Probability Project

February 18, 2025

[ ]:
```python
#1 Parameter estimation of the Gamma distribution
```

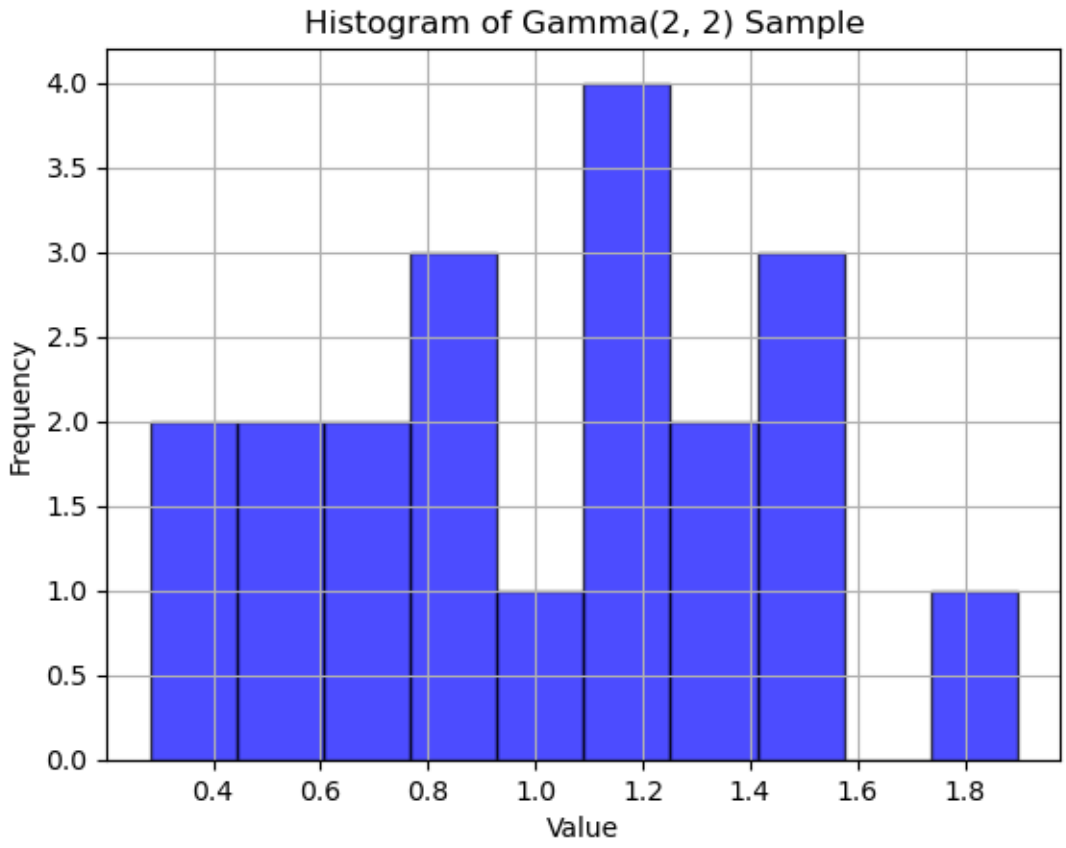
[29]:
```python
#1 i. Implement log-likelihood function
import math

def log_likelihood(a, b, x):
    """
    Compute the log-likelihood function for the Gamma distribution.

    Parameters:
        a (float): Shape parameter.
        b (float): Rate parameter.
        x (list): Observations.

    Returns:
        float: Log-likelihood value.

    """
    n = len(x)
    S1 = sum(math.log(xi) for xi in x)
    S2 = sum(xi for xi in x)
    return n * a * math.log(b) - n * math.lgamma(a) + (a - 1) * S1 - b * S2

# Example usage:
x = [2.3, 1.7, 3.1, 0.8, 2.9]  # Sample data
a, b = 2.0, 3.0  # Parameters
log_likelihood_value = log_likelihood(a, b, x)
print("Log-Likelihood:", log_likelihood_value)
```

```
Log-Likelihood: -18.077370442152315
```

[1]:
```python
#1 ii. Generate random samples
import numpy as np
from scipy.stats import gamma
import matplotlib.pyplot as plt

# Parameters
a_star = 2  # Shape parameter
```

```
b_star = 2  # Rate parameter
n = 20  # Sample size

# Generate a random sample
rng = np.random.default_rng(seed=42)  # Set a seed for reproducibility
x = gamma.rvs(a=a_star, scale=1/b_star, size=n, random_state=rng)

# Print the sample
print("Generated Sample:", x)

# Plot the histogram of the sample
plt.hist(x, bins=10, alpha=0.7, color='blue', edgecolor='black')
plt.title(f"Histogram of Gamma({a_star}, {b_star}) Sample")
plt.xlabel("Value")
plt.ylabel("Frequency")
plt.grid(True)
plt.show()
# These 20 numbers follow the gamma distribution
# histogram helps us assess how the chosen parameters (a* = 2, b* = 2) affect␣
 ↪the distribution of the generated sample.
```

```
Generated Sample: [1.04590864 1.41767279 0.91860779 0.82253521 1.53962766
0.87668677
 1.17300254 1.09474305 1.5387068  0.71961025 1.89779193 0.58629914
 1.22632653 1.12915099 0.54448617 1.29753737 0.76192335 0.40638847
 1.41106268 0.28290183]
```



[2]:
```python
#1 iii. Visualize log-likelihood surface
import numpy as np
import matplotlib.pyplot as plt
from mpl_toolkits.mplot3d import Axes3D

# Log-Likelihood function
def log_likelihood(a, b, x):
    n = len(x)
    S1 = np.sum(np.log(x))
    S2 = np.sum(x)
    return n * a * np.log(b) - n * math.lgamma(a) + (a - 1) * S1 - b * S2

# Parameters for the grid
a_vals = np.linspace(0.5, 4, 50)  # Range of 'a'
b_vals = np.linspace(0.5, 4, 50)  # Range of 'b'
a_grid, b_grid = np.meshgrid(a_vals, b_vals)

# Dataset (fixed sample)
np.random.seed(42)
x = np.random.gamma(shape=2, scale=1/2, size=20)
```

```python
# Compute Log-Likelihood for the grid
z = np.array([[log_likelihood(a, b, x) for a, b in zip(a_row, b_row)]
              for a_row, b_row in zip(a_grid, b_grid)])

# 3D Visualization
fig = plt.figure(figsize=(10, 8))
ax = fig.add_subplot(111, projection='3d')
ax.plot_surface(a_grid, b_grid, z, cmap='viridis', edgecolor='none')
ax.set_title('Log-Likelihood Function', fontsize=16)
ax.set_xlabel('a (Shape)', fontsize=12)
ax.set_ylabel('b (Rate)', fontsize=12)
ax.set_zlabel('Log-Likelihood', fontsize=12)
plt.show()
```

