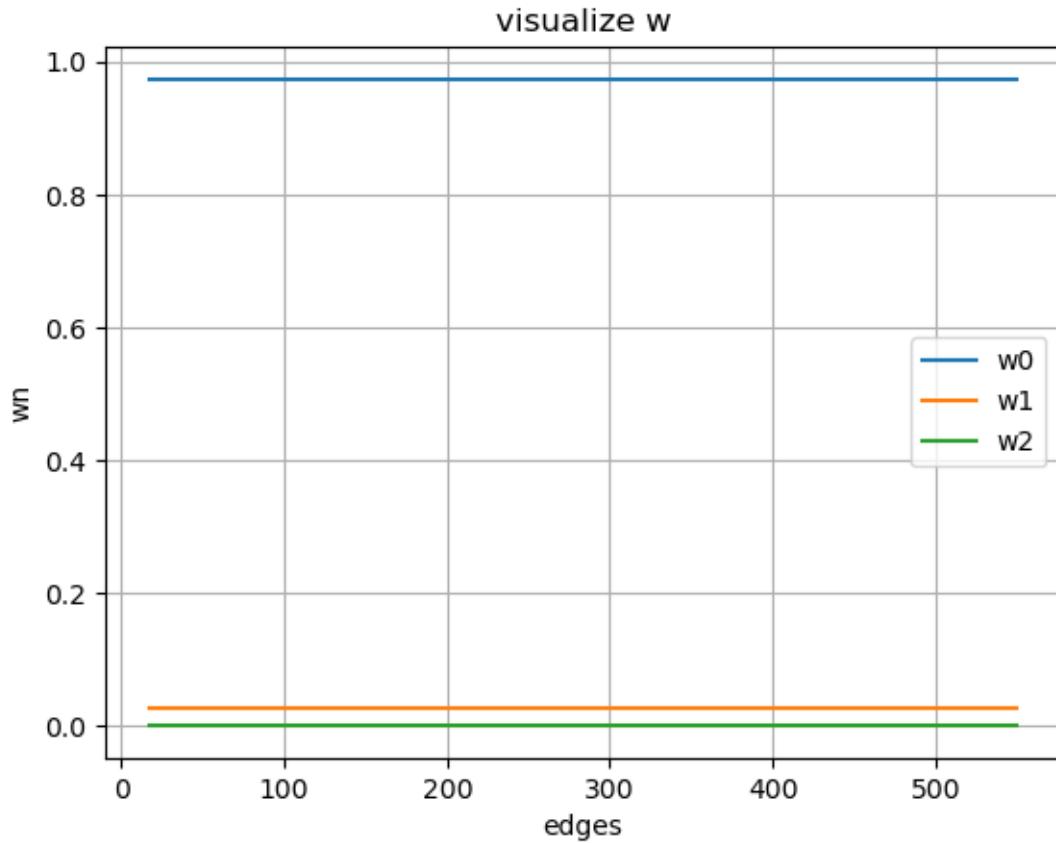


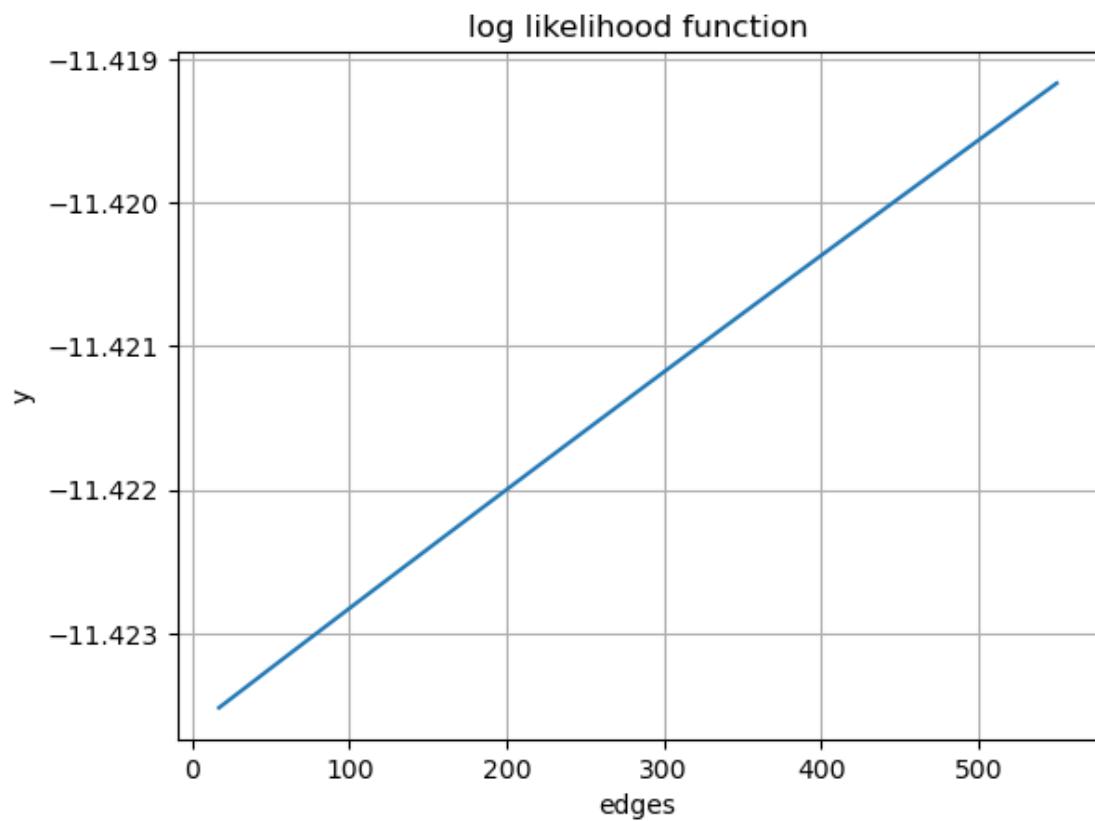


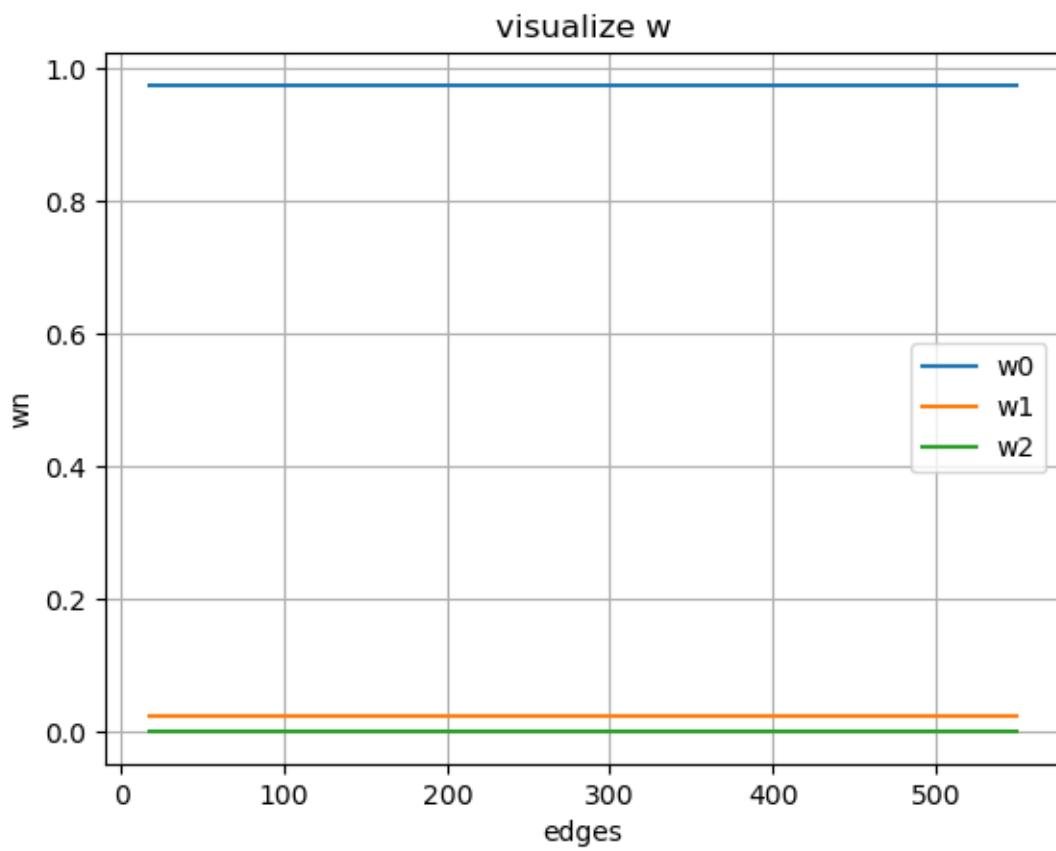


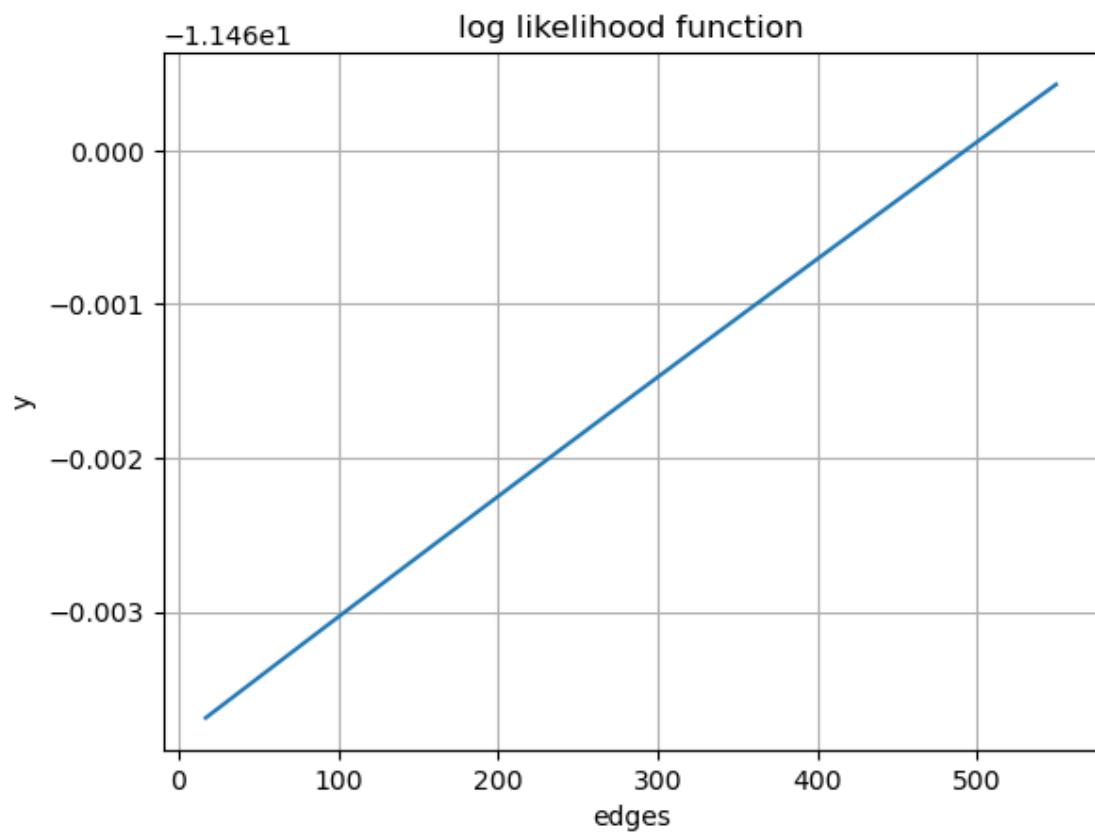


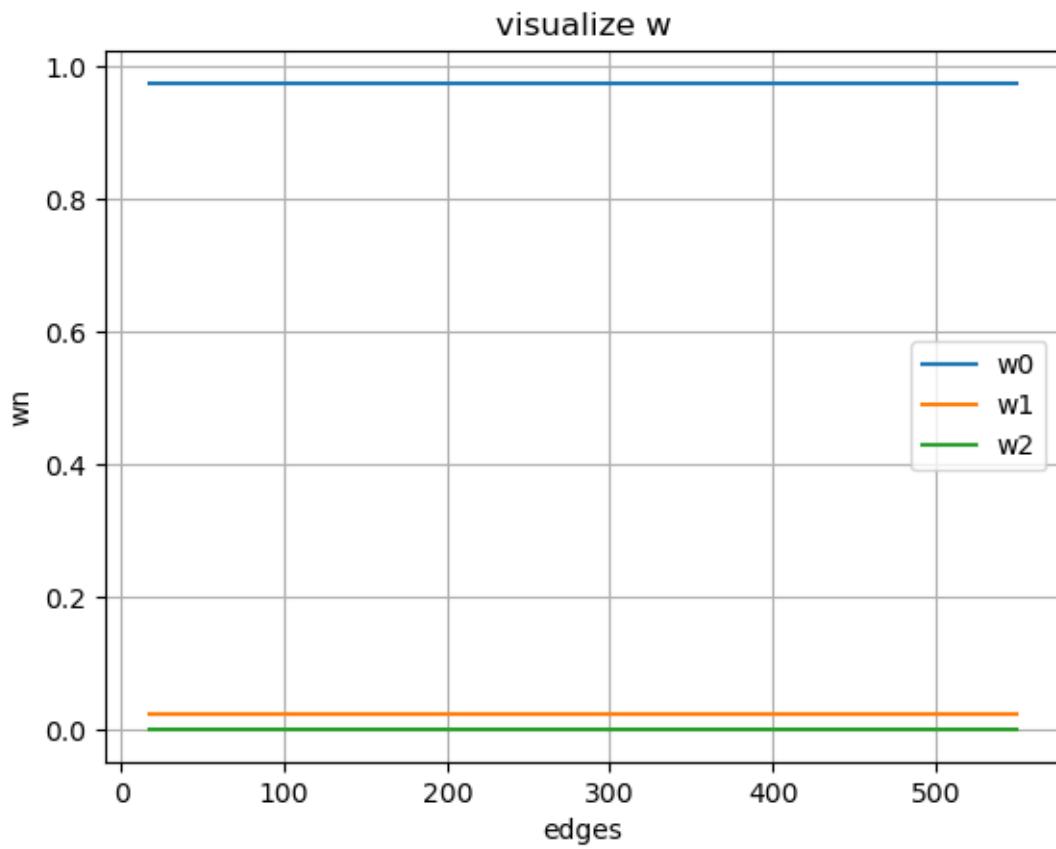


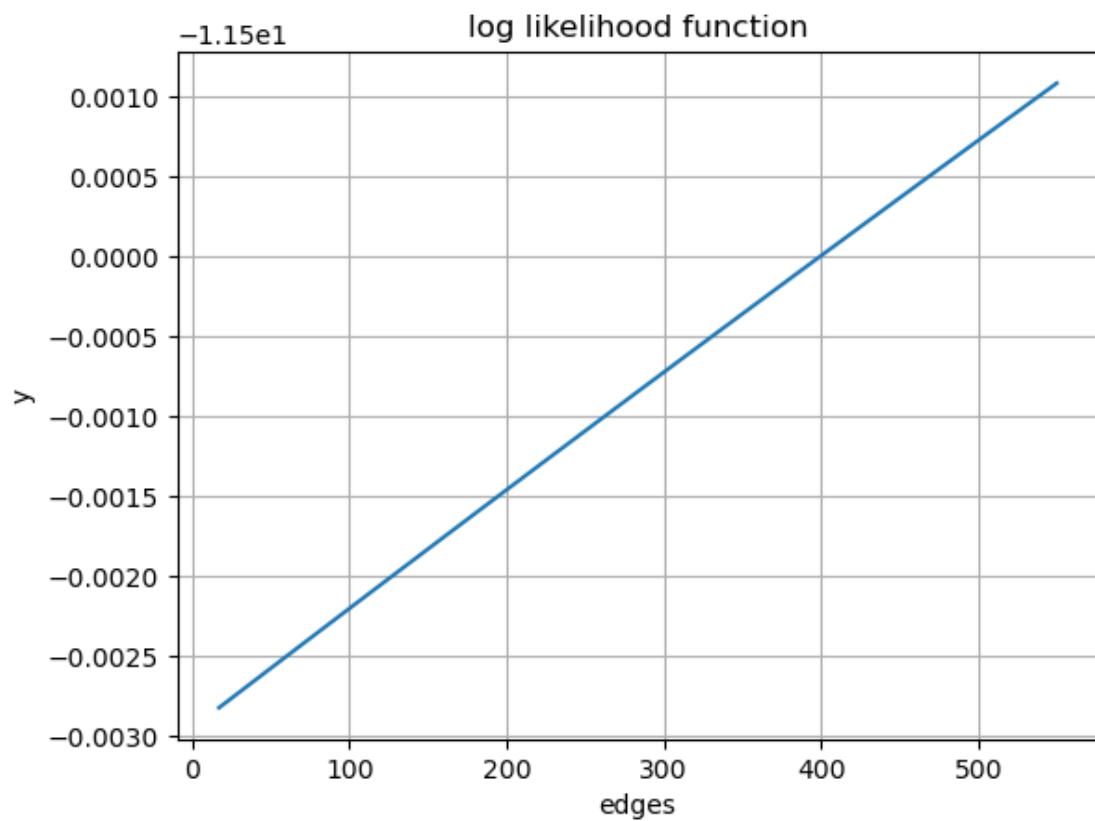


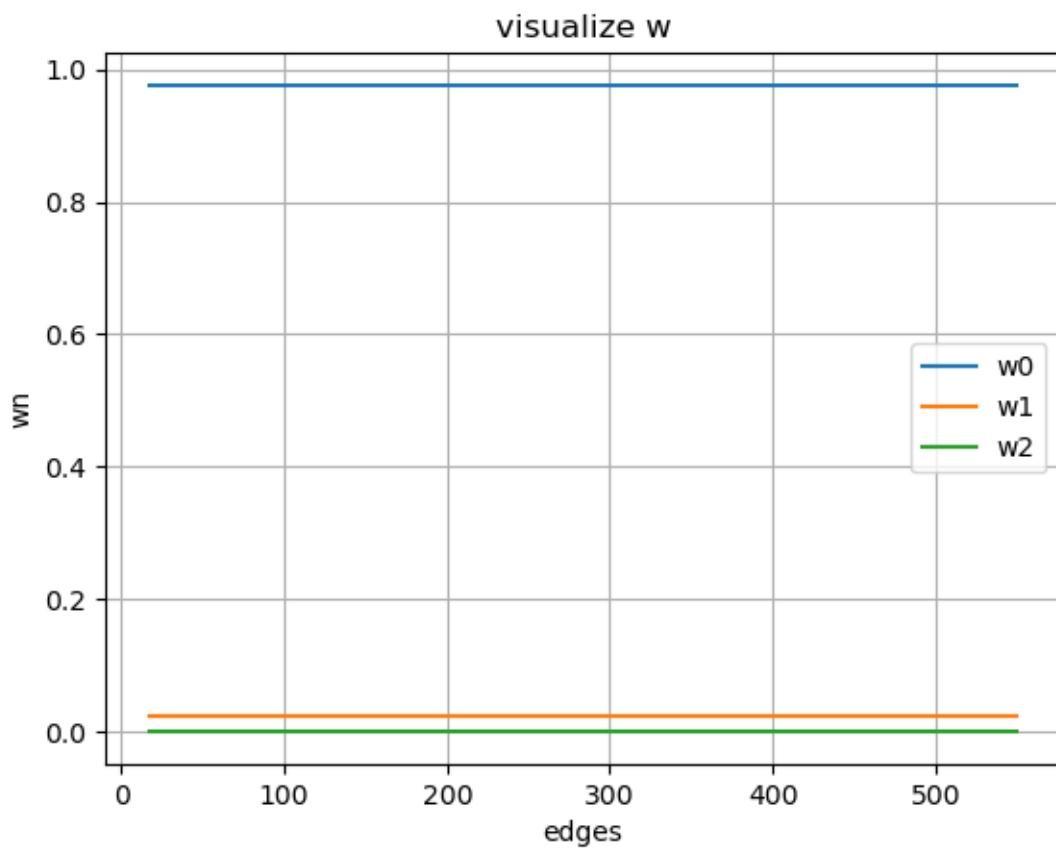


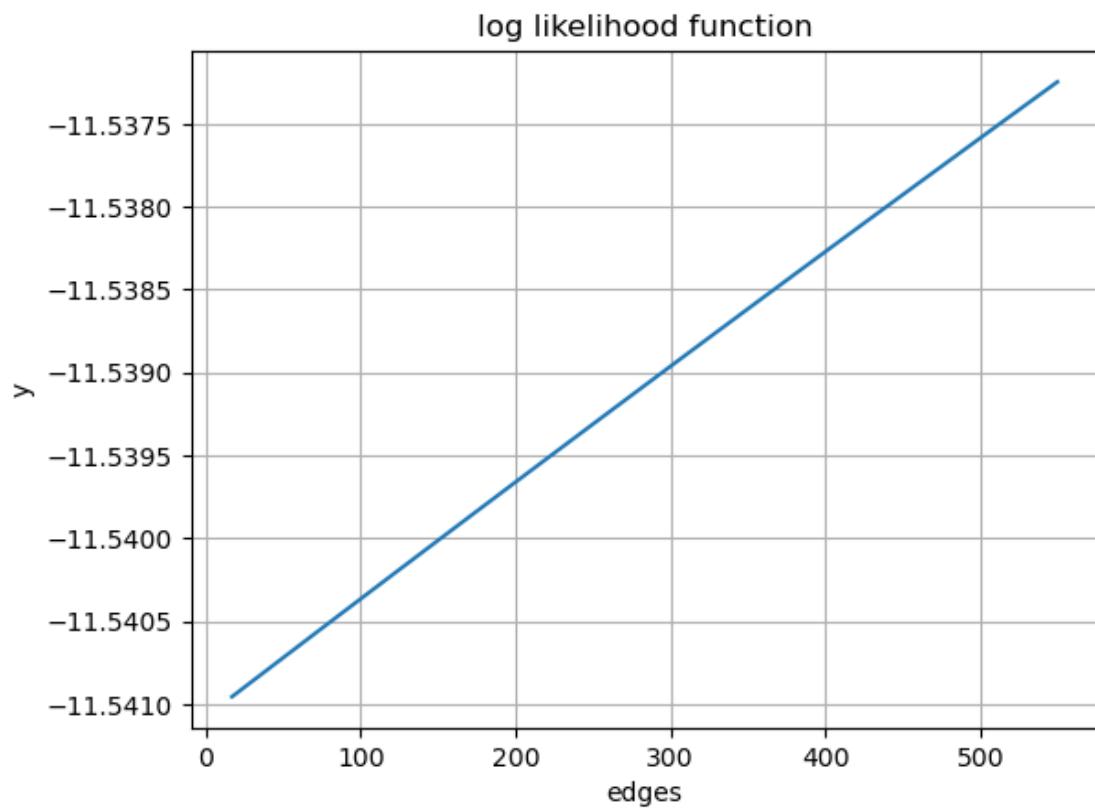


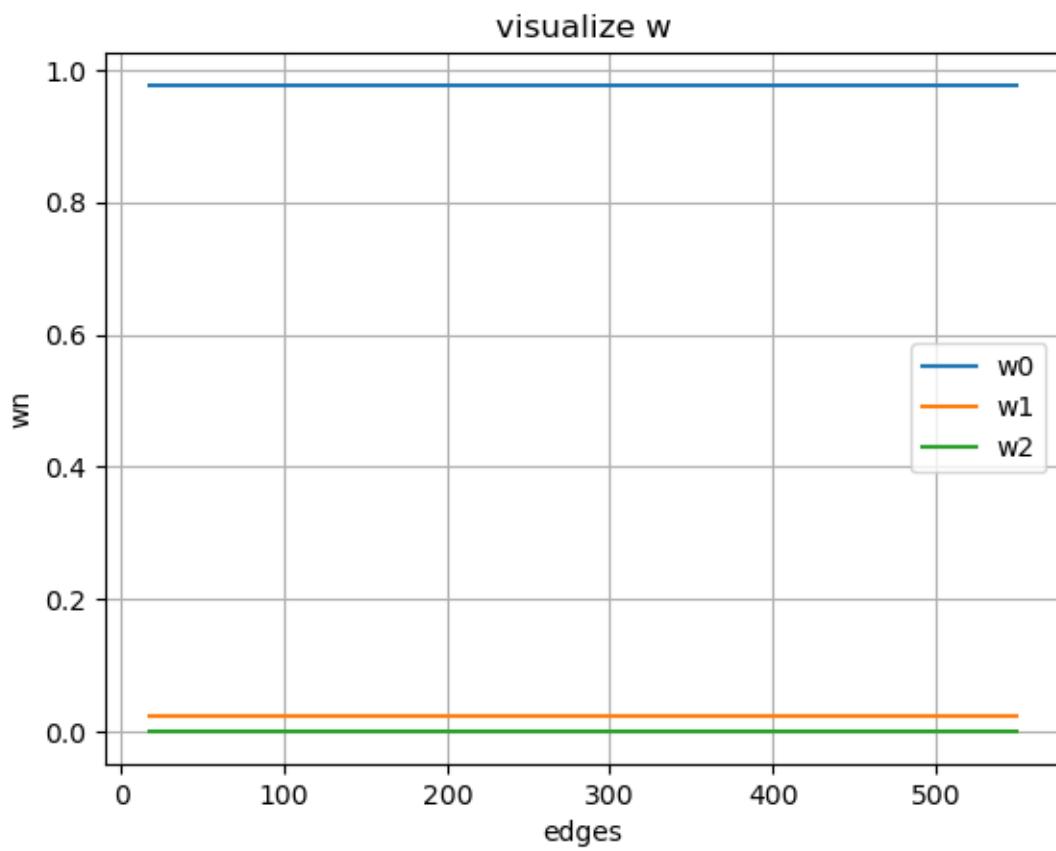


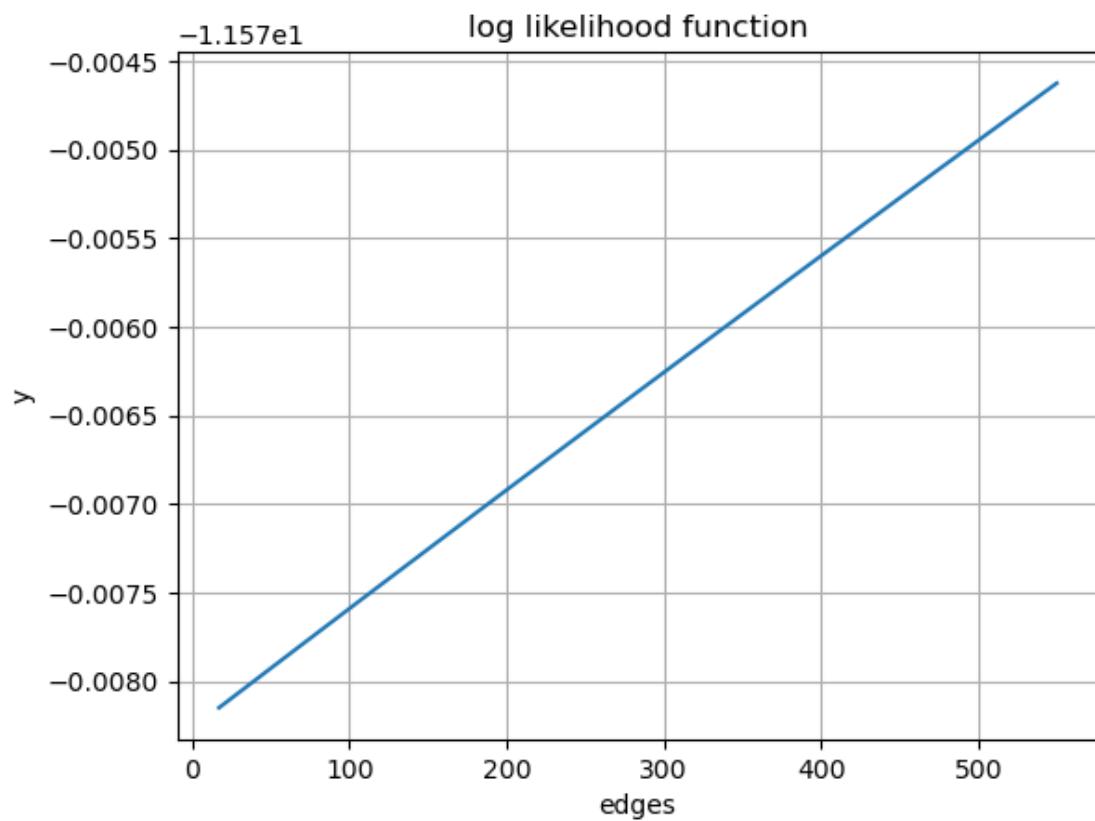


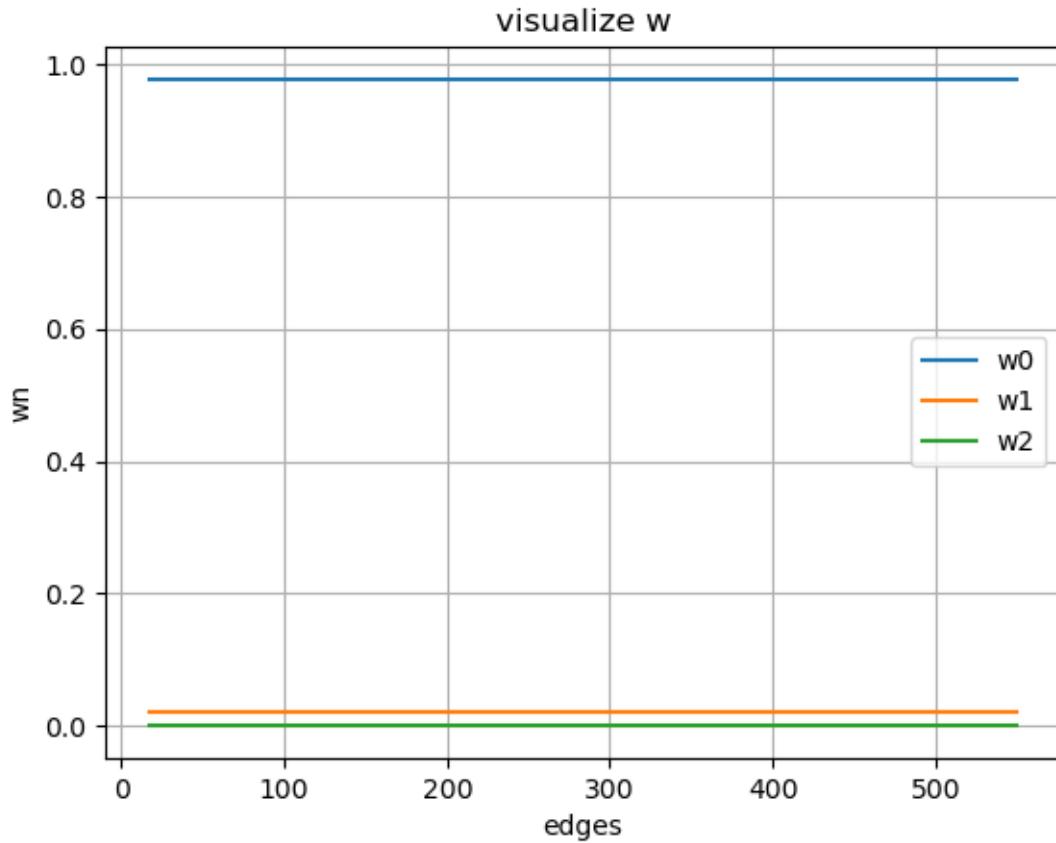


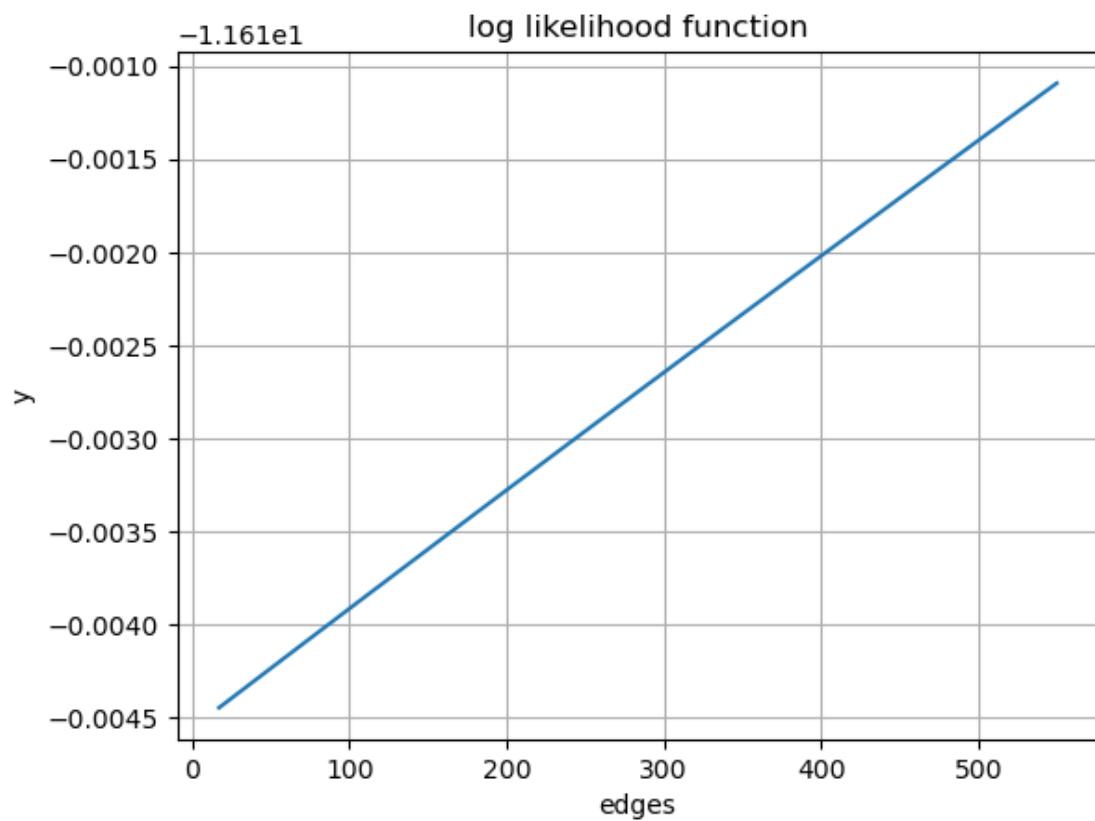


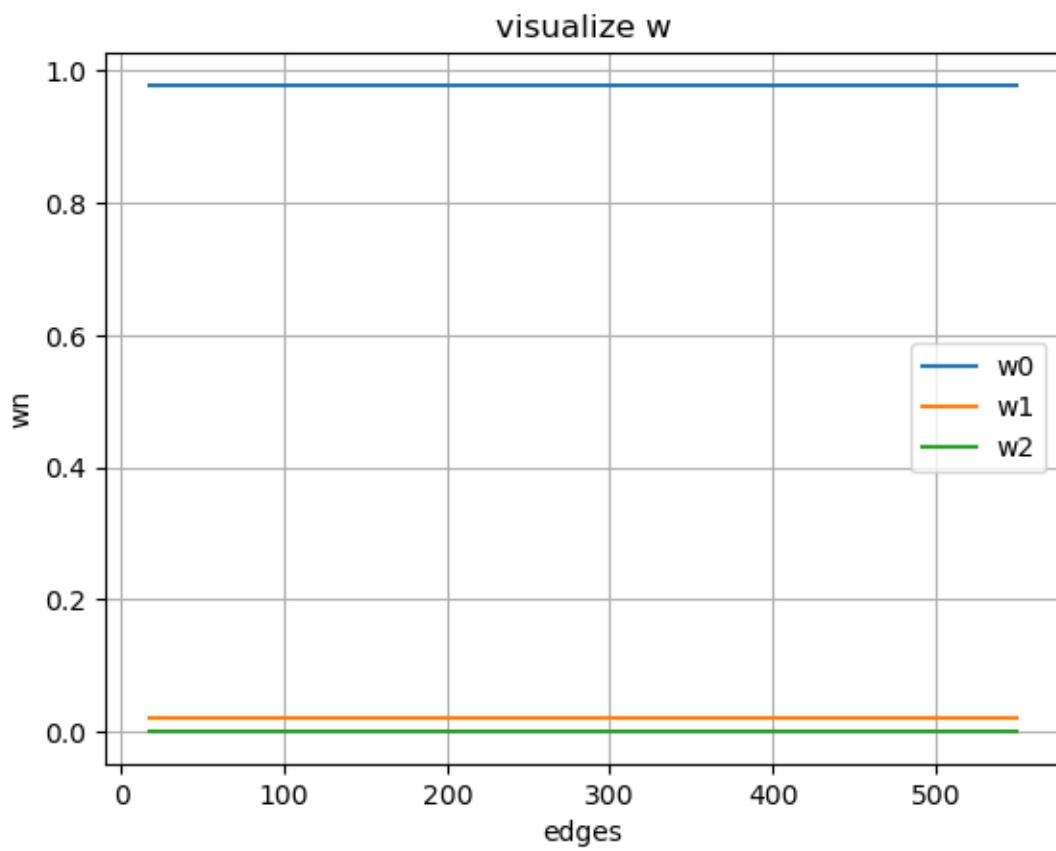


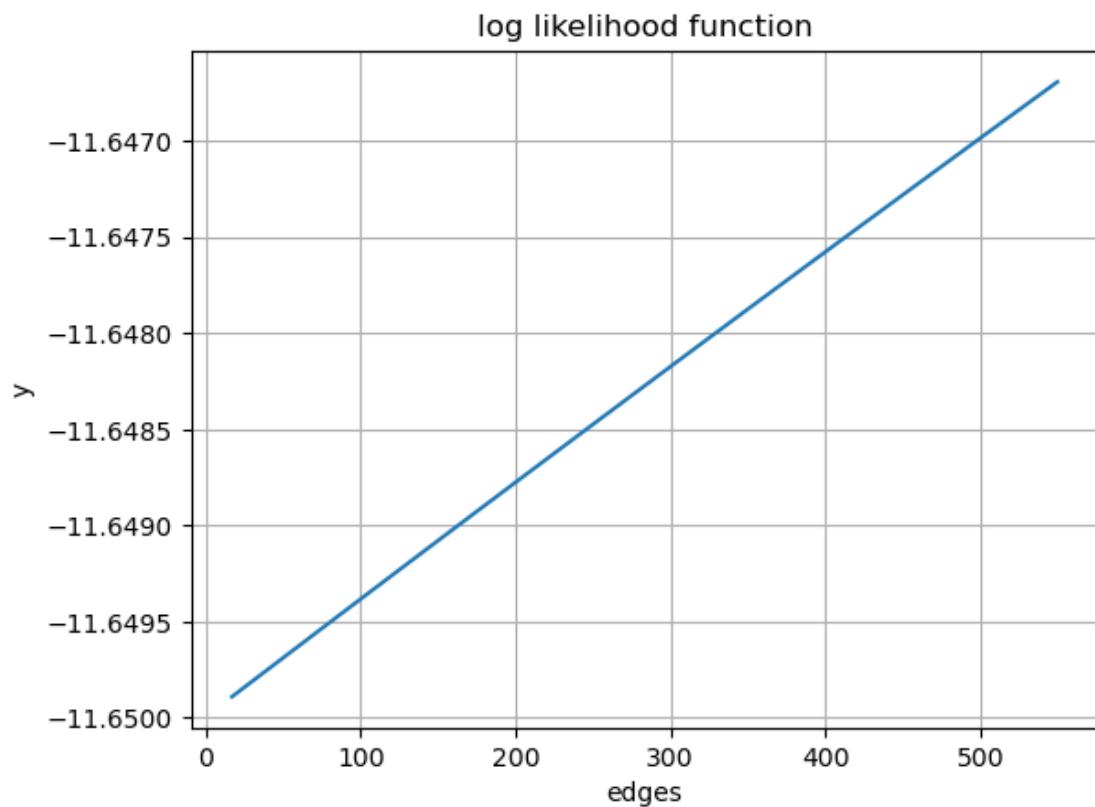


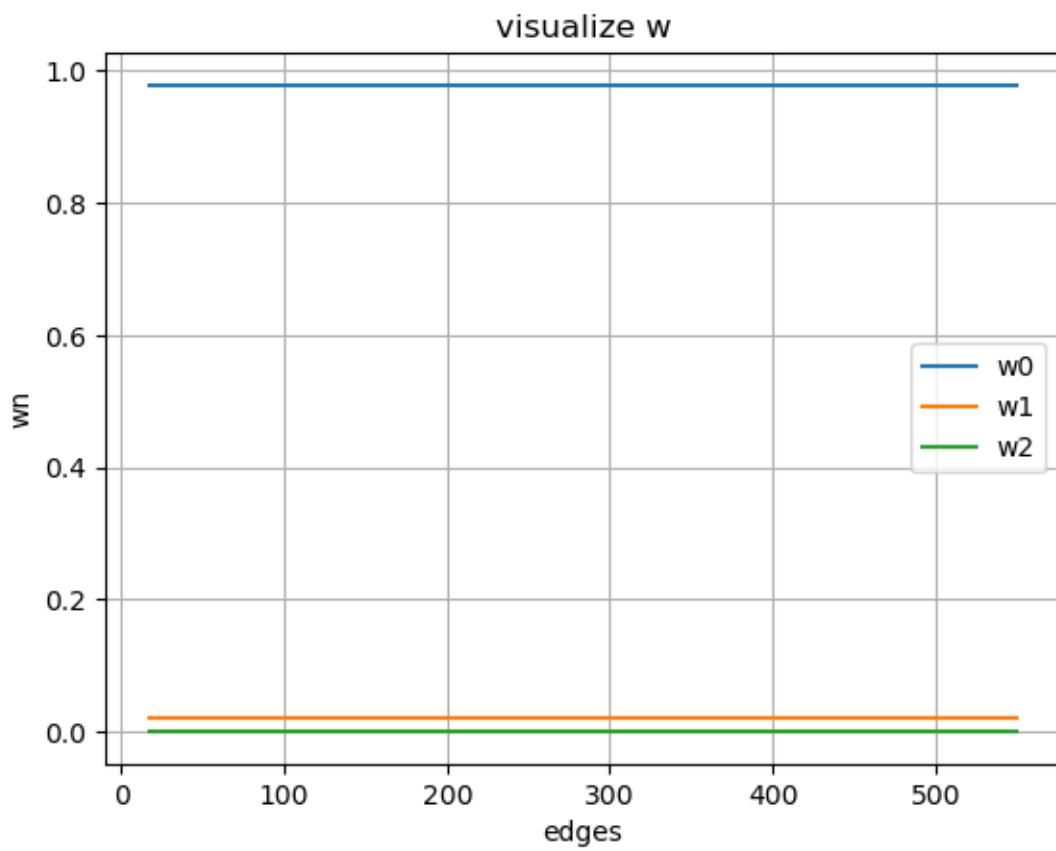


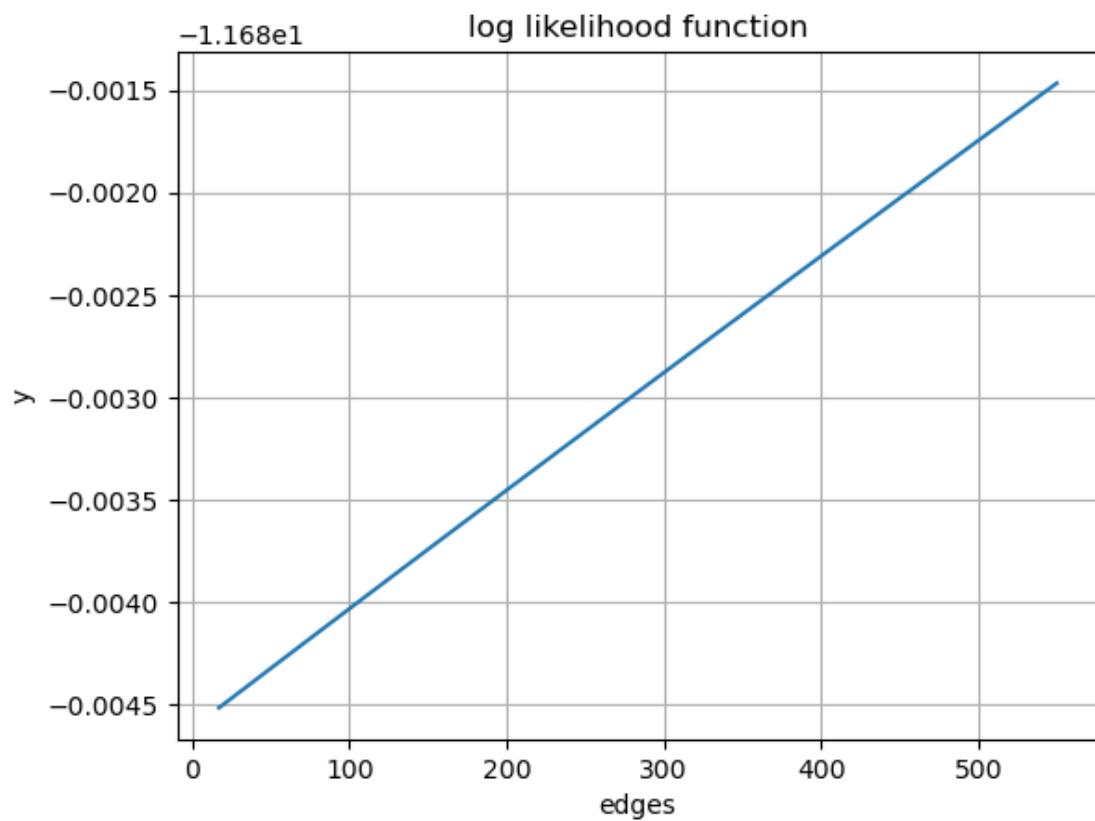


