Importing required packages

```
from google.colab import drive
drive.mount('/content/drive')
```

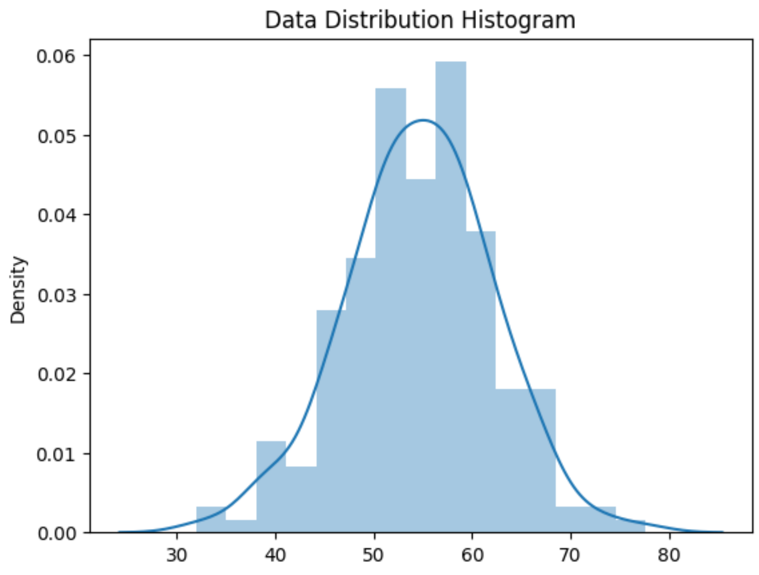
```
Drive already mounted at /content/drive; to attempt to forcibly remount, call drive.mount("/content/drive", force_remount=True).
```

```
import pandas as pd
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
from scipy.optimize import minimize
from scipy.stats import norm
```

```
df = pd.read_csv('/content/drive/MyDrive/sem 7/ID5055/Assignment 2/q4 Gene_expression.csv')
```

```
plt.title('Data Distribution Histogram')
sns.distplot(df)
```

```
<ipython-input-4-3fac749752ce>:2: UserWarning:

`distplot` is a deprecated function and will be removed in seaborn v0.14.0.

Please adapt your code to use either `displot` (a figure-level function with
similar flexibility) or `histplot` (an axes-level function for histograms).

For a guide to updating your code to use the new functions, please see
https://gist.github.com/mwaskom/de44147ed2974457ad6372750bbe5751

  sns.distplot(df)
<Axes: title={'center': 'Data Distribution Histogram'}, ylabel='Density'>
```



Assume the prior distribution of μ to be a normal distribution. You can take the sample mean of Day 1 samples and variance as prior parameters.

Given:

1. mean of the distribution μ_0 = mean of the Day 1 samples
2. variance of the distribution σ_0^2 = variance of the Day 1 samples

```
day1 = df['Day 1']
mu_0 = np.mean(day1, axis = 0)
sigma_0 = np.std(day1, axis = 0)

print(f"mean of the prior distribution is {mu_0}")
print(f"stanadrd deviation of the prior distribution is {sigma_0}")
```

```
mean of the prior distribution is 53.0472556695
stanadrd deviation of the prior distribution is 8.826980817204479
```

Estimate the posterior distribution of μ using samples from Day 1

Gene expression levels distribution is given by:

$$f(x;\mu,\sigma=8)=\frac{1}{8\sqrt{2\pi}}\exp\left(-\frac{(x-\mu)^2}{128}\right)$$

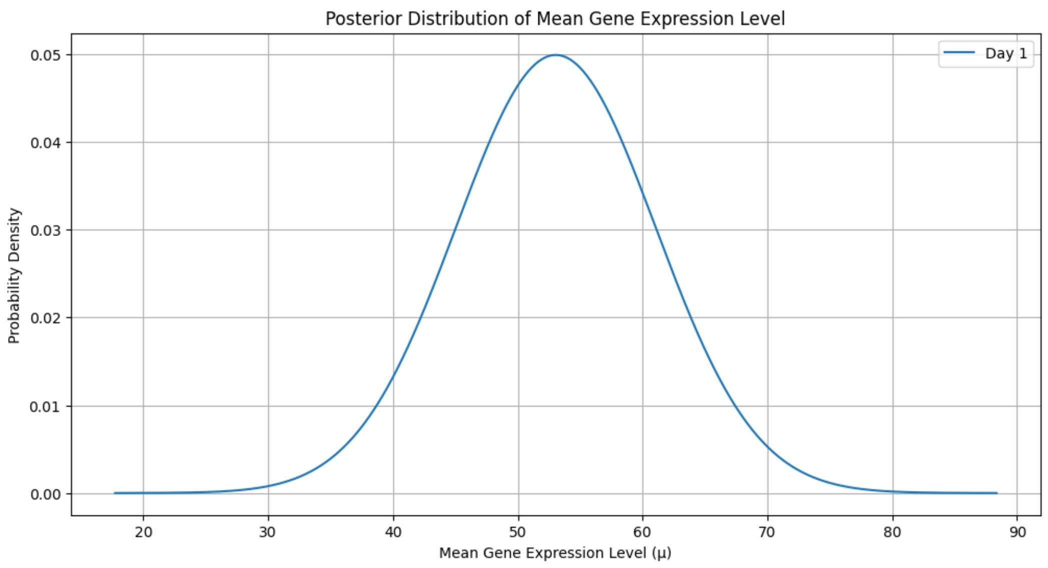
The prior distribution is given by:

$$f(\mu;\mu_0,\sigma_0)=\frac{1}{\sigma_0\sqrt{2\pi}}\exp\left(-\frac{(\mu-\mu_0)^2}{2\sigma_0^2}\right)$$

where μ_0 = 6.0337401566764175 and standard deviation σ_0 = 3.5503391410788043.

```
def map_log_likelihood(parameters, data, prior_mu, prior_std):
    mu = parameters
    if mu < 0:
        return np.inf
    log_likelihood = np.sum(np.log((1/(8*(2**0.5)*(np.pi)))*np.exp(-((data - mu)**2)/128))) + np.sum(np.log((1/(prior_std*(2**0.5)*(np.pi
    return -log_likelihood

initail_parameters = [1.0]

result = minimize(map_log_likelihood, initail_parameters, args = (df['Day 1'], mu_0, sigma_0))

# Estimated parameter
estimated_mu = result.x[0]
print("Estimated mu:", estimated_mu)

# Plot the probability distribution of the mean gene expression level each time after the update
plt.figure(figsize=(12, 6))
x = np.linspace(estimated_mu - 4*sigma_0, estimated_mu + 4*sigma_0, 1000)
y = norm.pdf(x, loc=estimated_mu, scale=8)
plt.plot(x, y, label=f'Day 1')

plt.xlabel('Mean Gene Expression Level (μ)')
plt.ylabel('Probability Density')
plt.title('Posterior Distribution of Mean Gene Expression Level')
plt.legend()
plt.grid()
plt.show()
```

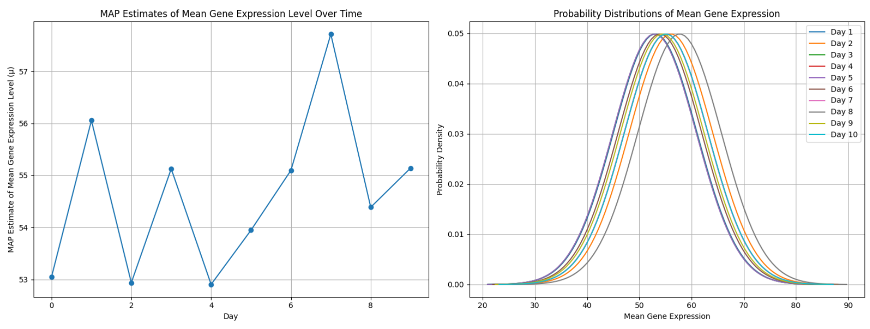
```
Estimated mu: 53.04723720260668
```



Update the priors and repeat the process using data from each of the days. Plot the probability distribution of the mean of gene expression level each time after the update

```
posteriori_mu = []
posteriori_sigma = []
num_days = 10
initial_paramters = [1.0]
```

```
for i in range(0, 10):
  day_data = df['Day '+ str(i+1)]

  mu_0 = np.mean(day_data, axis = 0)
  std_0 = np.std(day_data, axis = 0)

  result = minimize(map_log_likelihood, initial_paramters, args = (day_data, mu_0, sigma_0))

  estimated_mu = result.x[0]
  posteriori_mu.append(estimated_mu)

fig, axs = plt.subplots(1, 2, figsize=(16, 6))

# Plot the MAP estimates of the mean gene expression level
axs[0].plot(range(num_days), posteriori_mu, marker='o', linestyle='-')
axs[0].set_xlabel('Day')
axs[0].set_ylabel('MAP Estimate of Mean Gene Expression Level (μ)')
axs[0].set_title('MAP Estimates of Mean Gene Expression Level Over Time')
axs[0].grid()

# Plot individual normal distributions for each day
for i in range(num_days):
    day_data = df['Day ' + str(i+1)]
    x = np.linspace(posteriori_mu[i] - 4*8, posteriori_mu[i] + 4*8, 100)
    y = (1/(8 * np.sqrt(2 * np.pi))) * np.exp(-0.5 * ((x - posteriori_mu[i]) / 8)**2)
    axs[1].plot(x, y, label=f'Day {i+1}')

axs[1].set_xlabel('Mean Gene Expression')
axs[1].set_ylabel('Probability Density')
axs[1].set_title('Probability Distributions of Mean Gene Expression')
axs[1].legend()
axs[1].grid()

plt.tight_layout()
plt.show()
```



✓ 0s completed at 12:51 AM