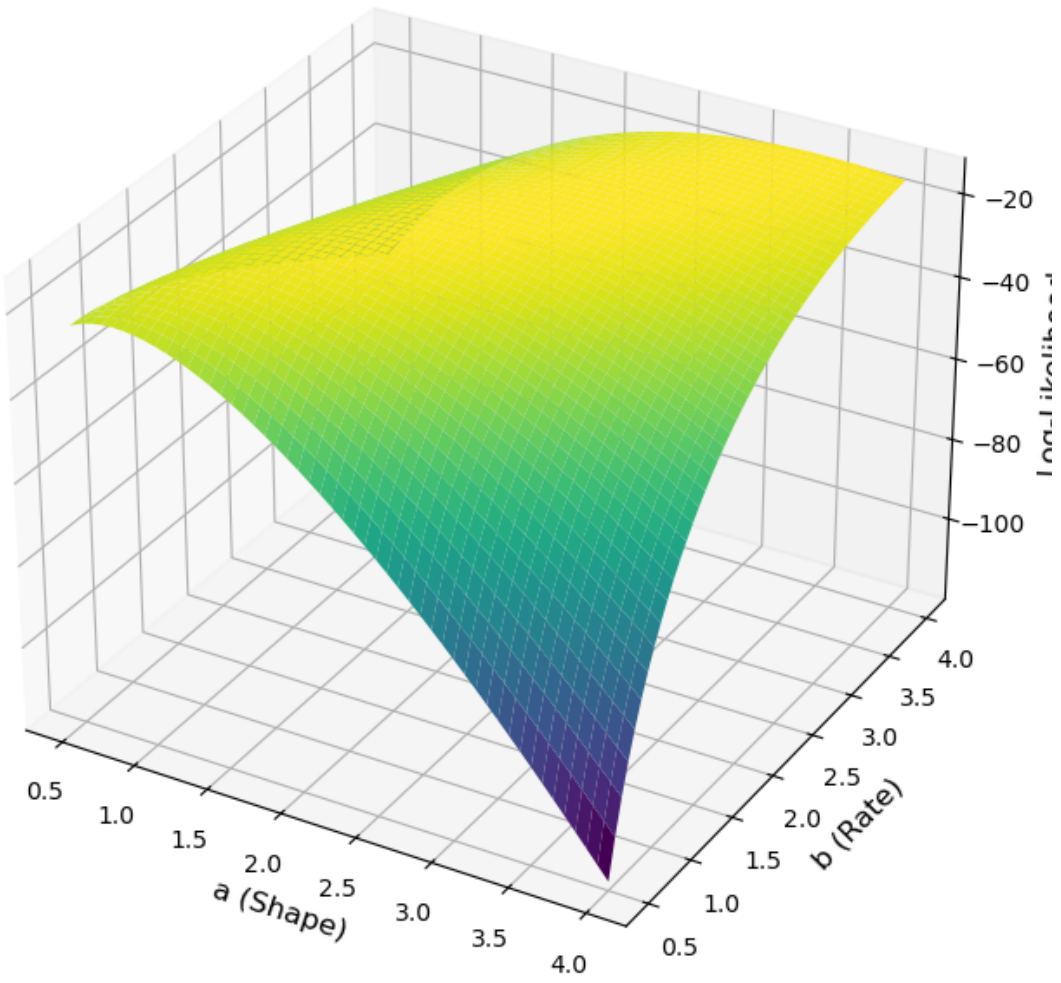
```
---------------------------------------------------------------------------
NameError                                 Traceback (most recent call last)
Cell In[2], line 23
     20 x = np.random.gamma(shape=2, scale=1/2, size=20)
     22 # Compute Log-Likelihood for the grid
---> 23 z = np.array([[log_likelihood(a, b, x) for a, b in zip(a_row, b_row)]
     24               for a_row, b_row in zip(a_grid, b_grid)])
     26 # 3D Visualization
     27 fig = plt.figure(figsize=(10, 8))

Cell In[2], line 23, in <listcomp>(.0)
     20 x = np.random.gamma(shape=2, scale=1/2, size=20)
     22 # Compute Log-Likelihood for the grid
---> 23 z = np.array([[log_likelihood(a, b, x) for a, b in zip(a_row, b_row)]
     24               for a_row, b_row in zip(a_grid, b_grid)])
     26 # 3D Visualization
     27 fig = plt.figure(figsize=(10, 8))

Cell In[2], line 23, in <listcomp>(.0)
     20 x = np.random.gamma(shape=2, scale=1/2, size=20)
     22 # Compute Log-Likelihood for the grid
---> 23 z = np.array([[log_likelihood(a, b, x) for a, b in zip(a_row, b_row)]
     24               for a_row, b_row in zip(a_grid, b_grid)])
     26 # 3D Visualization
     27 fig = plt.figure(figsize=(10, 8))

Cell In[2], line 11, in log_likelihood(a, b, x)
      9 S1 = np.sum(np.log(x))
     10 S2 = np.sum(x)
---> 11 return n * a * np.log(b) - n * math.lgamma(a) + (a - 1) * S1 - b * S2
```

```
NameError: name 'math' is not defined
```

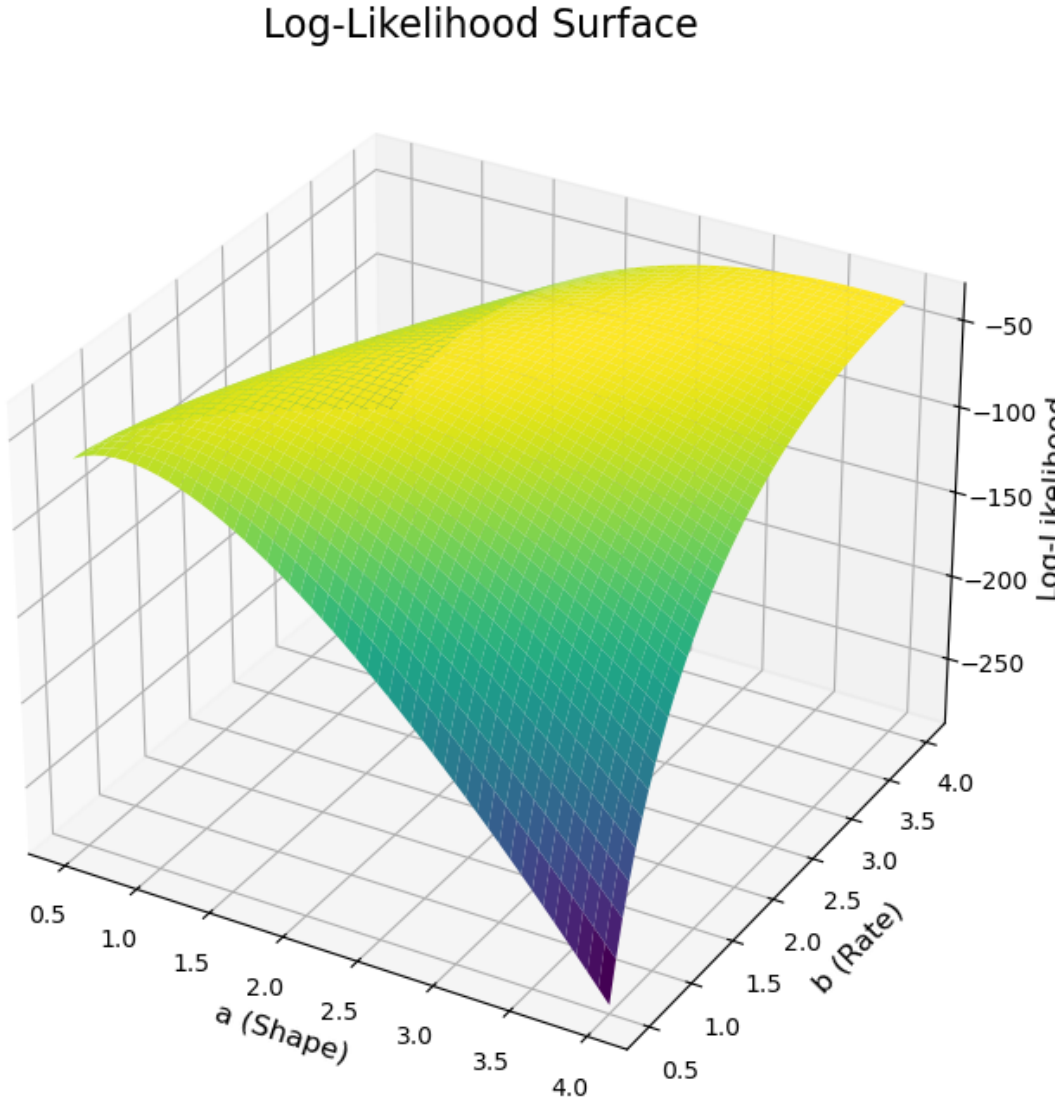
[31]:
```
#1. iv. What is the previous graphical representation for different simulated␣
 ↪data sets x of dif}ferent sizes and with different parameter values a* and␣
 ↪b* .
#1. v. What is the typical shape of the log-likelihood function? How many␣
 ↪critical points does it have? Where is the maximum of the function␣
 ↪apparently located ?

# Updated imports
import numpy as np
import matplotlib.pyplot as plt
from mpl_toolkits.mplot3d import Axes3D
import math

# Function to calculate log-likelihood
def log_likelihood(a, b, x):
    n = len(x)
    S1 = np.sum(np.log(x))
    S2 = np.sum(x)
    return n * a * np.log(b) - n * math.lgamma(a) + (a - 1) * S1 - b * S2

# Generate datasets with different parameters
def generate_gamma_data(a_star, b_star, n, seed=42):
    np.random.seed(seed)
    return np.random.gamma(shape=a_star, scale=1/b_star, size=n)

# Visualize log-likelihood for a dataset
def visualize_log_likelihood(x, a_range, b_range):
    a_vals = np.linspace(*a_range, 50)
    b_vals = np.linspace(*b_range, 50)
    a_grid, b_grid = np.meshgrid(a_vals, b_vals)
    z = np.array([[log_likelihood(a, b, x) for a, b in zip(a_row, b_row)]
                  for a_row, b_row in zip(a_grid, b_grid)])

    # 3D plot
    fig = plt.figure(figsize=(10, 8))
    ax = fig.add_subplot(111, projection='3d')
    ax.plot_surface(a_grid, b_grid, z, cmap='viridis', edgecolor='none')
    ax.set_title('Log-Likelihood Surface', fontsize=16)
    ax.set_xlabel('a (Shape)', fontsize=12)
    ax.set_ylabel('b (Rate)', fontsize=12)
    ax.set_zlabel('Log-Likelihood', fontsize=12)
    plt.show()

# Test cases with varying datasets
```

```
datasets = [
    (2, 2, 20),   # a* = 2, b* = 2, n = 20
    (2, 2, 50),   # a* = 2, b* = 2, n = 50
    (3, 1, 20),   # a* = 3, b* = 1, n = 20
    (1.5, 2.5, 100)  # a* = 1.5, b* = 2.5, n = 100
]

# Generate and visualize log-likelihood for each dataset
for a_star, b_star, n in datasets:
    x = generate_gamma_data(a_star, b_star, n)
    print(f"Dataset: a*={a_star}, b*={b_star}, n={n}")
    visualize_log_likelihood(x, (0.5, 4), (0.5, 4))

# a* = 2, b* = 2, n = 20: Broad peak near (2, 2) , Indicates parameter␣
 ↪uncertainty
# a* = 2, b* = 2, n = 50: Sharper peak closer to (2, 2) , Shows improved␣
 ↪estimation with larger sample
# a* = 3, b* = 1, n = 20: Elongated surface, Peak shifted towards higher 'a'␣
 ↪and lower 'b'
#a* = 1.5, b* = 2.5, n = 100: Very sharp, well-defined peak, Maximum close to␣
 ↪true values, Demonstrates benefit of large sample size
# The log-likelihood function typically has a smooth, concave surface. It forms␣
 ↪a "dome" shape.
# log-likelihood function appears to have a single critical point.
# This critical point is a global maximum, as evidenced by the single peak in␣
 ↪the surface plots.
# The maximum of the function is generally located near the true parameter␣
 ↪values used to generate the data.
```