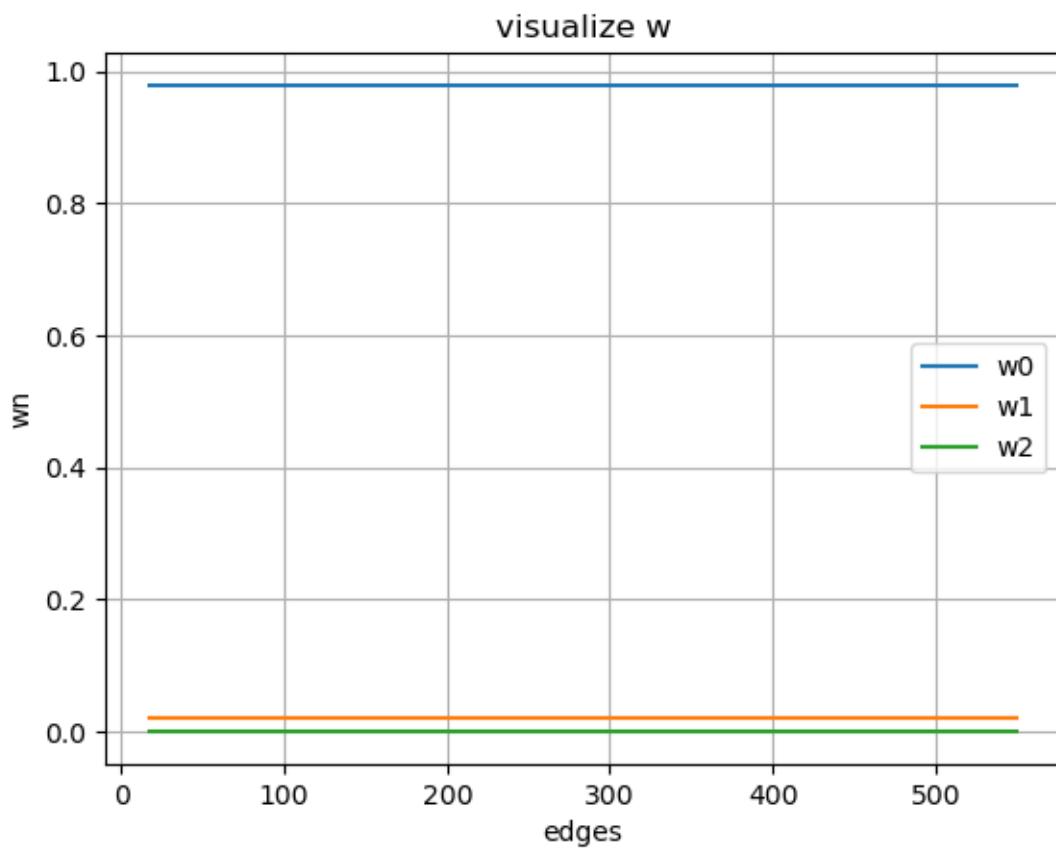


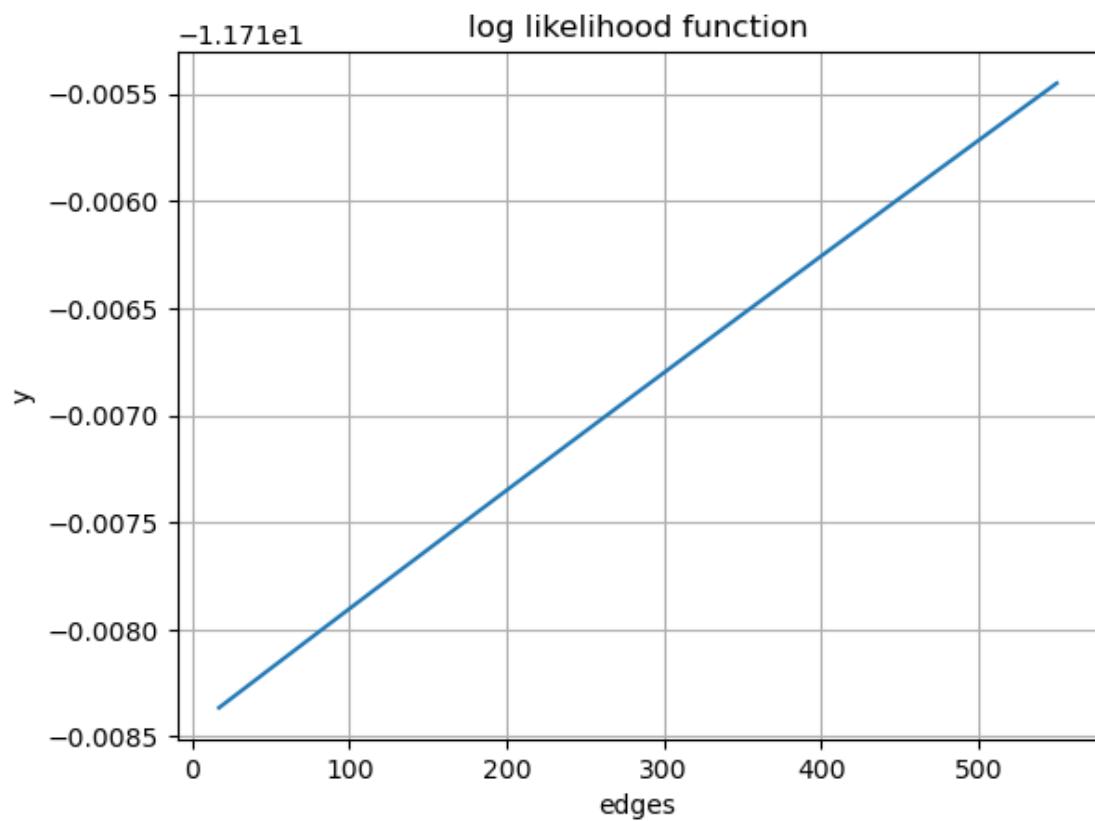


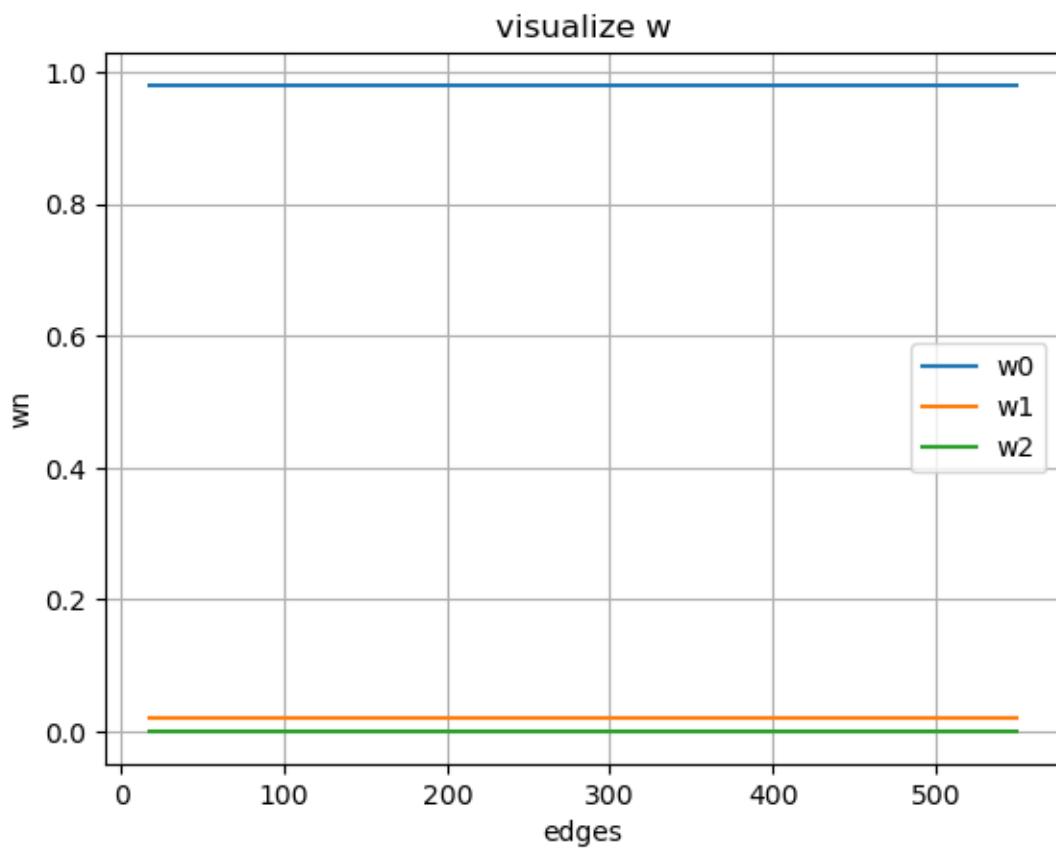




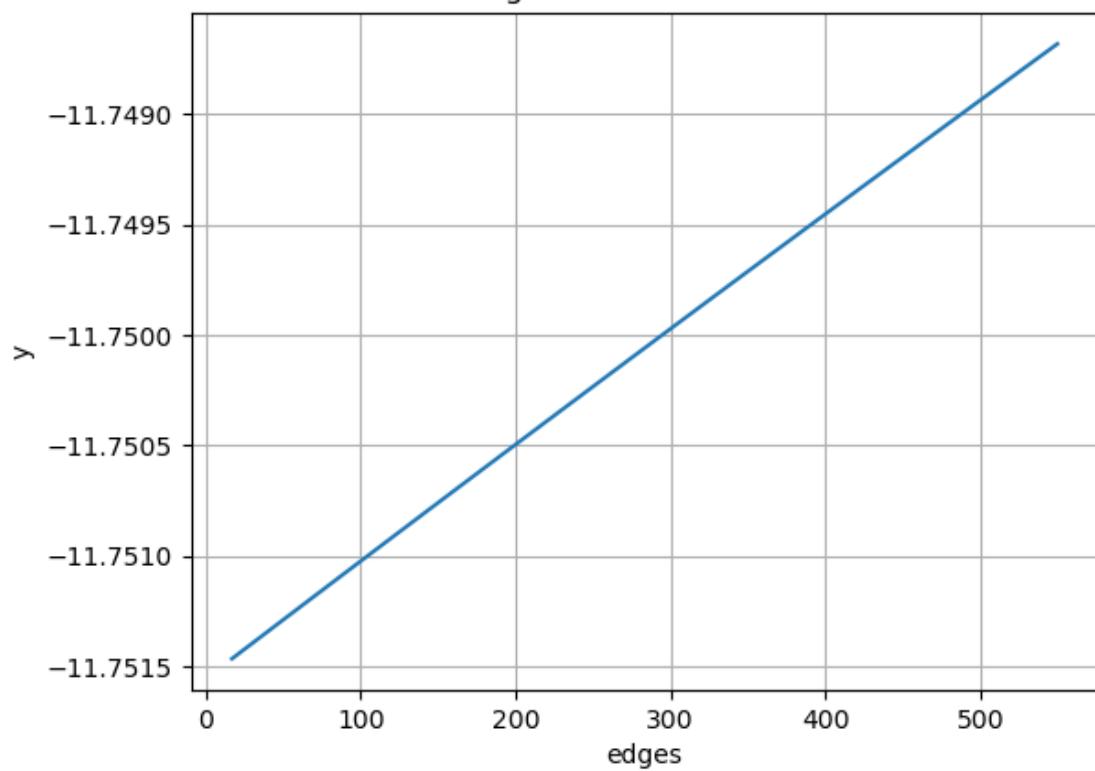


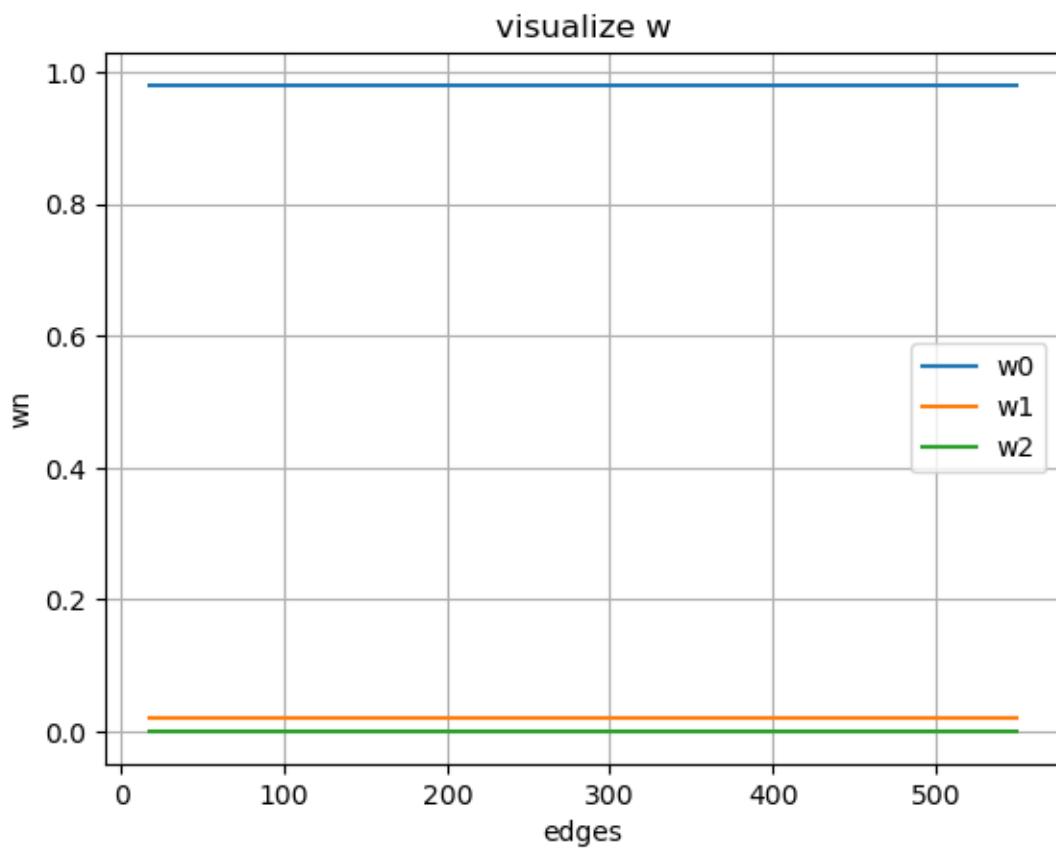


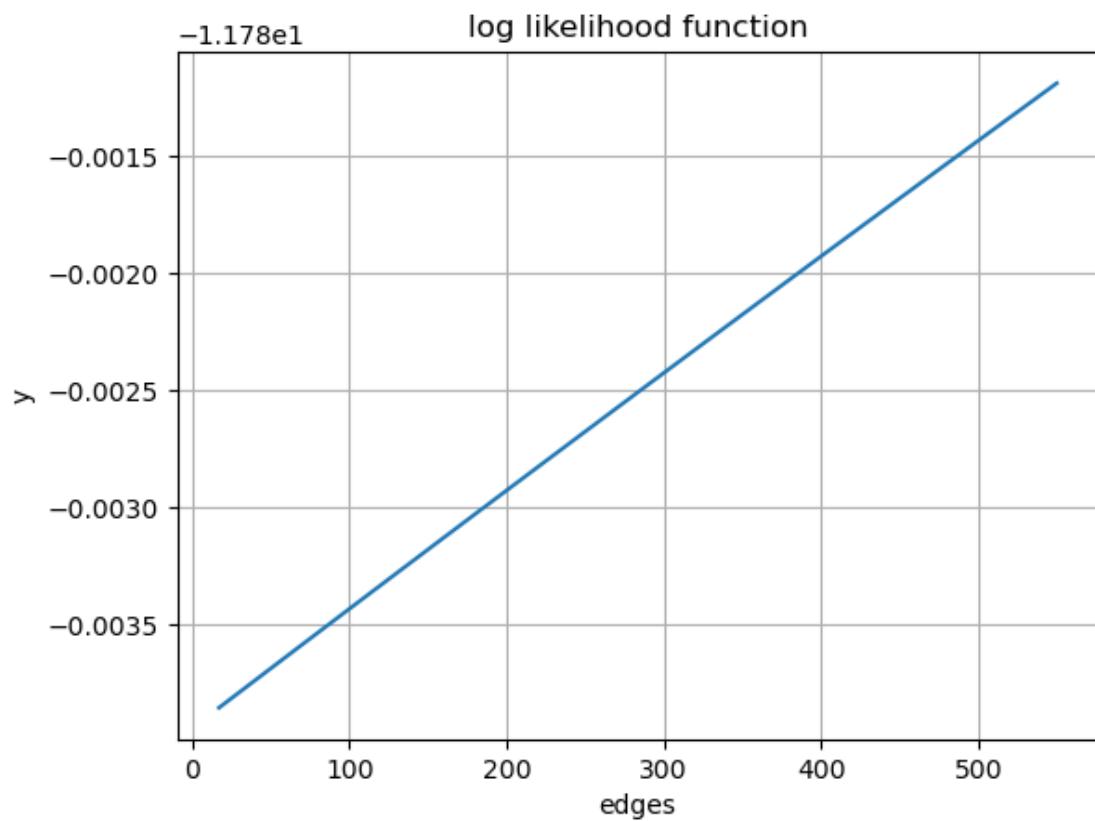


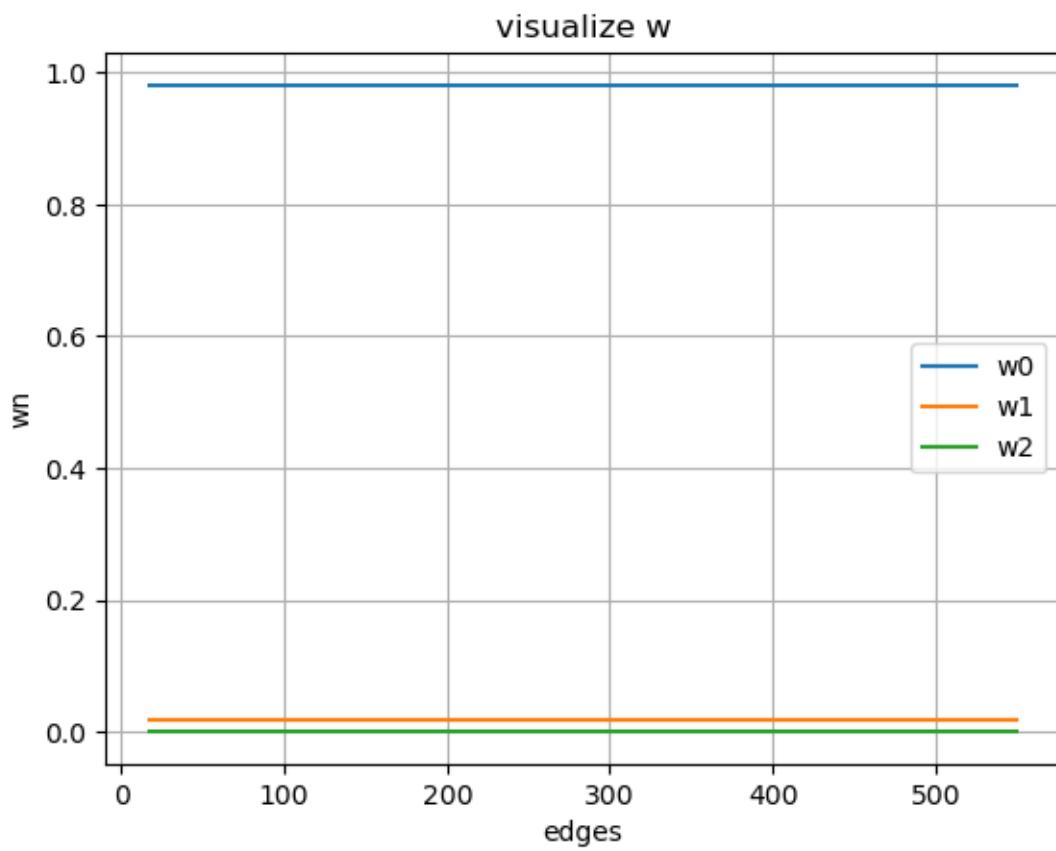


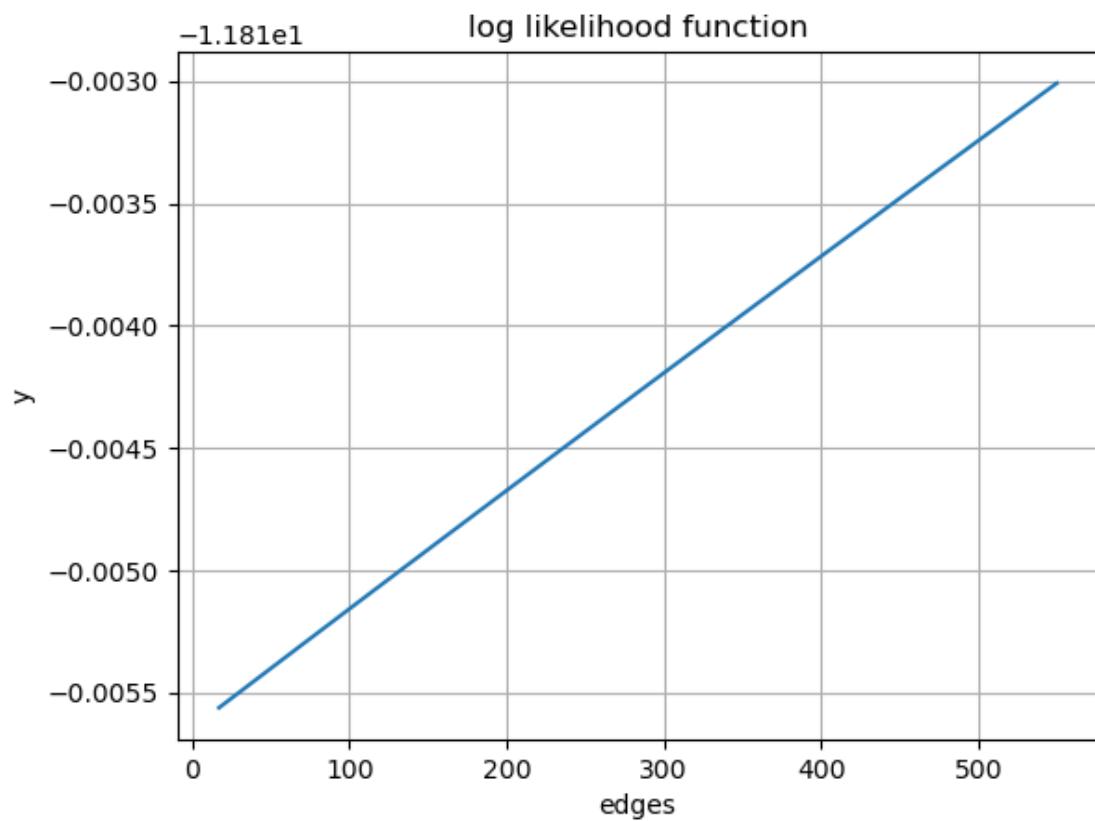
log likelihood function

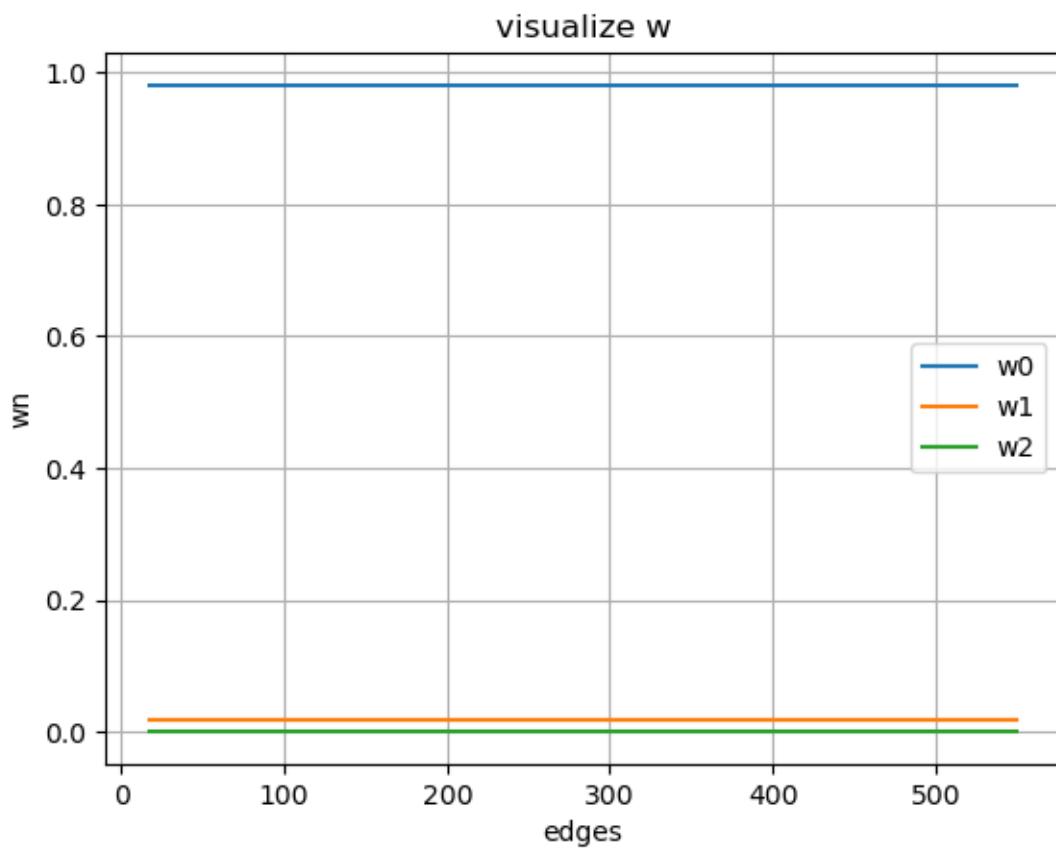




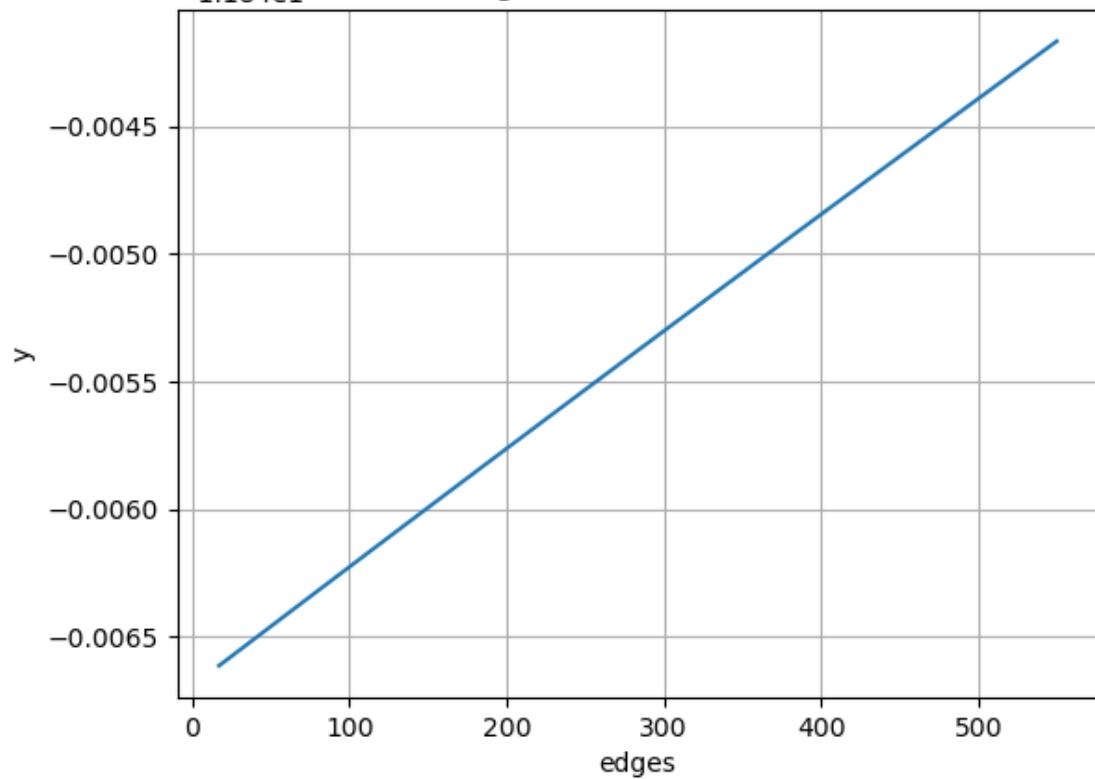


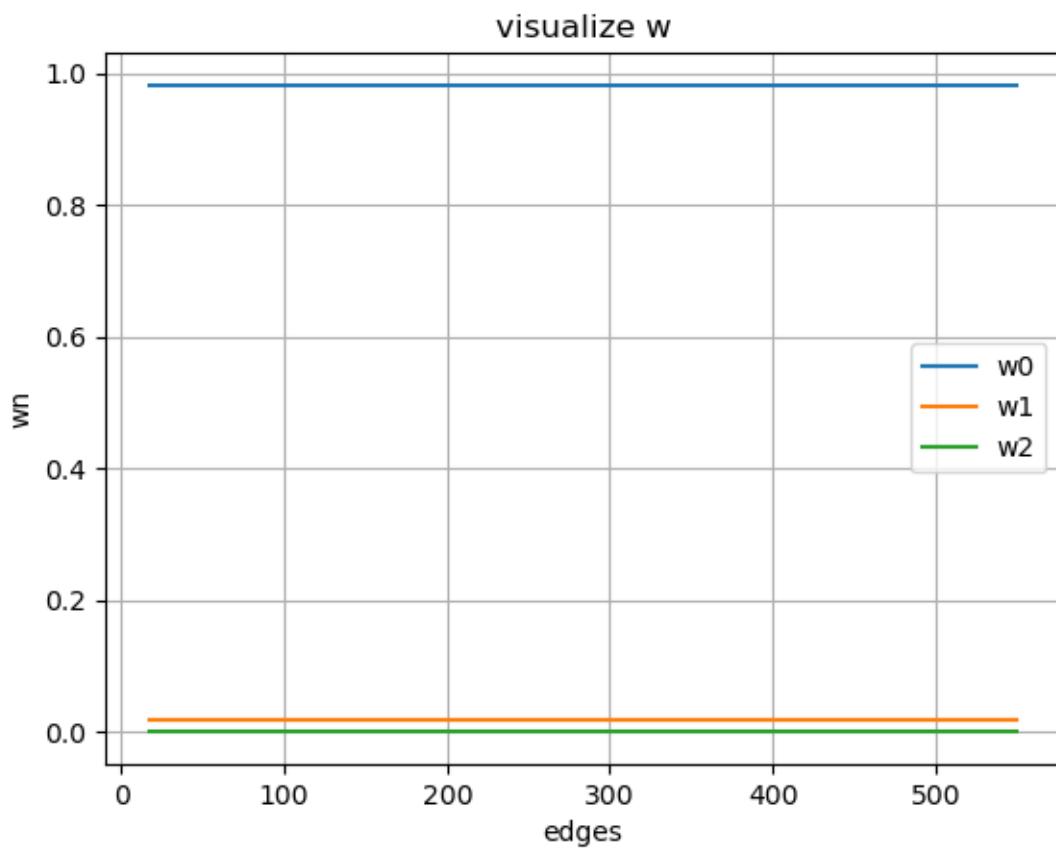


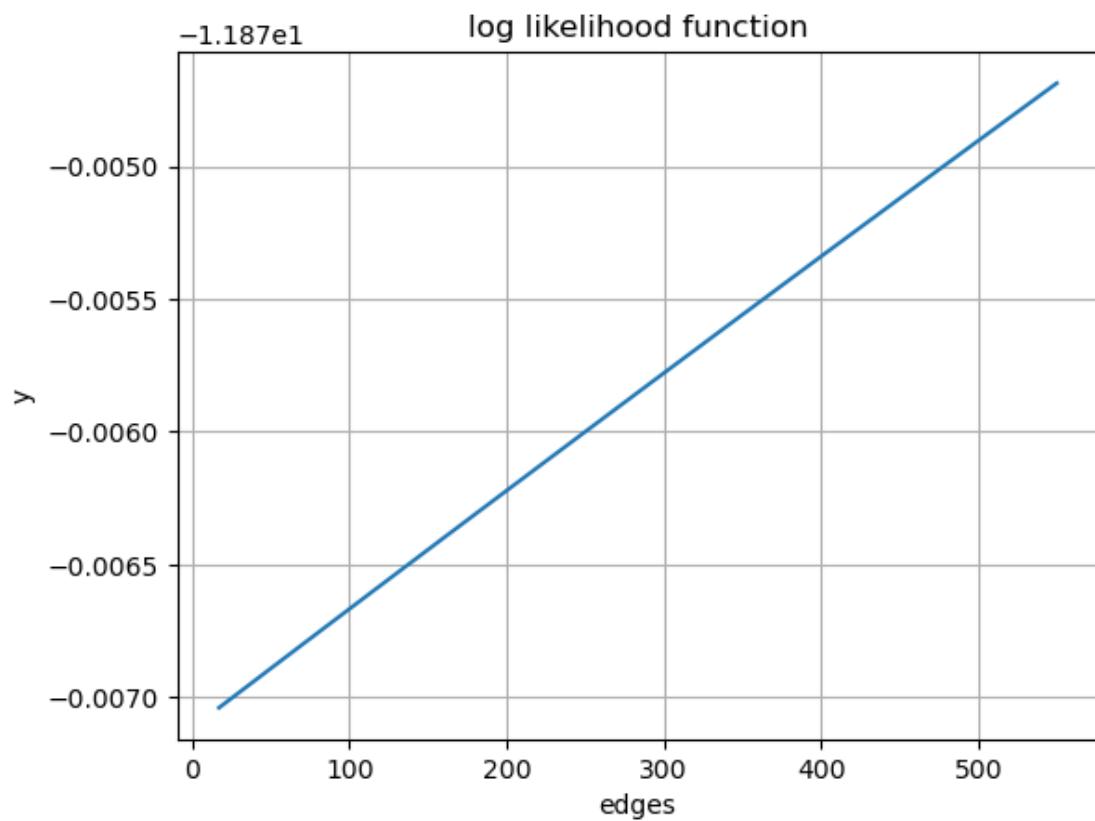


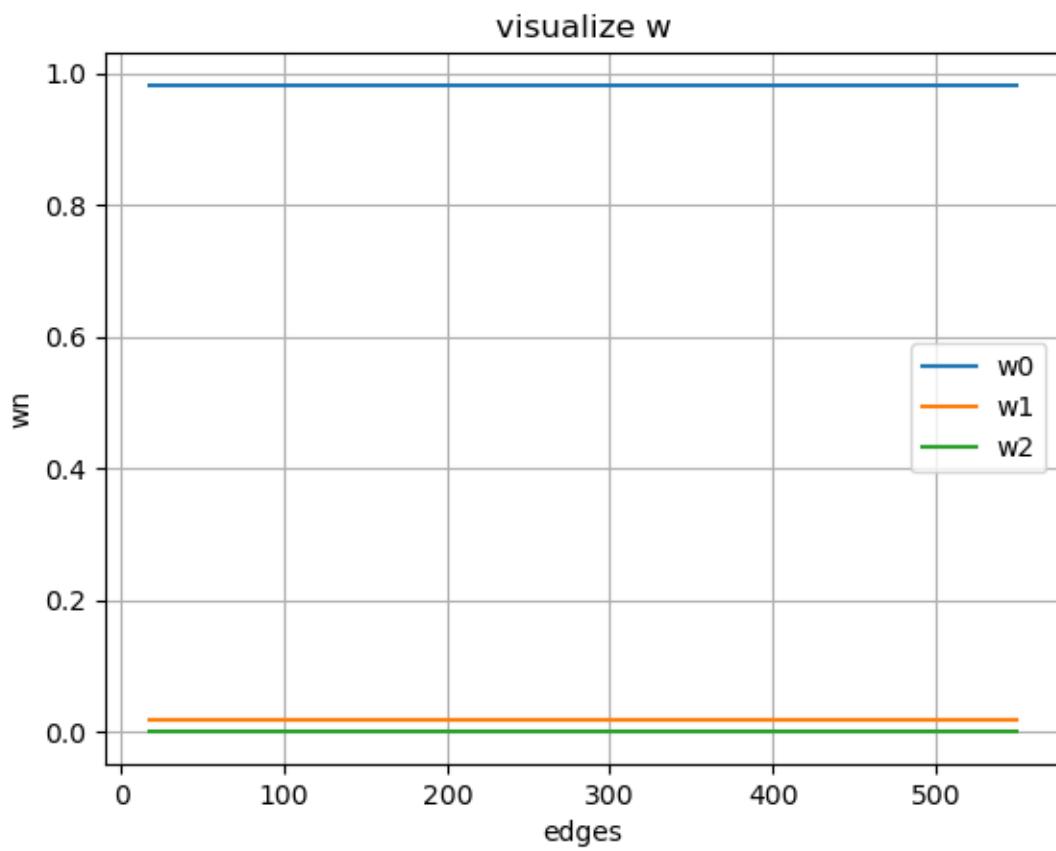


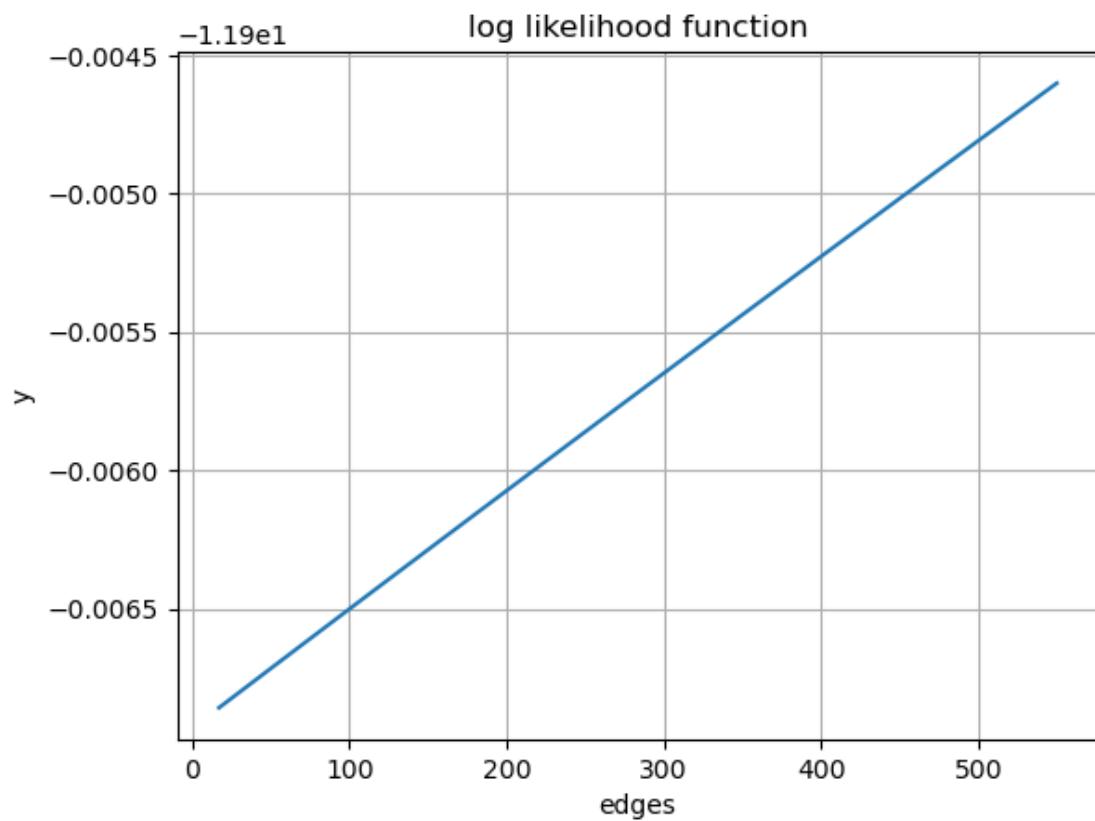
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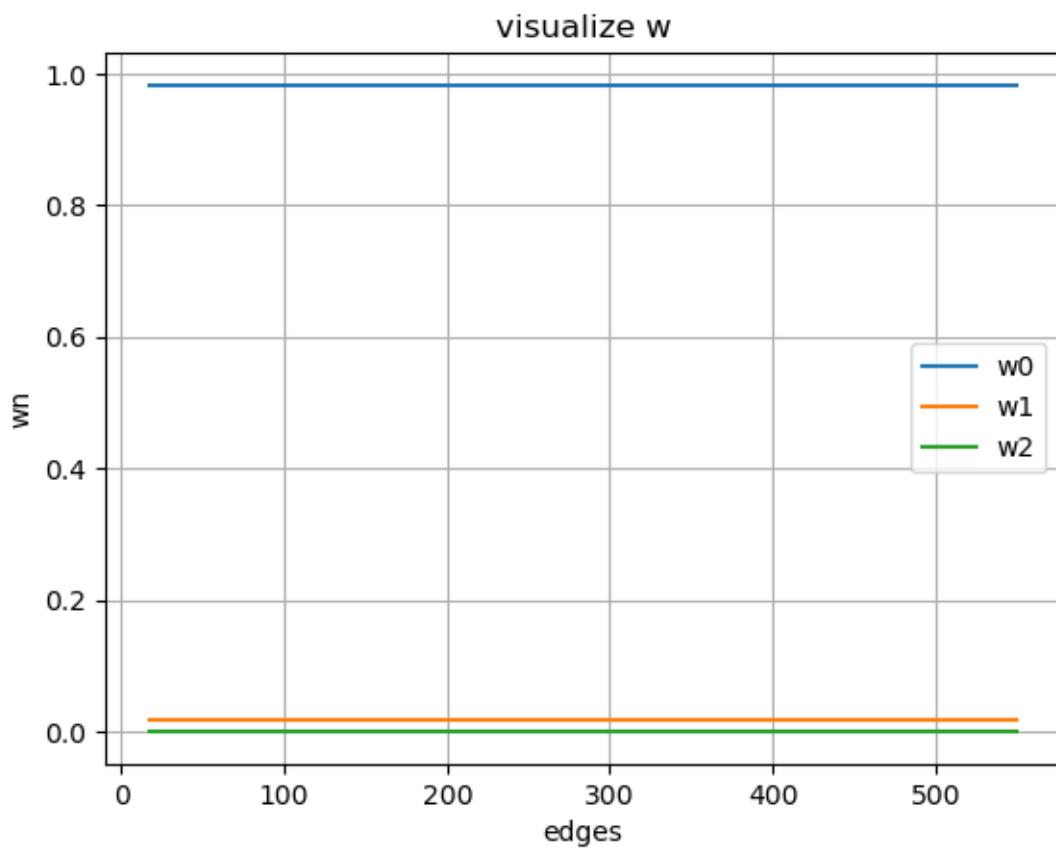


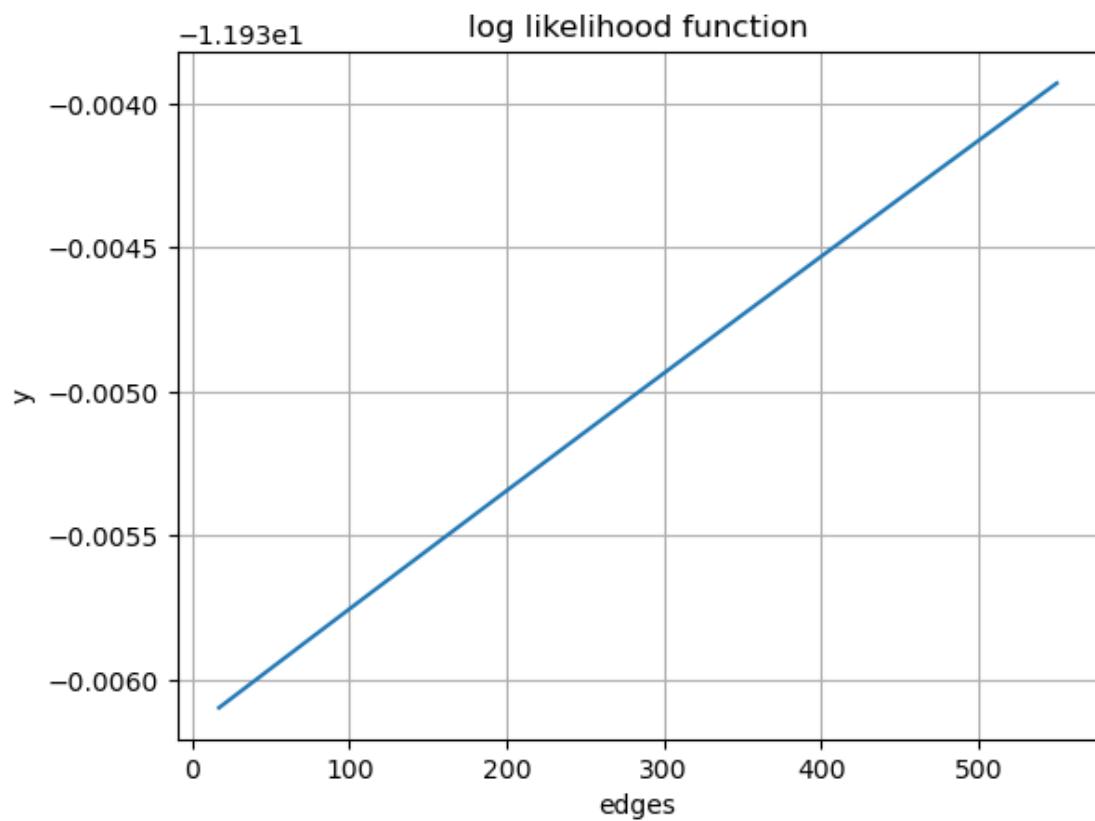


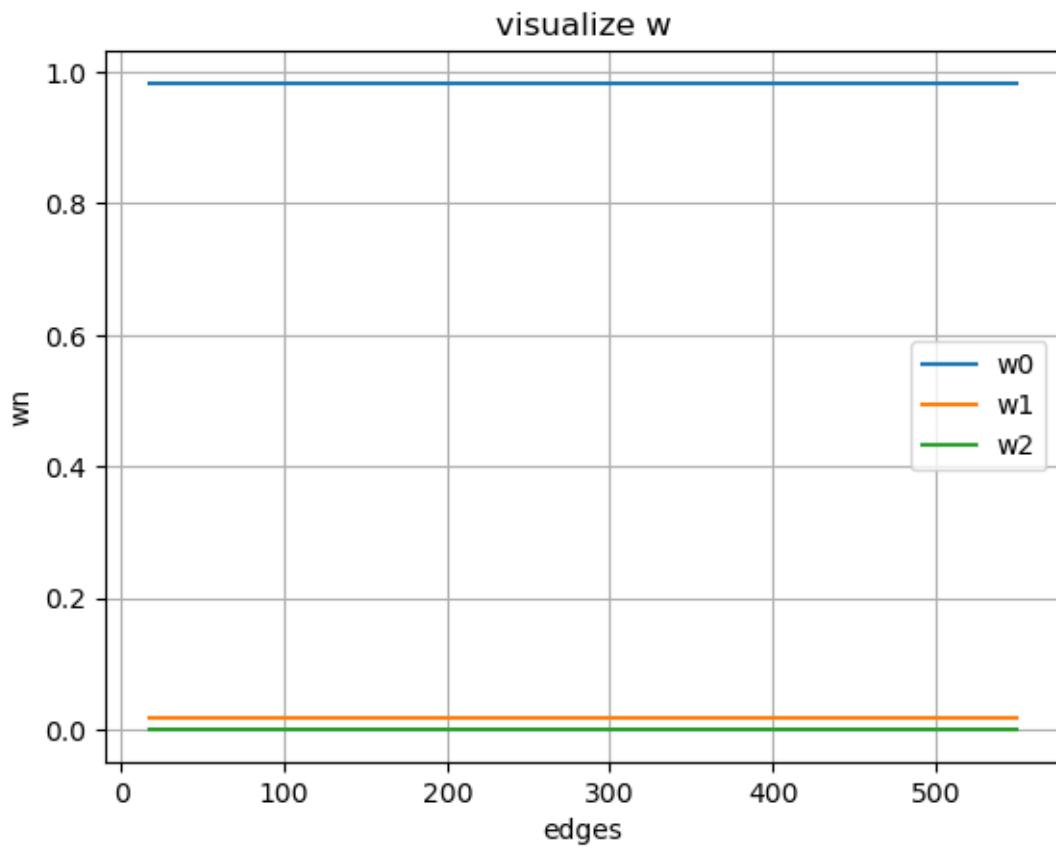


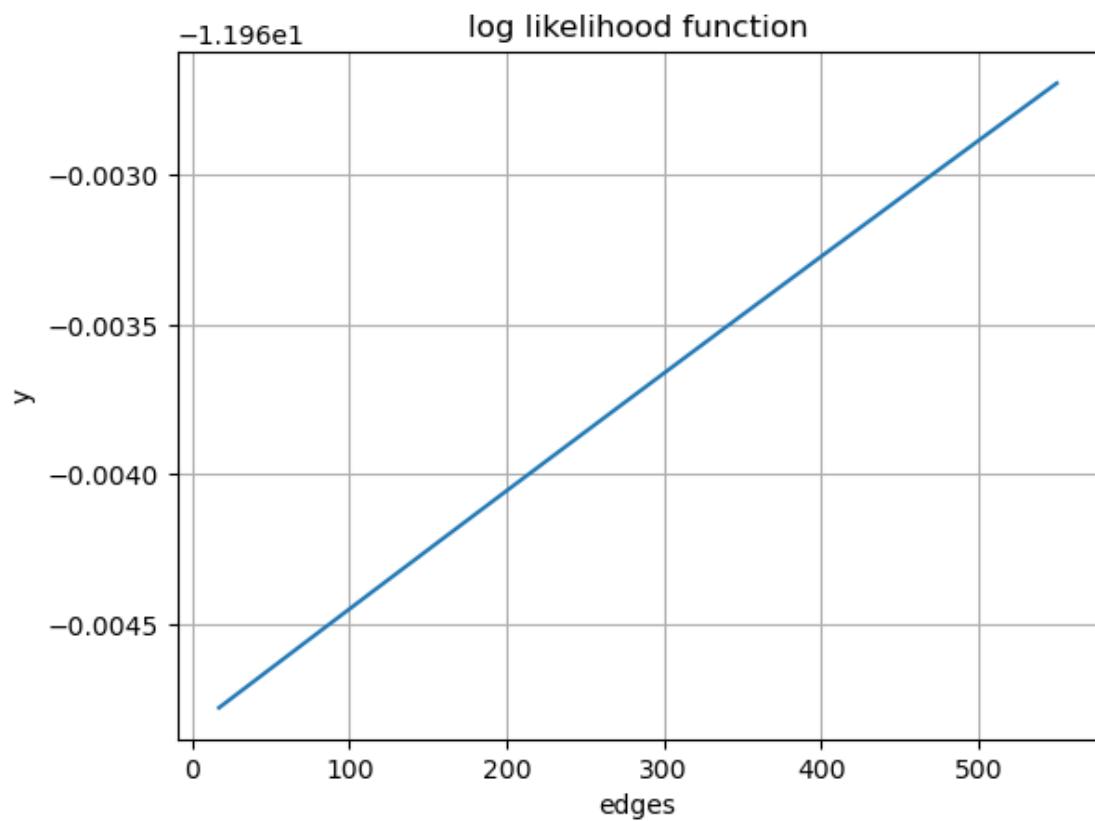


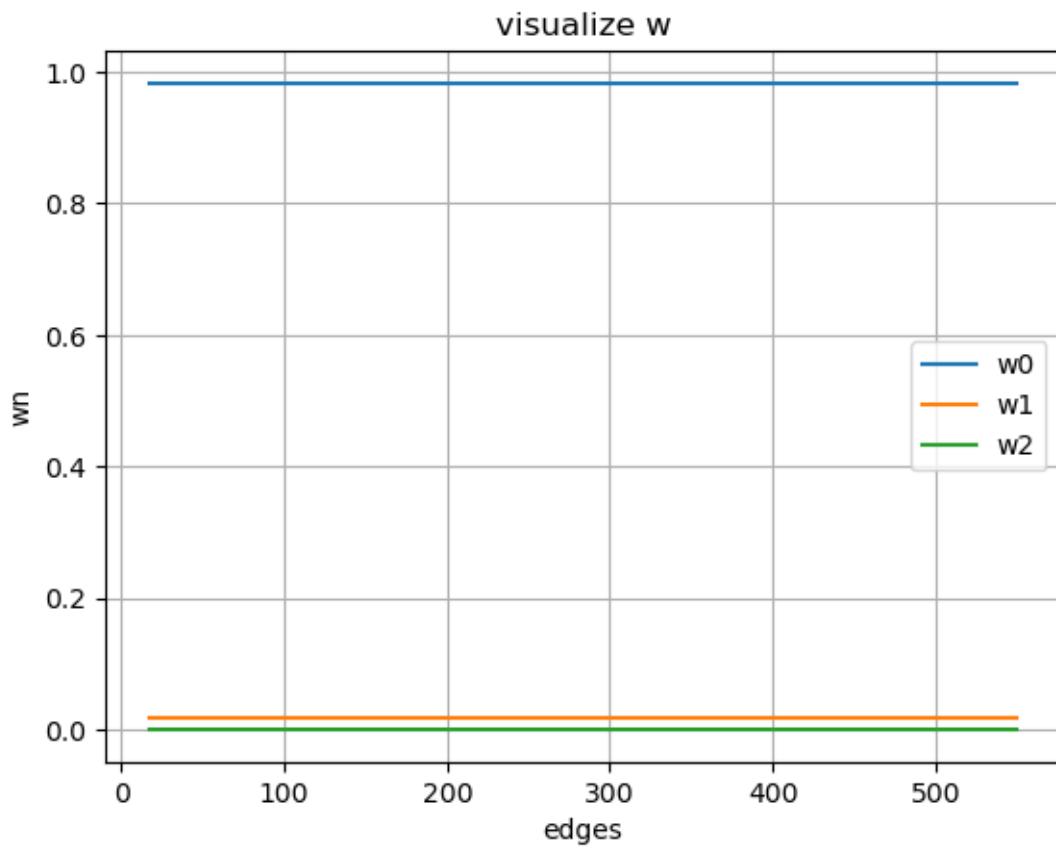


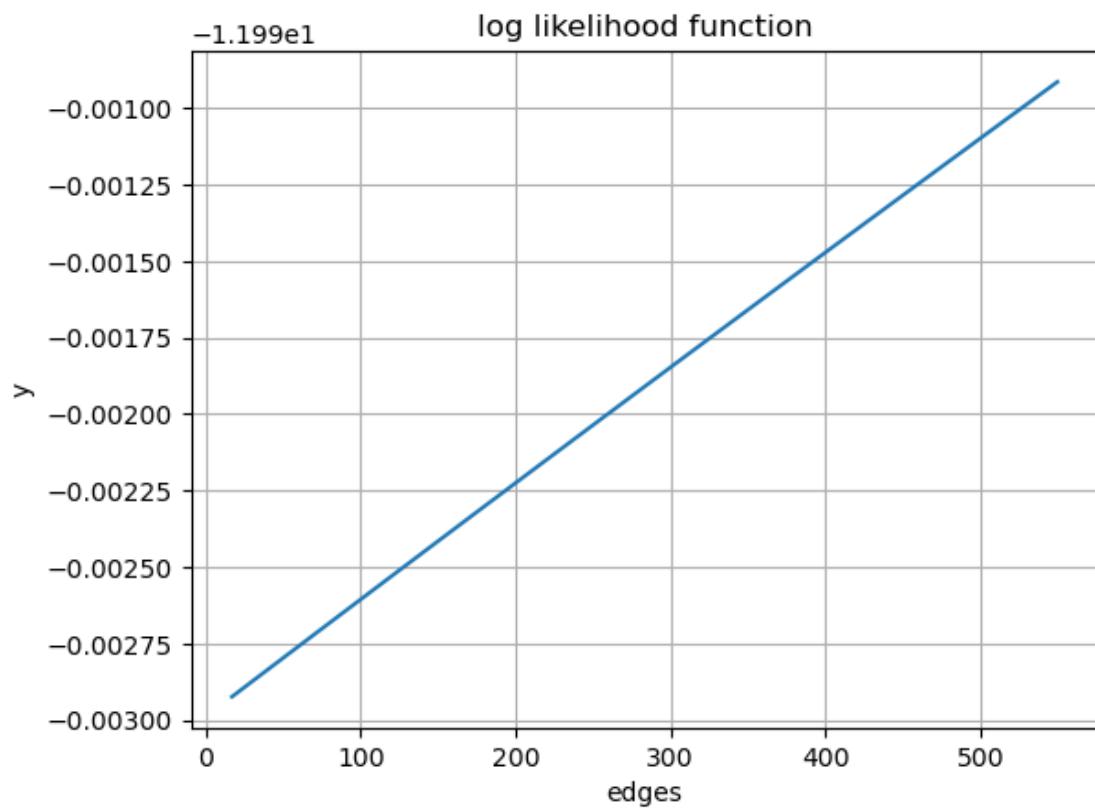


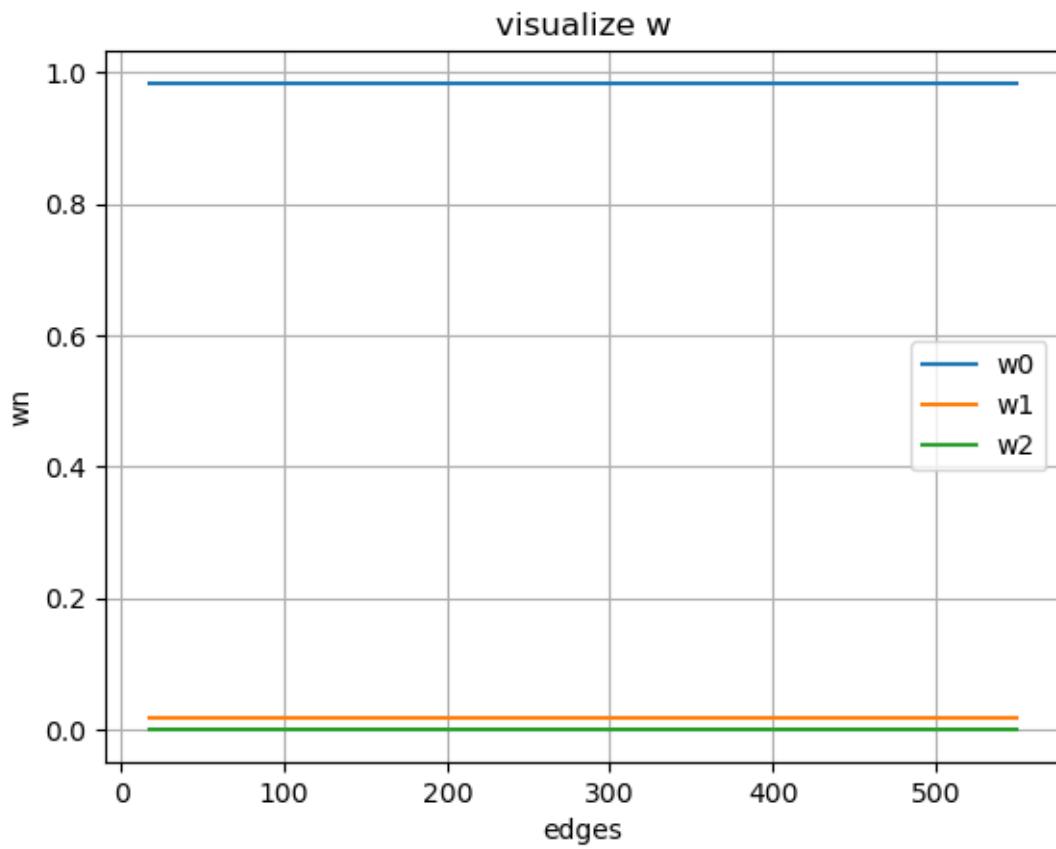


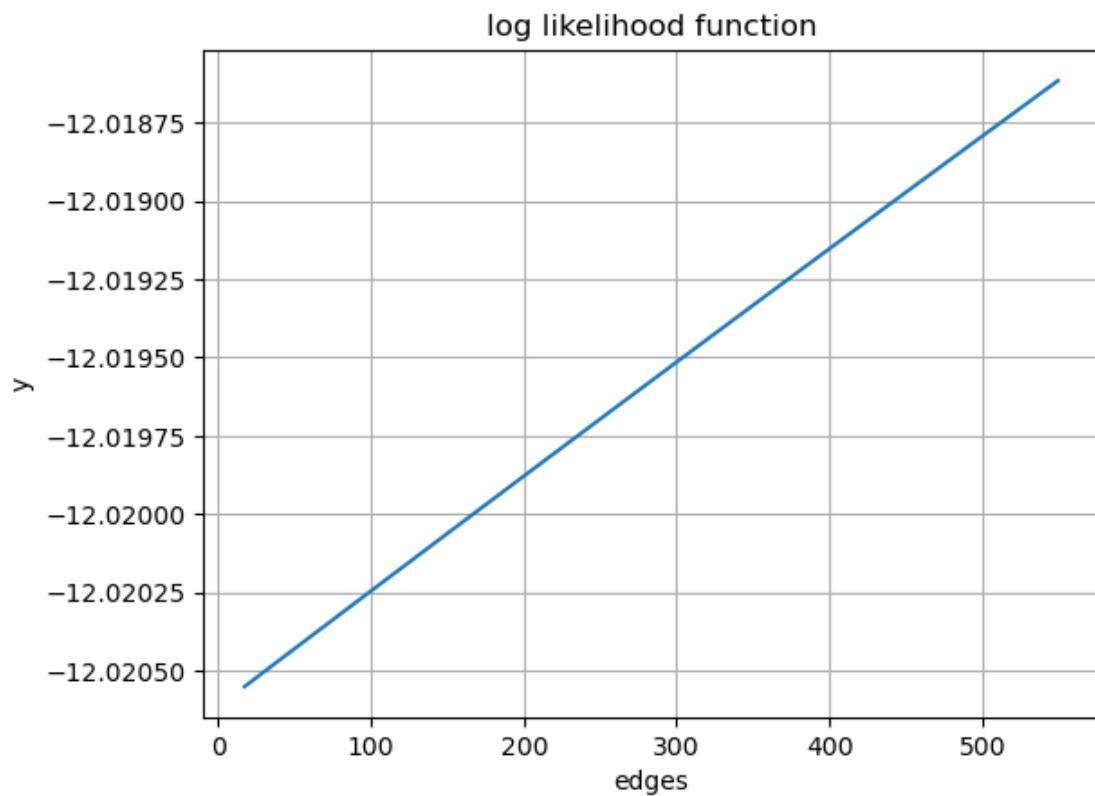


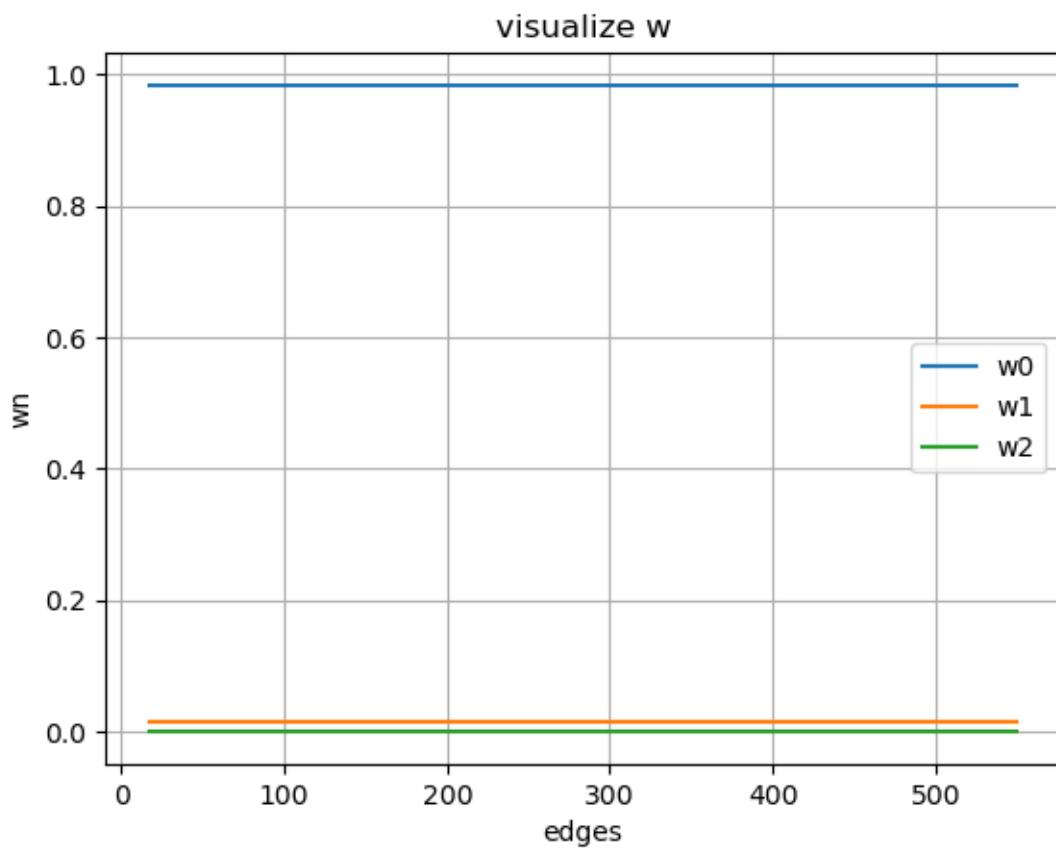


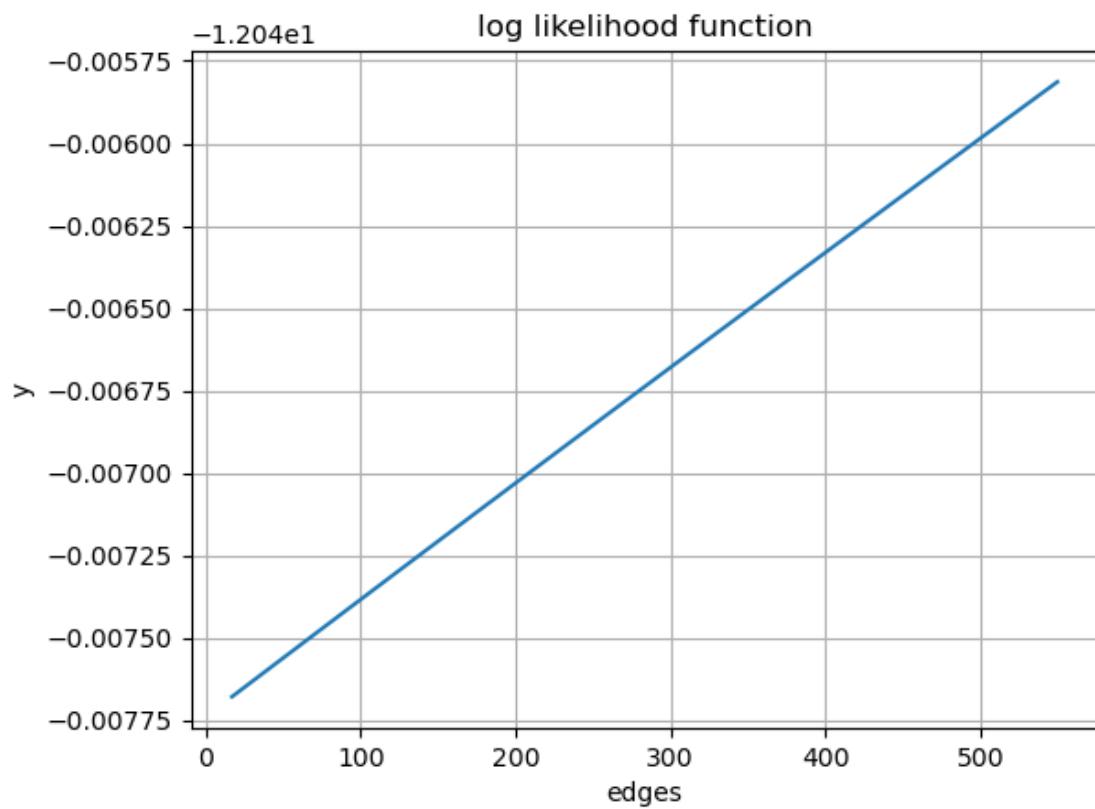


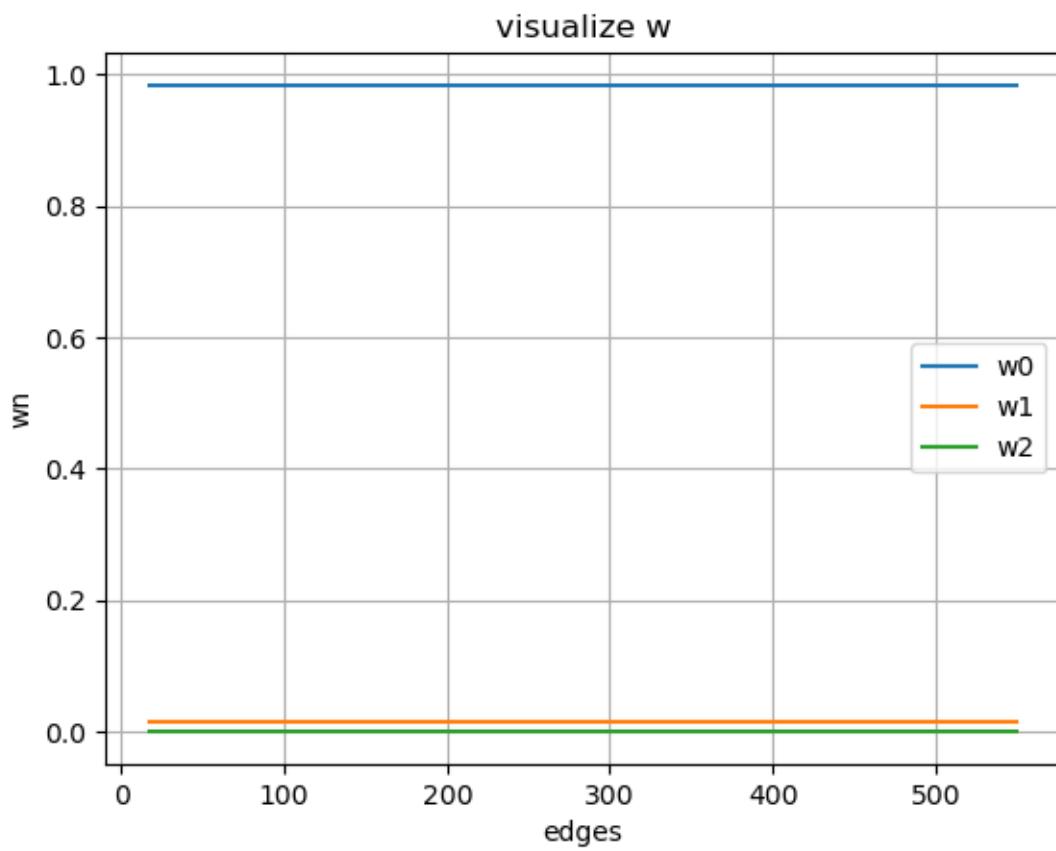


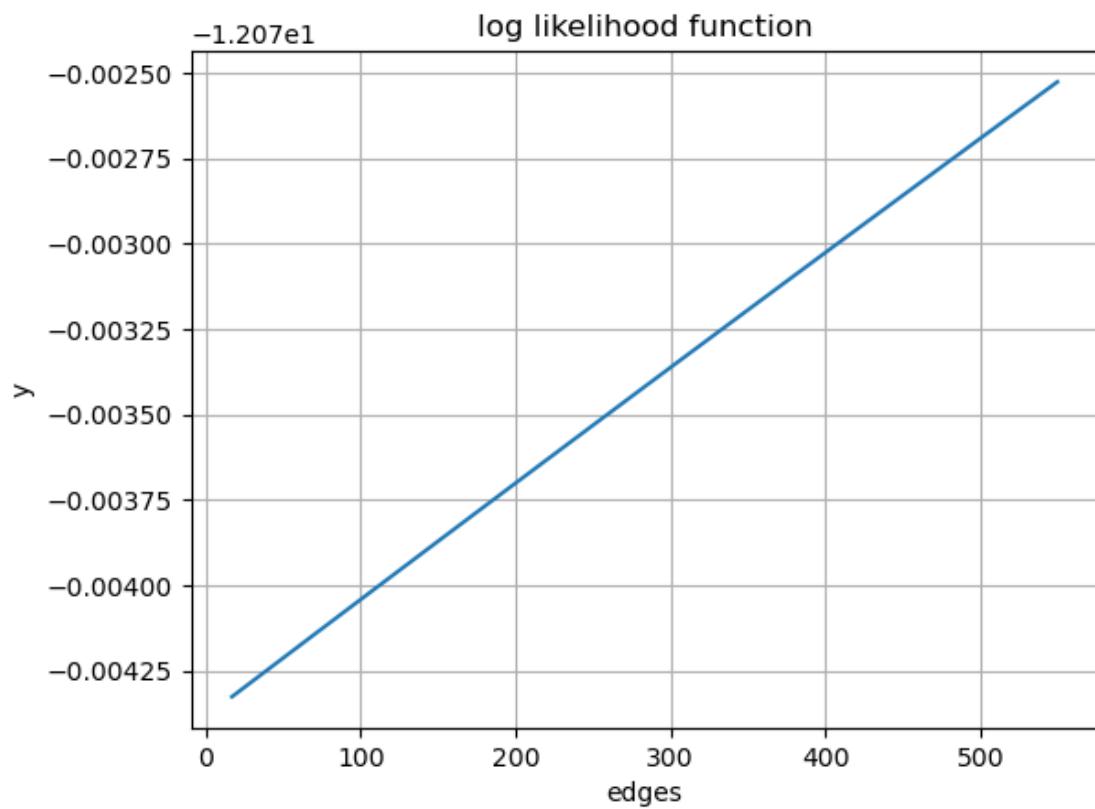


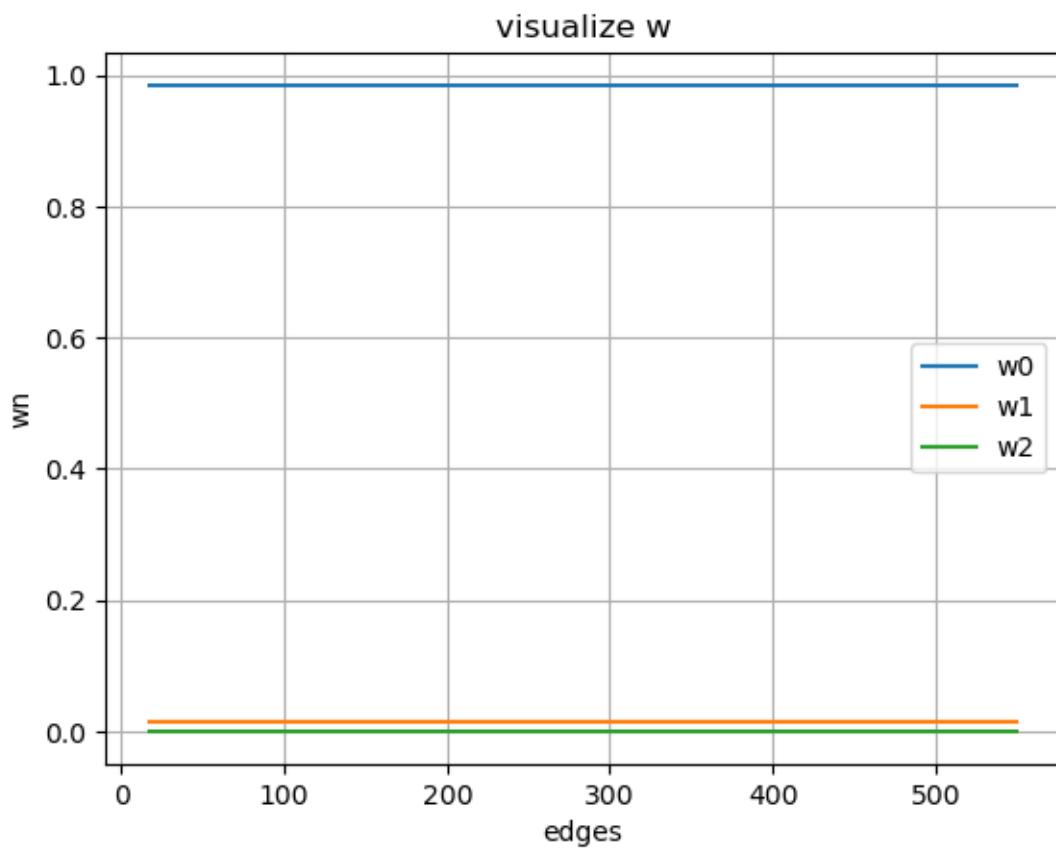


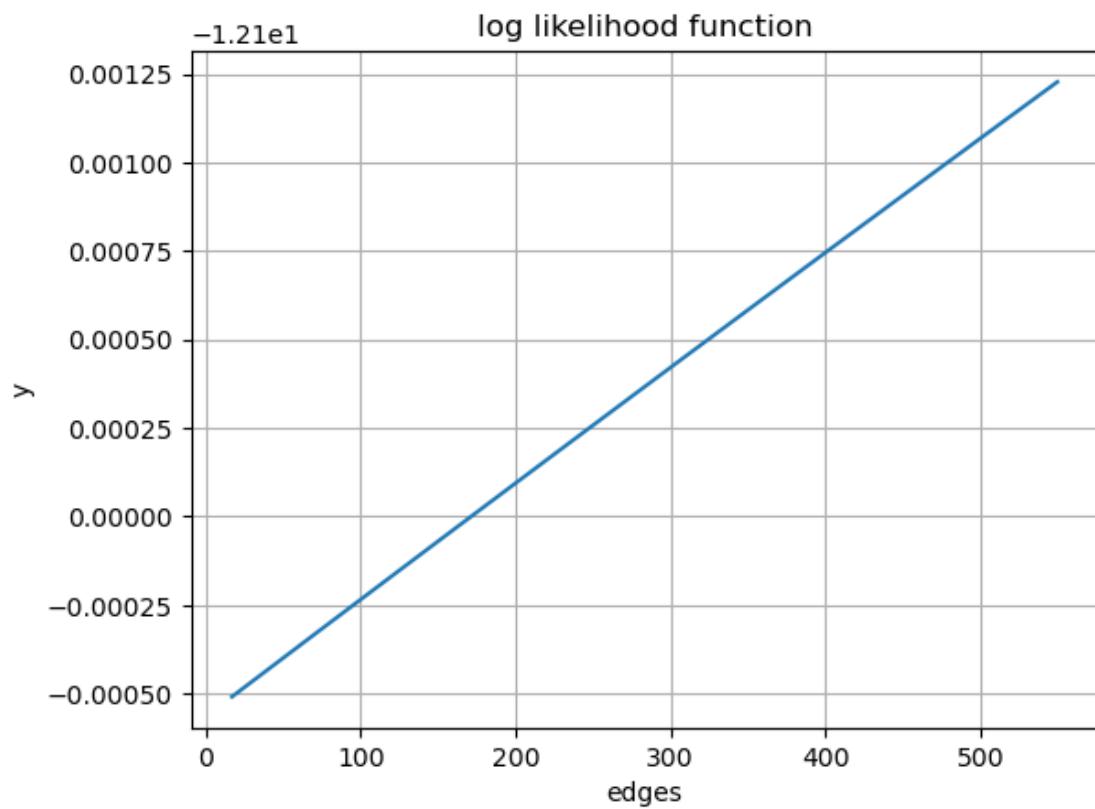


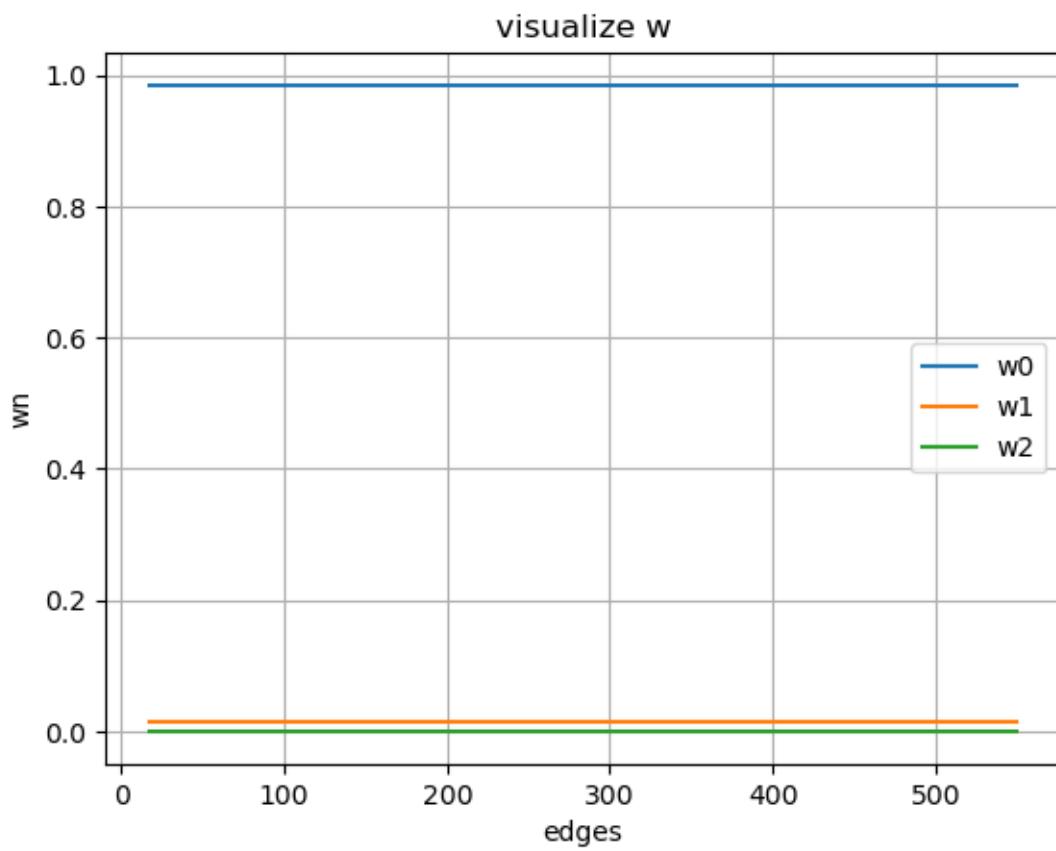


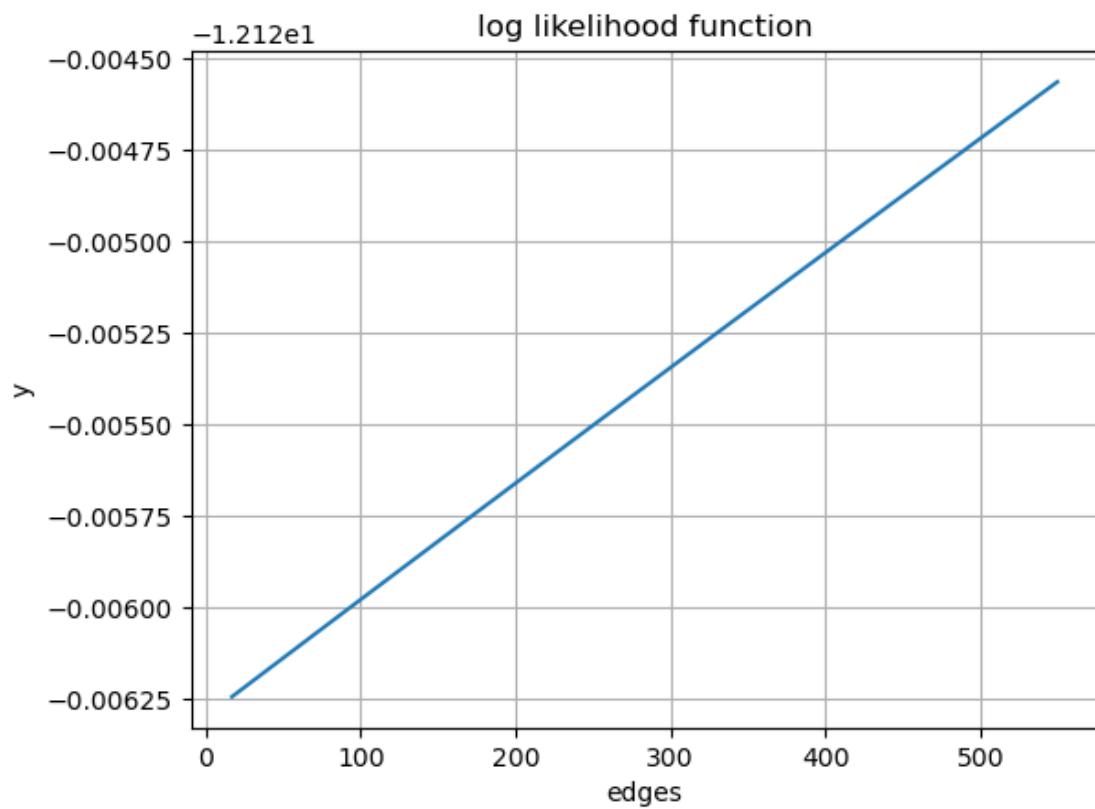


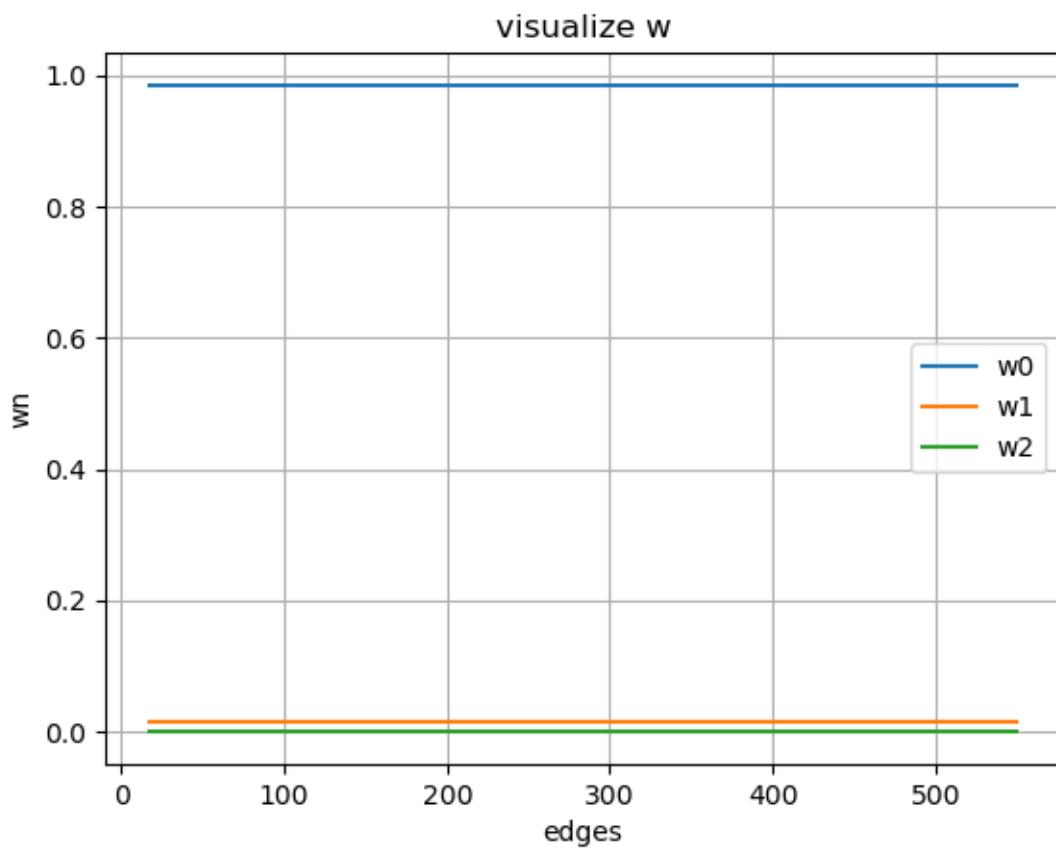


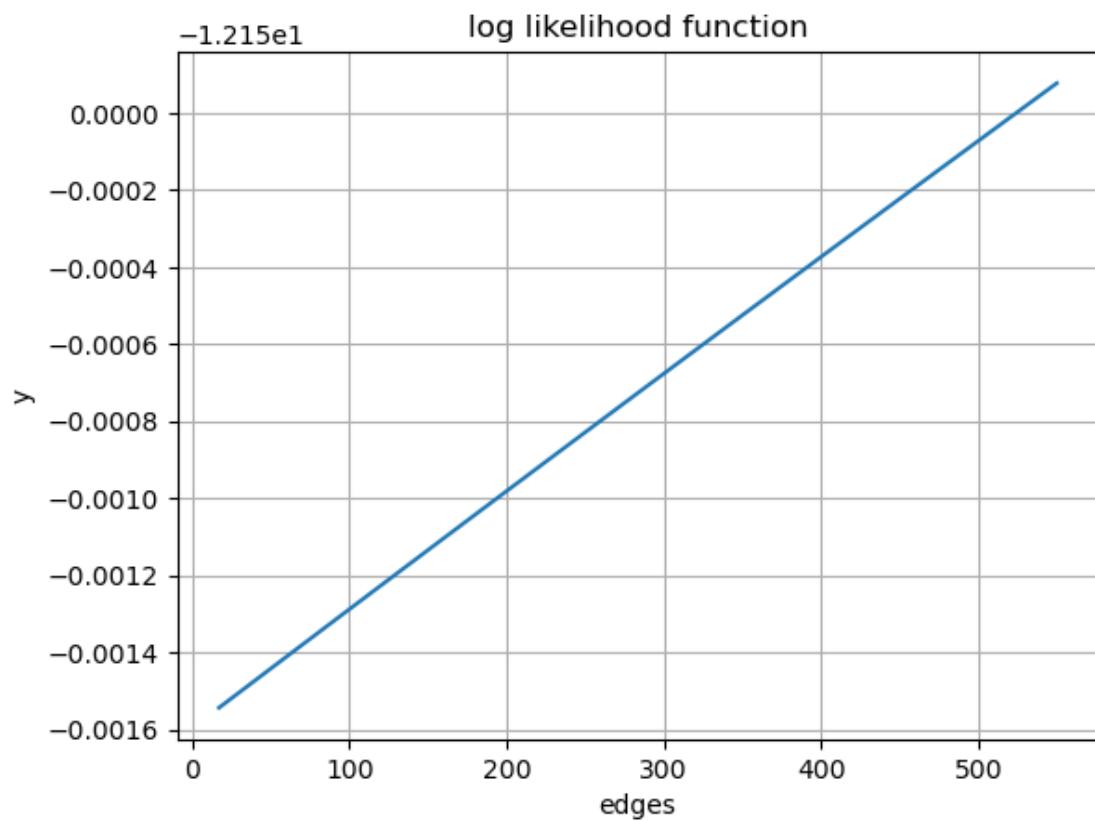


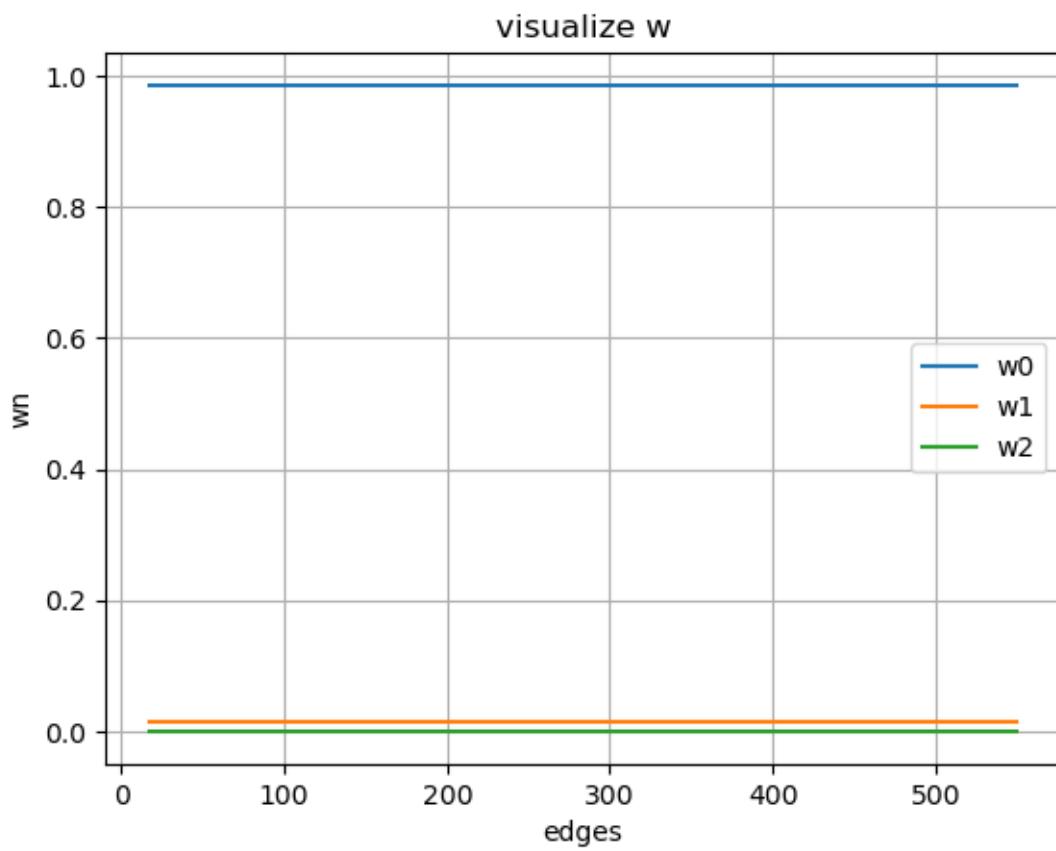


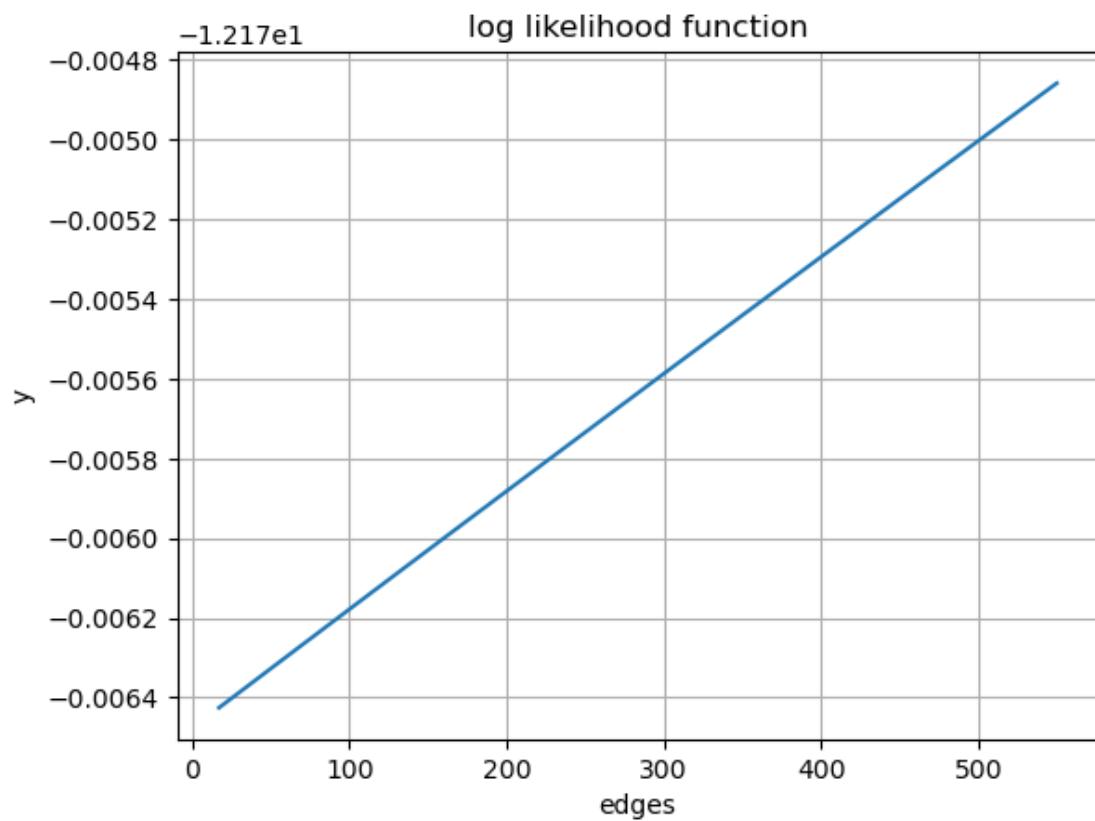


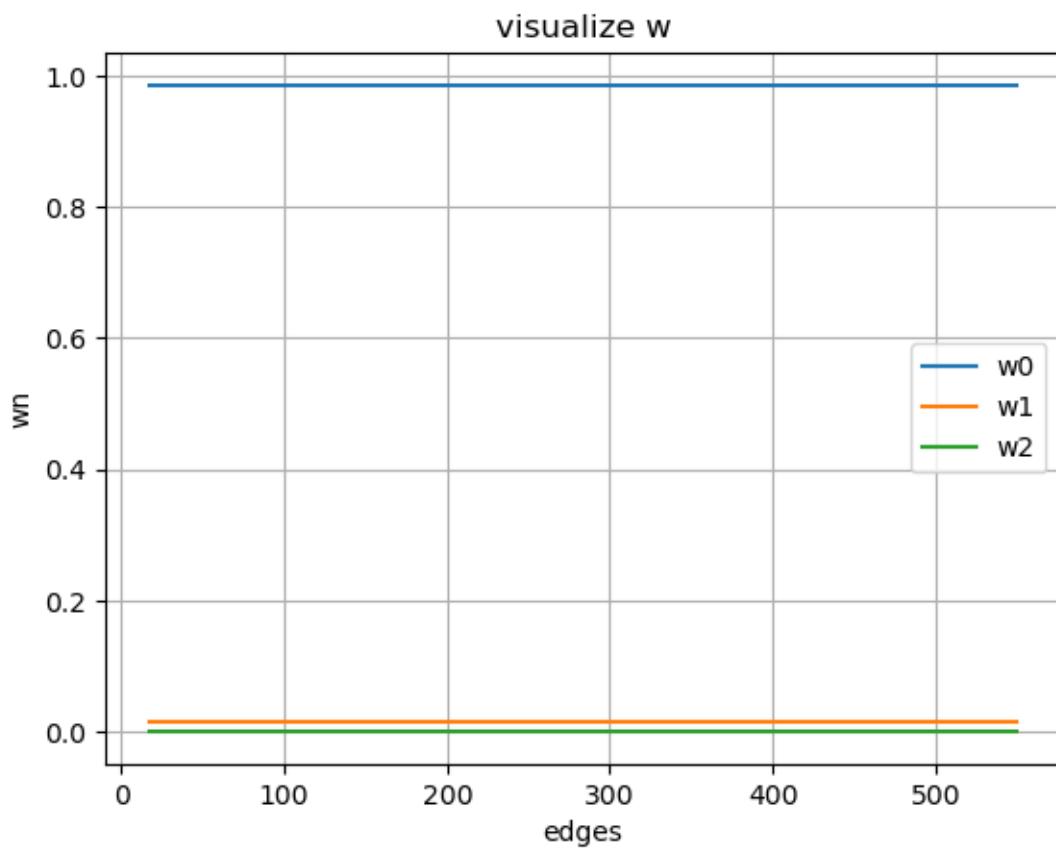


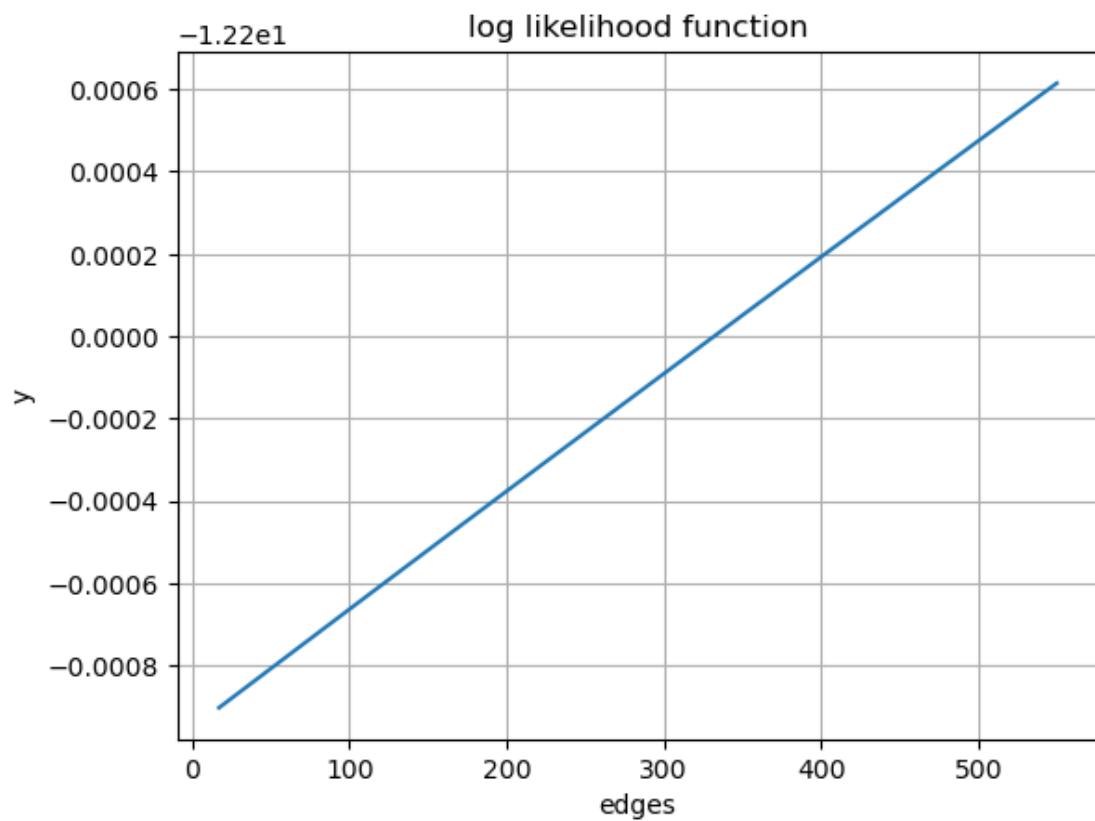


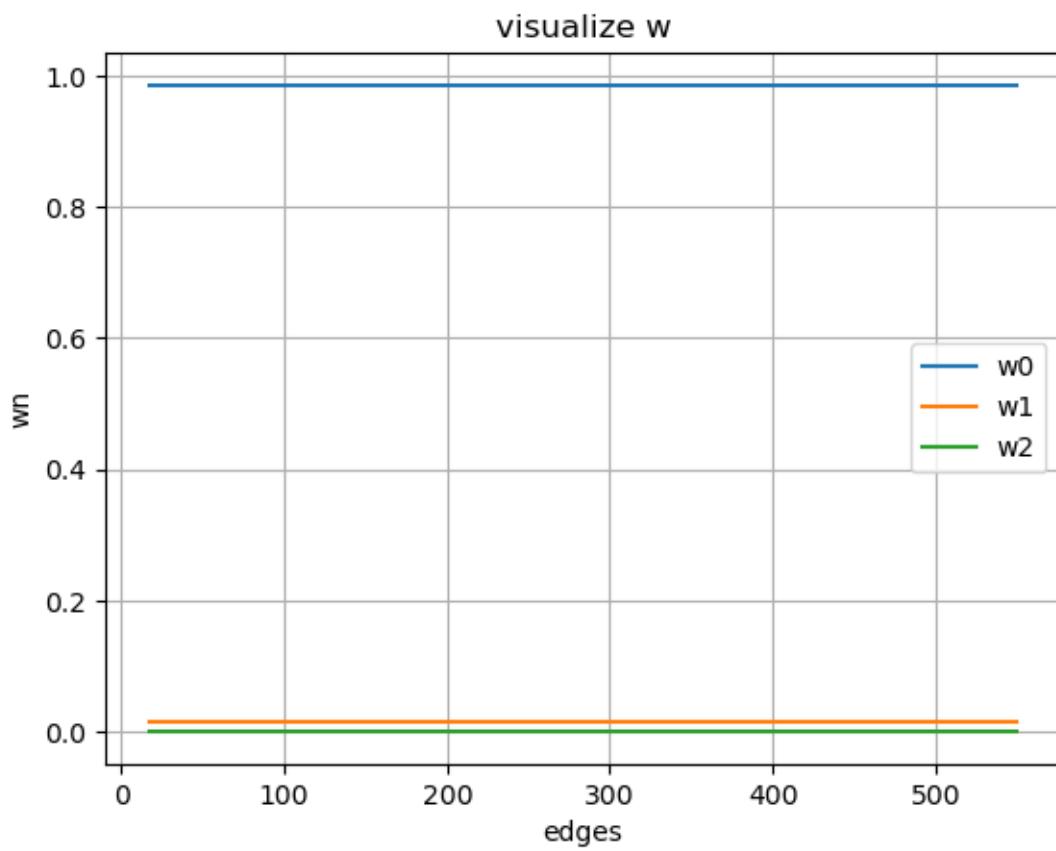


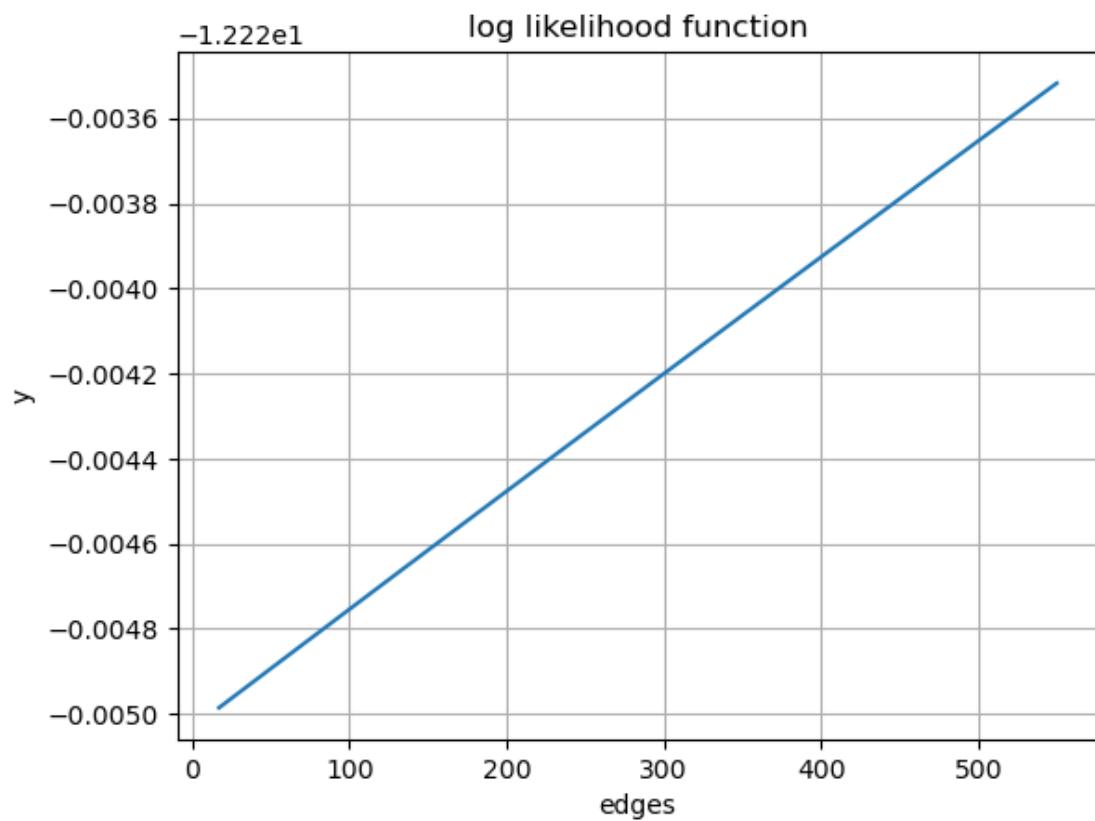


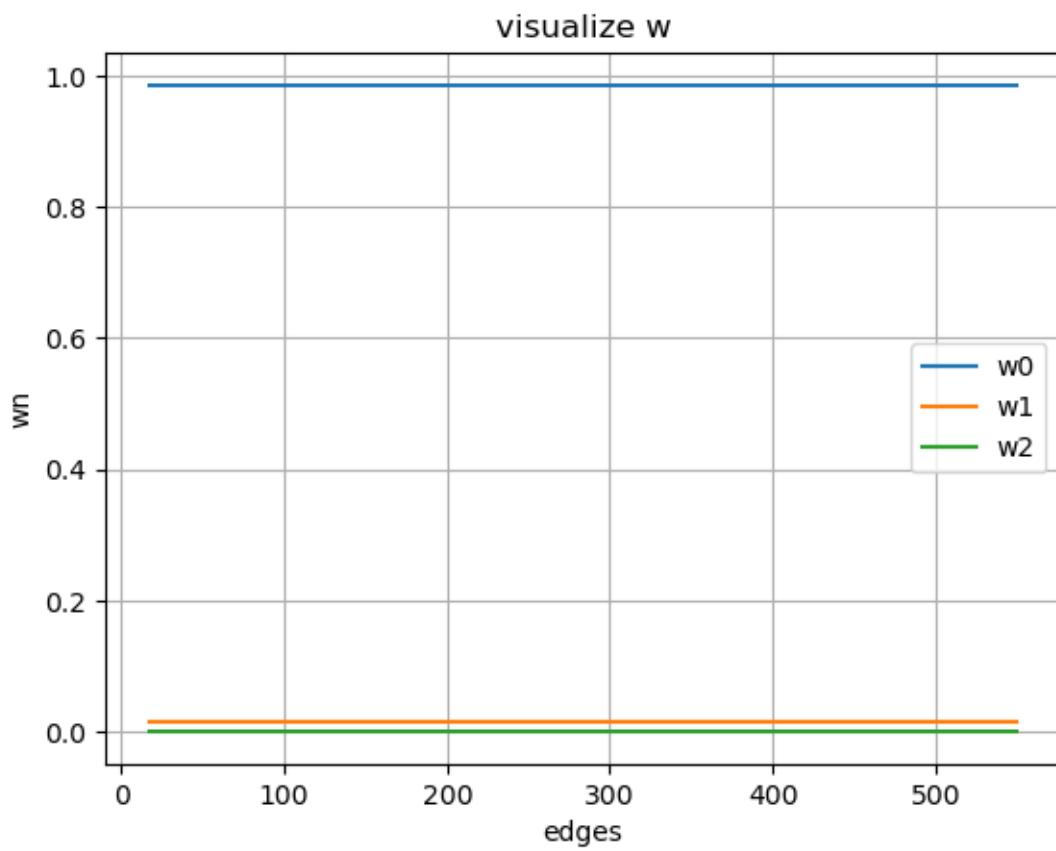


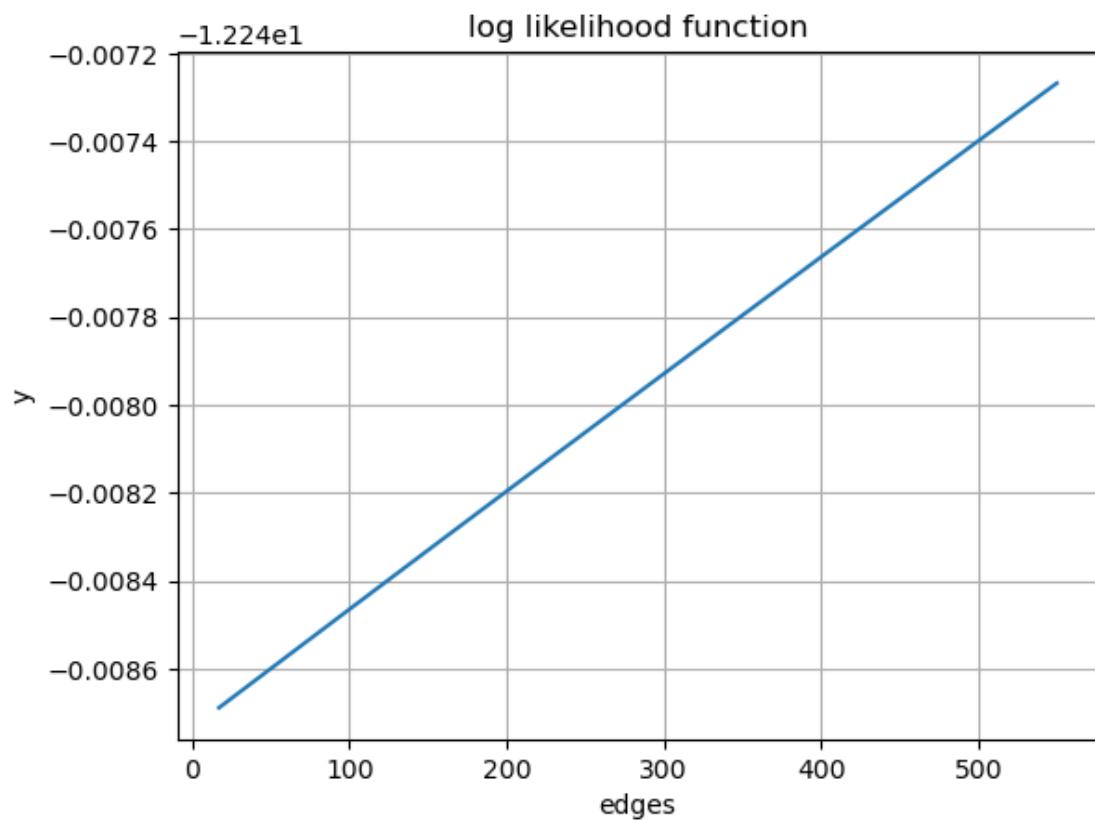


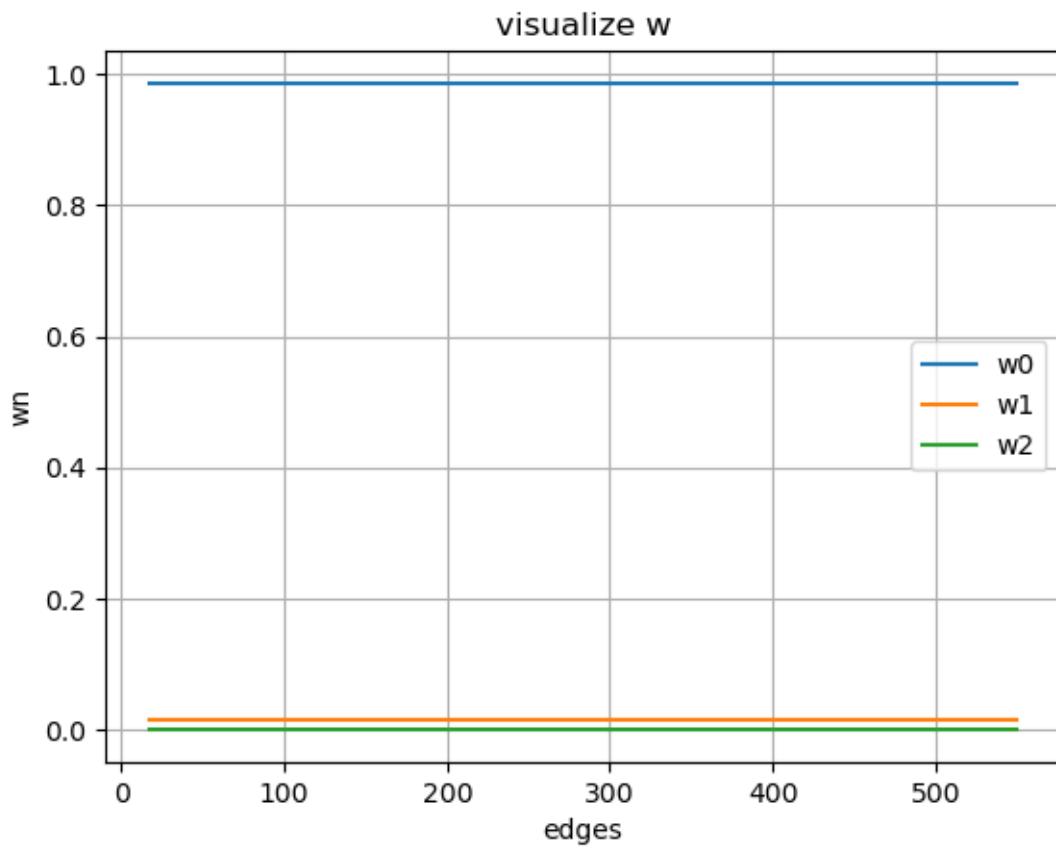


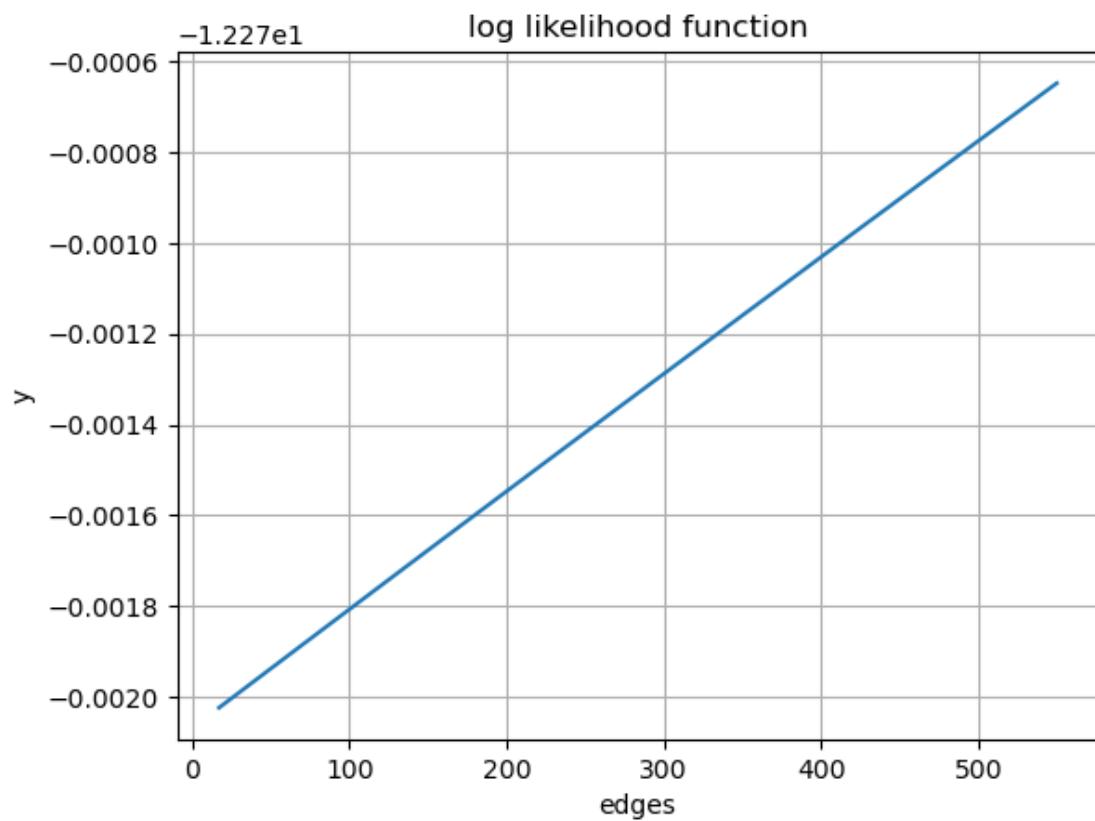


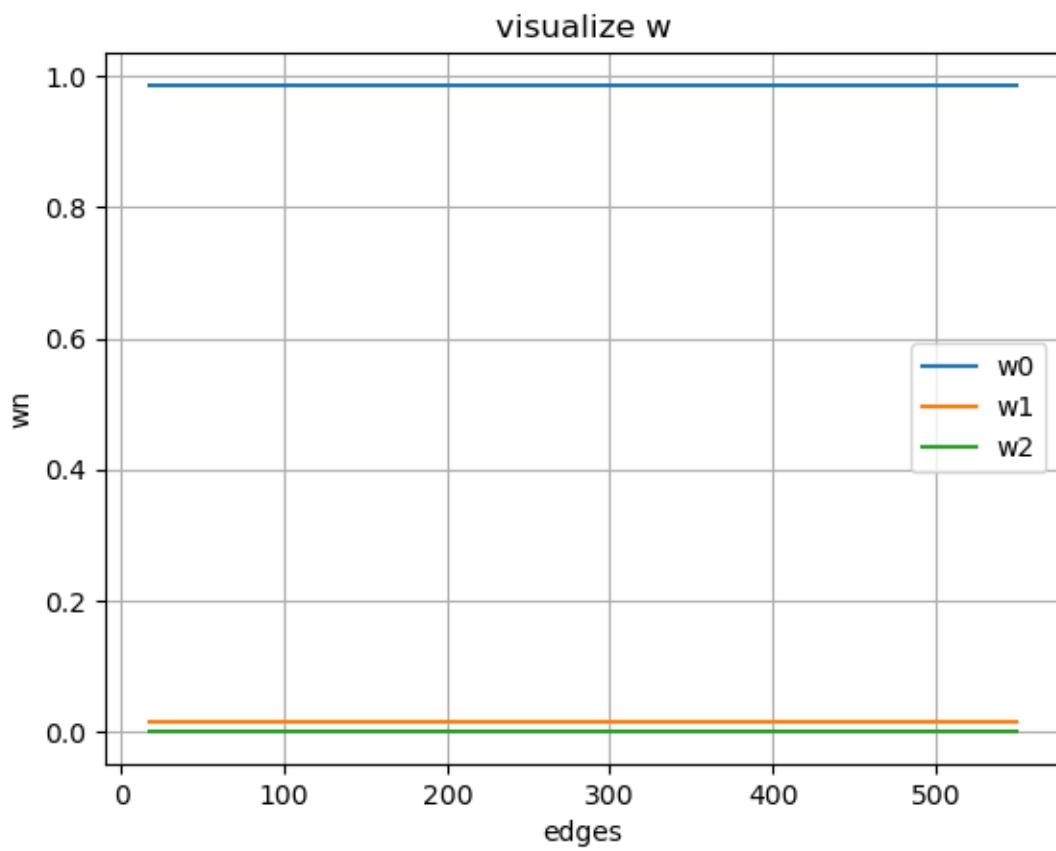


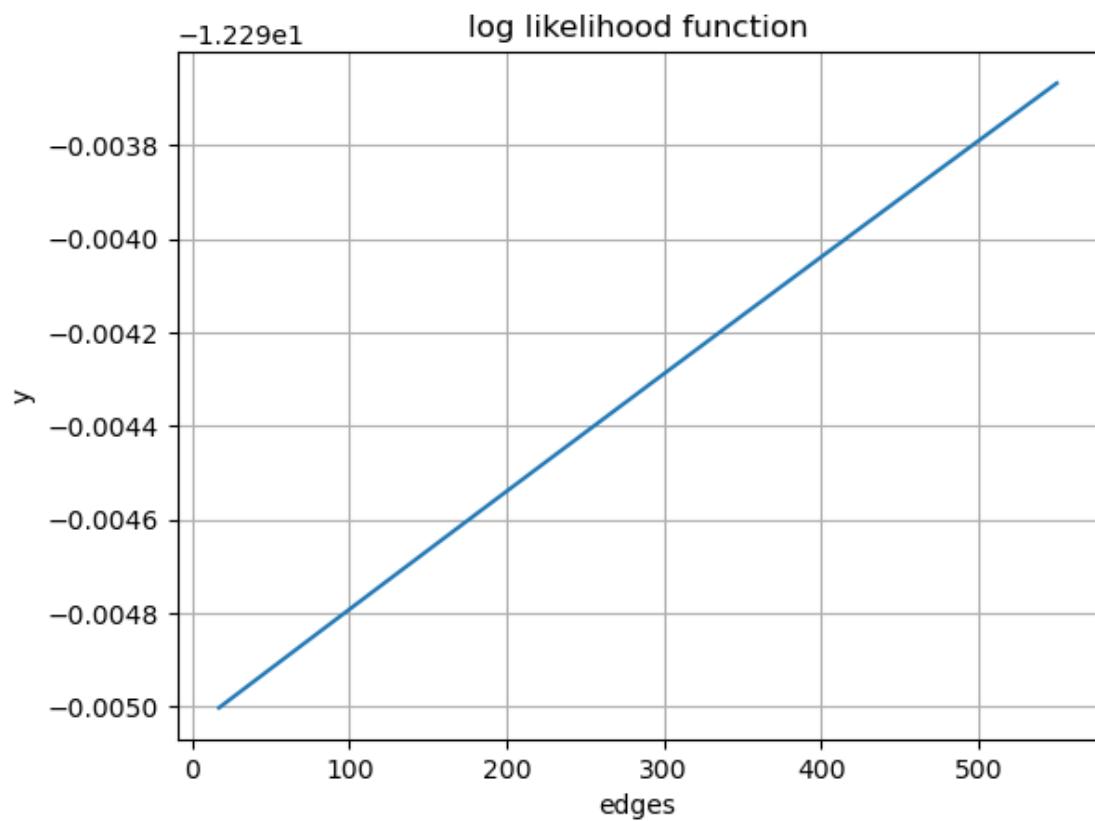


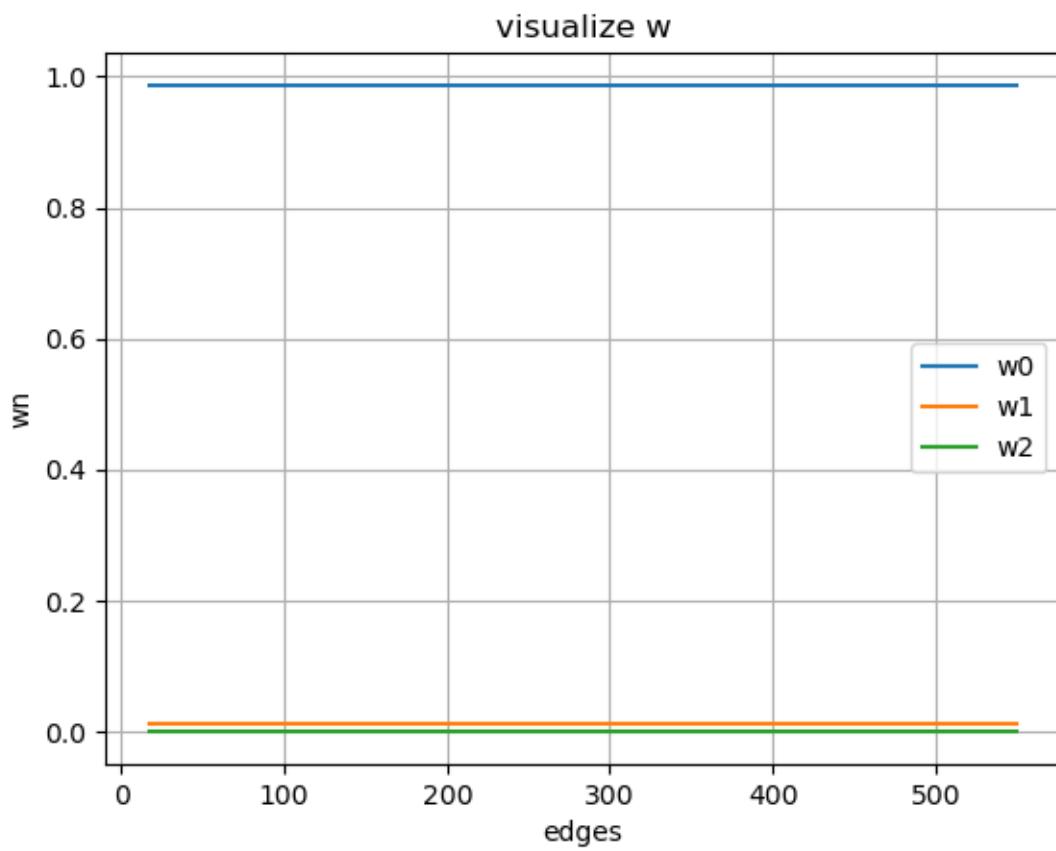


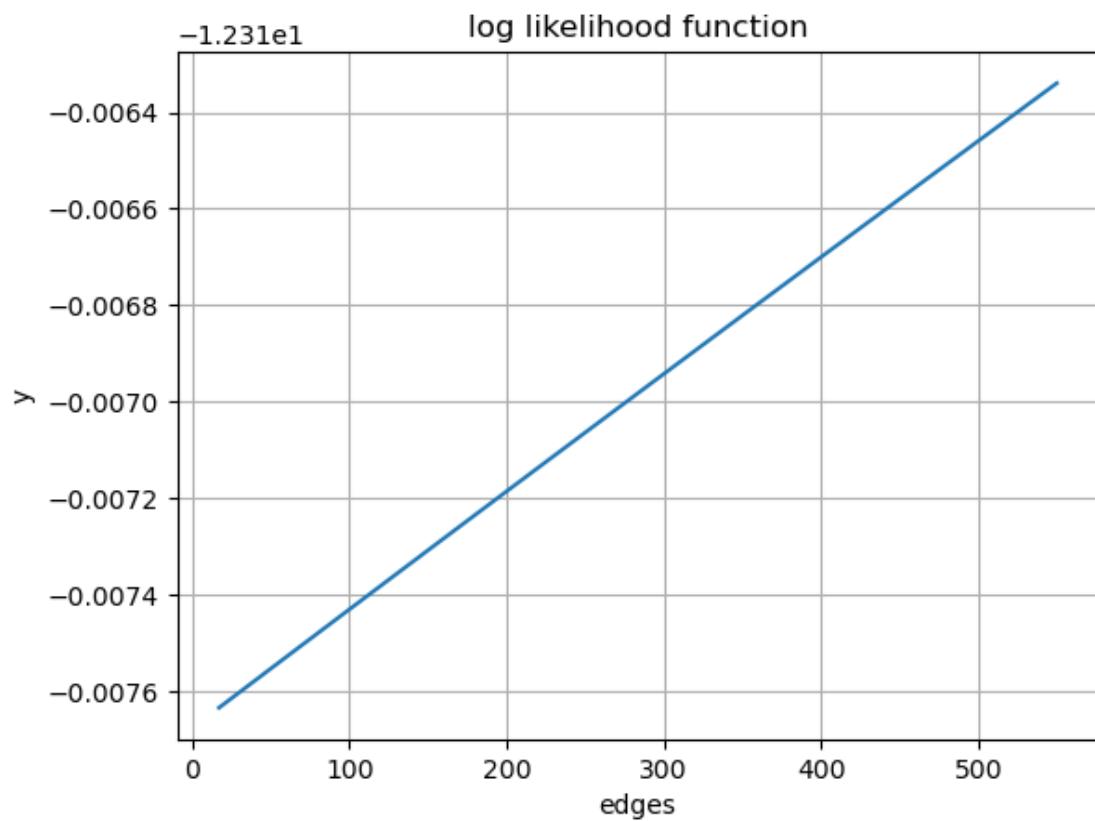


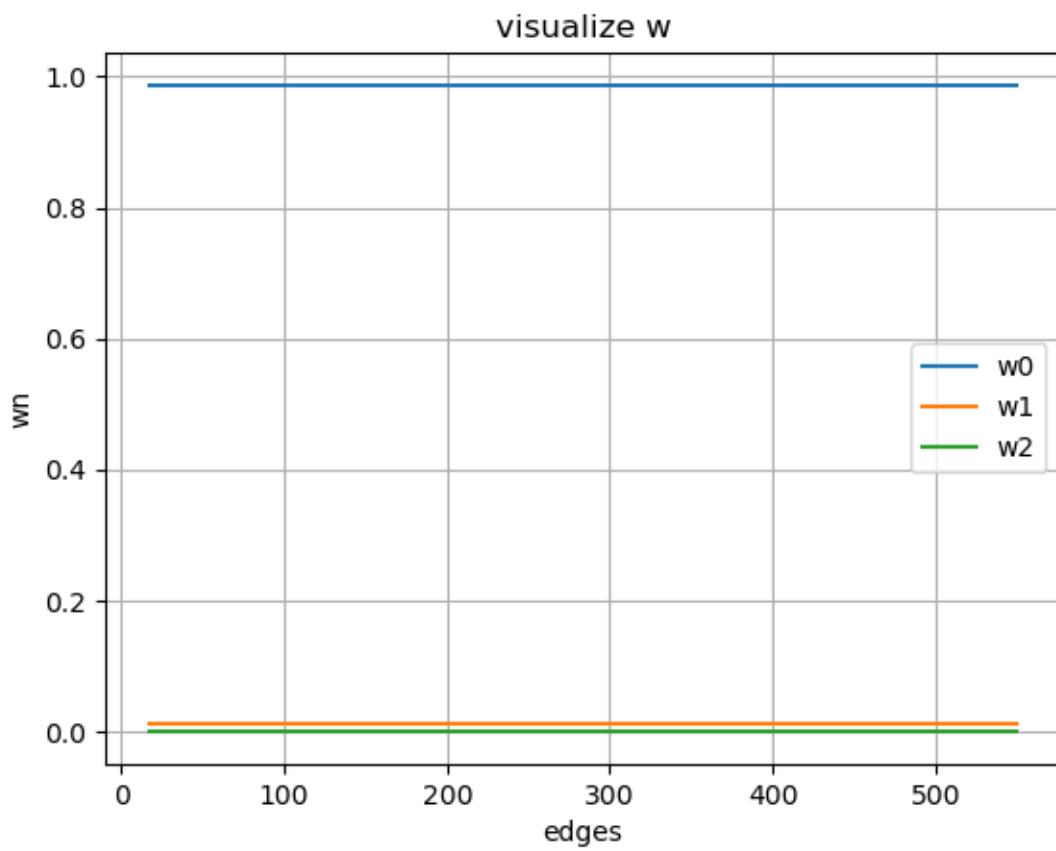