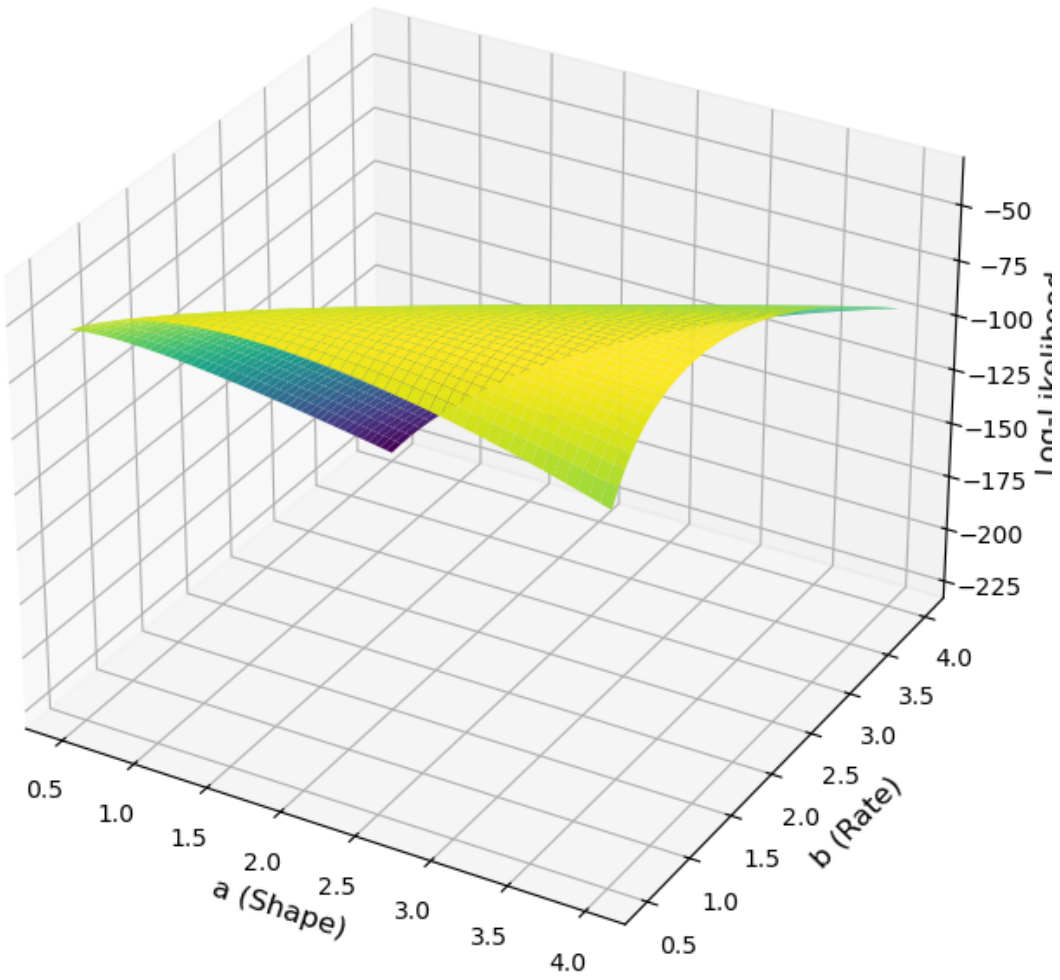
```
Dataset: a*=2, b*=2, n=20
```



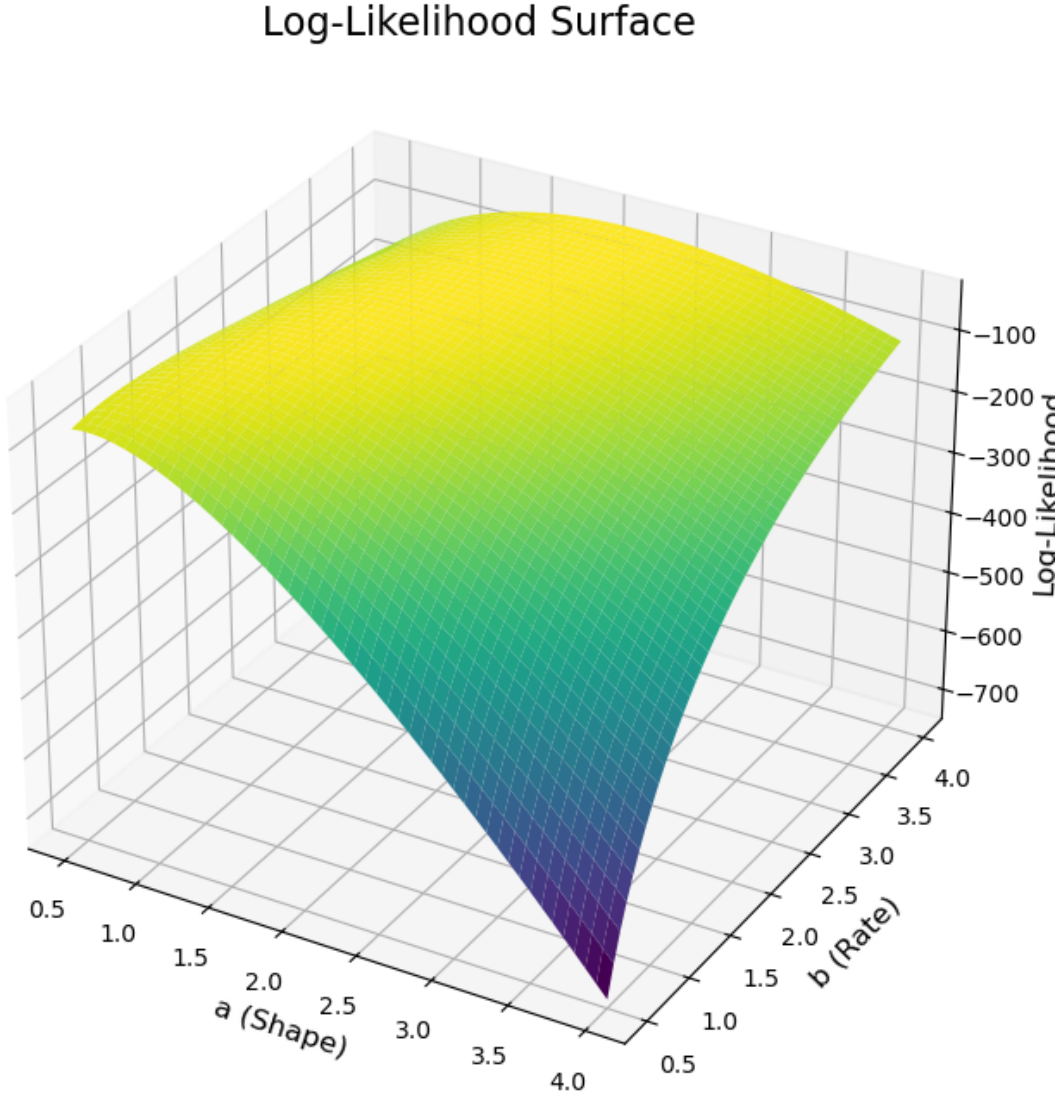
Dataset: a*=2, b*=2, n=50



Dataset: a*=3, b*=1, n=20



Dataset: a*=1.5, b*=2.5, n=100



[32]:
```
from scipy.special import digamma, polygamma
import numpy as np

def UpdateNewton(a, b, x):
    n = len(x)
    S1 = np.sum(np.log(x))
    S2 = np.sum(x)

    # Gradient
    grad_a = n * np.log(b) - n * digamma(a) + S1
    grad_b = (n * a / b) - S2
    grad = np.array([grad_a, grad_b])
```

```
    # Hessian
    hess_aa = -n * polygamma(1, a)  # polygamma(1, a) is the trigamma function
    hess_bb = -n * a / (b ** 2)
    hess_ab = n / b
    hessian = np.array([[hess_aa, hess_ab], [hess_ab, hess_bb]])

    # Compute the update step
    try:
        step = np.linalg.solve(hessian, grad)
    except np.linalg.LinAlgError:
        raise ValueError("Hessian is singular. Newton-Raphson update failed.")

    # Update parameters
    a_new = a - step[0]
    b_new = b - step[1]

    return a_new, b_new

def newton_raphson_gamma(x, tol=1e-6, max_iter=100):
    a, b = 1.0, 1.0  # Initial guesses
    for _ in range(max_iter):
        a_new, b_new = UpdateNewton(a, b, x)
        if np.linalg.norm([a_new - a, b_new - b]) < tol:
            return a_new, b_new
        a, b = a_new, b_new
    return a, b  # Return last values if max_iter is reached

# Example usage
x = np.random.gamma(shape=2, scale=1/2, size=20)
a_est, b_est = newton_raphson_gamma(x)
print(f"Estimated parameters: a={a_est:.4f}, b={b_est:.4f}")
```

```
Estimated parameters: a=2.9502, b=3.5605
```

[27]:
```
#1. VIII. 7. Write a function python UpdateNewton which performs an update of␣
 ↪the parameters.
# This function takes as arguments the current values of the parameters and the␣
 ↪data.
# It returns the new parameter values a^(t+1) and b^(t+1) obtained by (1).
# For the derivatives of log Γ(a) use the digamma and trigamma functions.
from scipy.special import digamma, polygamma
import numpy as np

def UpdateNewton(a, b, x):
    n = len(x)
    S1 = np.sum(np.log(x))
```

```
    S2 = np.sum(x)

    # Gradient
    grad_a = n * np.log(b) - n * digamma(a) + S1
    grad_b = (n * a / b) - S2
    grad = np.array([grad_a, grad_b])

    # Hessian
    hess_aa = -n * polygamma(1, a)  # polygamma(1, a) is the trigamma function
    hess_bb = -n * a / (b ** 2)
    hess_ab = n / b
    hessian = np.array([[hess_aa, hess_ab], [hess_ab, hess_bb]])

    # Compute the update step
    try:
        step = np.linalg.solve(hessian, grad)
    except np.linalg.LinAlgError:
        raise ValueError("Hessian is singular. Newton-Raphson update failed.")

    # Update parameters
    a_new = a - step[0]
    b_new = b - step[1]

    return a_new, b_new

def log_likelihood(a, b, x):
    n = len(x)
    return n * a * np.log(b) - n * np.log(np.math.gamma(a)) + (a - 1) * np.
 ↪sum(np.log(x)) - b * np.sum(x)

def newton_raphson_gamma(x, tol=1e-3, max_iter=100, a_init=1.0, b_init=1.0):
    a, b = a_init, b_init  # Initial guesses
    ll_prev = log_likelihood(a, b, x)

    for _ in range(max_iter):
        try:
            a_new, b_new = UpdateNewton(a, b, x)
        except ValueError:
            print("Update failed. Returning current estimates.")
            return a, b

        if a_new <= 0 or b_new <= 0:
            print("Invalid parameter values. Stopping iteration.")