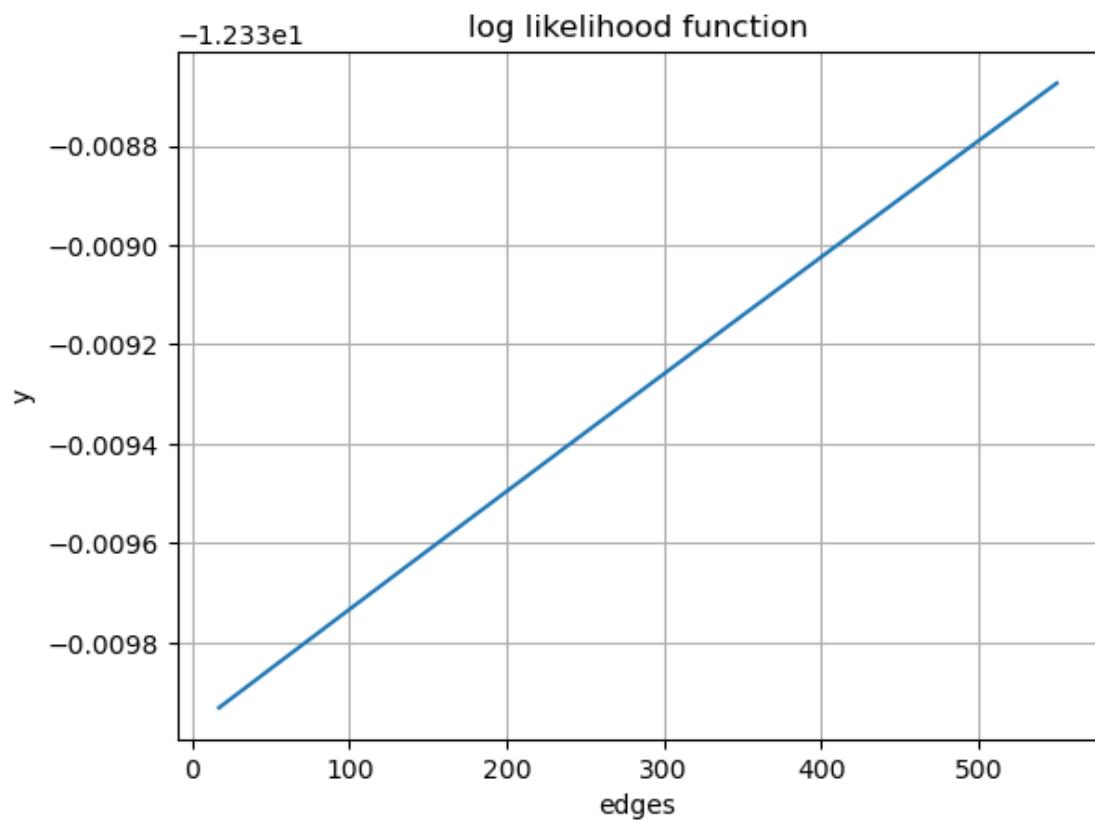


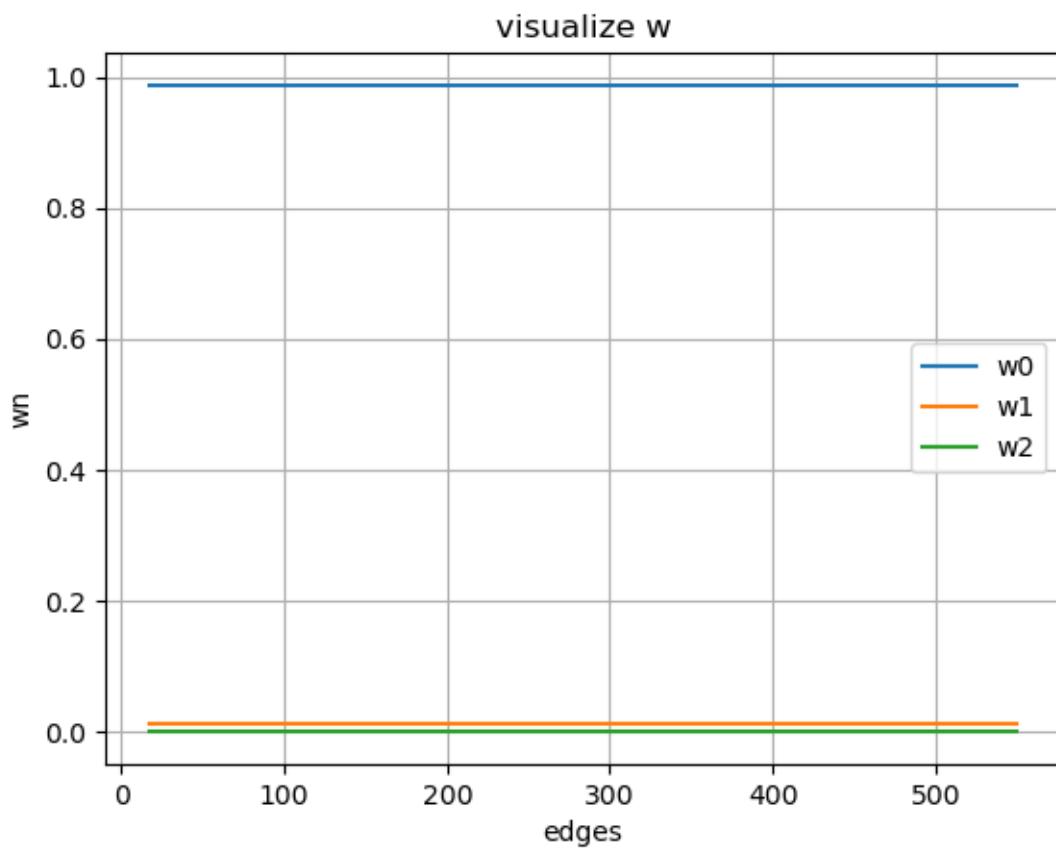


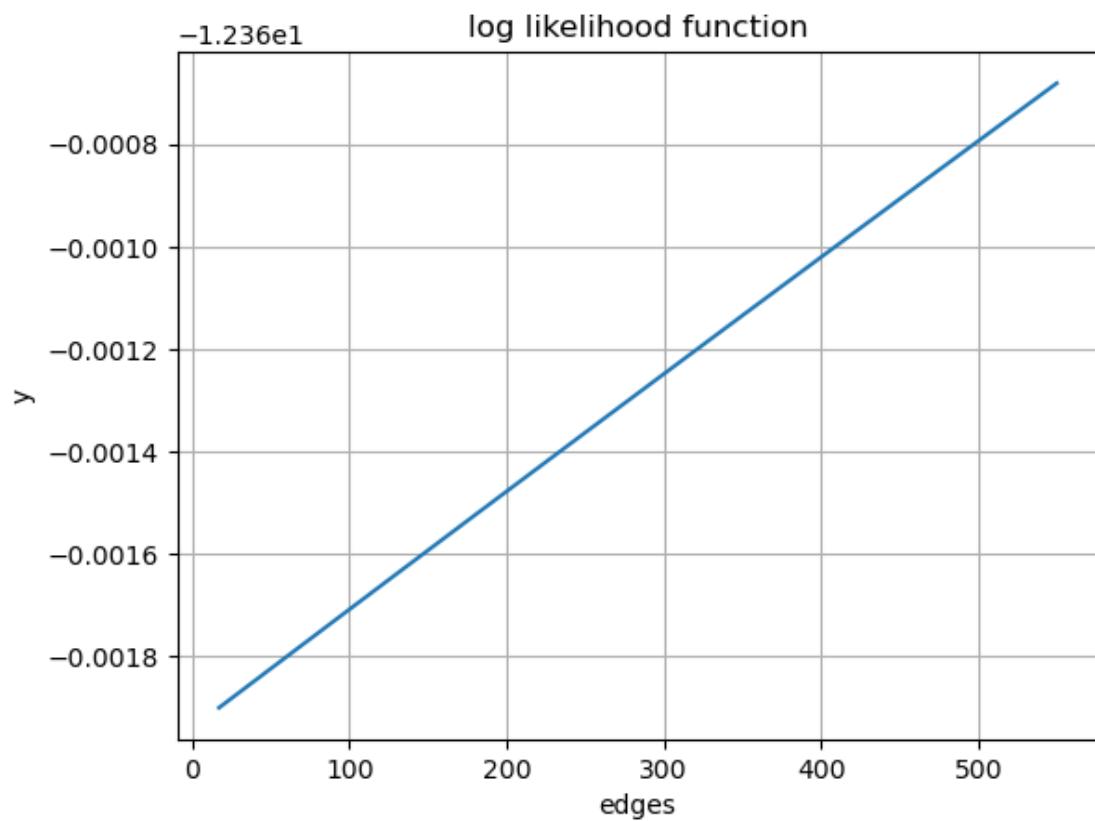


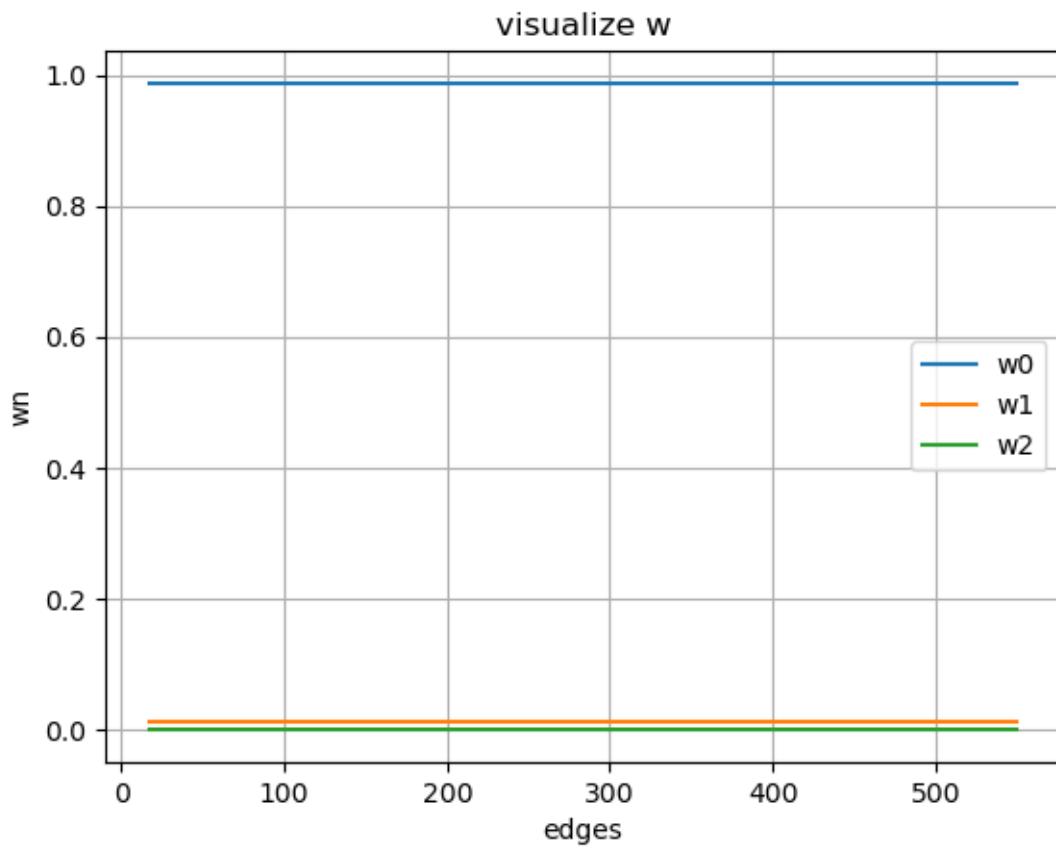


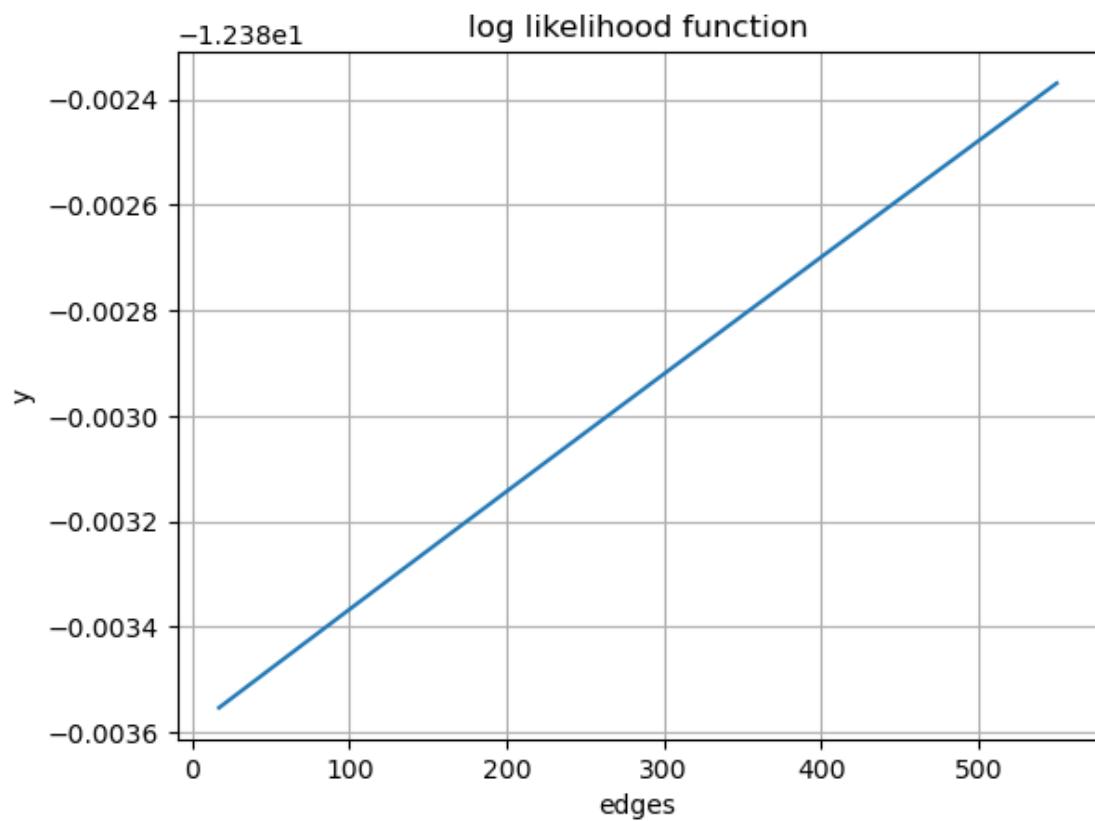


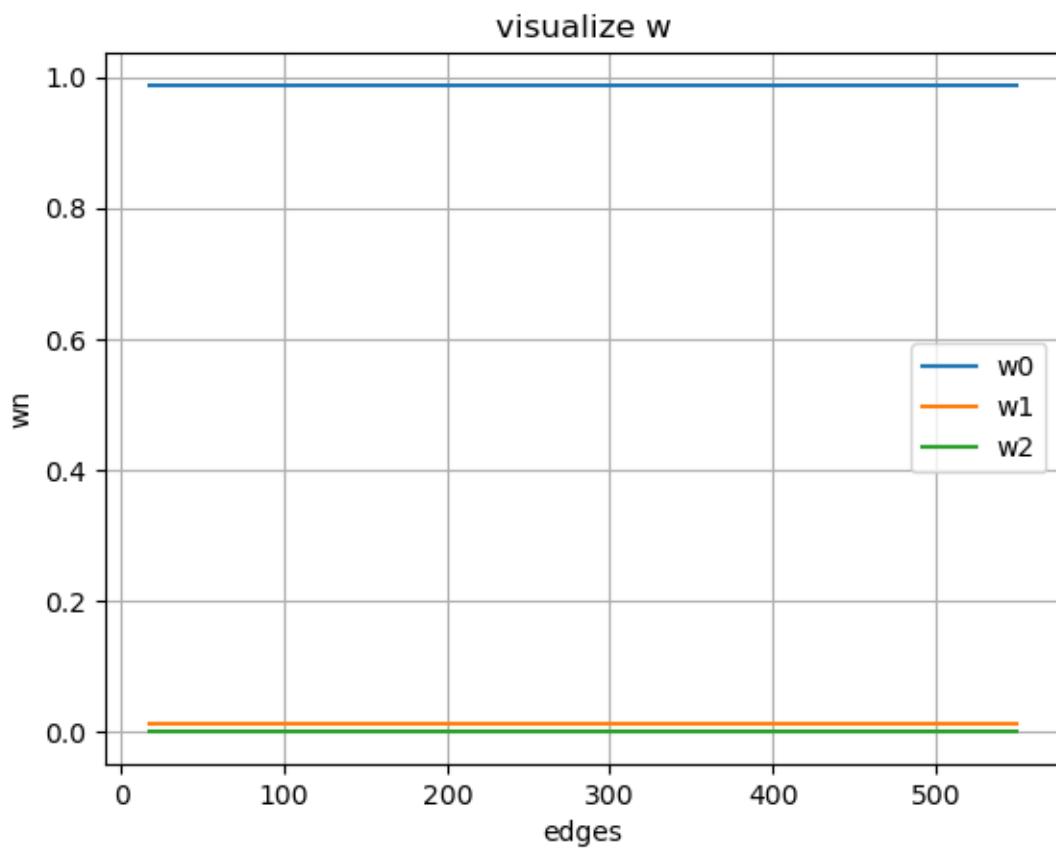


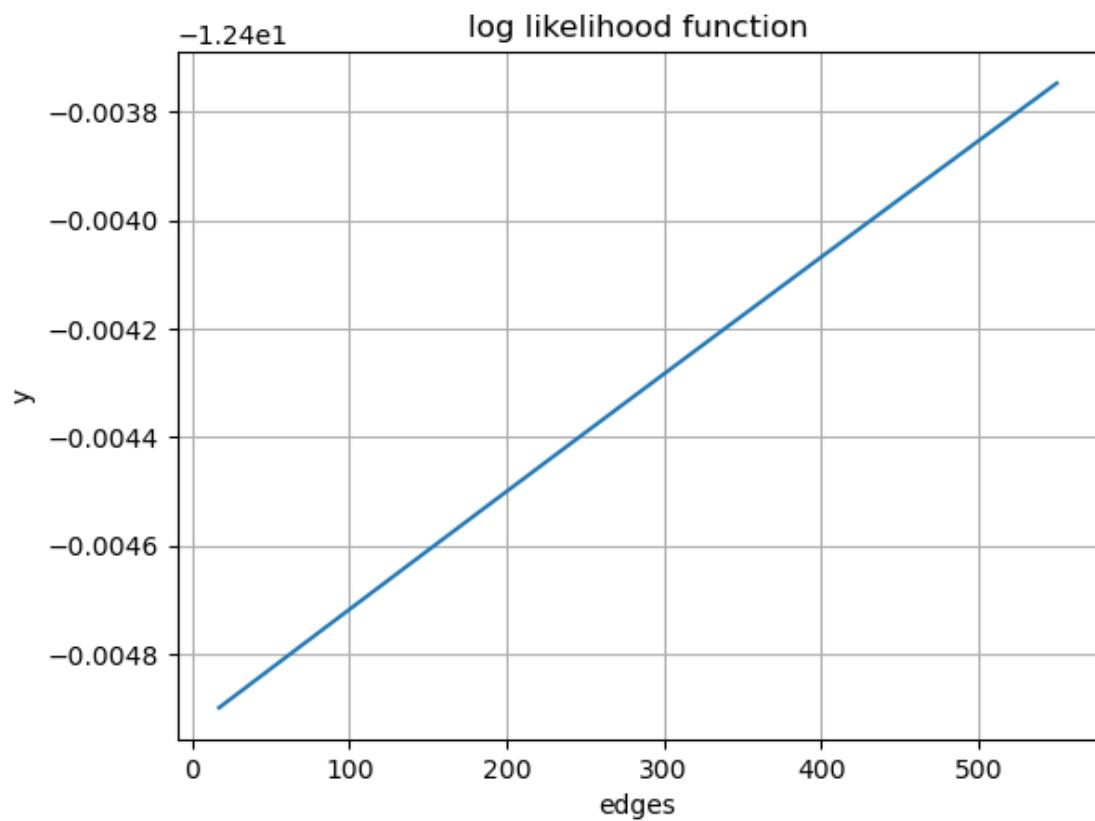


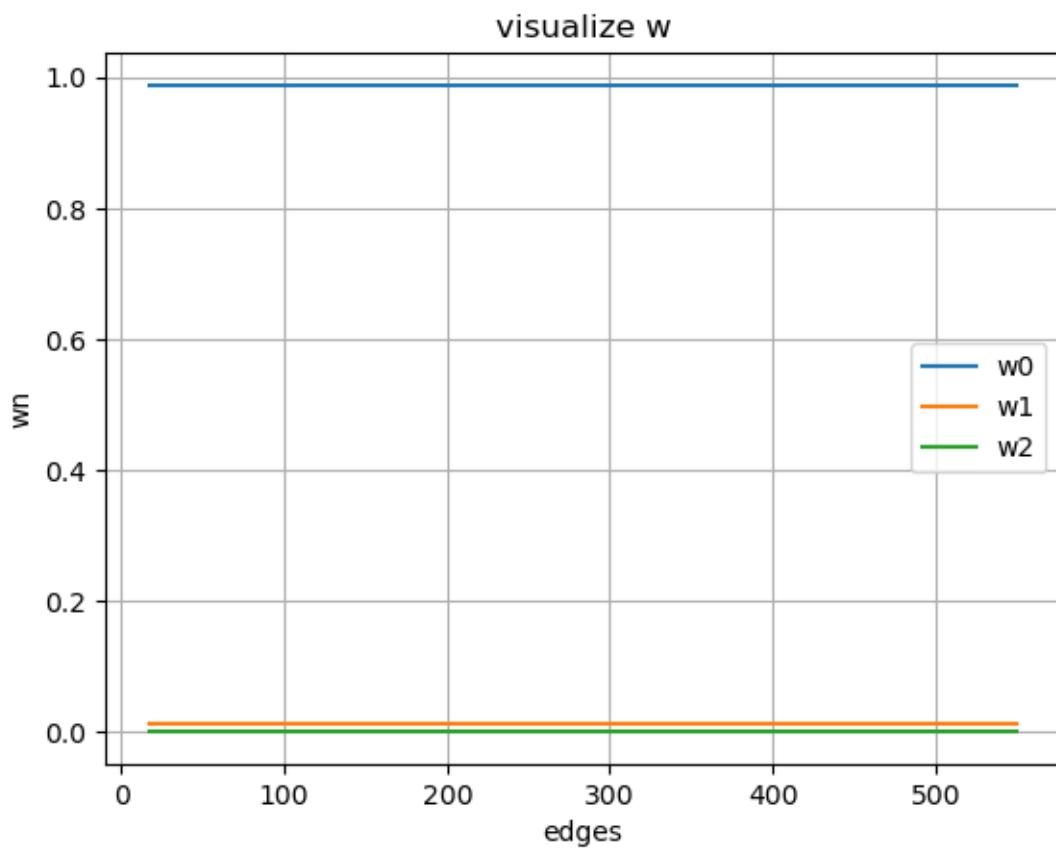


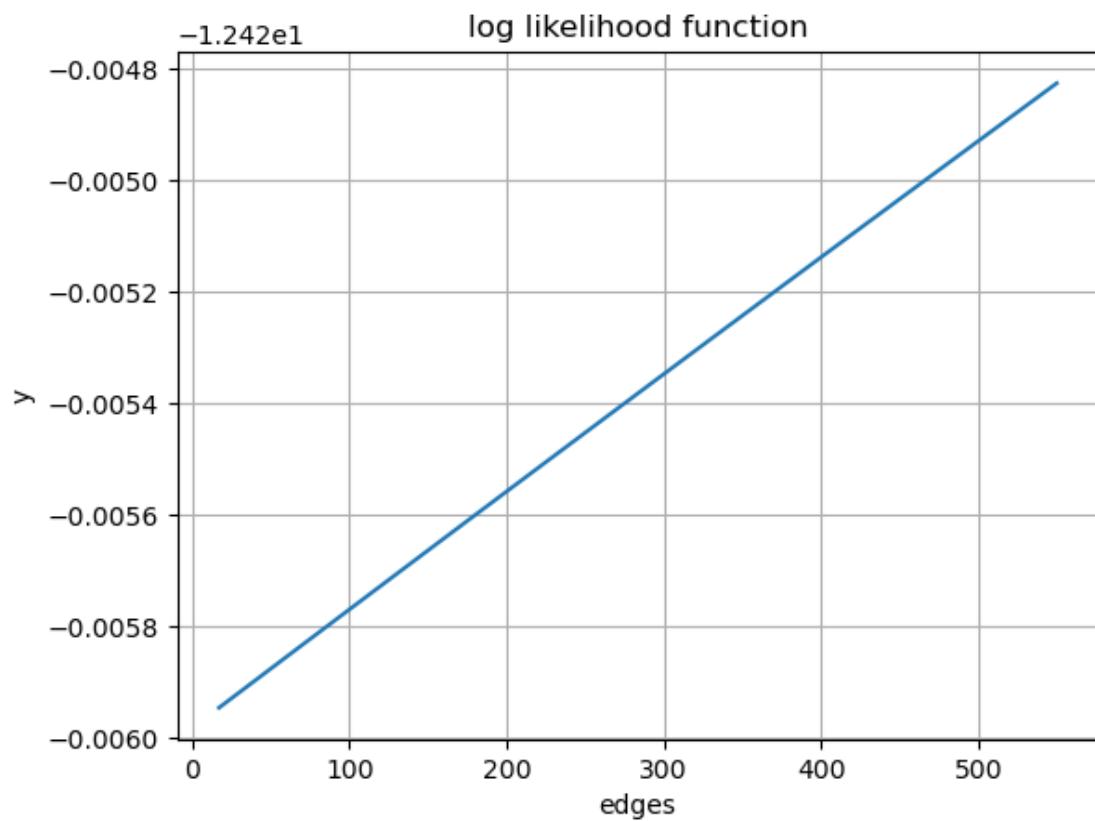


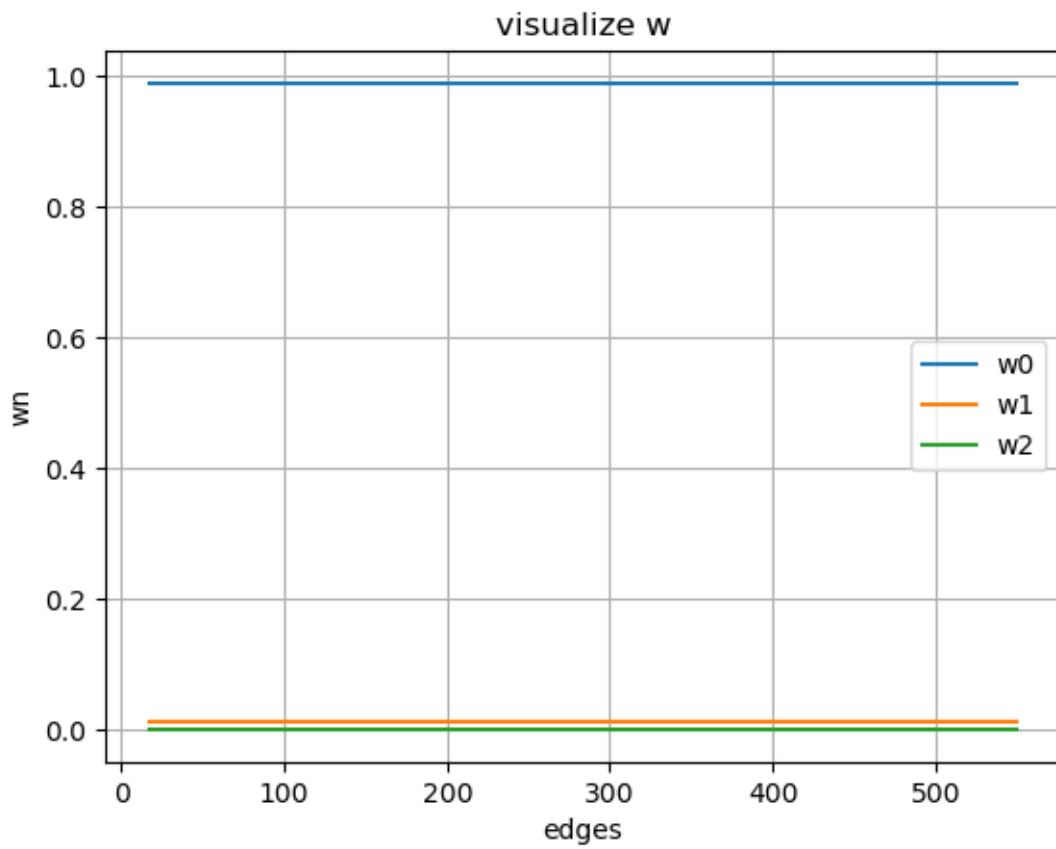


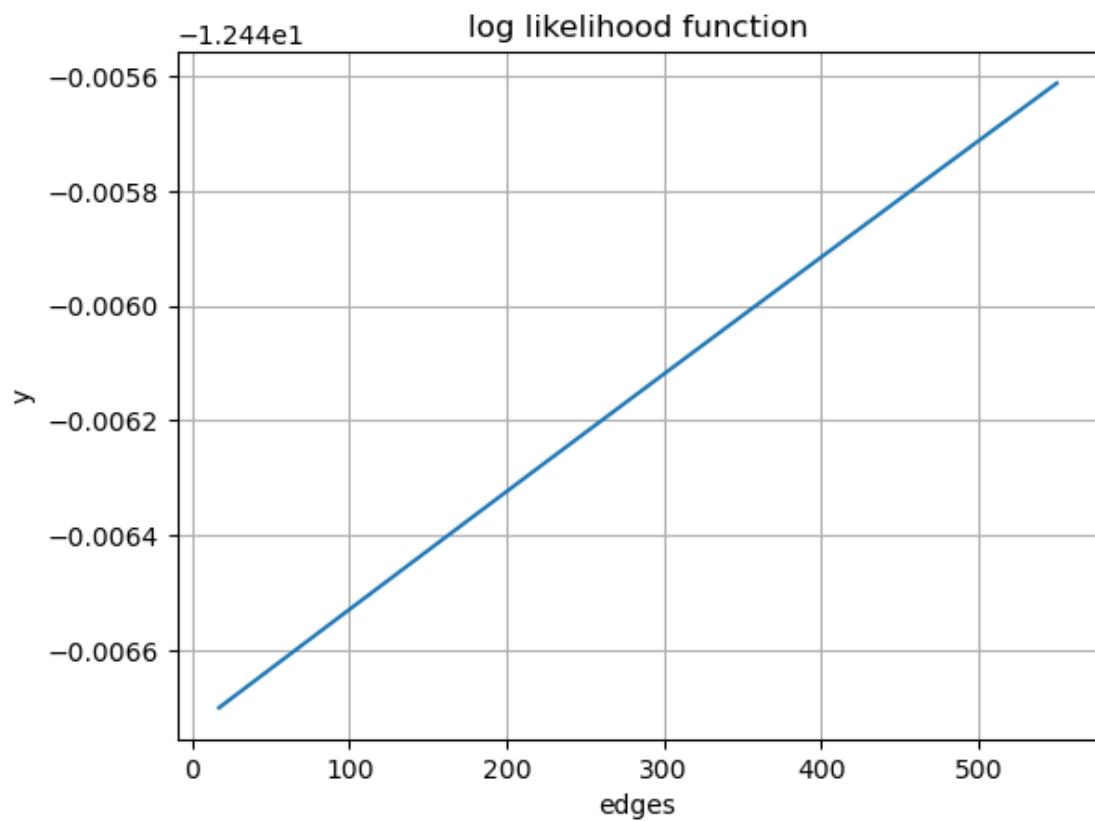


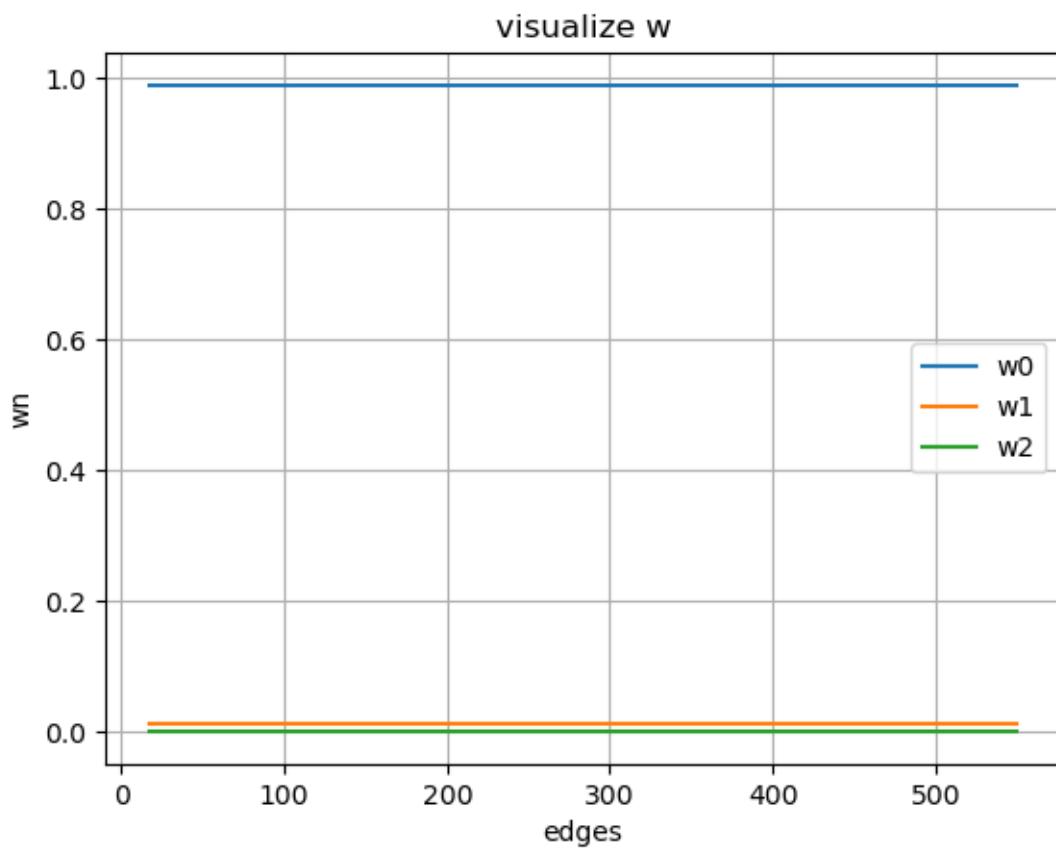


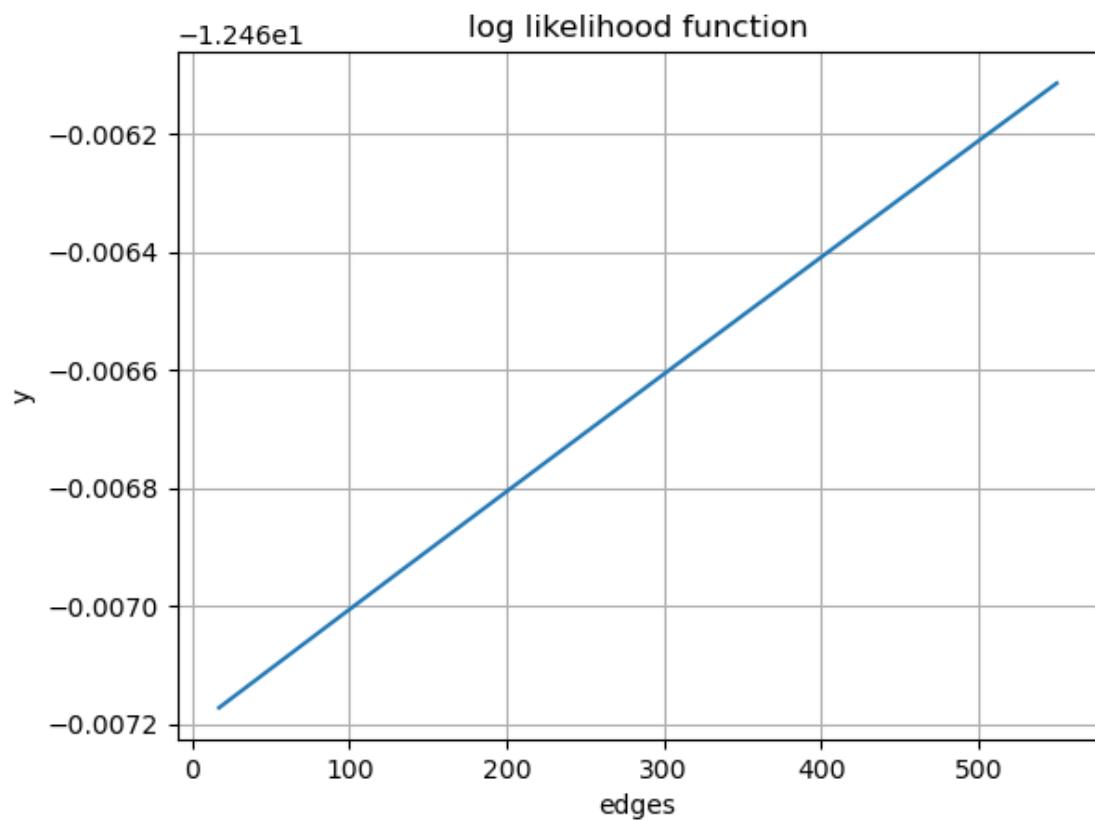


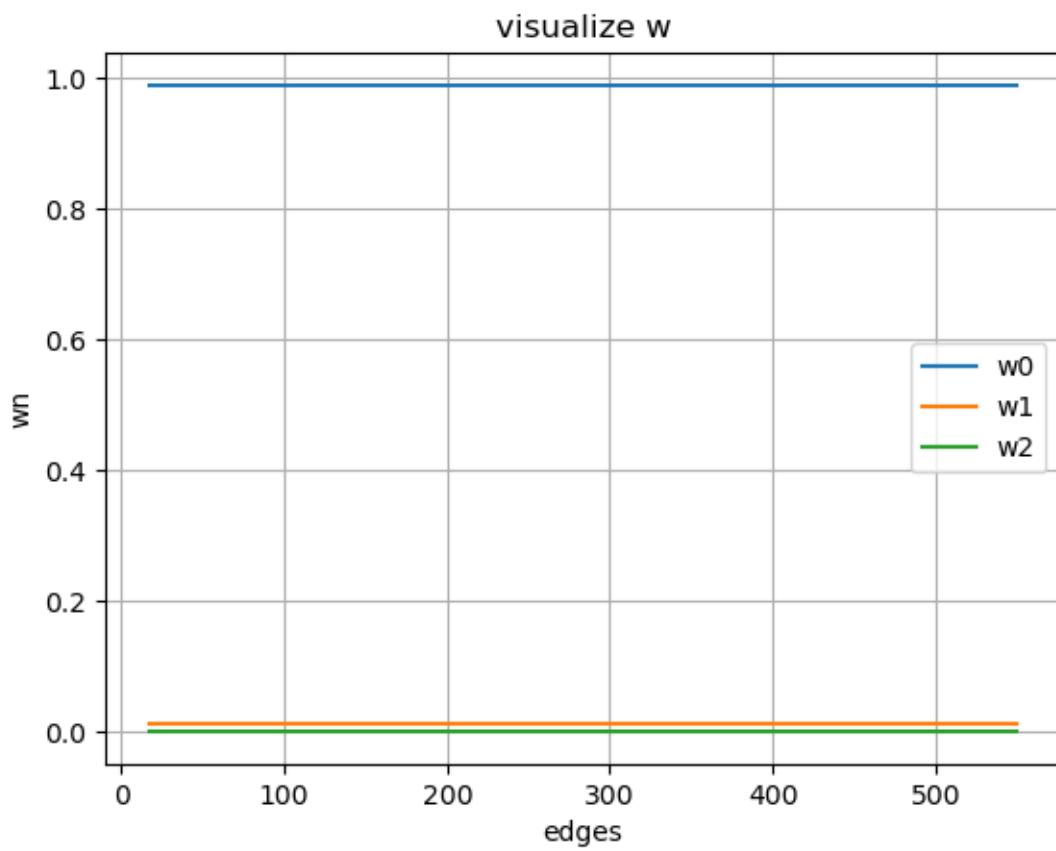


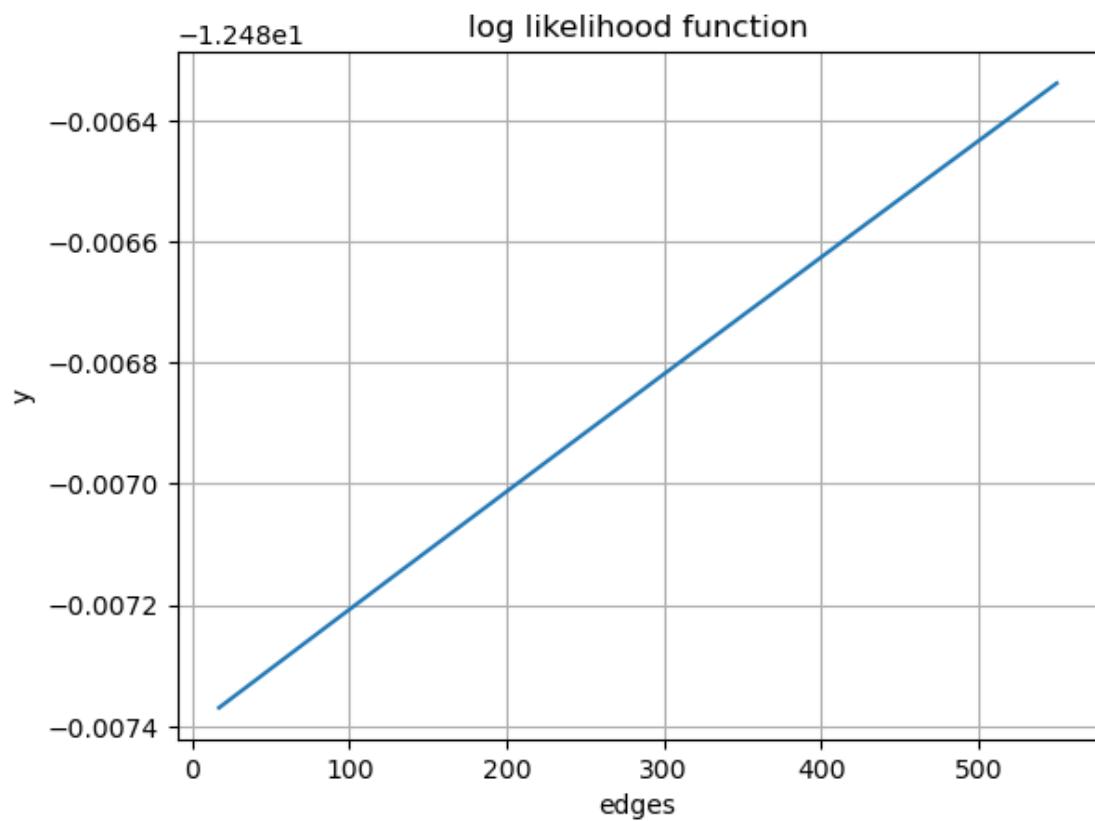


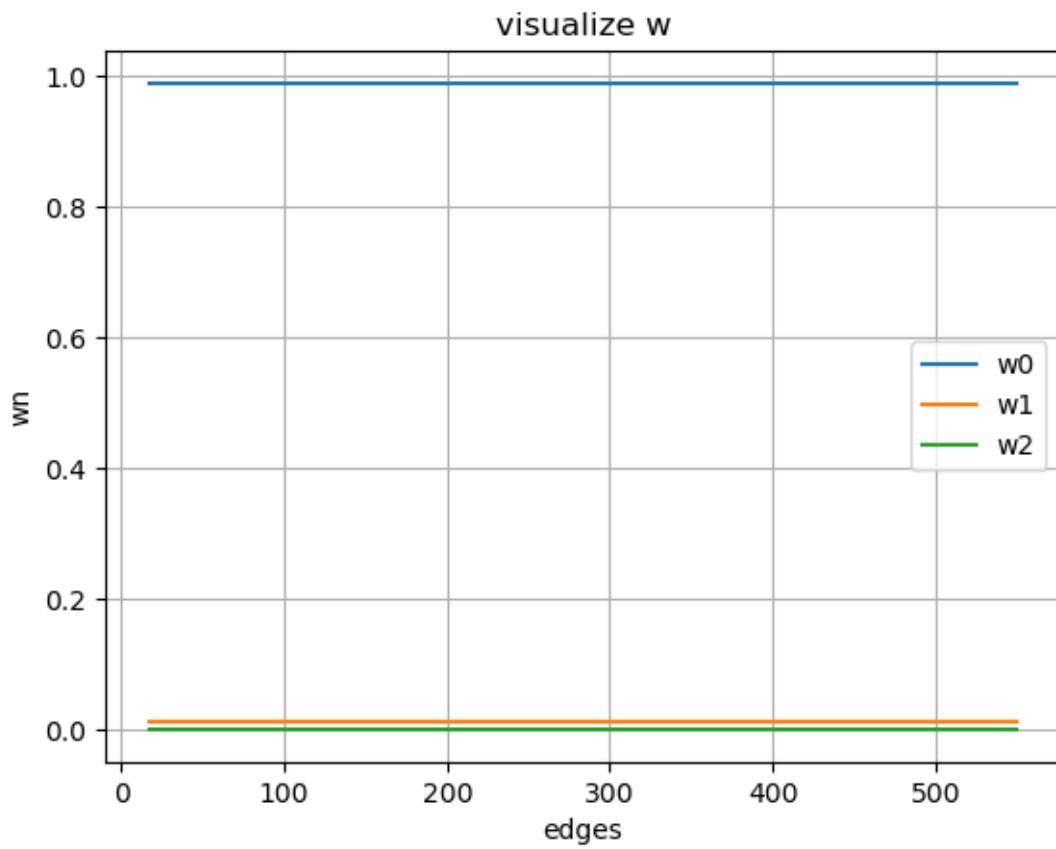


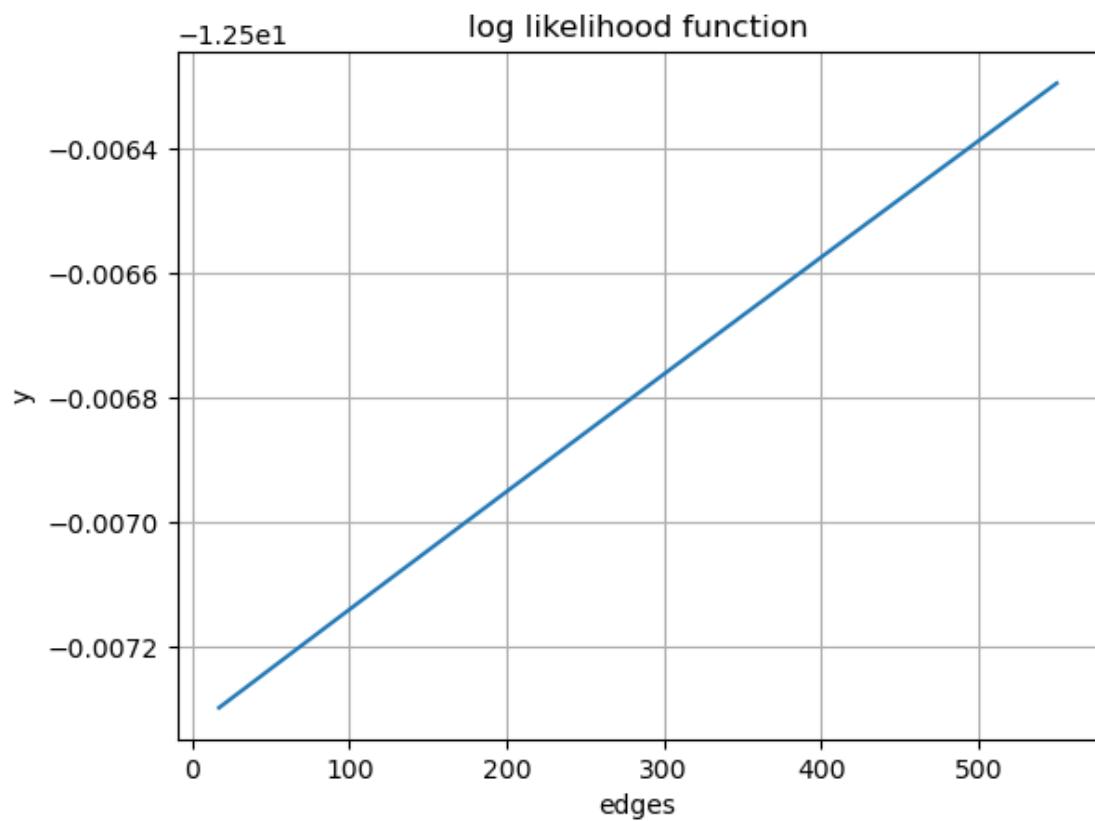


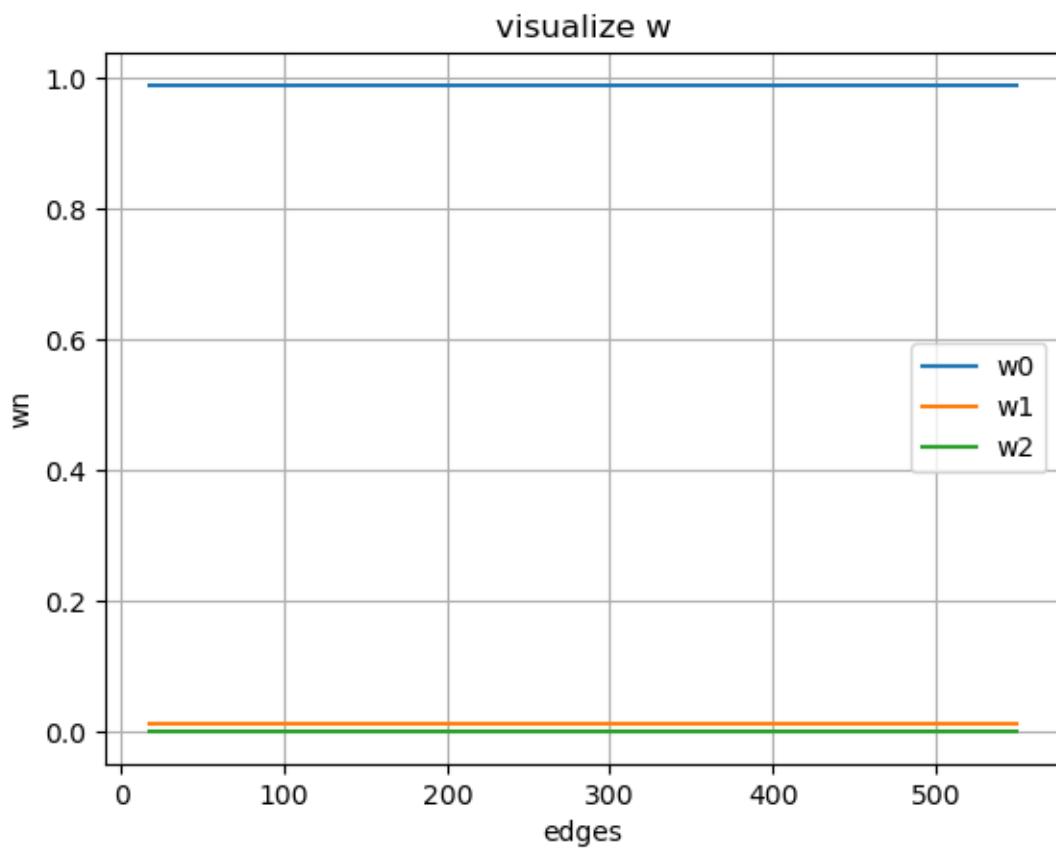


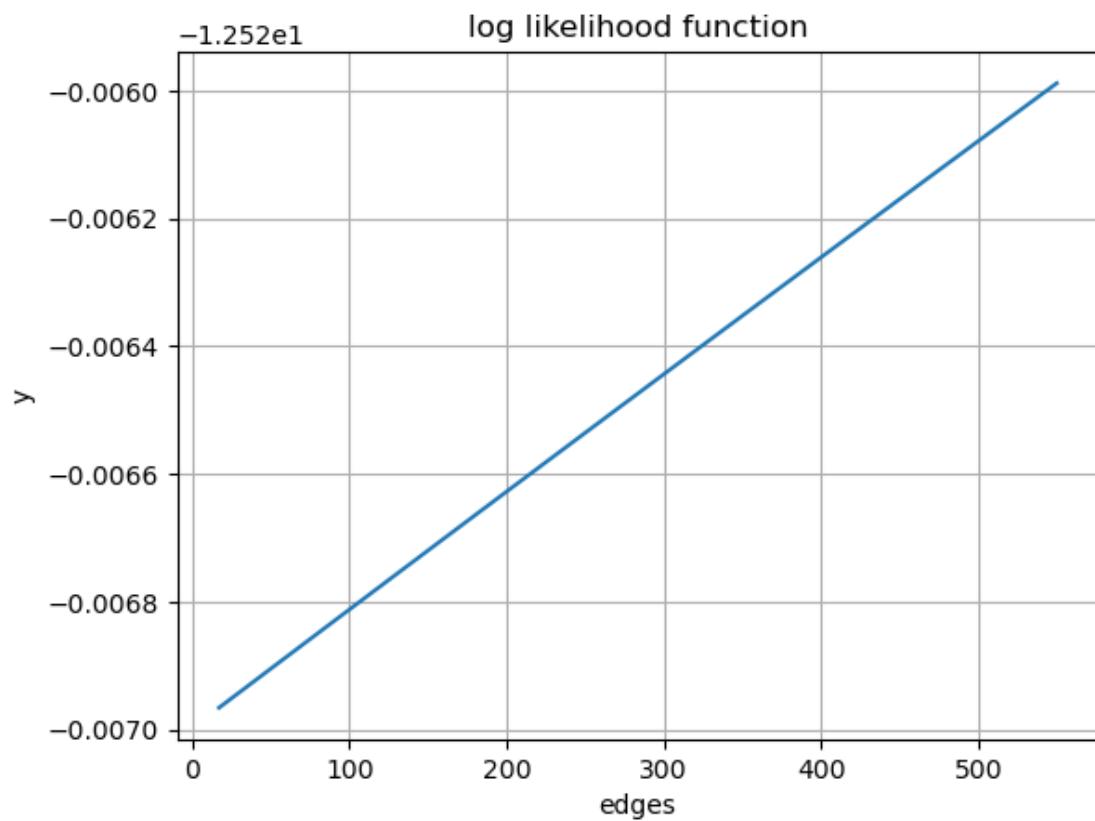


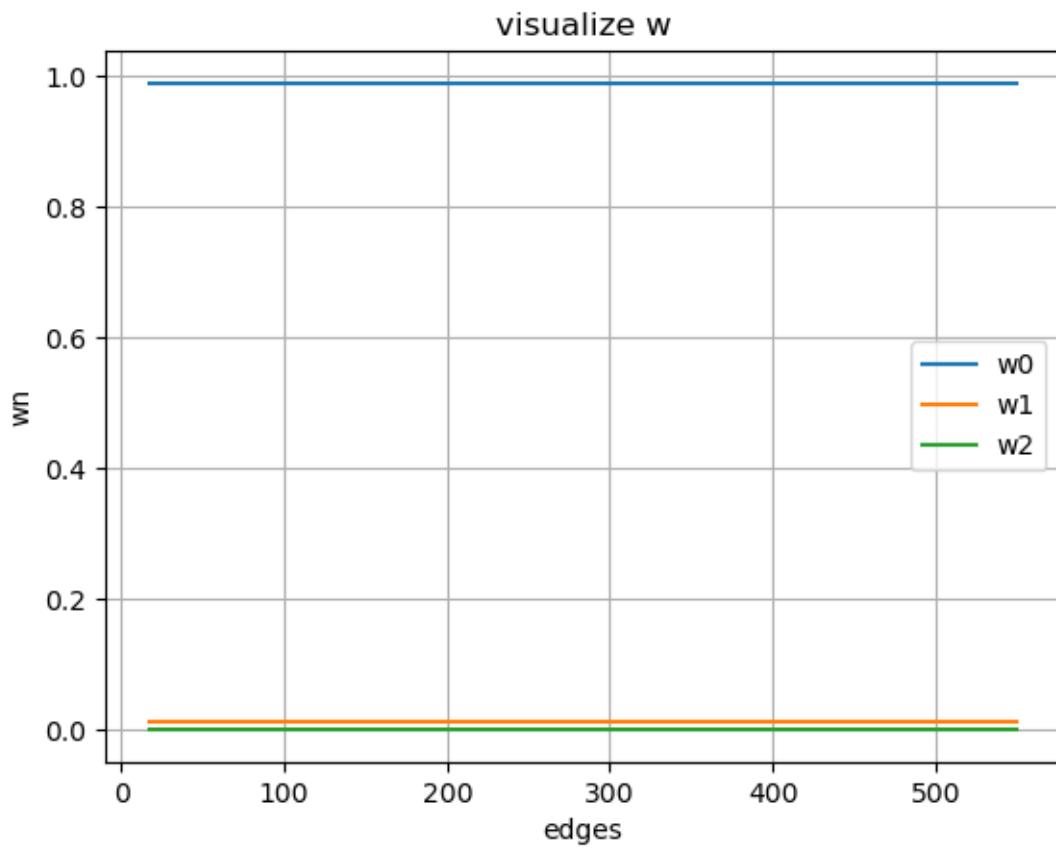


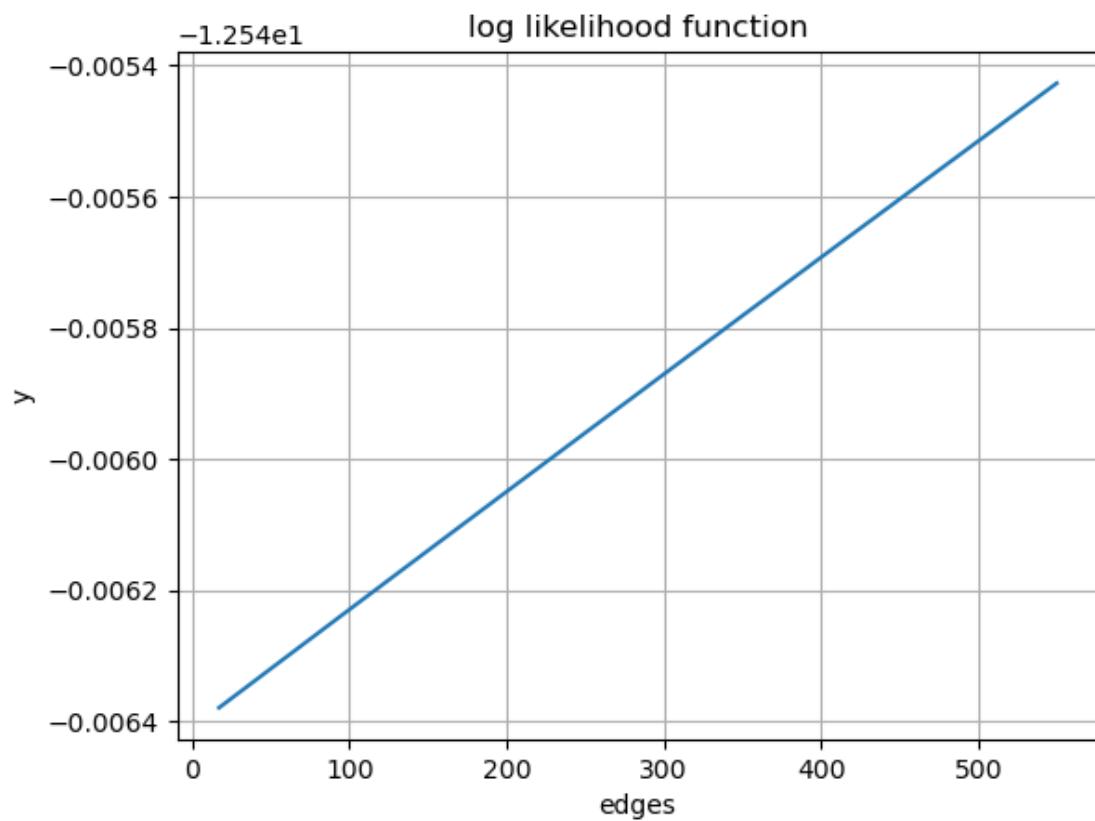


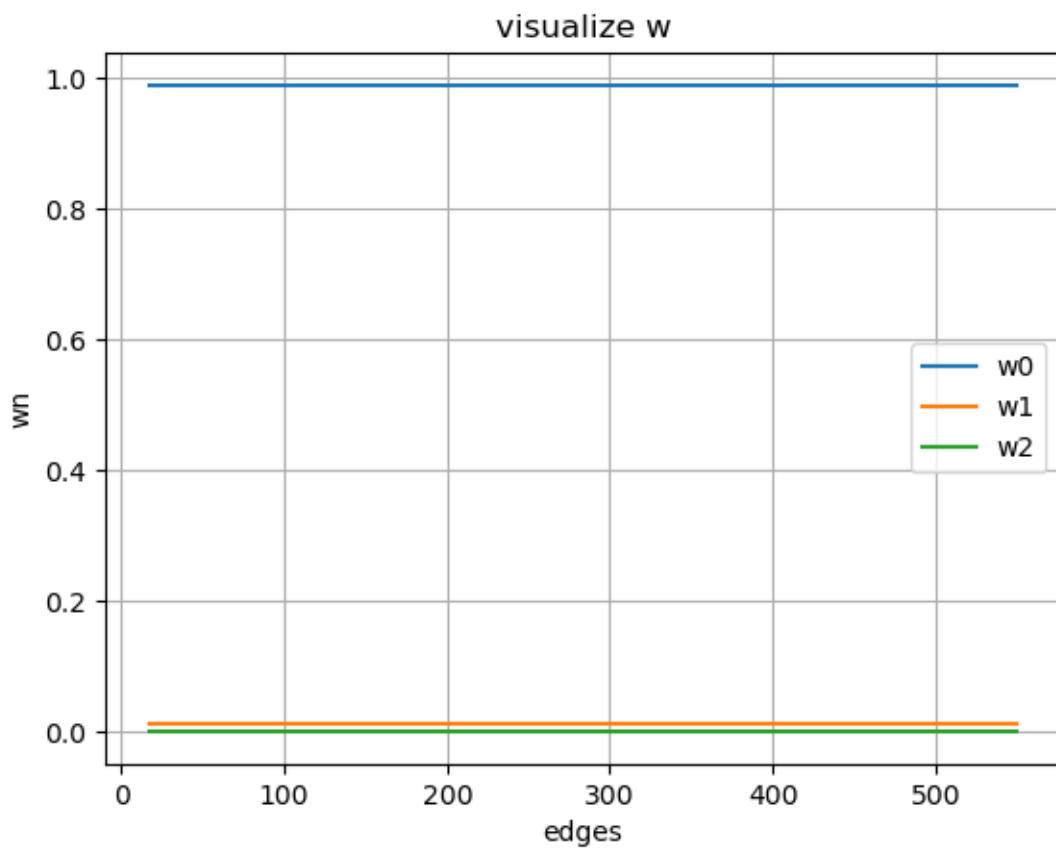


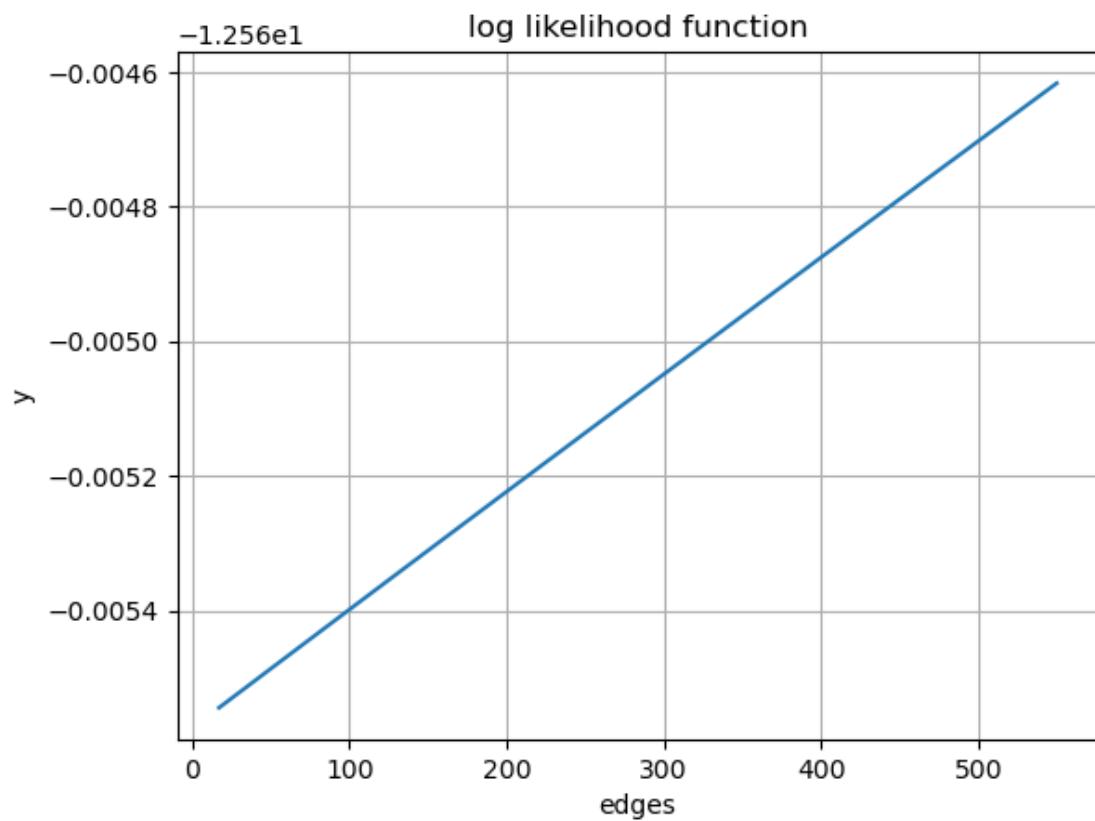


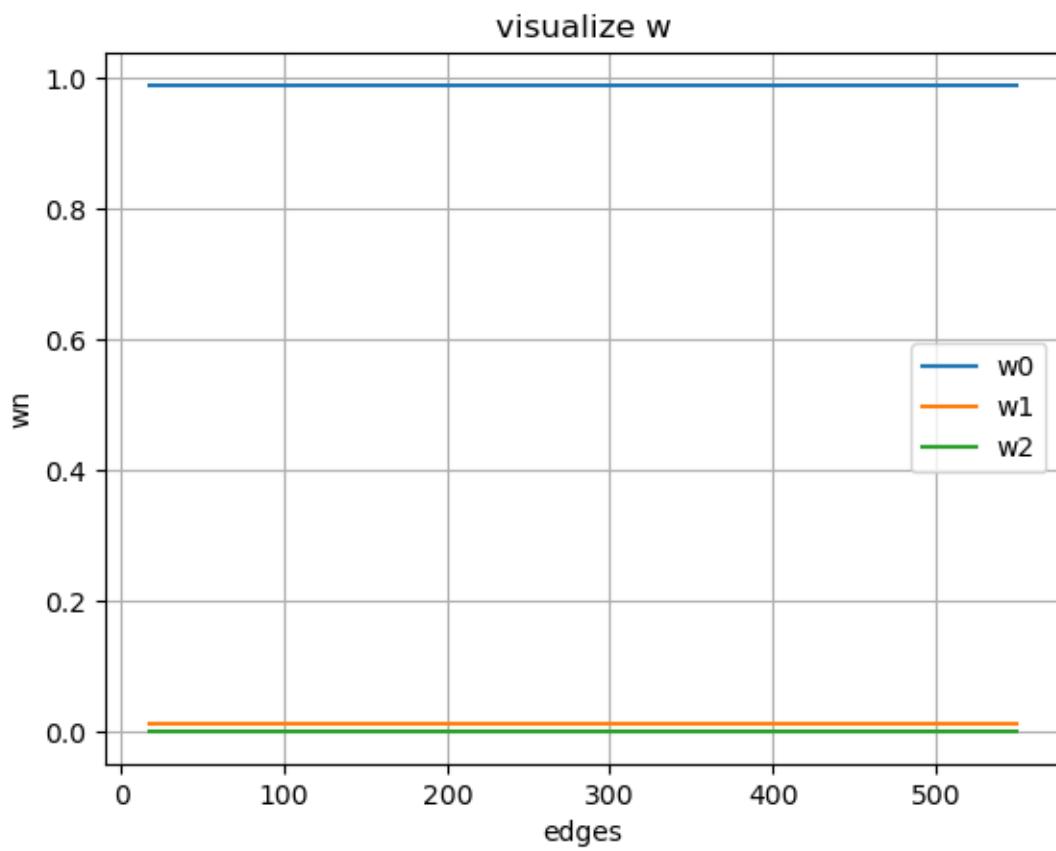


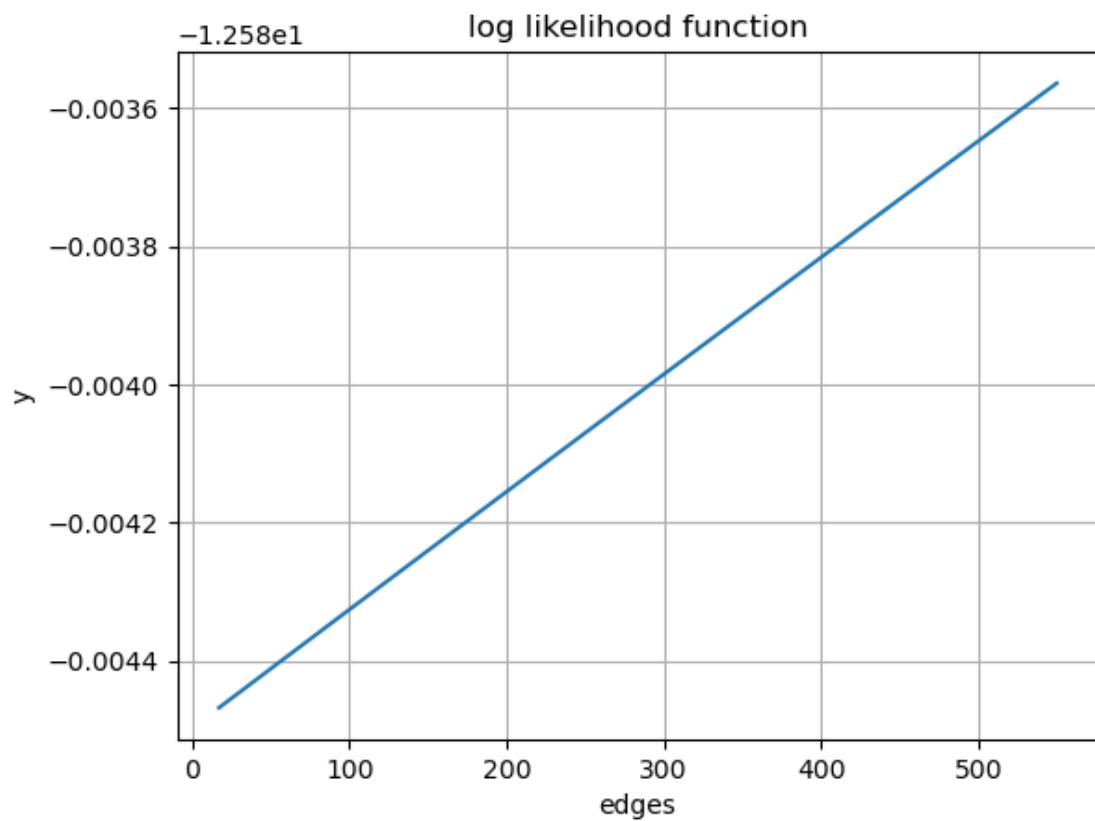


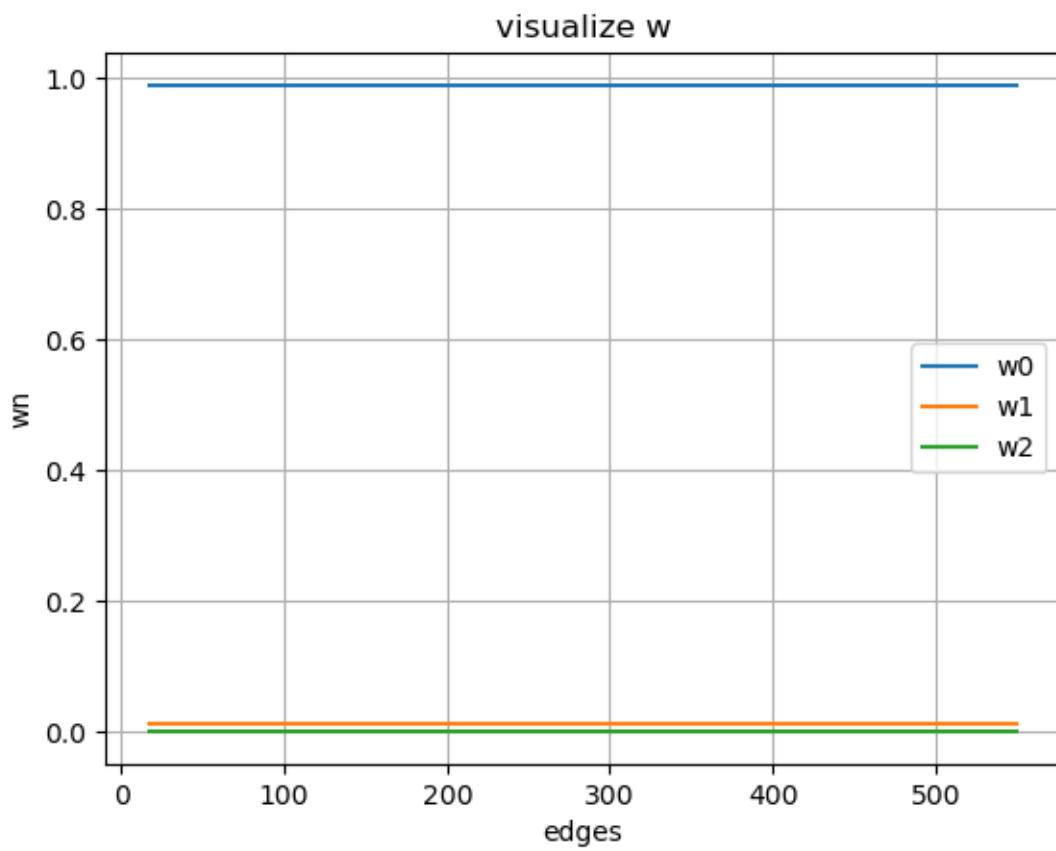


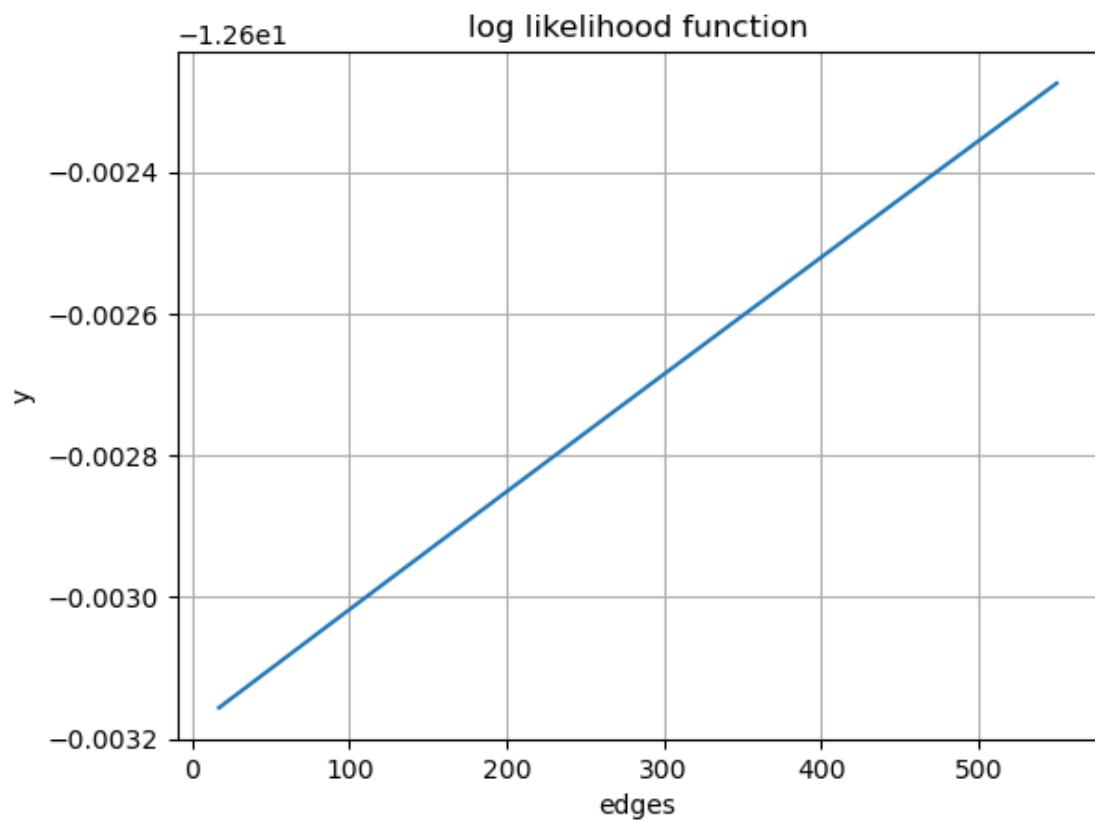


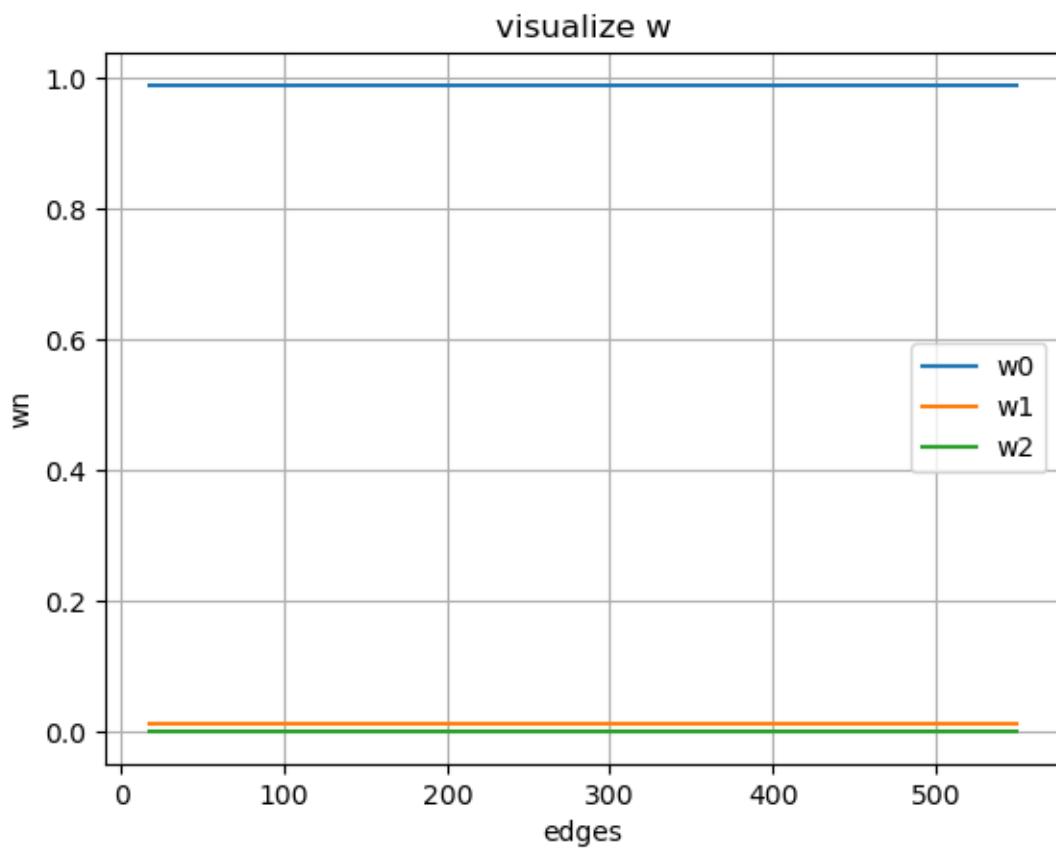


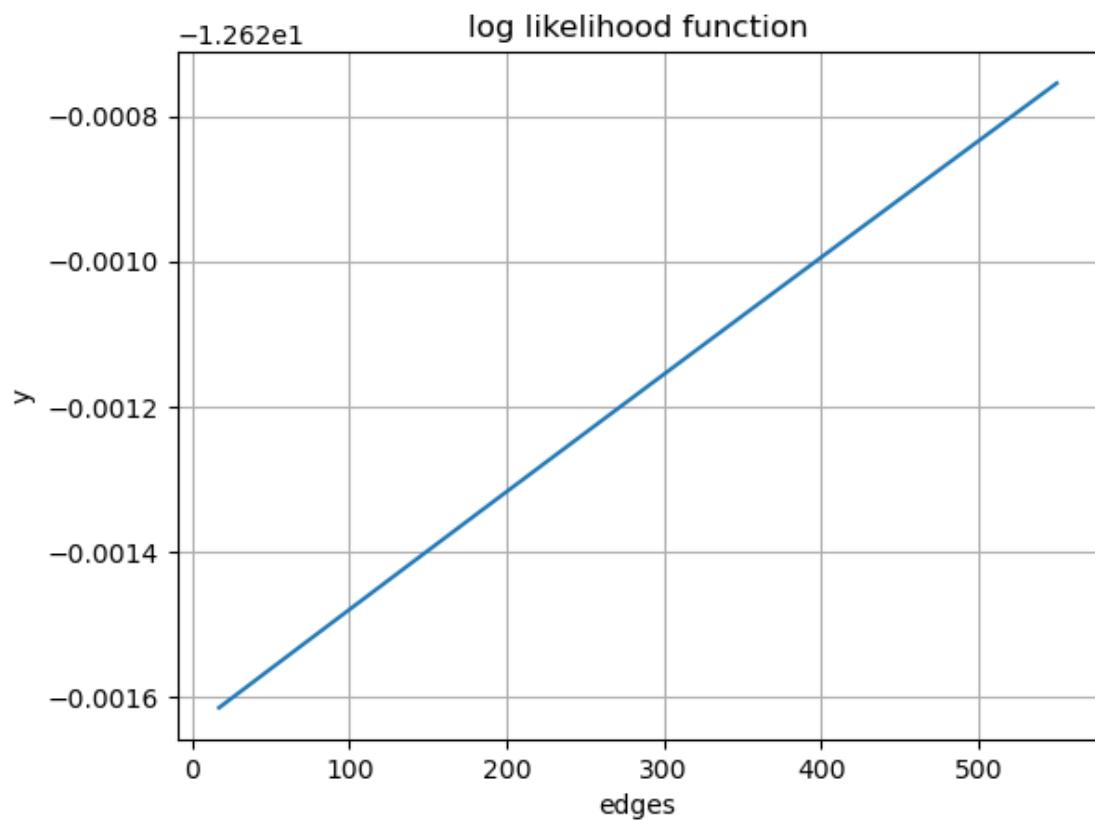


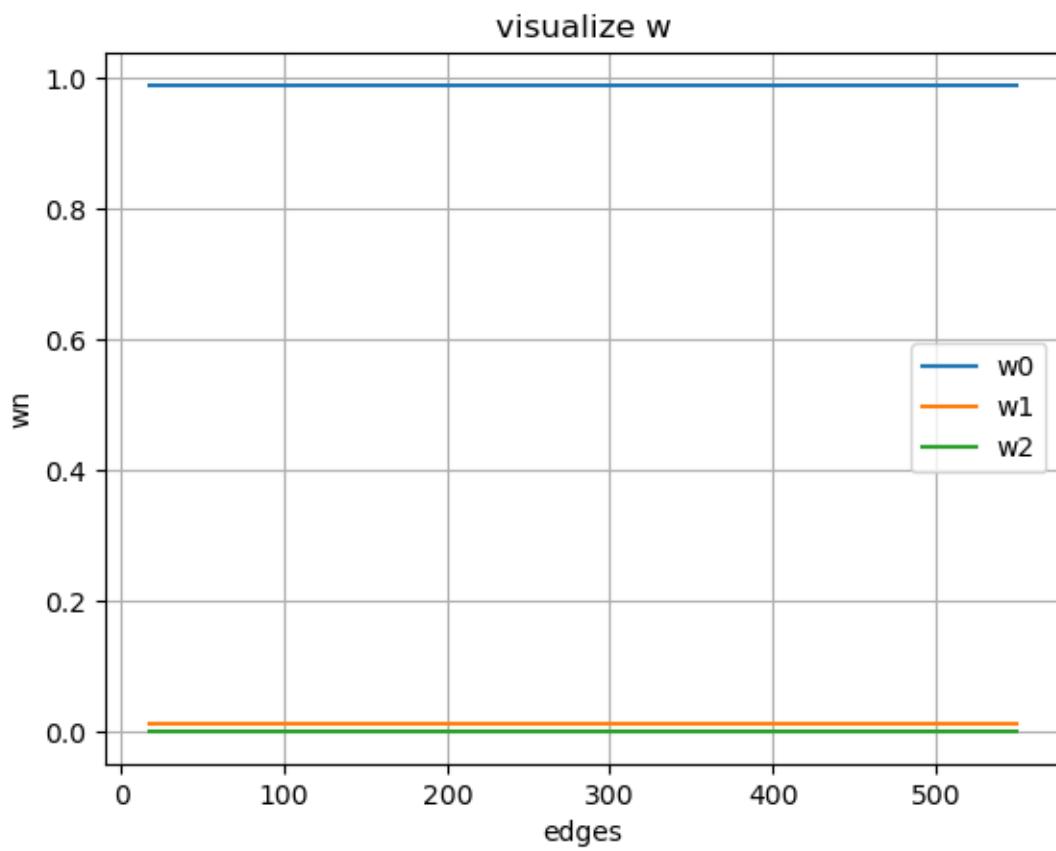


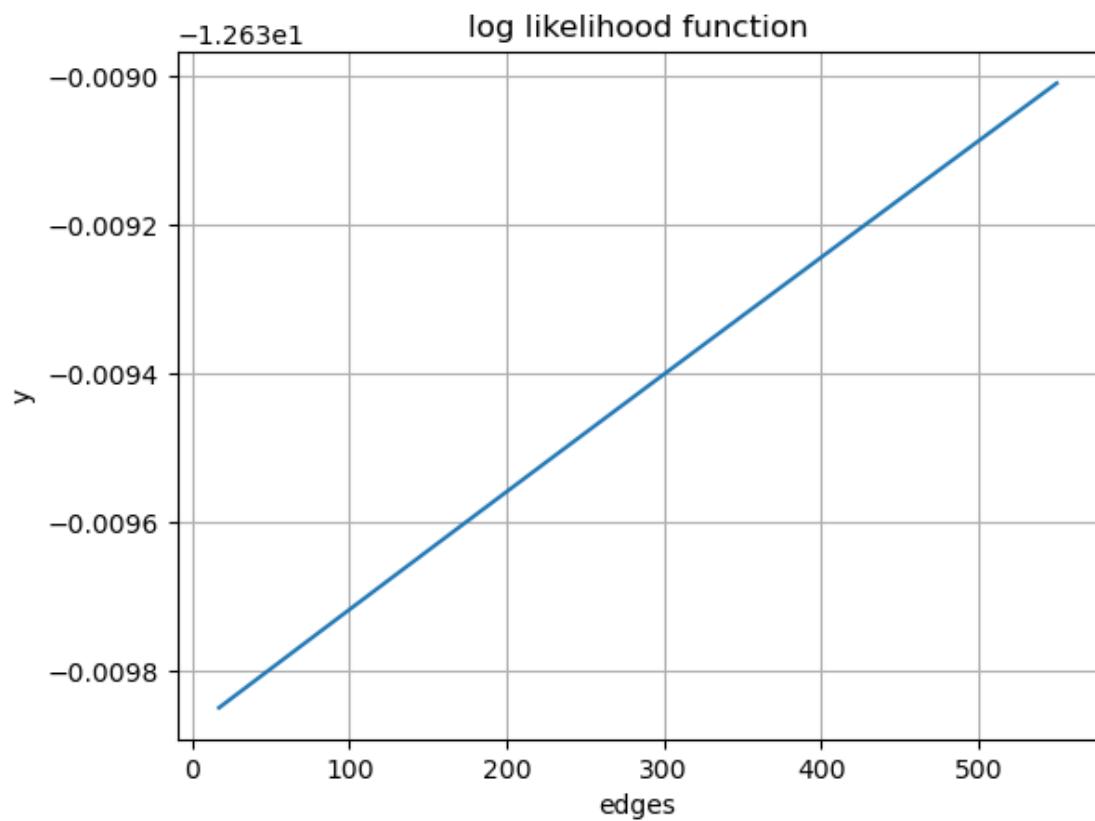


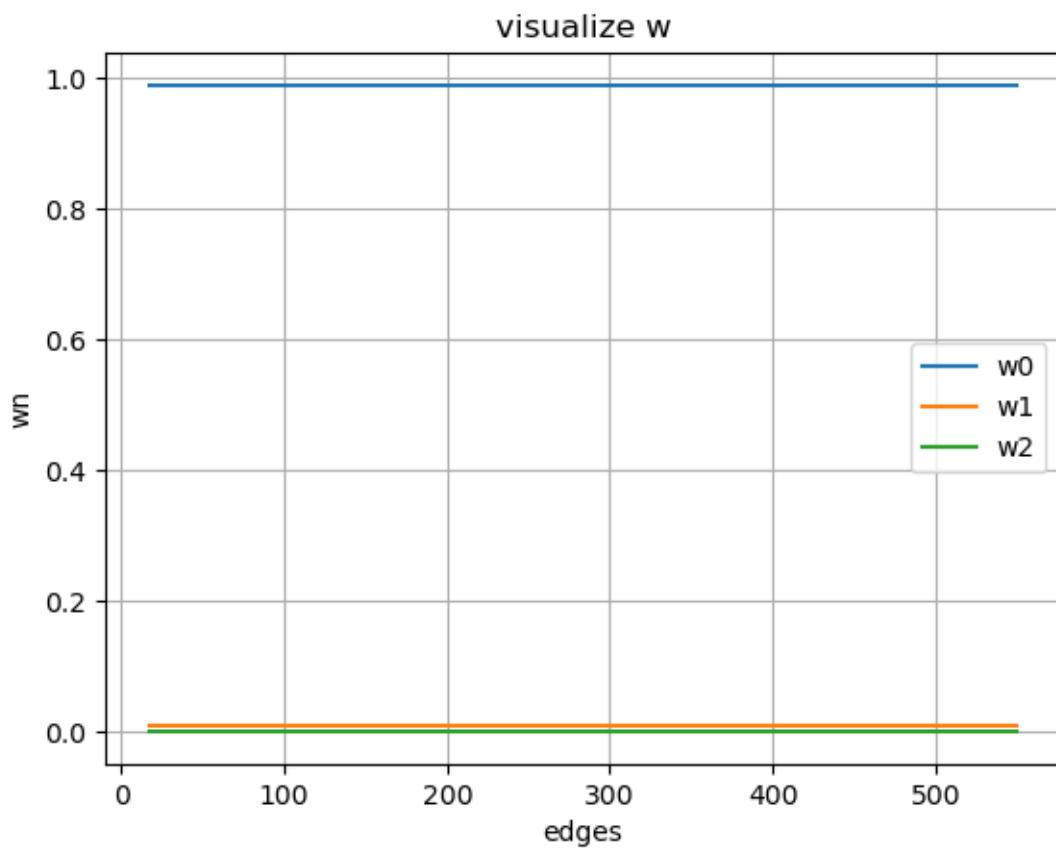




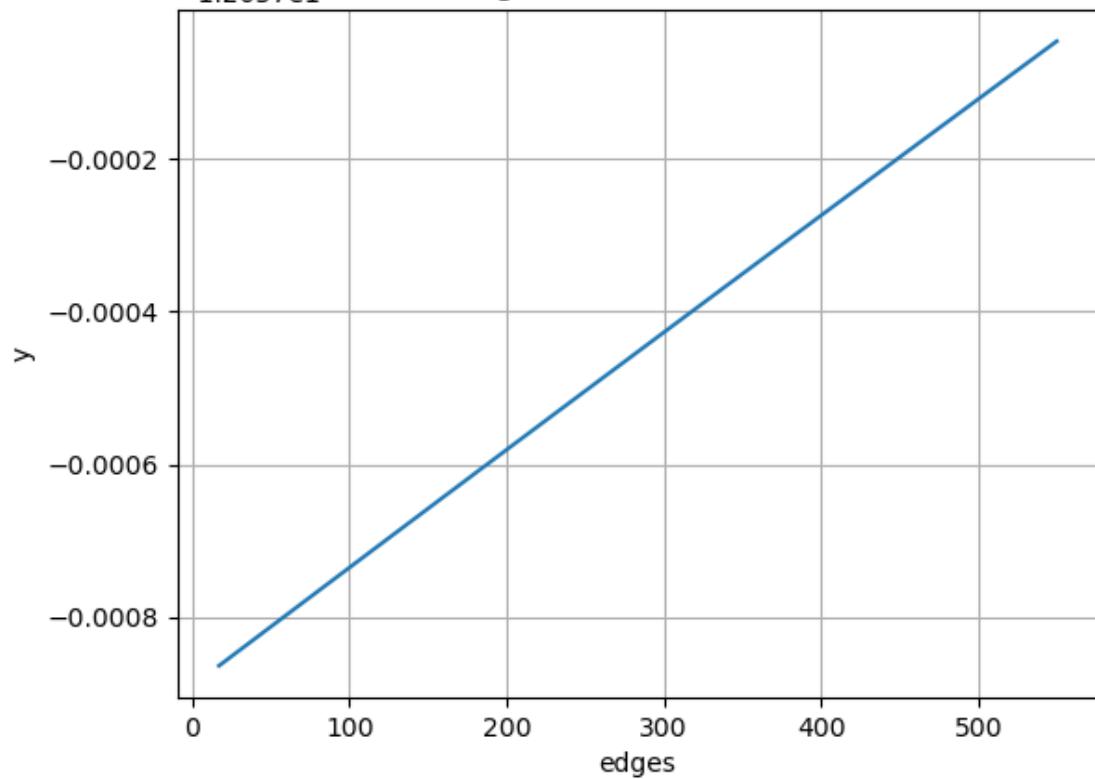