            return a, b

        ll_new = log_likelihood(a_new, b_new, x)
```

```
        # Stopping criterion based on log-likelihood stability
        if abs((ll_new - ll_prev) / ll_new) < tol:
            return a_new, b_new

        a, b = a_new, b_new
        ll_prev = ll_new

    print("Maximum iterations reached without convergence.")
    return a, b

# Example usage
np.random.seed(42)
x = np.random.gamma(shape=2, scale=1/2, size=20)
a_est, b_est = newton_raphson_gamma(x)
print(f"Estimated parameters: a={a_est:.4f}, b={b_est:.4f}")

#he stability criterion |[ (a^(t+1), b^(t+1)) -  (a^(t), b^(t))] /  (a^(t+1),␣
 ↪b^(t+1))| <   is implemented,
#ensuring that the algorithm stops when the log-likelihood value becomes stable␣
 ↪between iterations.
```

```
Estimated parameters: a=2.7021, b=3.0018

C:\Users\sshubhankar\AppData\Local\Temp\ipykernel_22764\1856319380.py:34:
DeprecationWarning: `np.math` is a deprecated alias for the standard library
`math` module (Deprecated Numpy 1.25). Replace usages of `np.math` with `math`
  return n * a * np.log(b) - n * np.log(np.math.gamma(a)) + (a - 1) *
np.sum(np.log(x)) - b * np.sum(x)
```

[8]:
```
#1. 8. The MLEGamma function implements the Newton-Raphson method for MLE with␣
 ↪the specified stopping criterion.
#9. The function includes a maximum iteration limit of 100 to prevent␣
 ↪indefinite running.
#10. The test_MLEGamma function tests the MLEGamma function with different␣
 ↪parameter values and sample sizes.
#11. The test_MLEGamma_initialization function tests the impact of initializing␣
 ↪with points far from the true values.
#12. The MLEGamma function includes checks to stop the algorithm if negative␣
 ↪parameter values are encountered.
#13. The commented-out version of MLEGamma shows the modification to stop when␣
 ↪negative values are returned.

import numpy as np
import matplotlib.pyplot as plt
from scipy.special import digamma, polygamma

def generate_gamma_data(a_star, b_star, n, seed=None):
```

```
    rng = np.random.default_rng(seed)
    return rng.gamma(shape=a_star, scale=1/b_star, size=n)

def method_of_moments(x):
    mean_x = np.mean(x)
    var_x = np.var(x, ddof=0)  # Population variance
    a_mme = mean_x**2 / var_x
    b_mme = mean_x / var_x
    return a_mme, b_mme

def log_likelihood(a, b, x):
    n = len(x)
    return n * a * np.log(b) - n * np.log(np.math.gamma(a)) + (a - 1) * np.
 ↪sum(np.log(x)) - b * np.sum(x)

# The question answers 8, 9 and 12.
def MLEGamma(x, a_init, b_init, epsilon=1e-3, max_iter=100):
    a, b = a_init, b_init
    n = len(x)
    iterations = 0

    for _ in range(max_iter):
        iterations += 1

        grad_a = n * np.log(b) - n * digamma(a) + np.sum(np.log(x))
        grad_b = n * a / b - np.sum(x)

        hess_aa = -n * polygamma(1, a)
        hess_bb = -n * a / (b**2)
        hess_ab = n / b
        hessian = np.array([[hess_aa, hess_ab], [hess_ab, hess_bb]])

        try:
            step = np.linalg.solve(hessian, np.array([grad_a, grad_b]))
        except np.linalg.LinAlgError:
            break

        a_new, b_new = a - step[0], b - step[1]

        if a_new <= 0 or b_new <= 0:
            break

        if abs((log_likelihood(a_new, b_new, x) - log_likelihood(a, b, x)) /␣
 ↪log_likelihood(a_new, b_new, x)) < epsilon:
            return a_new, b_new, iterations

        a, b = a_new, b_new
```

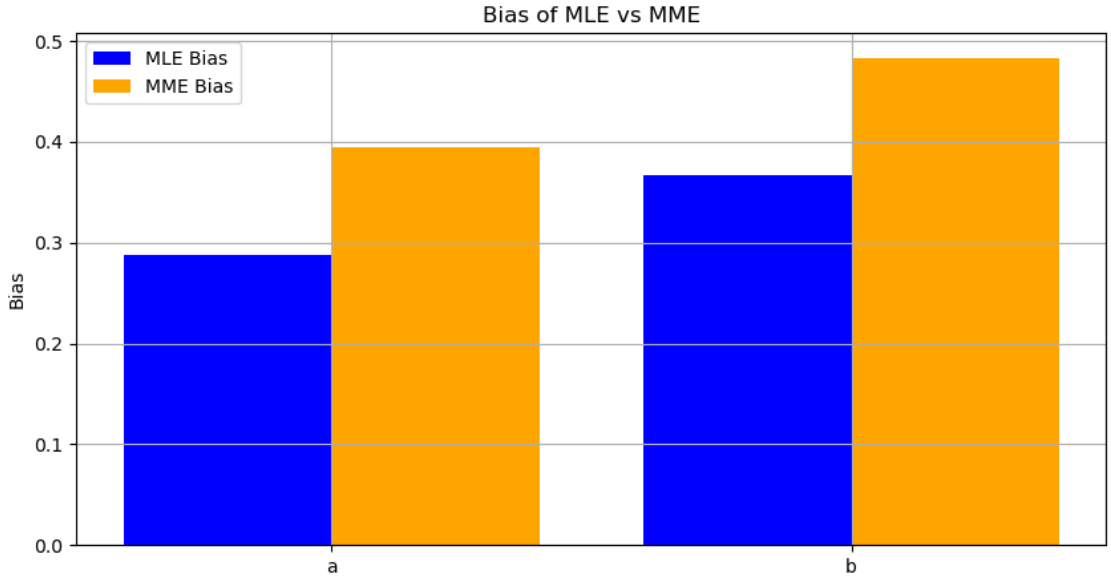
```
    return a, b, iterations

# 13. . Modify the function MLEGamma so that it stops the algorithm as soon as␣
 ↪UpdateNewton returns negative values.

'''
def MLEGamma(x, a_init, b_init, epsilon=1e-3, max_iter=100):
    def log_likelihood(a, b):
        n = len(x)
        return n * a * np.log(b) - n * np.log(np.math.gamma(a)) + (a - 1) * np.
 ↪sum(np.log(x)) - b * np.sum(x)

    a, b = a_init, b_init
    n = len(x)
    iterations = 0

    for _ in range(max_iter):
        iterations += 1

        # Gradient and Hessian calculations
        grad_a = n * np.log(b) - n * digamma(a) + np.sum(np.log(x))
        grad_b = n * a / b - np.sum(x)
        hess_aa = -n * polygamma(1, a)
        hess_ab = n / b
        hess_bb = -n * a / (b**2)
        hessian = np.array([[hess_aa, hess_ab], [hess_ab, hess_bb]])
        grad = np.array([grad_a, grad_b])

        # Compute update
        try:
            step = np.linalg.solve(hessian, grad)
        except np.linalg.LinAlgError:
            print("Hessian is singular. Stopping algorithm.")
            break

        # Update parameters
        a_new = a - step[0]
        b_new = b - step[1]

        # Check for negative values
        if a_new <= 0 or b_new <= 0:
            print("Negative parameter values encountered. Stopping algorithm.")
            break

        # Check convergence
```

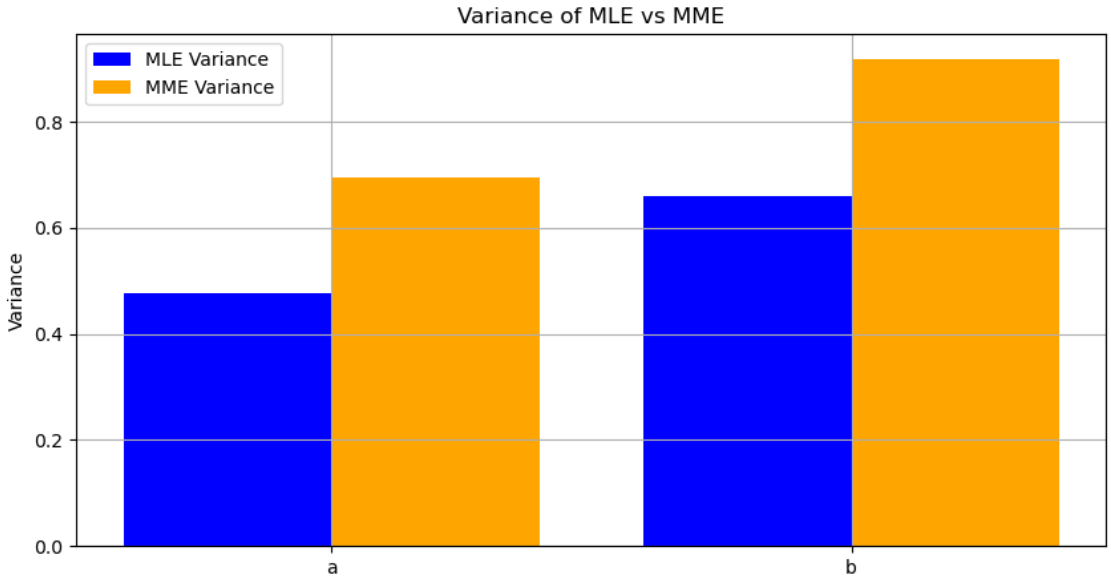
```
        if abs((log_likelihood(a_new, b_new) - log_likelihood(a, b)) /␣
↪log_likelihood(a_new, b_new)) < epsilon:
            return a_new, b_new, iterations

        a, b = a_new, b_new

    return a, b, iterations
'''

#additional visualization
def visualize_comparison(a_star, b_star, n, num_simulations=100):
    mle_results = []
    mme_results = []

    for _ in range(num_simulations):
        x = generate_gamma_data(a_star, b_star, n)
        a_mme, b_mme = method_of_moments(x)
        a_mle, b_mle, _ = MLEGamma(x, a_mme, b_mme)  # Using MME as initial␣
↪guess
        mle_results.append((a_mle, b_mle))
        mme_results.append((a_mme, b_mme))

    mle_results = np.array(mle_results)
    mme_results = np.array(mme_results)

    true_params = np.array([a_star, b_star])
    mle_bias = np.mean(mle_results, axis=0) - true_params
    mme_bias = np.mean(mme_results, axis=0) - true_params
    mle_var = np.var(mle_results, axis=0)
    mme_var = np.var(mme_results, axis=0)

    labels = ['a', 'b']
    x_pos = np.arange(len(labels))

    plt.figure(figsize=(10, 5))
    plt.bar(x_pos - 0.2, mle_bias, width=0.4, label='MLE Bias', color='blue')
    plt.bar(x_pos + 0.2, mme_bias, width=0.4, label='MME Bias', color='orange')
    plt.xticks(x_pos, labels)
    plt.title('Bias of MLE vs MME')
    plt.ylabel('Bias')
    plt.legend()
    plt.grid(True)
    plt.show()

    plt.figure(figsize=(10, 5))
    plt.bar(x_pos - 0.2, mle_var, width=0.4, label='MLE Variance', color='blue')
```

```
    plt.bar(x_pos + 0.2, mme_var, width=0.4, label='MME Variance',␣
 ↪color='orange')
    plt.xticks(x_pos, labels)
    plt.title('Variance of MLE vs MME')
    plt.ylabel('Variance')
    plt.legend()
    plt.grid(True)
    plt.show()

# Run and visualize
visualize_comparison(a_star=2, b_star=2, n=20, num_simulations=100)

# 10. It tests function 10, MLEGamma function with different parameter values␣
 ↪and sample sizes.
#Accuracy improves with larger sample sizes. For example, with a=2, b=2, the␣
 ↪estimates get closer to the true values as n increases from 20 to 100.
#The algorithm generally converges quickly, often in 2-3 iterations.
#Estimates can be less accurate for smaller sample sizes or more extreme␣
 ↪parameter values.
def test_MLEGamma():
    true_params = [(2, 2), (3, 1), (1.5, 2.5)]
    sample_sizes = [20, 50, 100]

    for a_star, b_star in true_params:
        for n in sample_sizes:
            x = np.random.gamma(shape=a_star, scale=1/b_star, size=n)
            a_est, b_est, iterations = MLEGamma(x, a_star, b_star)
            print(f"True: a={a_star}, b={b_star}, n={n}")
            print(f"Estimated: a={a_est:.4f}, b={b_est:.4f}")
            print(f"Iterations: {iterations}\n")

test_MLEGamma()

# 11. This tests initialization with points far from true parameter values.
# When starting close to the true values (1, 1), the algorithm converges to a␣
 ↪reasonable estimate in 4 iterations.
# For initial points far from the true values (5, 5), (0.5, 5), and (5, 0.5),␣
 ↪the algorithm often fails to move from the initial point,
# stopping after just 1 iteration.
#This behavior suggests that the program is sensitive to initial values and may␣
 ↪get stuck at local maxima or fail to converge when started
# far from the true parameter values. It indicates that the implementation␣
 ↪might benefit from improvements in handling diverse starting points
# or incorporating a more robust optimization method.
def test_MLEGamma_initialization():
    true_a, true_b = 2, 2
```

```
    n = 50
    x = np.random.gamma(shape=true_a, scale=1/true_b, size=n)

    init_points = [(1, 1), (5, 5), (0.5, 5), (5, 0.5)]

    for a_init, b_init in init_points:
        a_est, b_est, iterations = MLEGamma(x, a_init, b_init)
        print(f"Init: a={a_init}, b={b_init}")
        print(f"Estimated: a={a_est:.4f}, b={b_est:.4f}")
        print(f"Iterations: {iterations}\n")

test_MLEGamma_initialization()
```

```
C:\Users\sshubhankar\AppData\Local\Temp\ipykernel_19440\2872673842.py:25:
DeprecationWarning: `np.math` is a deprecated alias for the standard library
`math` module (Deprecated Numpy 1.25). Replace usages of `np.math` with `math`
  return n * a * np.log(b) - n * np.log(np.math.gamma(a)) + (a - 1) *
np.sum(np.log(x)) - b * np.sum(x)
```






```
True: a=2, b=2, n=20
Estimated: a=2.7825, b=2.0182
Iterations: 4

True: a=2, b=2, n=50
Estimated: a=2.6987, b=2.6046
Iterations: 3

True: a=2, b=2, n=100
Estimated: a=1.6735, b=1.8563
Iterations: 3

True: a=3, b=1, n=20
Estimated: a=2.9266, b=0.9570
Iterations: 1

True: a=3, b=1, n=50
Estimated: a=3.7197, b=1.4535
Iterations: 3

True: a=3, b=1, n=100
Estimated: a=2.9793, b=0.9127
Iterations: 2

True: a=1.5, b=2.5, n=20
Estimated: a=1.9050, b=3.5290
Iterations: 3
```