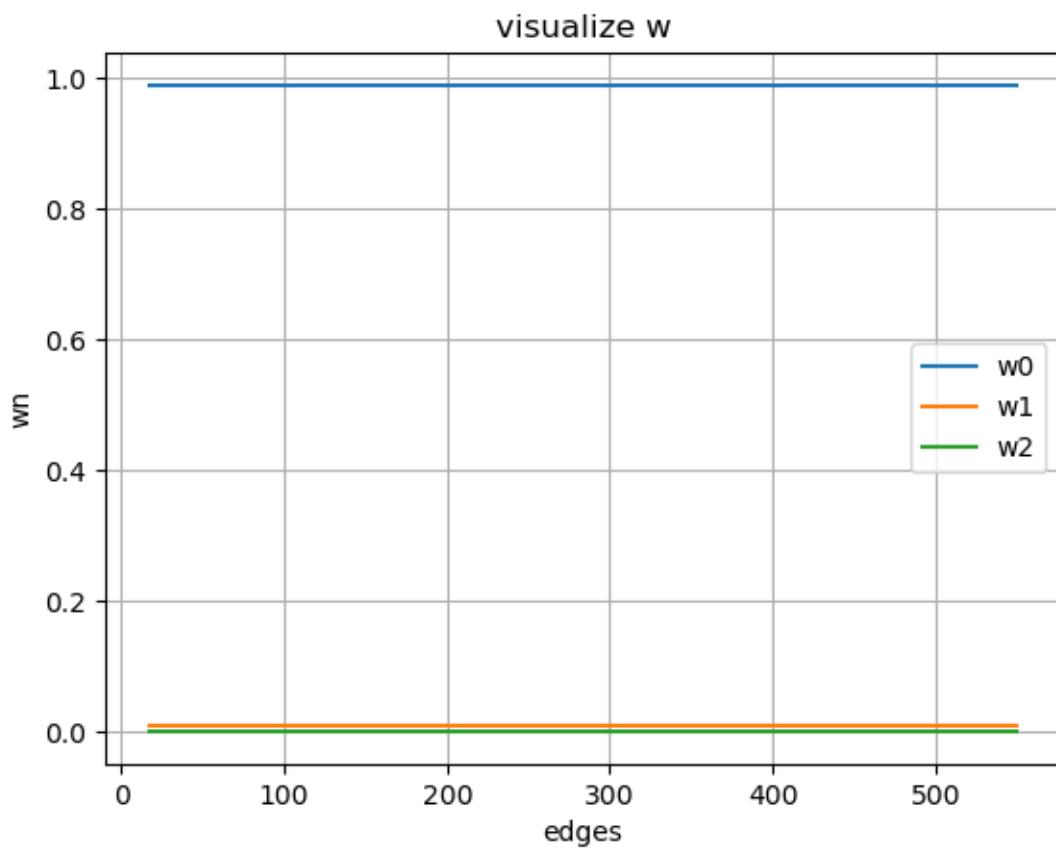


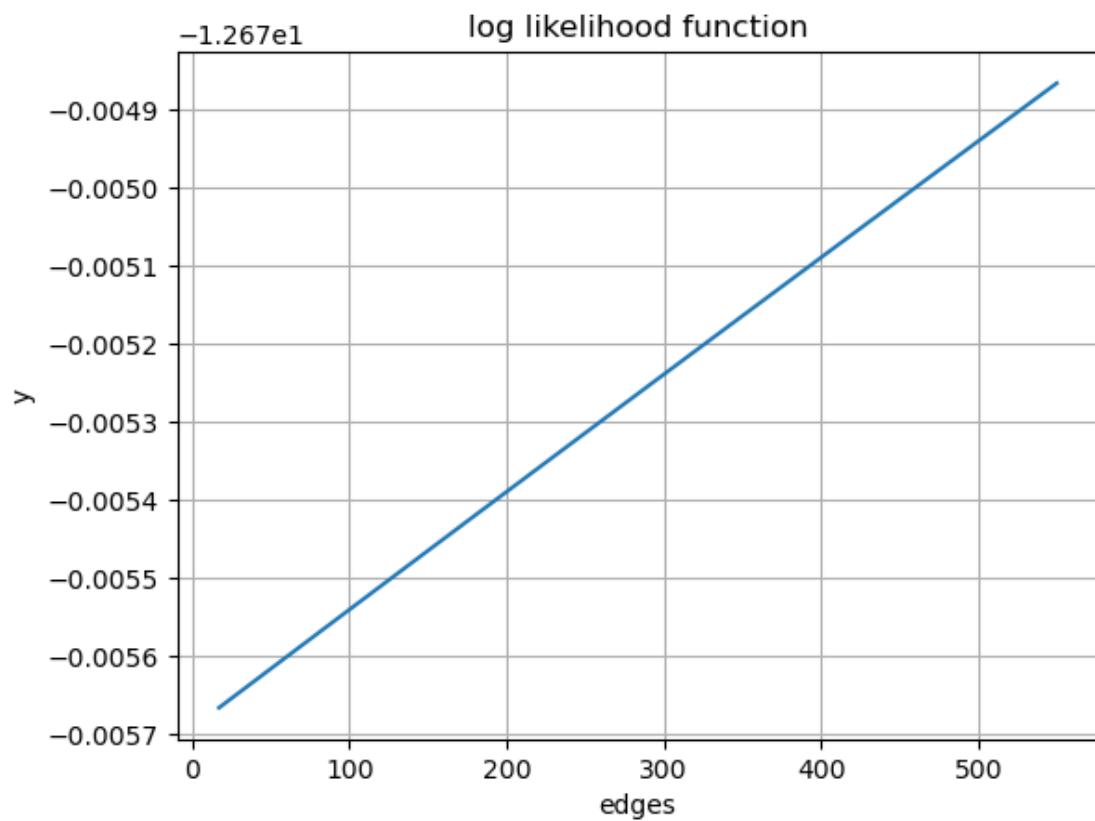


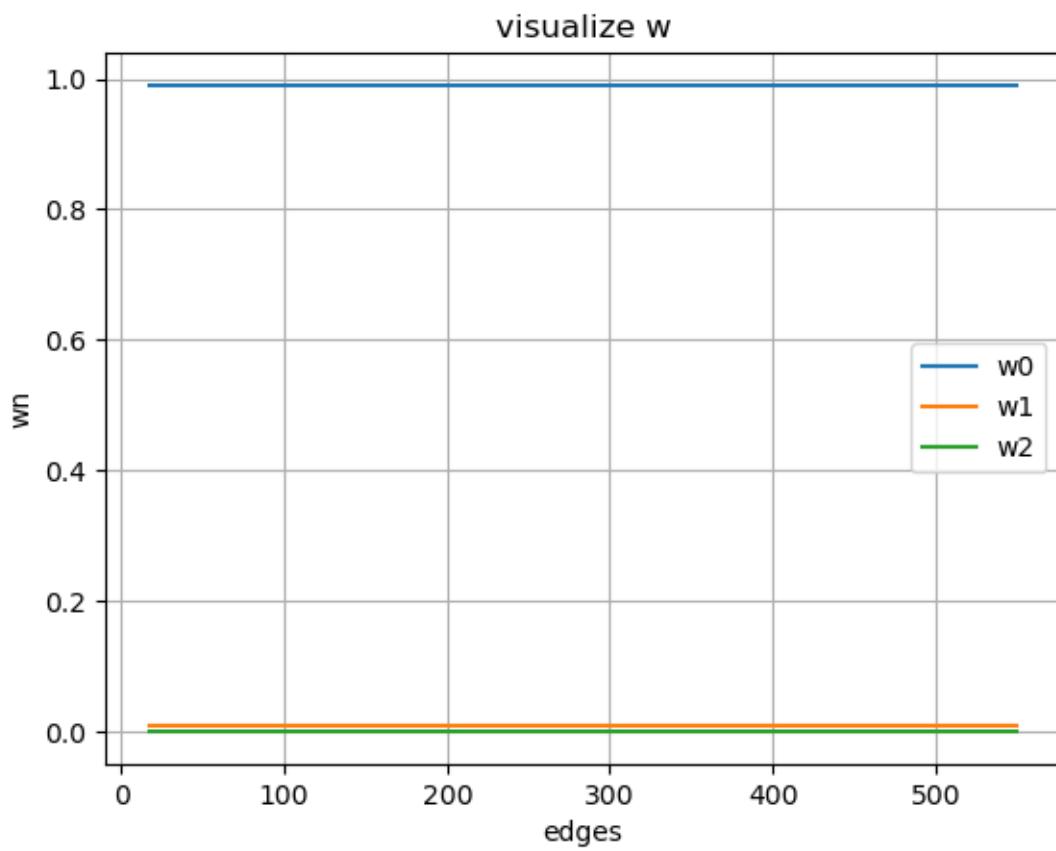


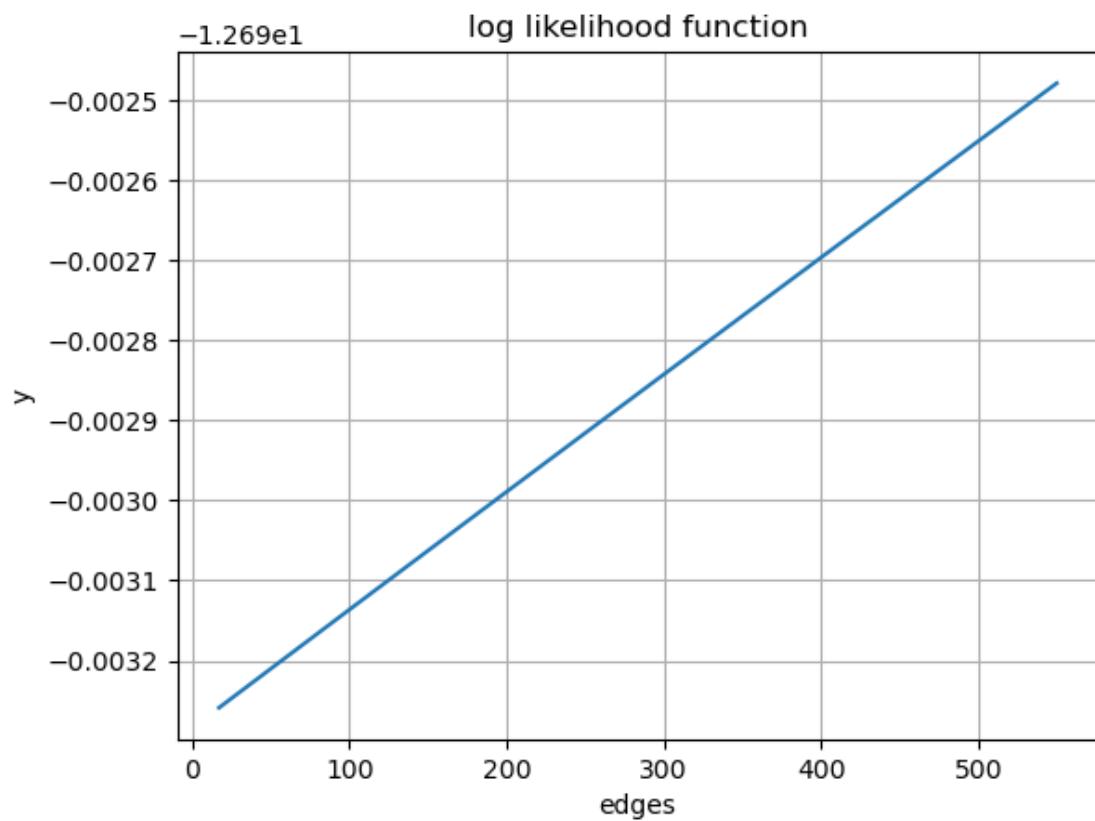
-1.2657e1 log likelihood function

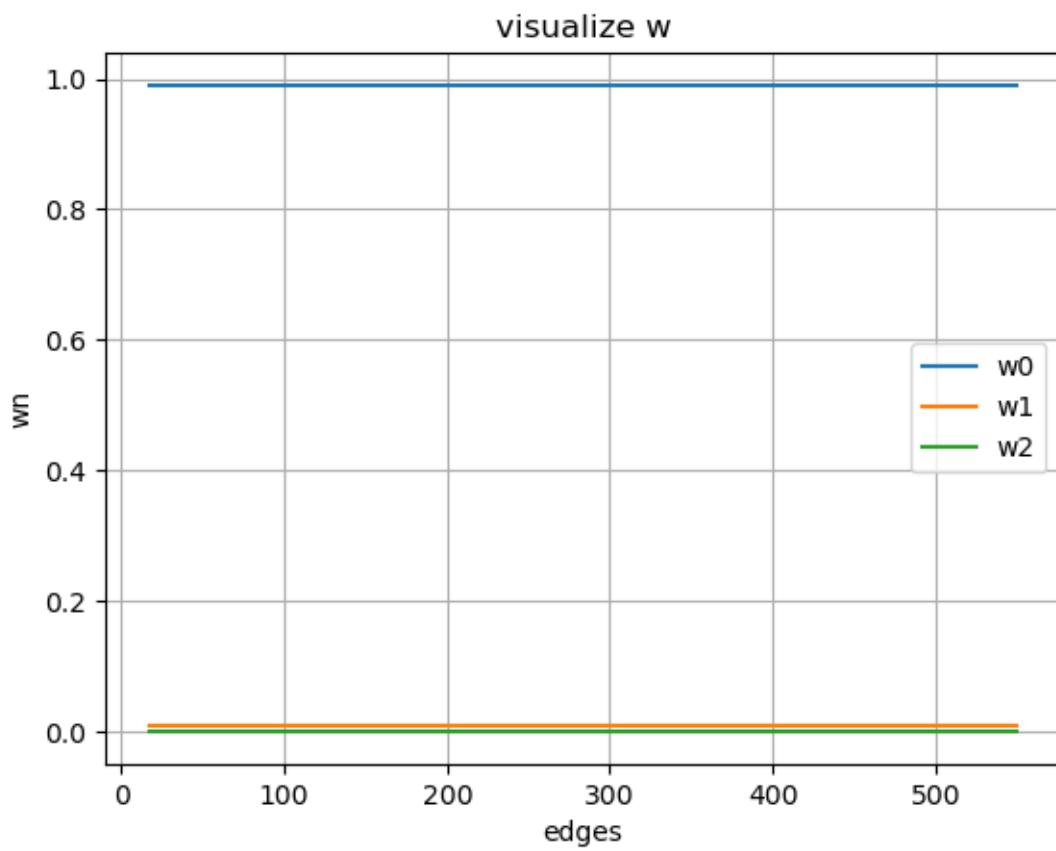


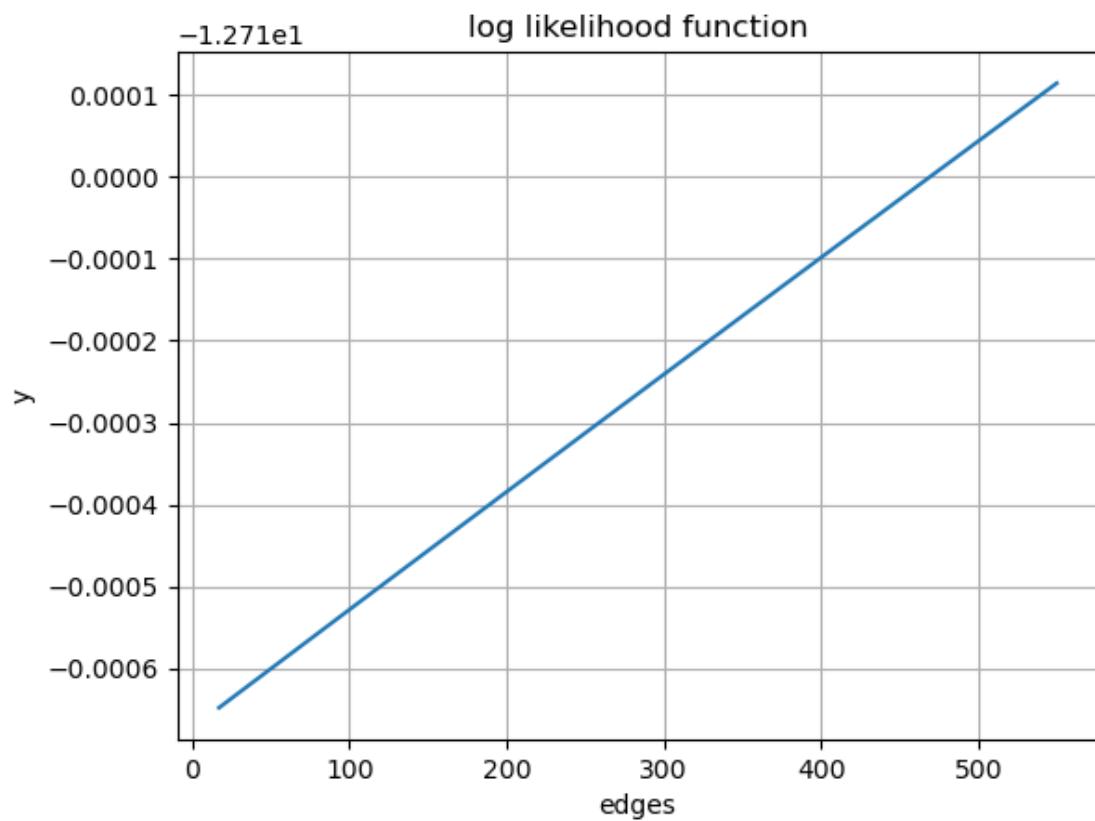


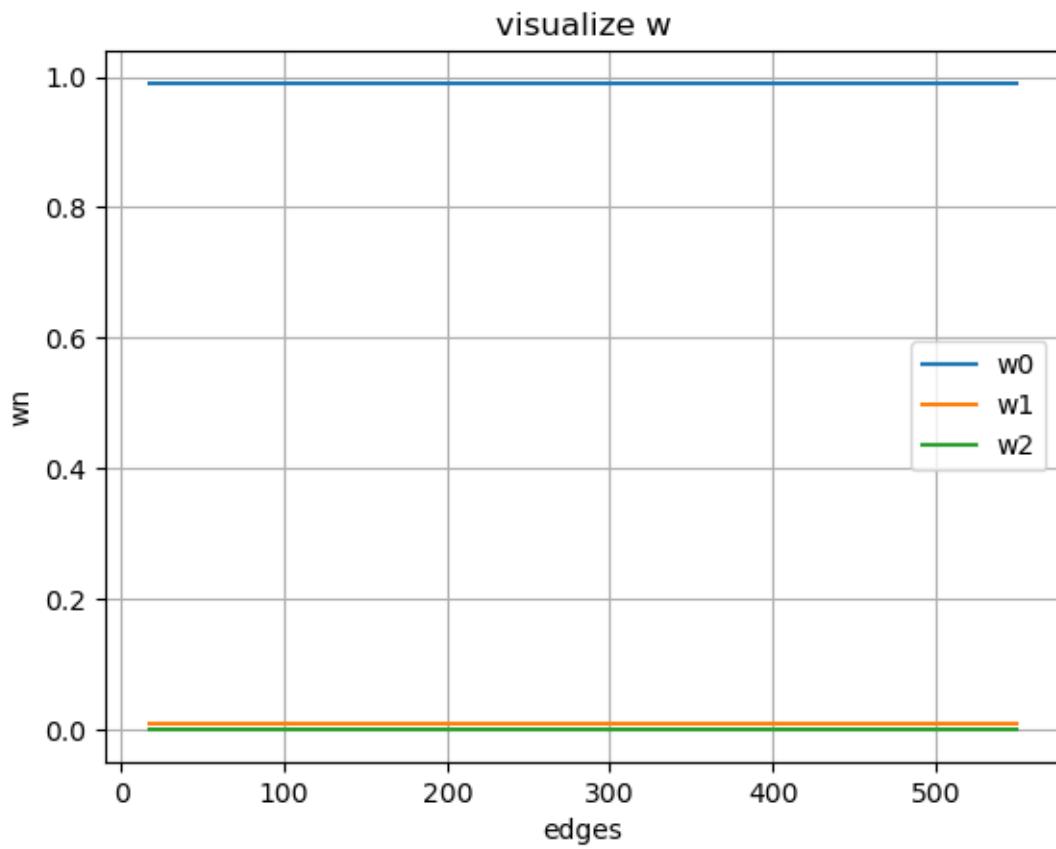


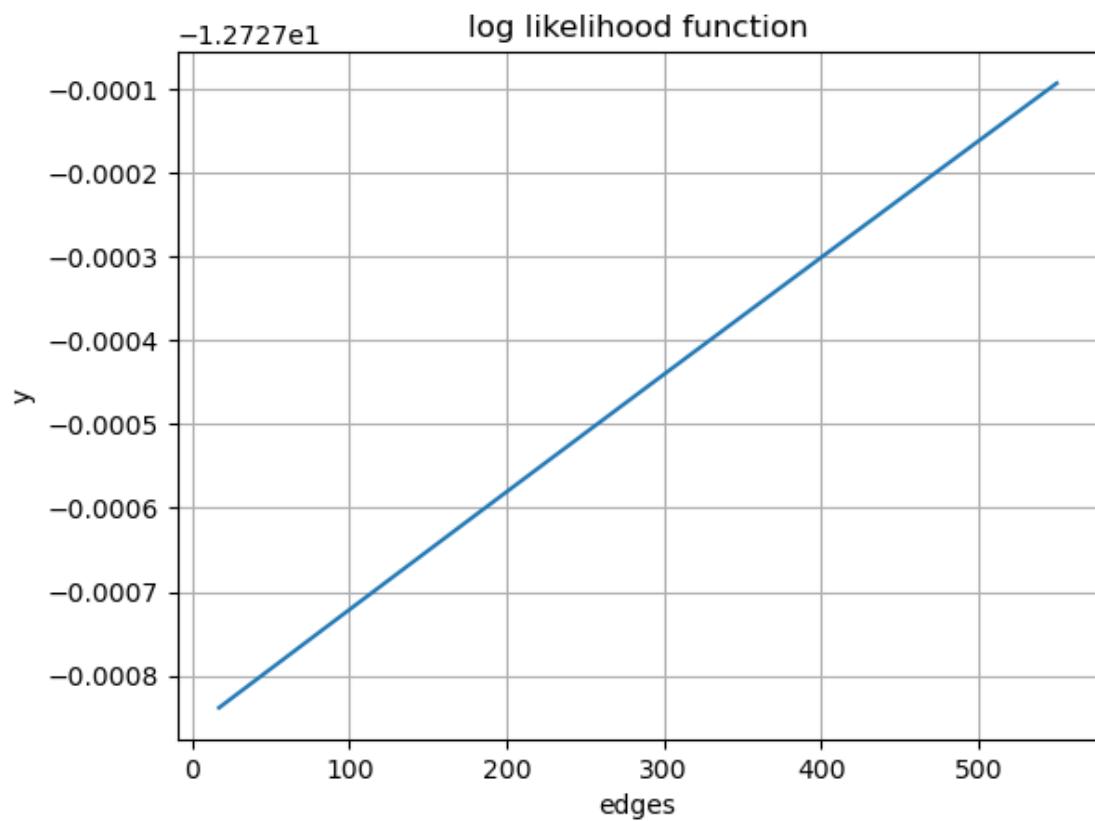


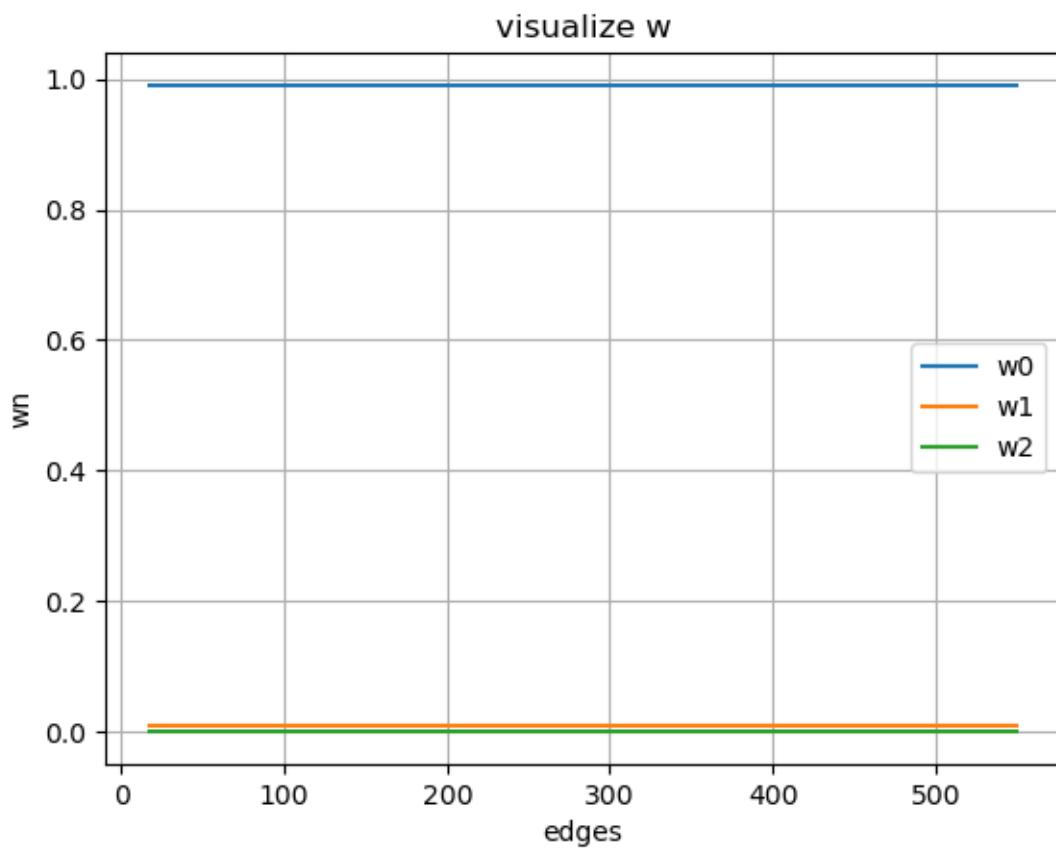


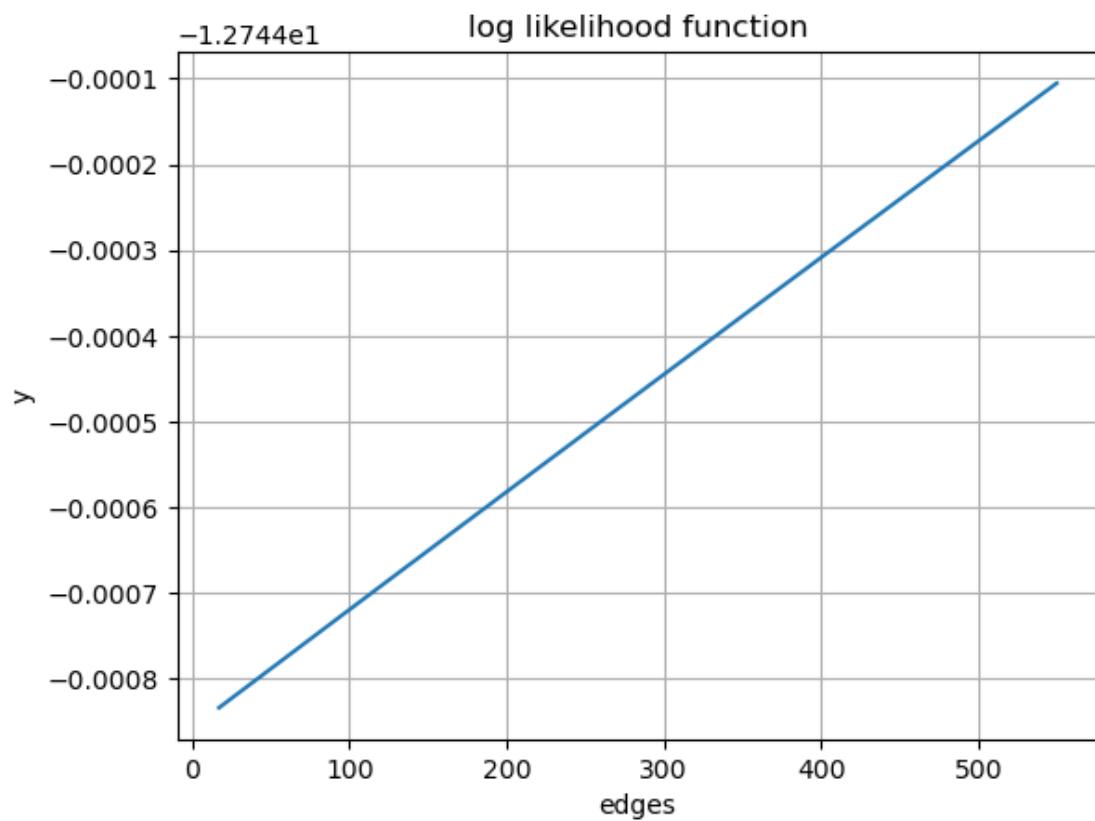


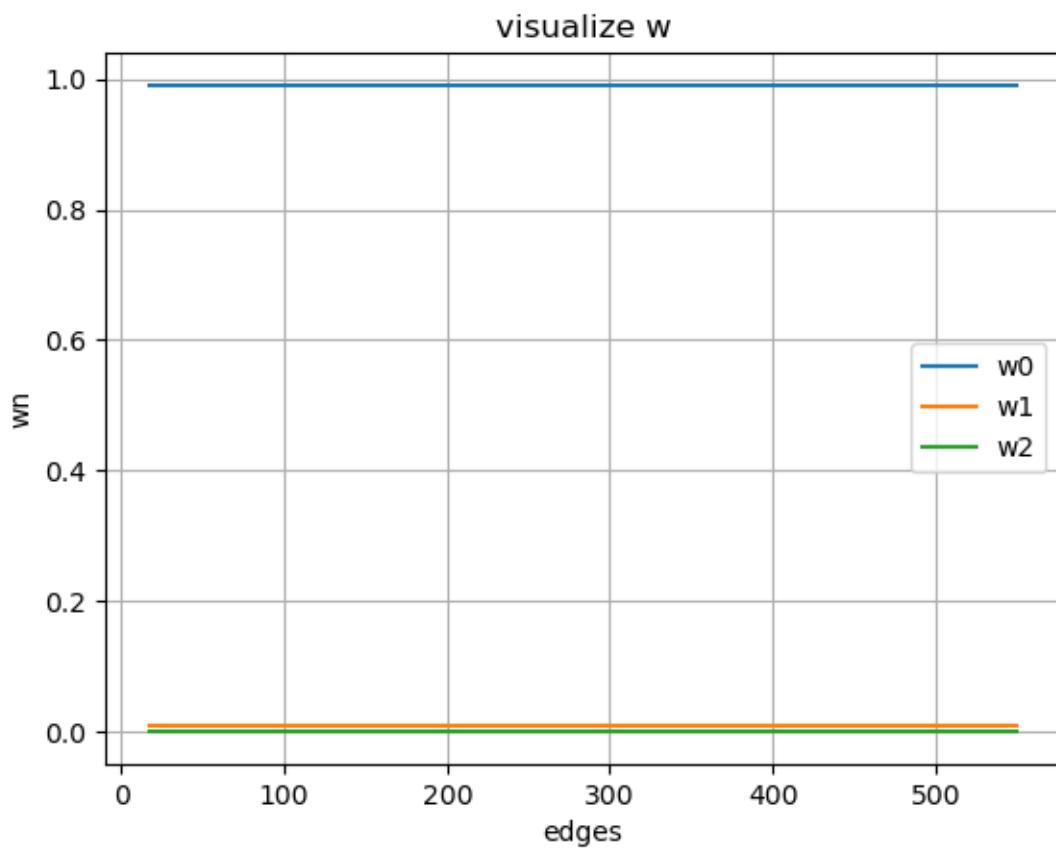


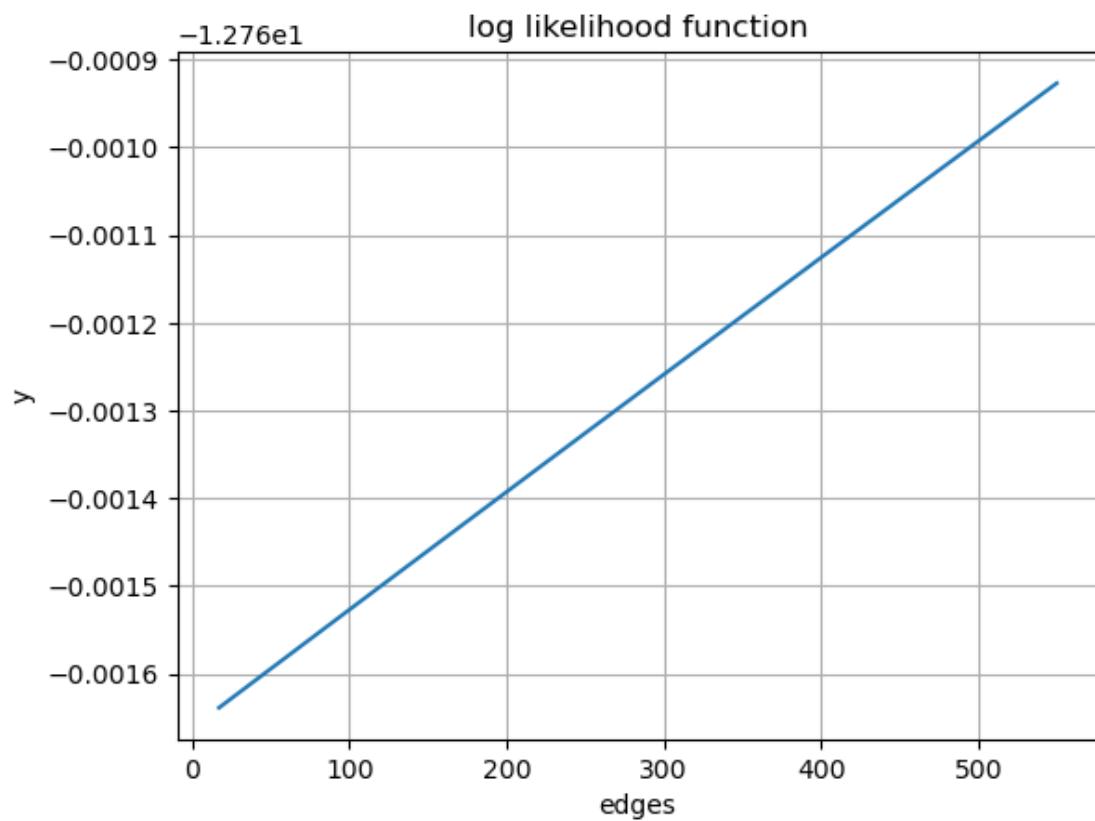


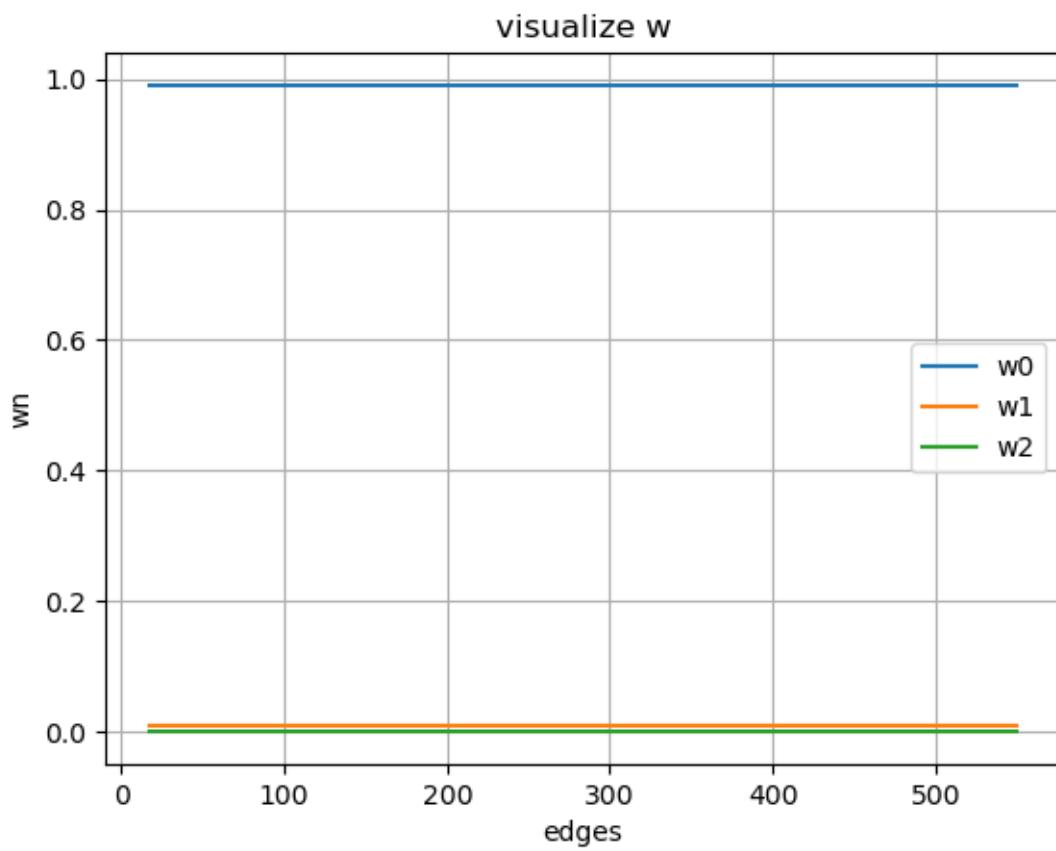


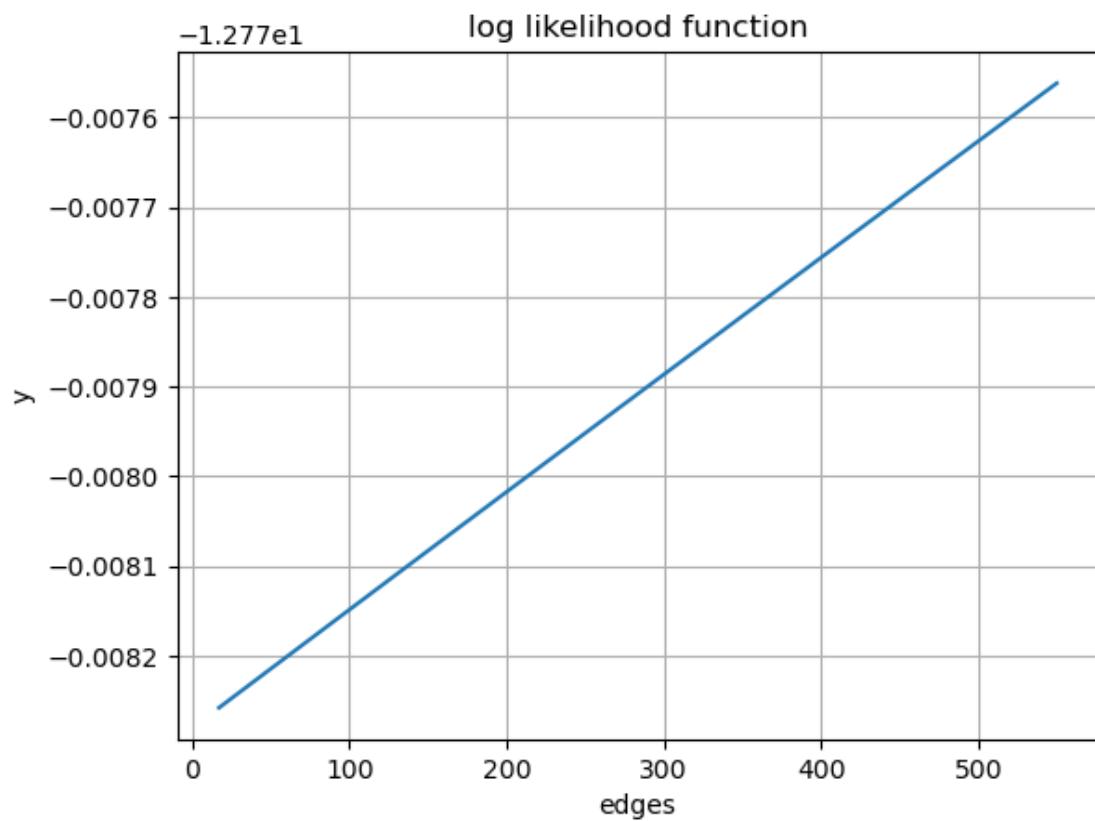


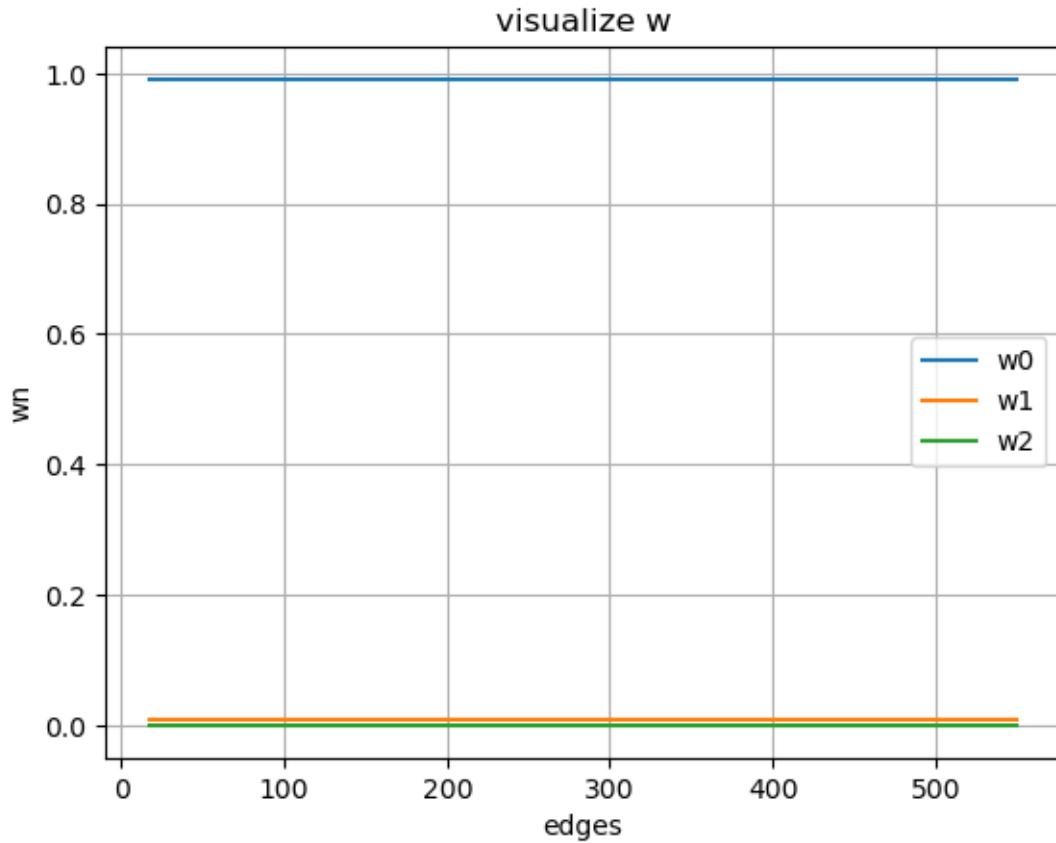


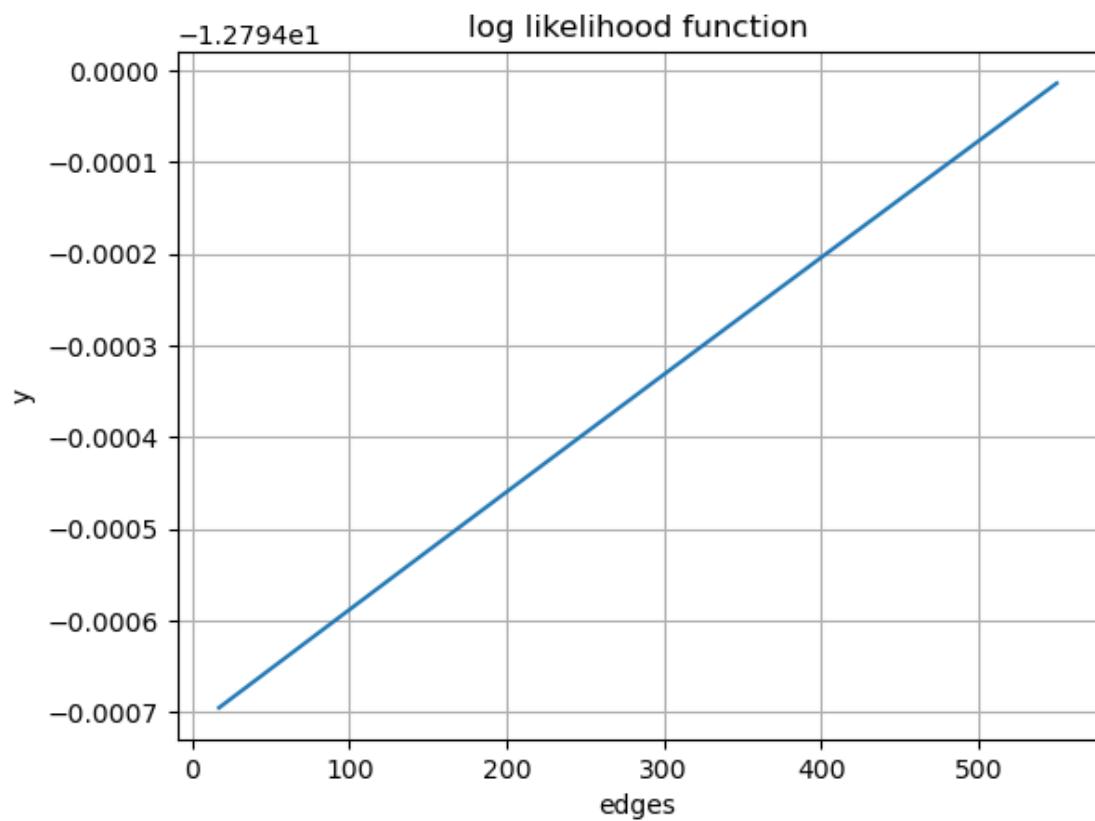


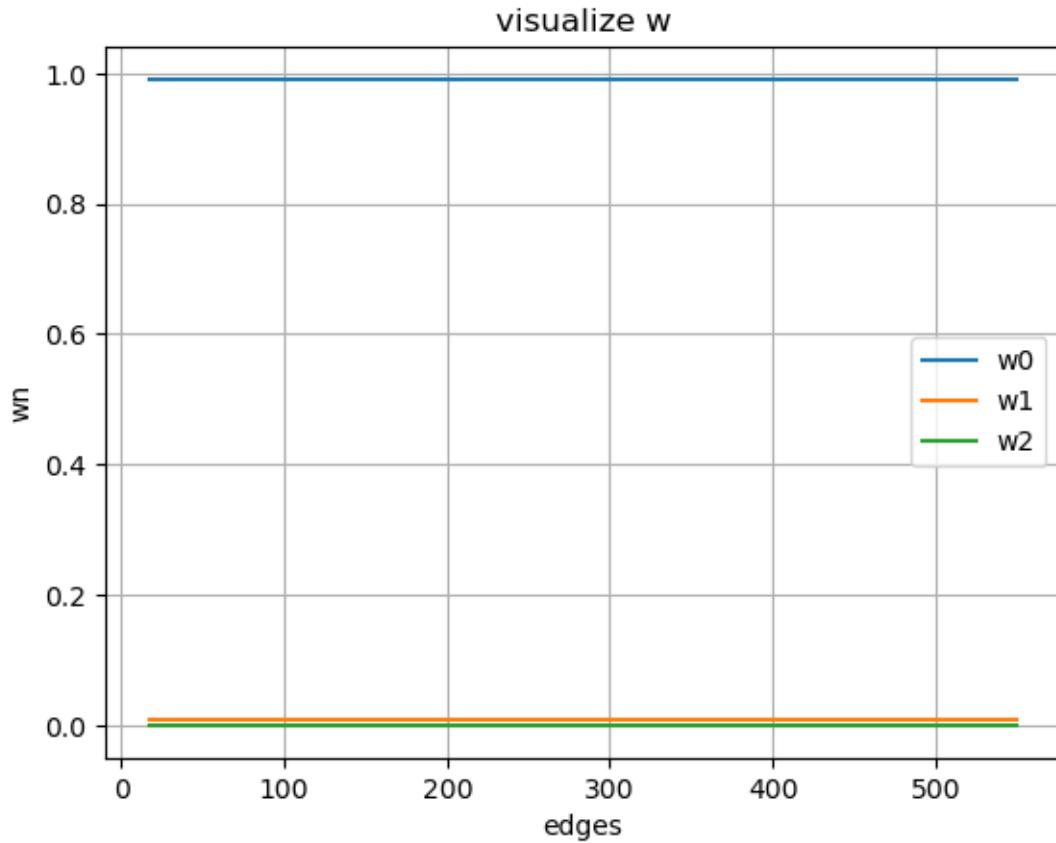


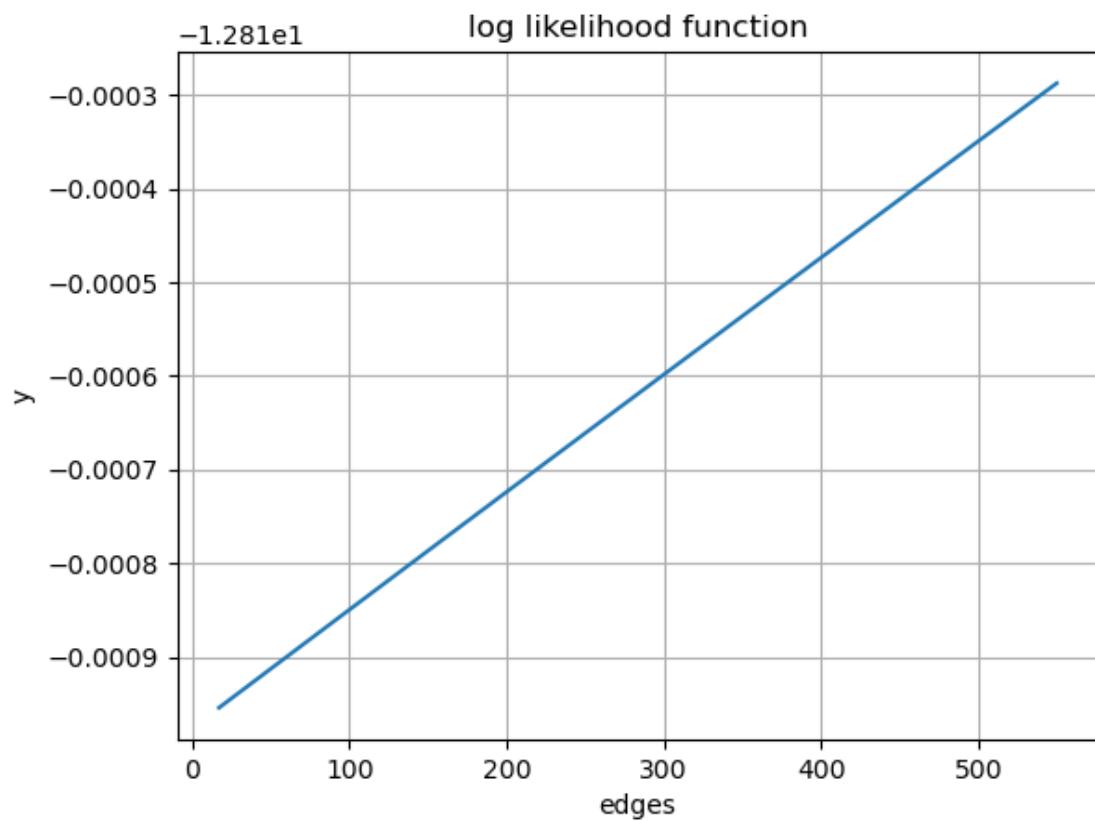


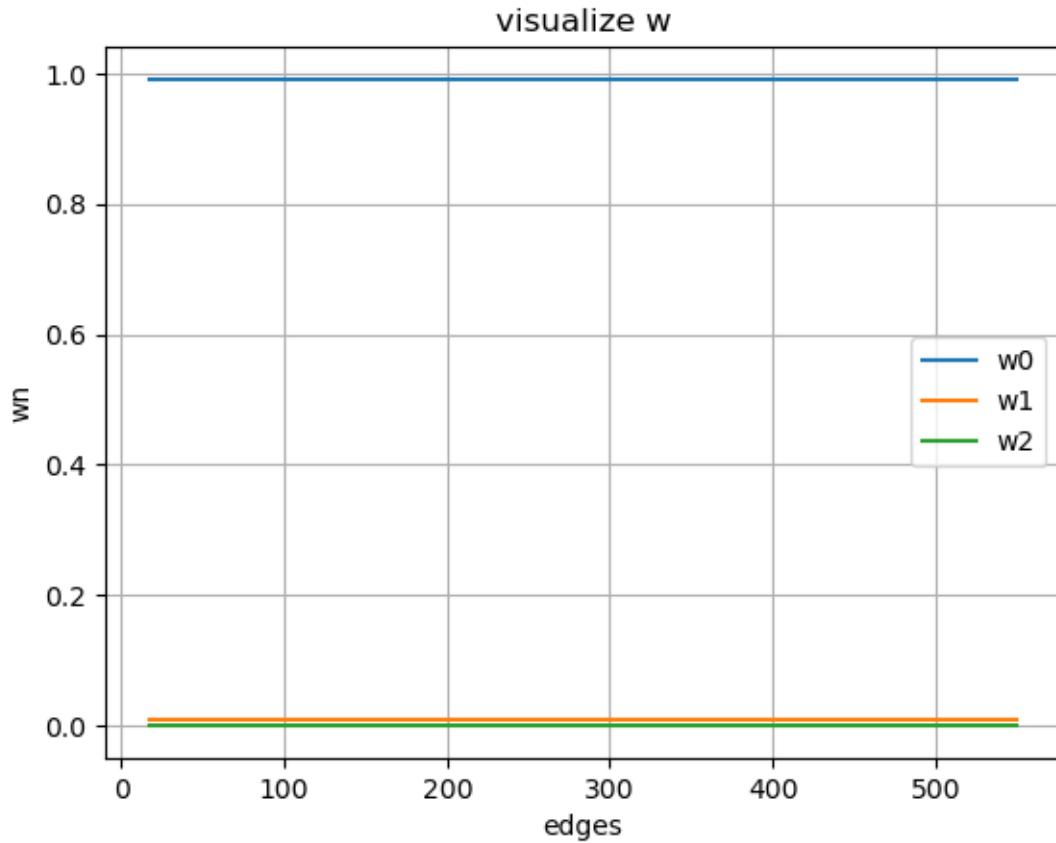


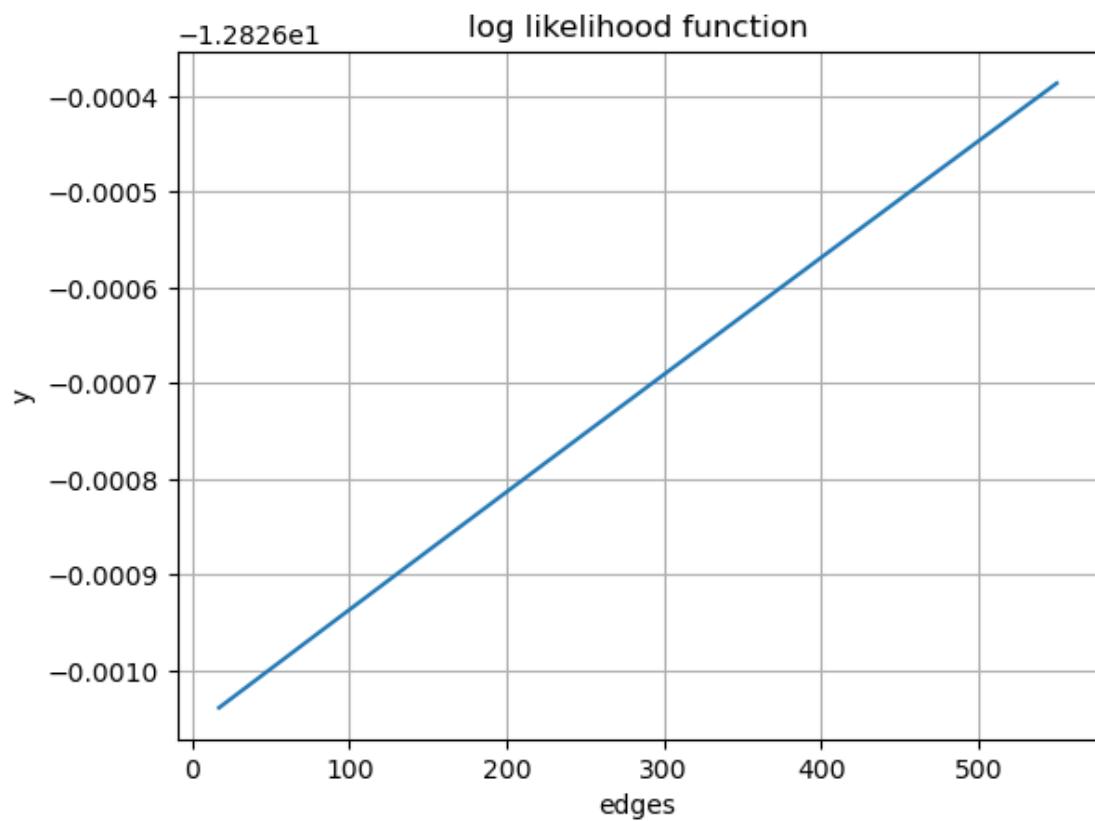


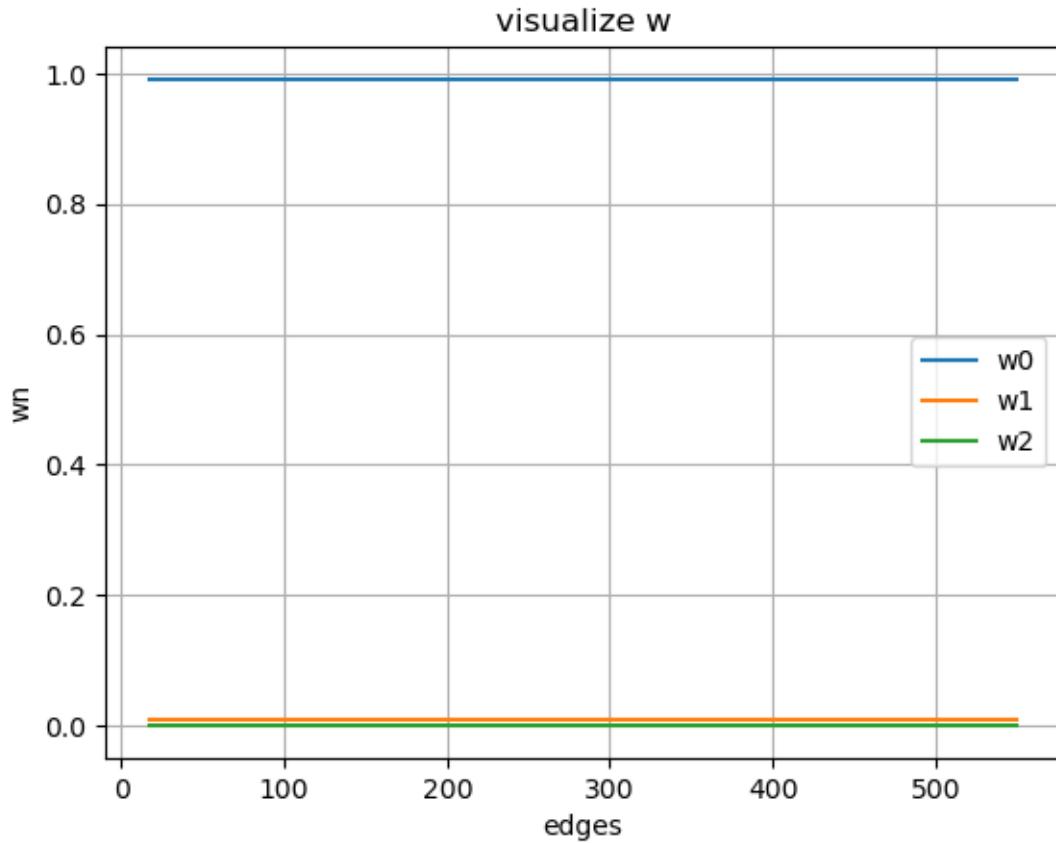


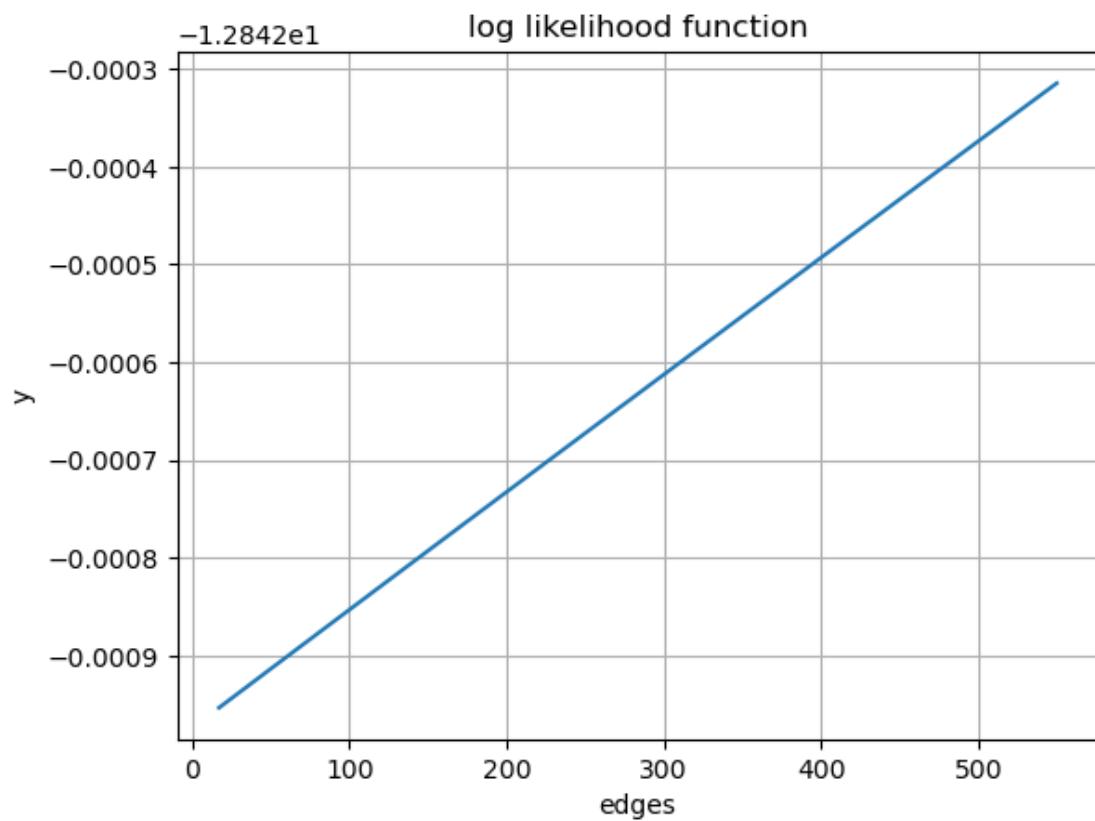


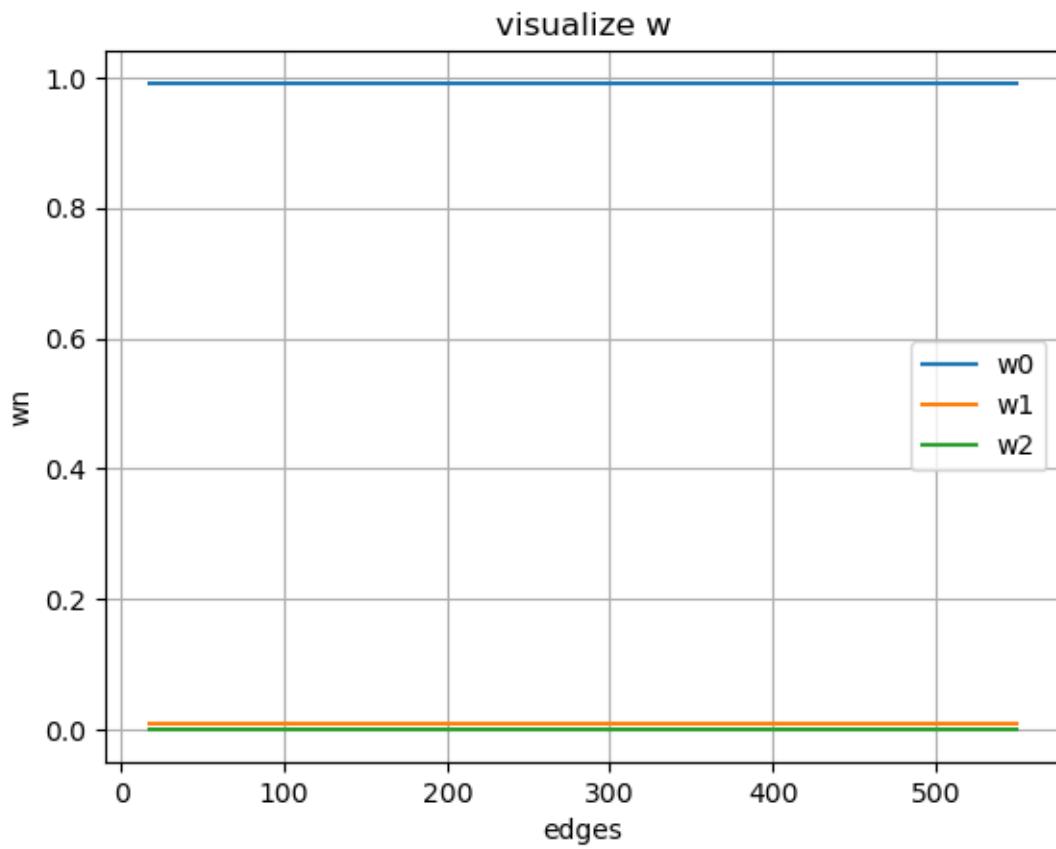


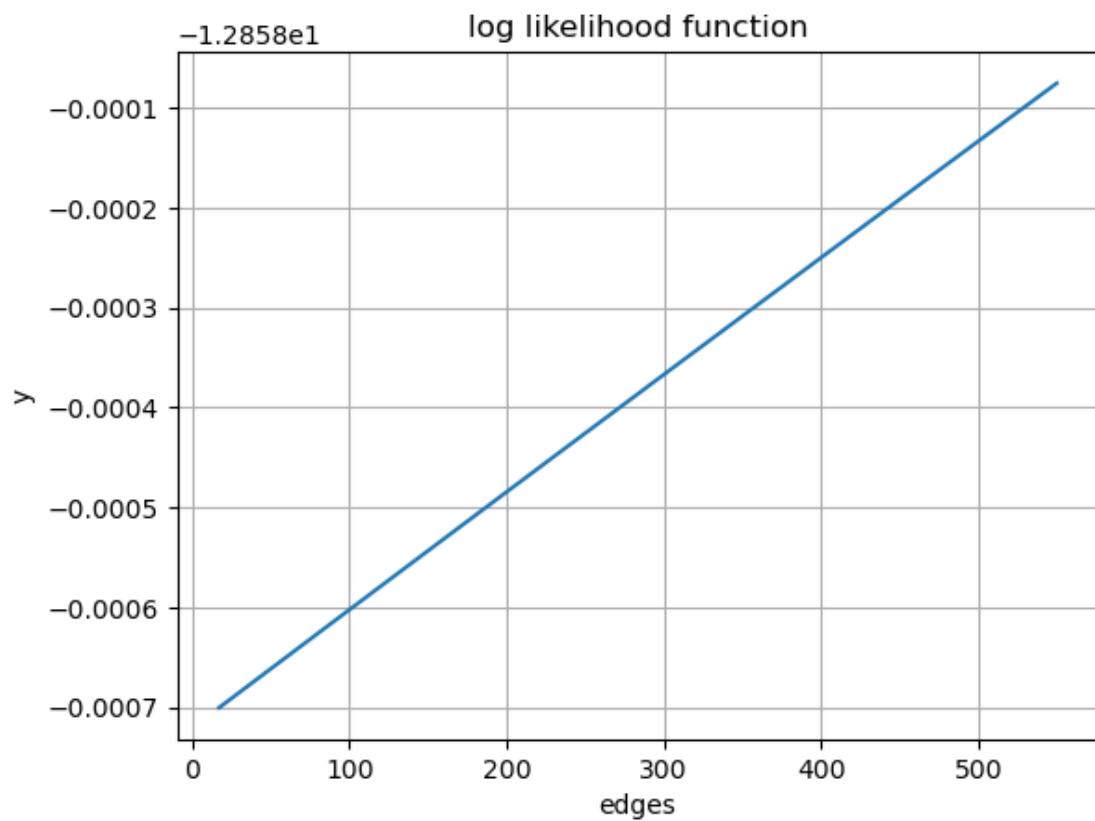


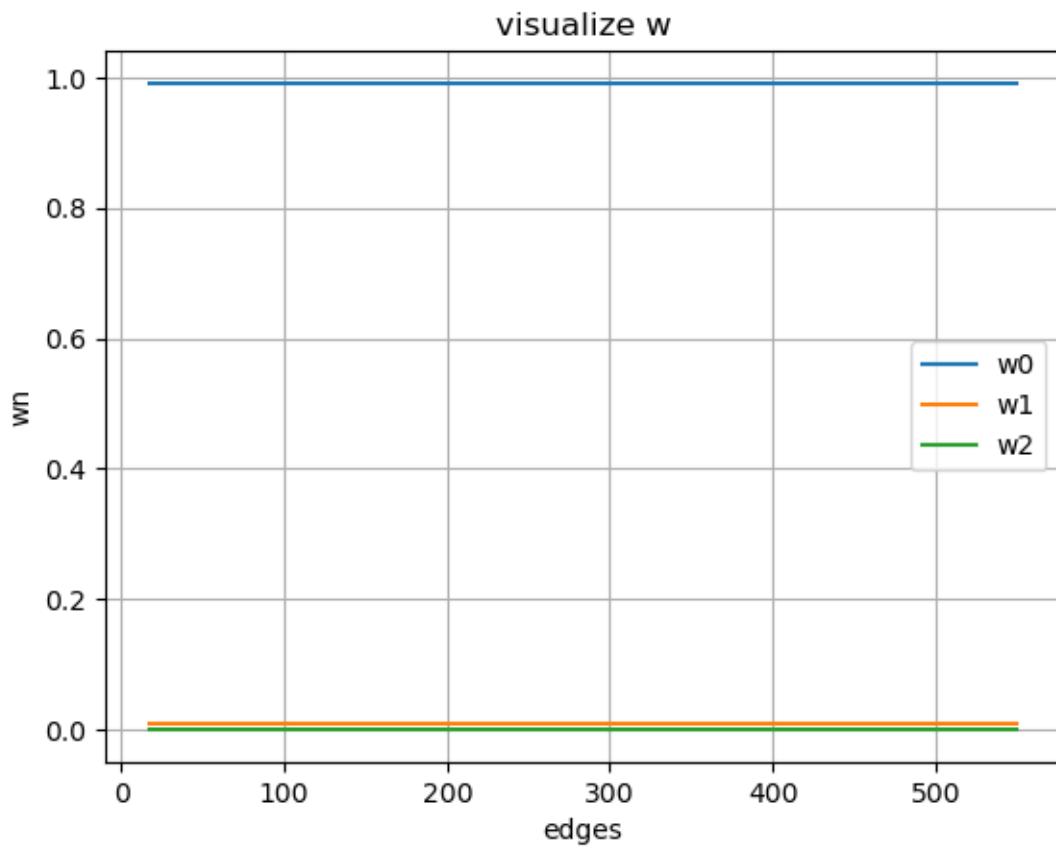


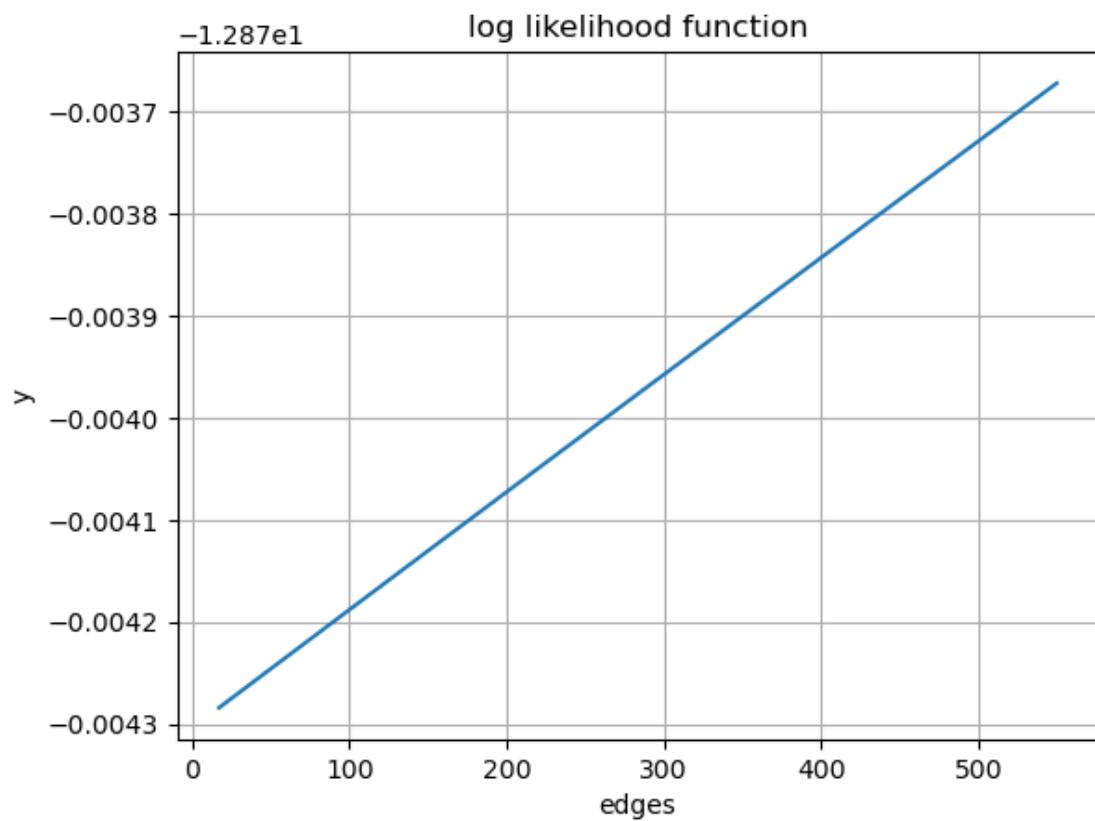


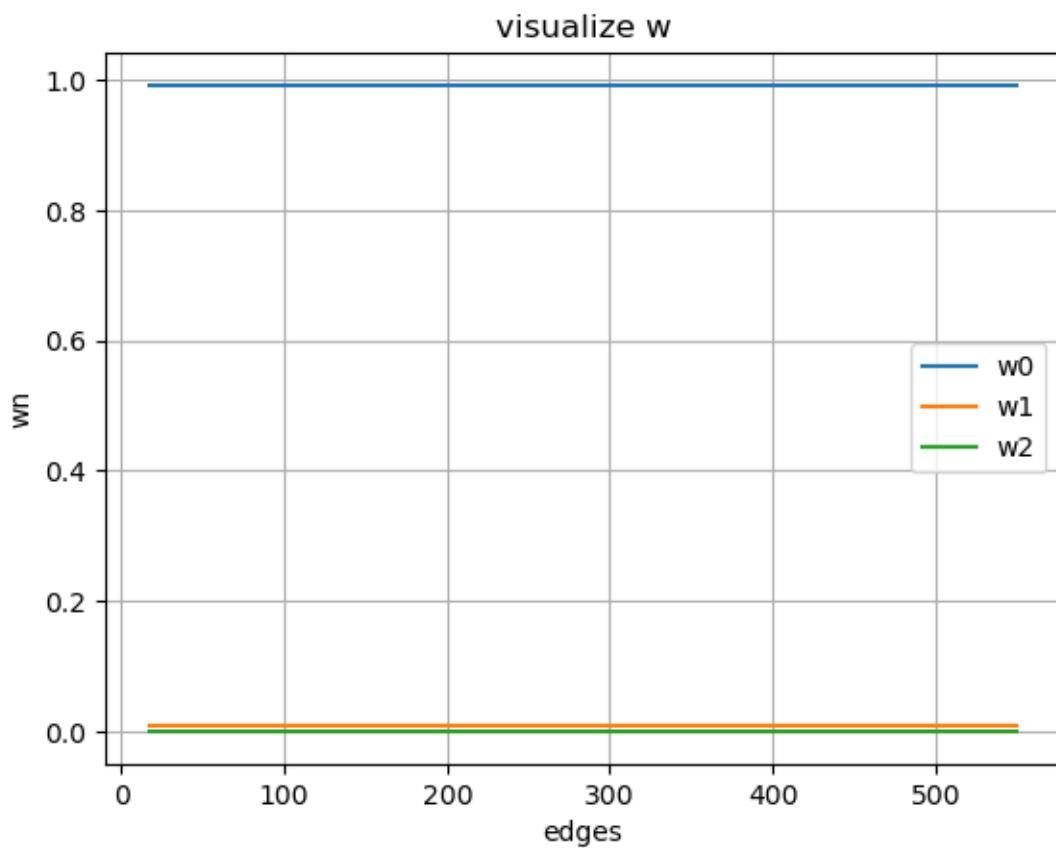


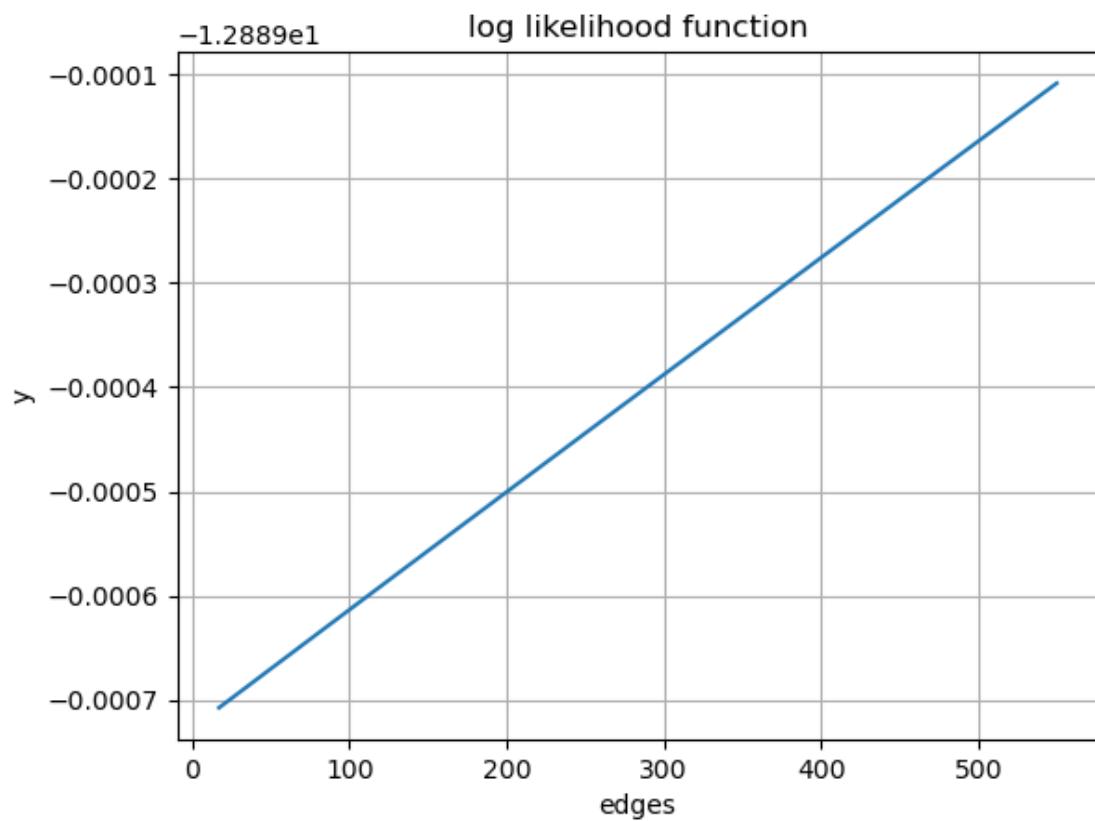


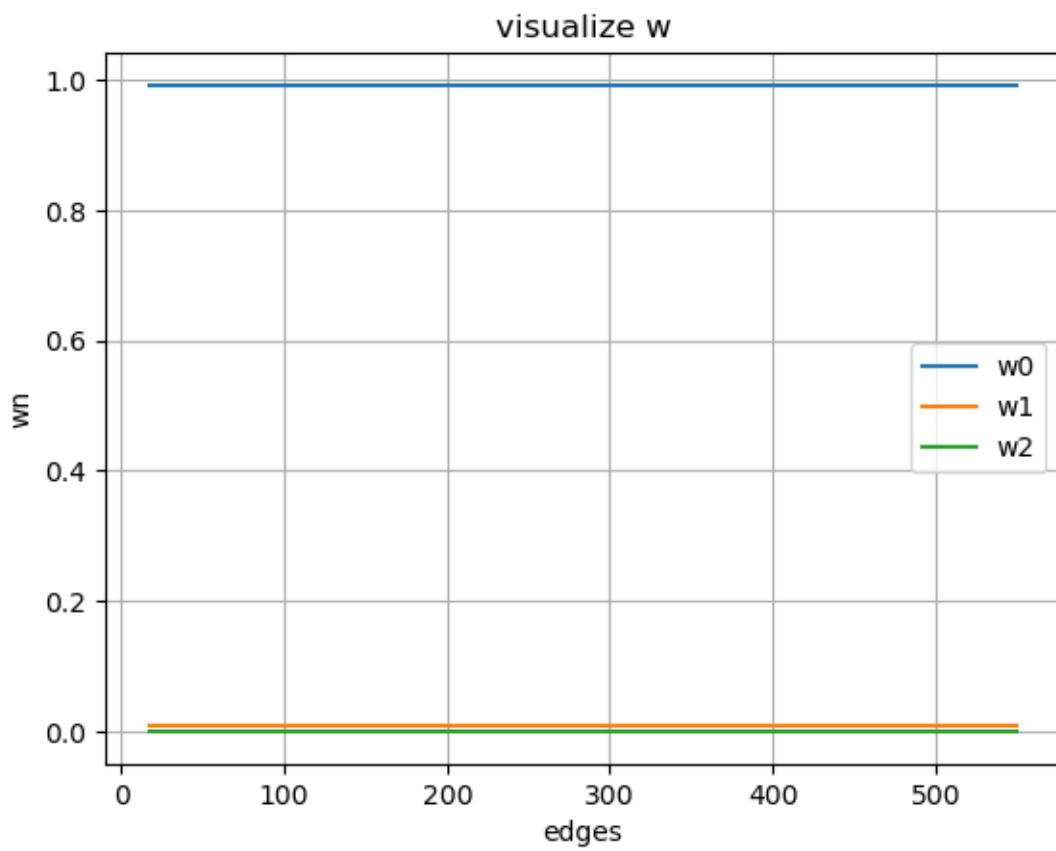


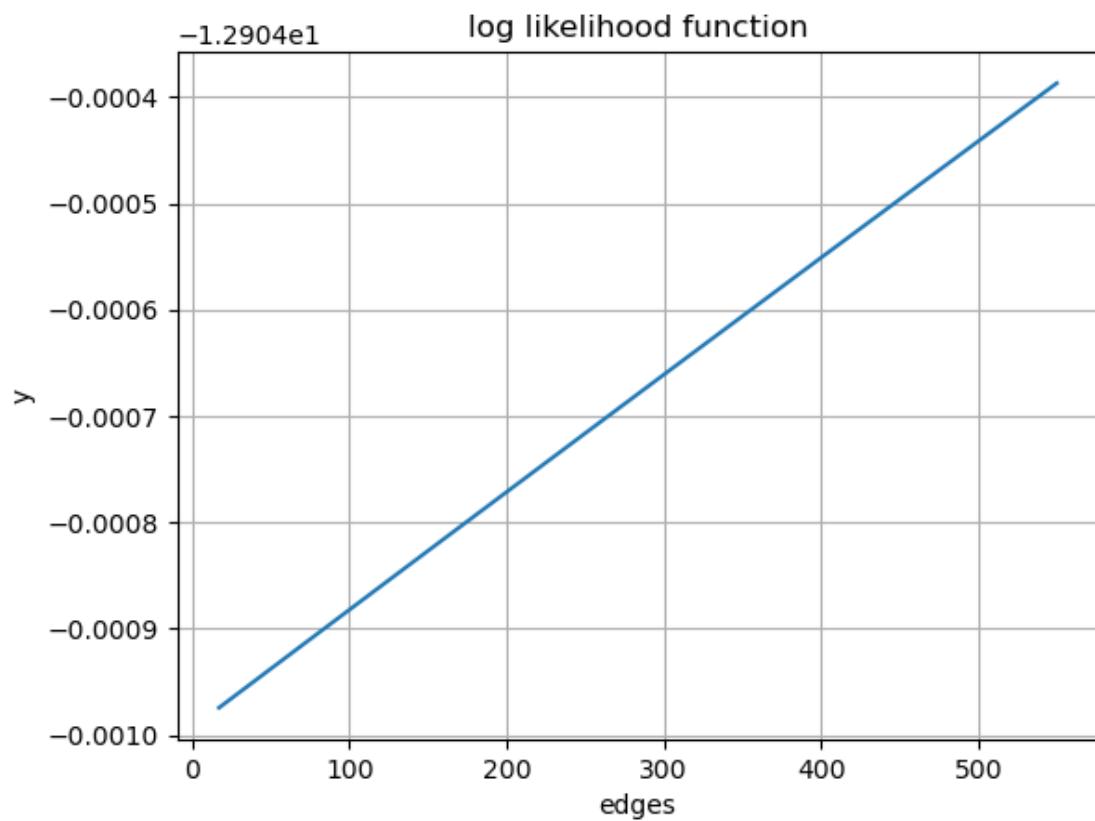


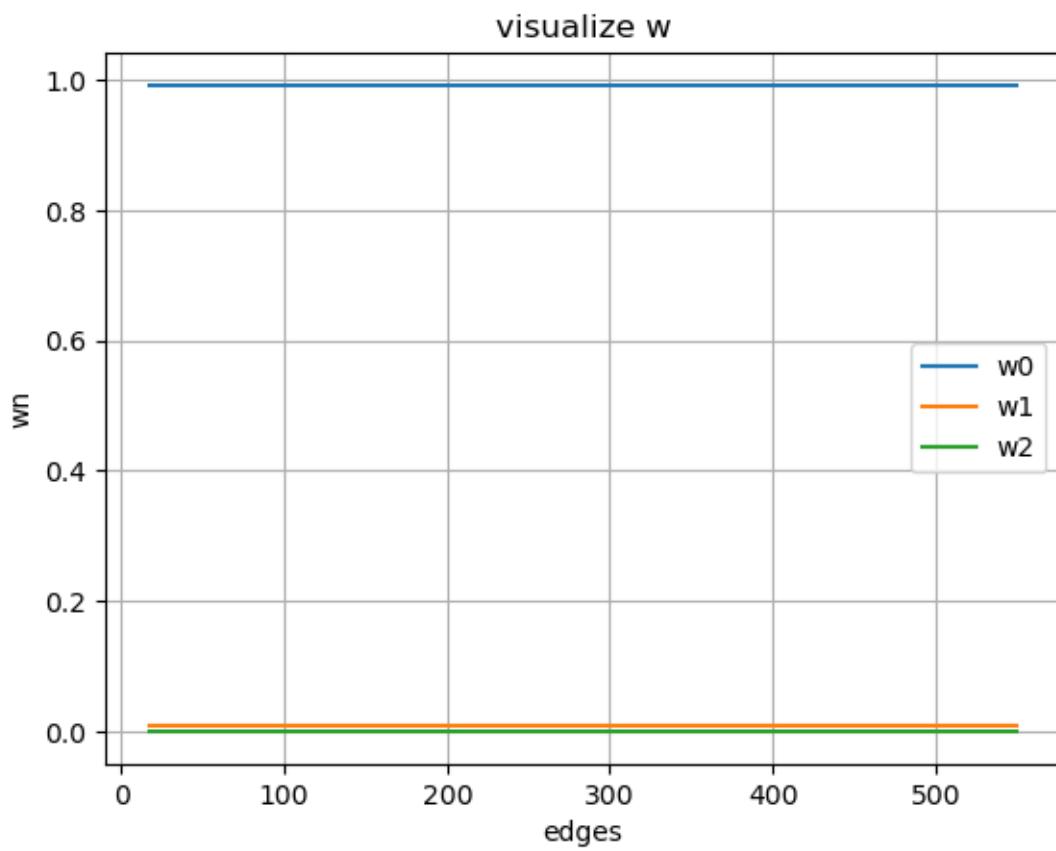