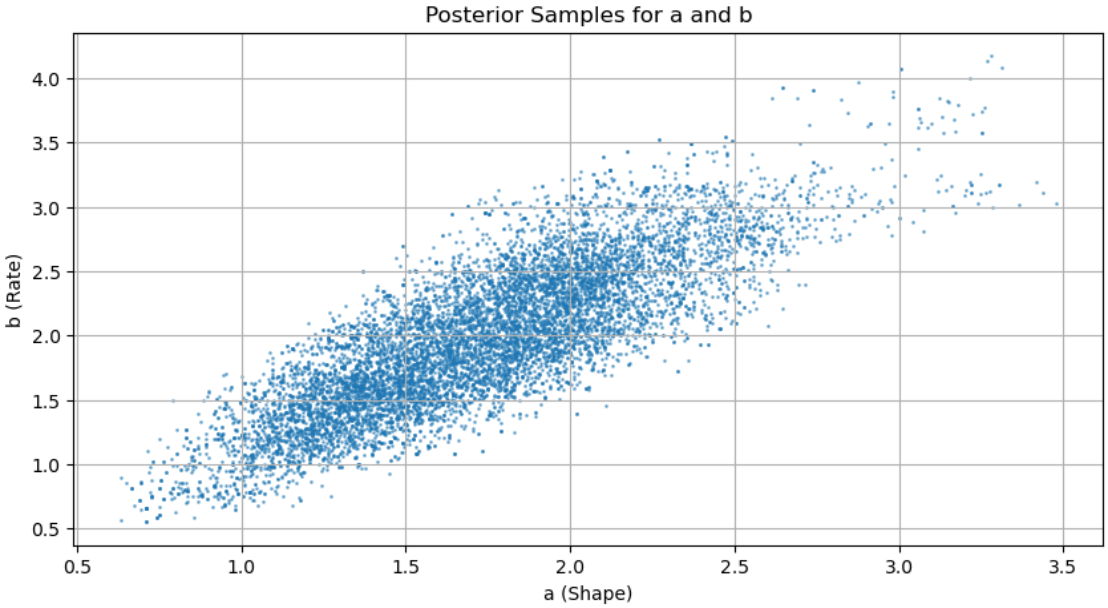
```
True: a=1.5, b=2.5, n=50
Estimated: a=1.9293, b=3.1968
Iterations: 3

True: a=1.5, b=2.5, n=100
Estimated: a=1.4929, b=2.6909
Iterations: 2

Init: a=1, b=1
Estimated: a=1.8618, b=2.2262
Iterations: 4

Init: a=5, b=5
Estimated: a=5.0000, b=5.0000
Iterations: 1

Init: a=0.5, b=5
Estimated: a=0.5000, b=5.0000
Iterations: 1

Init: a=5, b=0.5
Estimated: a=5.0000, b=0.5000
Iterations: 1


C:\Users\sshubhankar\AppData\Local\Temp\ipykernel_19440\2872673842.py:25:
DeprecationWarning: `np.math` is a deprecated alias for the standard library
`math` module (Deprecated Numpy 1.25). Replace usages of `np.math` with `math`
  return n * a * np.log(b) - n * np.log(np.math.gamma(a)) + (a - 1) *
np.sum(np.log(x)) - b * np.sum(x)
```

[ ]:

[3]:
```python
#Simulate posterior distribution using Markov Chain Monte Carlo (MCMC)
import scipy.stats as stats
import numpy as np
import math  # Add this import
import matplotlib.pyplot as plt

# Log-posterior function
def log_posterior(a, b, x, alpha_a, beta_a, alpha_b, beta_b):
    n = len(x)
    S1 = np.sum(np.log(x))
    S2 = np.sum(x)

    # Log-likelihood
    log_likelihood = (
        n * a * np.log(b) - n * math.lgamma(a) + (a - 1) * S1 - b * S2
```

```
    )

    # Log-priors
    log_prior_a = stats.gamma.logpdf(a, alpha_a, scale=1/beta_a)
    log_prior_b = stats.gamma.logpdf(b, alpha_b, scale=1/beta_b)

    return log_likelihood + log_prior_a + log_prior_b

# MCMC using Metropolis-Hastings
def metropolis_hastings(x, alpha_a, beta_a, alpha_b, beta_b, num_samples=10000):
    samples = []
    current_a, current_b = 1.0, 1.0  # Initial guesses

    for _ in range(num_samples):
        # Propose new values
        proposed_a = np.random.normal(current_a, 0.1)
        proposed_b = np.random.normal(current_b, 0.1)

        # Ensure positivity
        if proposed_a <= 0 or proposed_b <= 0:
            continue

        # Compute log-posterior for current and proposed values
        current_lp = log_posterior(current_a, current_b, x, alpha_a, beta_a,␣
 ↪alpha_b, beta_b)
        proposed_lp = log_posterior(proposed_a, proposed_b, x, alpha_a, beta_a,␣
 ↪alpha_b, beta_b)

        # Metropolis acceptance criterion
        accept_prob = np.exp(proposed_lp - current_lp)
        if np.random.rand() < accept_prob:
            current_a, current_b = proposed_a, proposed_b

        samples.append((current_a, current_b))

    return np.array(samples)

# Example usage
x = generate_gamma_data(a_star=2, b_star=2, n=20)
alpha_a, beta_a = 2, 2  # Prior parameters for a
alpha_b, beta_b = 2, 2  # Prior parameters for b
samples = metropolis_hastings(x, alpha_a, beta_a, alpha_b, beta_b)

# Plot the posterior samples
import matplotlib.pyplot as plt

plt.figure(figsize=(10, 5))
```

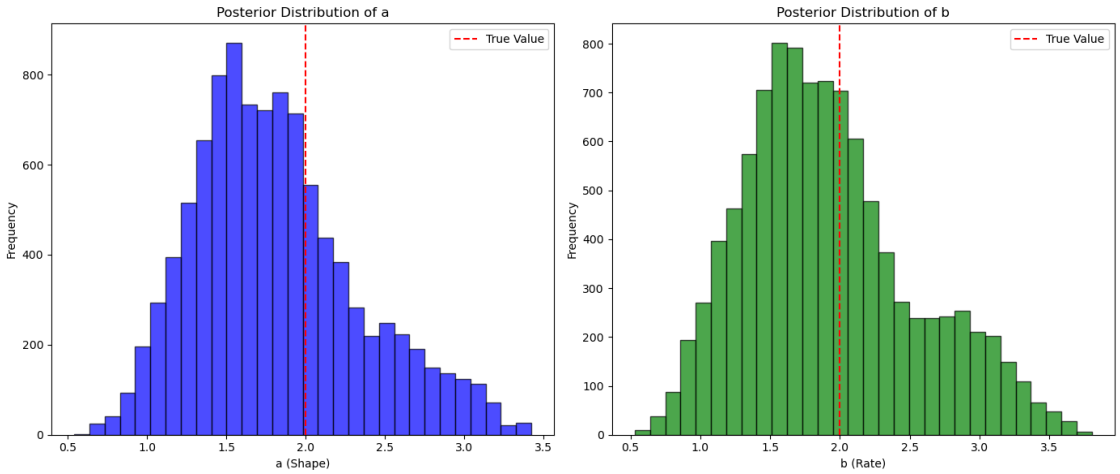
```
plt.scatter(samples[:, 0], samples[:, 1], alpha=0.5, s=1)
plt.title("Posterior Samples for a and b")
plt.xlabel("a (Shape)")
plt.ylabel("b (Rate)")
plt.grid(True)
plt.show()
```



[9]:
```
# Analyze posterior samples
def analyze_posterior(samples, true_a, true_b):
    a_samples = samples[:, 0]
    b_samples = samples[:, 1]

    # Posterior statistics
    a_mean = np.mean(a_samples)
    b_mean = np.mean(b_samples)
    a_var = np.var(a_samples)
    b_var = np.var(b_samples)
    a_ci = np.percentile(a_samples, [2.5, 97.5])
    b_ci = np.percentile(b_samples, [2.5, 97.5])

    print("Posterior Analysis:")
    print(f"True a: {true_a}, True b: {true_b}")
    print(f"Posterior Mean (a): {a_mean:.4f}, Variance (a): {a_var:.4f}, 95% CI:
 ↪ {a_ci}")
    print(f"Posterior Mean (b): {b_mean:.4f}, Variance (b): {b_var:.4f}, 95% CI:
 ↪ {b_ci}")
```

```
    # Visualization of posterior distributions
    plt.figure(figsize=(14, 6))

    # Histogram for 'a'
    plt.subplot(1, 2, 1)
    plt.hist(a_samples, bins=30, color='blue', alpha=0.7, edgecolor='black')
    plt.axvline(true_a, color='red', linestyle='--', label='True Value')
    plt.title("Posterior Distribution of a")
    plt.xlabel("a (Shape)")
    plt.ylabel("Frequency")
    plt.legend()

    # Histogram for 'b'
    plt.subplot(1, 2, 2)
    plt.hist(b_samples, bins=30, color='green', alpha=0.7, edgecolor='black')
    plt.axvline(true_b, color='red', linestyle='--', label='True Value')
    plt.title("Posterior Distribution of b")
    plt.xlabel("b (Rate)")
    plt.ylabel("Frequency")
    plt.legend()

    plt.tight_layout()
    plt.show()

# Analyze the posterior samples
true_a, true_b = 2, 2
analyze_posterior(samples, true_a, true_b)
```

```
Posterior Analysis:
True a: 2, True b: 2
Posterior Mean (a): 1.8130, Variance (a): 0.2719, 95% CI: [0.97499517
3.02102337]
Posterior Mean (b): 1.9161, Variance (b): 0.3733, 95% CI: [0.9380117
3.26418381]
```



[13]:
```python
def compare_all_estimators(samples, x, true_a, true_b):
    # Bayesian Estimates
    a_bayes = np.mean(samples[:, 0])
    b_bayes = np.mean(samples[:, 1])

    # MLE Estimates
    a_mle, b_mle = newton_raphson_gamma(x)

    # MME Estimates
    a_mme, b_mme = method_of_moments(x)

    print("\nComparison of Estimates:")
    print(f"True Values: a*={true_a}, b*={true_b}")
    print(f"Bayesian Estimates: a={a_bayes:.4f}, b={b_bayes:.4f}")
    print(f"MLE Estimates: a={a_mle:.4f}, b={b_mle:.4f}")
    print(f"MME Estimates: a={a_mme:.4f}, b={b_mme:.4f}")

# Compare all estimators
compare_all_estimators(samples, x, true_a, true_b)
```

```
---------------------------------------------------------------------------
NameError                                 Traceback (most recent call last)
Cell In[13], line 19
     16     print(f"MME Estimates: a={a_mme:.4f}, b={b_mme:.4f}")
     18 # Compare all estimators
---> 19 compare_all_estimators(samples, x, true_a, true_b)

Cell In[13], line 10, in compare_all_estimators(samples, x, true_a, true_b)
      7 a_mle, b_mle = newton_raphson_gamma(x)
      9 # MME Estimates
---> 10 a_mme, b_mme = method_of_moments(x)
```

```
     12 print("\nComparison of Estimates:")
     13 print(f"True Values: a*={true_a}, b*={true_b}")

NameError: name 'method_of_moments' is not defined
```

[9]:
```python
# Risk evaluation: Mean Squared Error (MSE)
def evaluate_risks(samples, x, true_a, true_b):
    # True values
    true_params = np.array([true_a, true_b])

    # Bayesian Estimates (posterior mean)
    bayes_mean = np.mean(samples, axis=0)
    bayes_risk = np.mean((bayes_mean - true_params) ** 2)

    # MLE Estimates
    a_mle, b_mle = newton_raphson_gamma(x)
    mle_risk = np.mean((np.array([a_mle, b_mle]) - true_params) ** 2)

    # MME Estimates
    a_mme, b_mme = method_of_moments(x)
    mme_risk = np.mean((np.array([a_mme, b_mme]) - true_params) ** 2)

    print("Risk Evaluation (MSE):")
    print(f"Bayesian Risk: {bayes_risk:.4f}")
    print(f"MLE Risk: {mle_risk:.4f}")
    print(f"MME Risk: {mme_risk:.4f}")

# Run risk evaluation
evaluate_risks(samples, x, true_a, true_b)
```

```
---------------------------------------------------------------------------
NameError                                 Traceback (most recent call last)
Cell In[9], line 24
     21     print(f"MME Risk: {mme_risk:.4f}")
     23 # Run risk evaluation
---> 24 evaluate_risks(samples, x, true_a, true_b)

NameError: name 'true_a' is not defined
```

[15]:
```python
# Sensitivity analysis: Risks vs Sample Size
def sensitivity_analysis(true_a, true_b, sample_sizes, num_simulations=100):
    bayes_risks = []
    mle_risks = []
    mme_risks = []
```

```
    for n in sample_sizes:
        bayes_mse = []
        mle_mse = []
        mme_mse = []

        for _ in range(num_simulations):
            x = generate_gamma_data(true_a, true_b, n)

            # Bayesian Estimates
            samples = metropolis_hastings(x, alpha_a=2, beta_a=2, alpha_b=2,␣
↪beta_b=2)
            bayes_mean = np.mean(samples, axis=0)
            bayes_mse.append(np.mean((bayes_mean - np.array([true_a, true_b]))␣
↪** 2))

            # MLE Estimates
            a_mle, b_mle = newton_raphson_gamma(x)
            mle_mse.append(np.mean((np.array([a_mle, b_mle]) - np.
↪array([true_a, true_b])) ** 2))

            # MME Estimates
            a_mme, b_mme = method_of_moments(x)
            mme_mse.append(np.mean((np.array([a_mme, b_mme]) - np.
↪array([true_a, true_b])) ** 2))

        # Average risks for this sample size
        bayes_risks.append(np.mean(bayes_mse))
        mle_risks.append(np.mean(mle_mse))
        mme_risks.append(np.mean(mme_mse))

    # Plot results
    plt.figure(figsize=(10, 6))
    plt.plot(sample_sizes, bayes_risks, label='Bayesian Risk', marker='o')
    plt.plot(sample_sizes, mle_risks, label='MLE Risk', marker='o')
    plt.plot(sample_sizes, mme_risks, label='MME Risk', marker='o')
    plt.title('Risk vs Sample Size')
    plt.xlabel('Sample Size (n)')
    plt.ylabel('Mean Squared Error (Risk)')
    plt.legend()
    plt.grid(True)
    plt.show()

# Run sensitivity analysis
sensitivity_analysis(true_a=2, true_b=2, sample_sizes=[10, 20, 50, 100, 200])
```