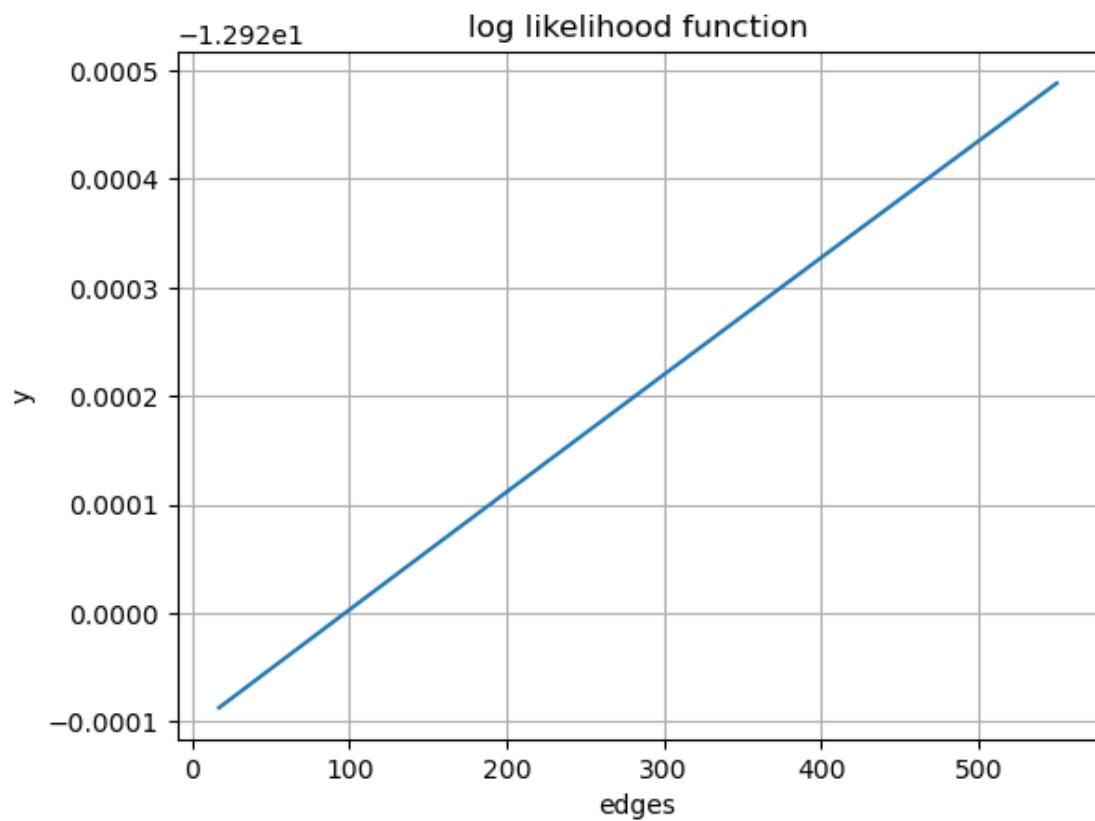


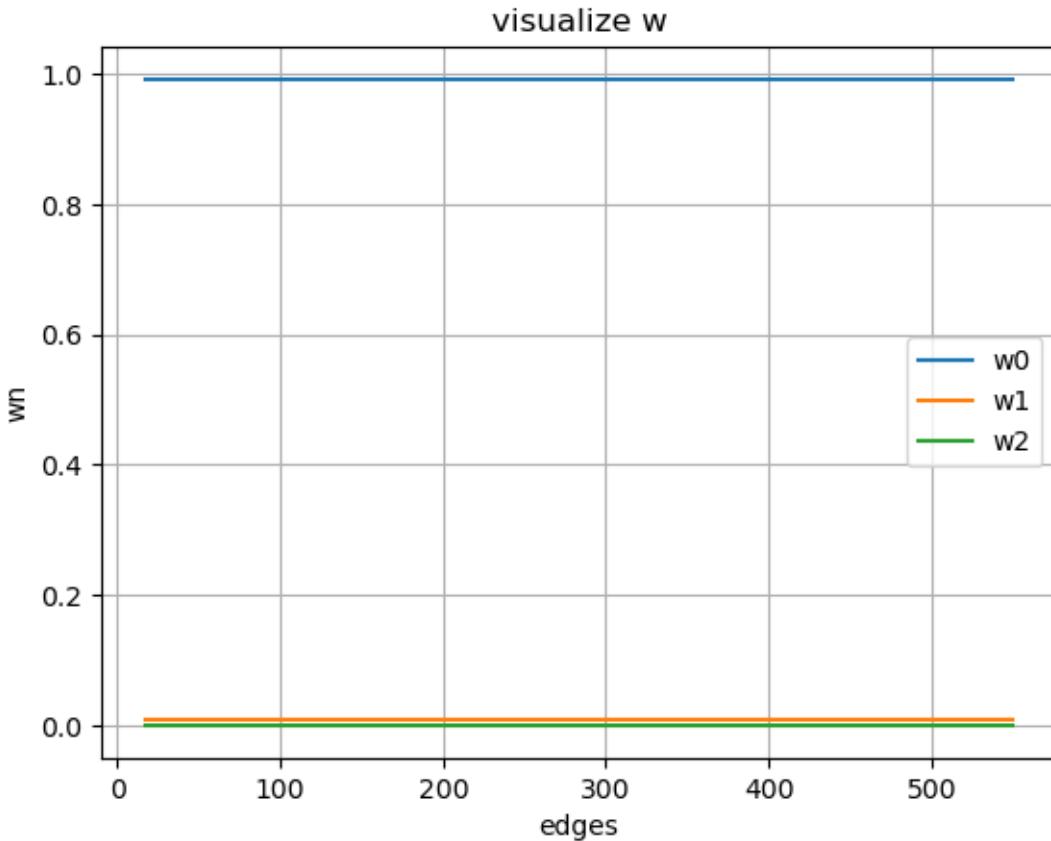












2.6 Task 6: Vary only one model parameter

Keeping all other parameters fixed to their estimated values, vary only μ_2 (the mean of the middle Gaussian distribution) between the estimated values of μ_1 and μ_3 in about 100 steps, and plot for each step the log likelihood function.

```
[42]: mu_final = u.copy()
sigma_final = [math.sqrt(sig[0]), math.sqrt(sig[1]), math.sqrt(sig[2])]
pi_final = pi.copy()
w_final = [w0, w1, w2]

steps = 100
mu_2_range = np.linspace(mu_final[0], mu_final[2], steps)
log_likelihoods = []

for mu_2 in mu_2_range:
    mu = mu_final.copy()
    mu[1] = mu_2

    pdf0 = pi_final[0] * stats.norm.pdf(edges, mu[0], sigma_final[0])
```

```

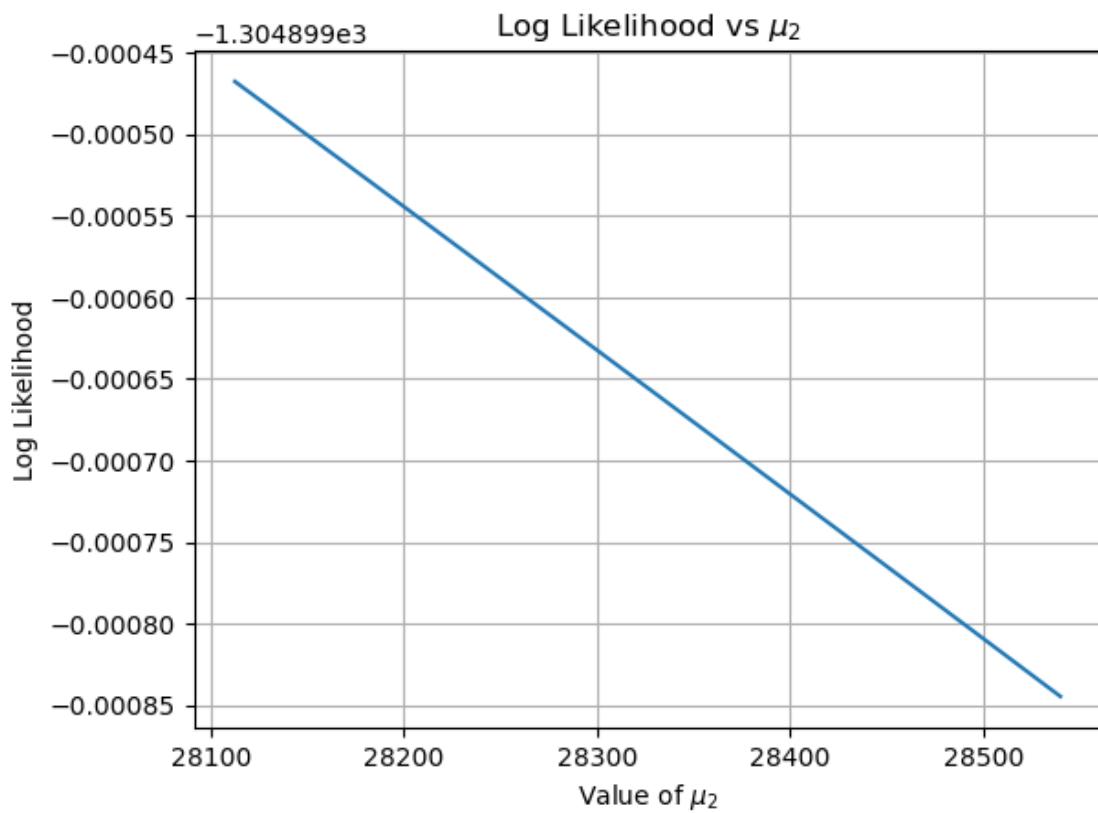
pdf1 = pi_final[1] * stats.norm.pdf(edges, mu[1], sigma_final[1])
pdf2 = pi_final[2] * stats.norm.pdf(edges, mu[2], sigma_final[2])

pdf_total = pdf0 + pdf1 + pdf2
w0 = pdf0 / pdf_total
w1 = pdf1 / pdf_total
w2 = pdf2 / pdf_total

log_likelihood = np.sum(np.log(pdf_total))
log_likelihoods.append(log_likelihood)

plt.plot(mu_2_range, log_likelihoods)
plt.xlabel('Value of  $\mu_2$ ')
plt.ylabel('Log Likelihood')
plt.title('Log Likelihood vs  $\mu_2$ ')
plt.grid(True)
plt.show()

```



2.7 Task 7: Locate Lower bound

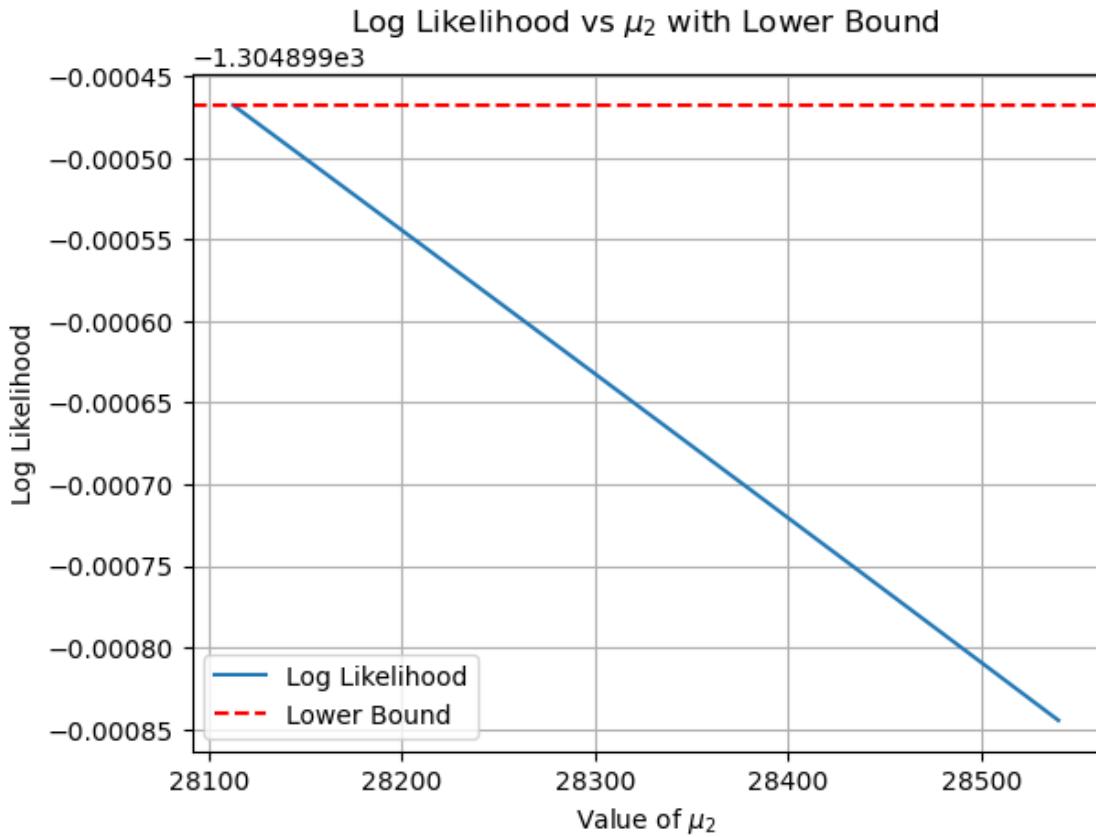
On the same figure, also plot the lower bound corresponding to the parameter vector in which all parameters are set to their estimated values, except μ_2 which is set to the estimated value of μ_1 .

```
[43]: mu_lower_bound = mu_final.copy()
mu_lower_bound[1] = mu_lower_bound[0]

pdf0 = pi_final[0] * stats.norm.pdf(edges, mu_lower_bound[0], sigma_final[0])
pdf1 = pi_final[1] * stats.norm.pdf(edges, mu_lower_bound[1], sigma_final[1])
pdf2 = pi_final[2] * stats.norm.pdf(edges, mu_lower_bound[2], sigma_final[2])

pdf_total = pdf0 + pdf1 + pdf2
w0 = pdf0 / pdf_total
w1 = pdf1 / pdf_total
w2 = pdf2 / pdf_total

log_likelihood_lower_bound = np.sum(np.log(pdf_total))
plt.plot(mu_2_range, log_likelihoods, label='Log Likelihood')
plt.axhline(y=log_likelihood_lower_bound, color='r', linestyle='--',  
            label='Lower Bound')
plt.xlabel('Value of $\mu_2$')
plt.ylabel('Log Likelihood')
plt.title('Log Likelihood vs $\mu_2$ with Lower Bound')
plt.grid(True)
plt.legend()
plt.show()
```



2.8 Task 8: Maximize lower bound

Compute the value for μ_2 that maximizes this lower bound (first line of eq. 3.35), indicate its location on the figure, and comment on the result.

Formulate the lower bound as

$$\begin{aligned}
 Q(\theta|\tilde{\theta}) = & -\frac{1}{2} \sum_{k=1}^K \left[\frac{1}{\sigma_k^2} \sum_{n=1}^N w_{n,k} (d_n - \mu_k - \sum_{m=1}^M c_m \phi_{n,m})^2 + \left(\sum_{n=1}^N w_{n,k} \right) \log \sigma_k^2 \right] \\
 & + \sum_{k=1}^K \left[\left(\sum_{n=1}^N w_{n,k} \right) \log \pi_k \right] \\
 & - \sum_{n=1}^N \sum_{k=1}^K w_{n,k} \log w_{n,k} - \frac{N}{2} \log(2\pi)
 \end{aligned}$$

```
[44]: mu_upper_bound = mu_final.copy()
mu_upper_bound[1] = mu_upper_bound[2]
```

```

pdf0_upper = pi_final[0] * stats.norm.pdf(edges, mu_upper_bound[0],  

                                         sigma_final[0])  

pdf1_upper = pi_final[1] * stats.norm.pdf(edges, mu_upper_bound[1],  

                                         sigma_final[1])  

pdf2_upper = pi_final[2] * stats.norm.pdf(edges, mu_upper_bound[2],  

                                         sigma_final[2])  

pdf_total_upper = pdf0_upper + pdf1_upper + pdf2_upper  

w0_upper = pdf0_upper / pdf_total_upper  

w1_upper = pdf1_upper / pdf_total_upper  

w2_upper = pdf2_upper / pdf_total_upper  

log_likelihood_upper_bound = np.sum(np.log(pdf_total_upper))  

plt.plot(mu_2_range, log_likelihoods, label='Log Likelihood')  

plt.axhline(y=log_likelihood_lower_bound, color='r', linestyle='--',  

            label='Lower Bound')  

plt.axhline(y=log_likelihood_upper_bound, color='g', linestyle='--',  

            label='Upper Bound')  

plt.xlabel('Value of $\mu_2$')  

plt.ylabel('Log Likelihood')  

plt.title('Log Likelihood vs $\mu_2$ with Lower and Upper Bounds')  

plt.grid(True)  

plt.legend()  

plt.show()

```