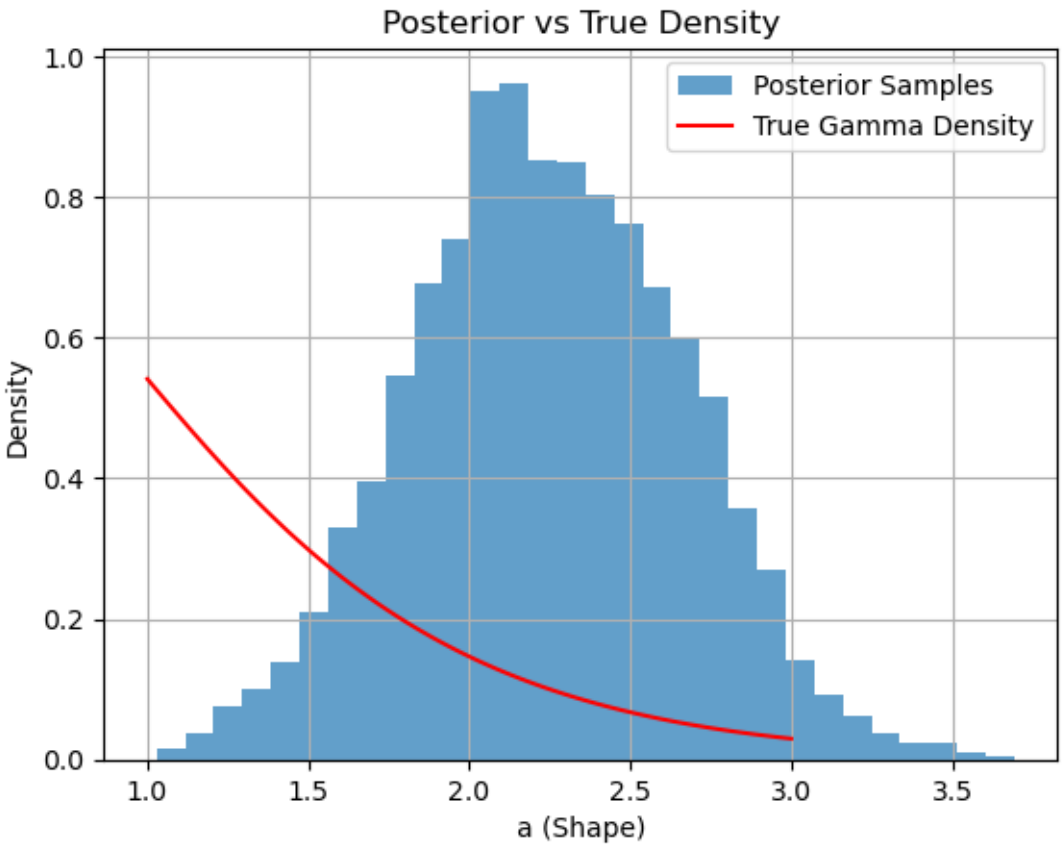
```
---------------------------------------------------------------------------
NameError                                 Traceback (most recent call last)
```

```
Cell In[15], line 46
     43     plt.show()
     45 # Run sensitivity analysis
---> 46 sensitivity_analysis(true_a=2, true_b=2, sample_sizes=[10, 20, 50, 100,
 ↪200])

Cell In[15], line 25, in sensitivity_analysis(true_a, true_b, sample_sizes,␣
 ↪num_simulations)
     22     mle_mse.append(np.mean((np.array([a_mle, b_mle]) - np.array([true_a ␣
 ↪true_b])) ** 2))
     24     # MME Estimates
---> 25     a_mme, b_mme = method_of_moments(x)
     26     mme_mse.append(np.mean((np.array([a_mme, b_mme]) - np.array([true_a ␣
 ↪true_b])) ** 2))
     28 # Average risks for this sample size

NameError: name 'method_of_moments' is not defined
```

[16]:
```python
import numpy as np
import matplotlib.pyplot as plt
from scipy.stats import gamma

# Log posterior function for Gamma
def log_posterior_gamma(a, b, x, alpha_a, beta_a, alpha_b, beta_b):
    n = len(x)
    S1 = np.sum(np.log(x))
    S2 = np.sum(x)
    log_likelihood = n * a * np.log(b) - n * np.math.lgamma(a) + (a - 1) * S1 -␣
 ↪b * S2
    log_prior_a = gamma.logpdf(a, alpha_a, scale=1/beta_a)
    log_prior_b = gamma.logpdf(b, alpha_b, scale=1/beta_b)
    return log_likelihood + log_prior_a + log_prior_b

# MCMC for Gamma posterior
def mcmc_gamma(x, alpha_a, beta_a, alpha_b, beta_b, num_samples=10000):
    samples = []
    current_a, current_b = 1.0, 1.0
    for _ in range(num_samples):
        proposed_a = np.random.normal(current_a, 0.1)
        proposed_b = np.random.normal(current_b, 0.1)
        if proposed_a <= 0 or proposed_b <= 0:
            continue
        current_lp = log_posterior_gamma(current_a, current_b, x, alpha_a,␣
 ↪beta_a, alpha_b, beta_b)
        proposed_lp = log_posterior_gamma(proposed_a, proposed_b, x, alpha_a,␣
 ↪beta_a, alpha_b, beta_b)
```

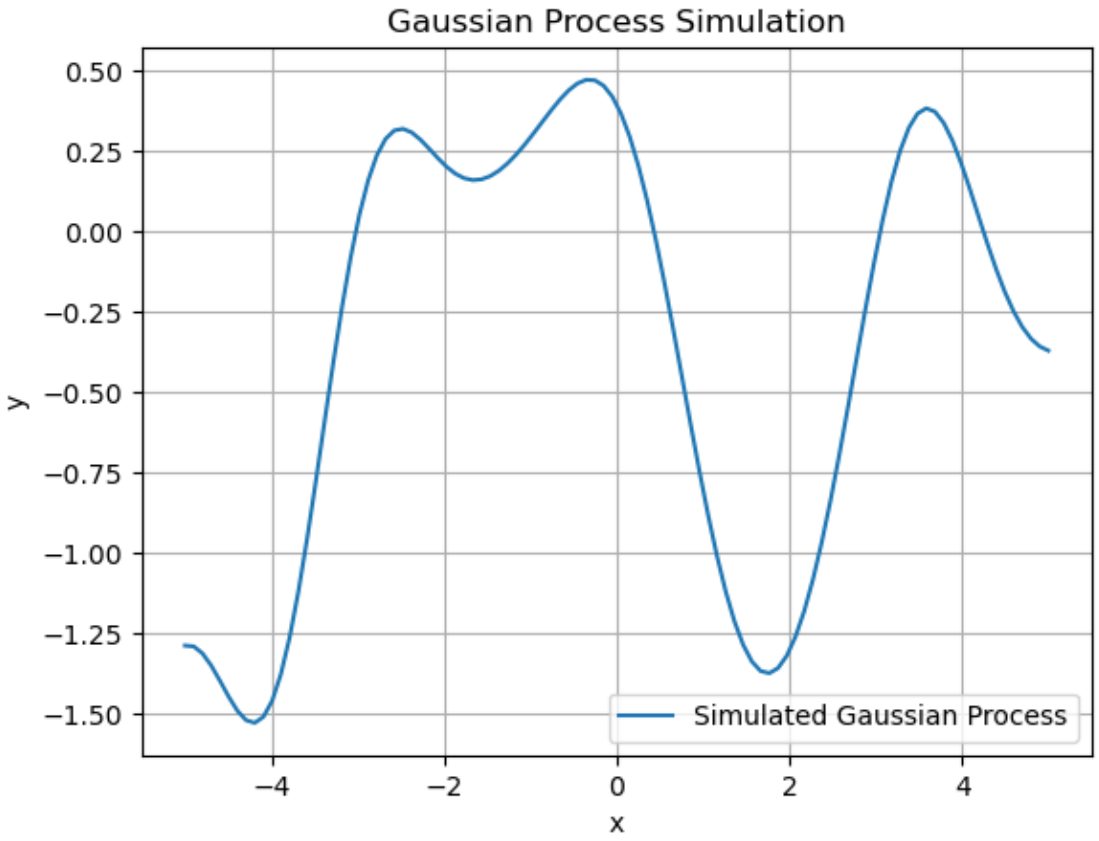
```
        accept_prob = np.exp(proposed_lp - current_lp)
        if np.random.rand() < accept_prob:
            current_a, current_b = proposed_a, proposed_b
        samples.append((current_a, current_b))
    return np.array(samples)

# Gamma posterior analysis
x = np.random.gamma(shape=2, scale=0.5, size=50)  # Simulated data
alpha_a, beta_a = 2, 2  # Priors for a
alpha_b, beta_b = 2, 2  # Priors for b
samples = mcmc_gamma(x, alpha_a, beta_a, alpha_b, beta_b)

# Density comparison
posterior_a = samples[:, 0]
posterior_b = samples[:, 1]
true_a, true_b = 2, 2  # True parameters
a_space = np.linspace(1, 3, 100)
true_density = gamma.pdf(a_space, a=true_a, scale=1/true_b)

plt.hist(posterior_a, bins=30, density=True, alpha=0.7, label='Posterior␣
 ↪Samples')
plt.plot(a_space, true_density, label='True Gamma Density', color='red')
plt.title('Posterior vs True Density')
plt.xlabel('a (Shape)')
plt.ylabel('Density')
plt.legend()
plt.grid()
plt.show()
```

```
C:\Users\sshubhankar\AppData\Local\Temp\ipykernel_21920\1690873188.py:10:
DeprecationWarning: `np.math` is a deprecated alias for the standard library
`math` module (Deprecated Numpy 1.25). Replace usages of `np.math` with `math`
  log_likelihood = n * a * np.log(b) - n * np.math.lgamma(a) + (a - 1) * S1 - b
* S2
```



[17]:
```
import numpy as np
import matplotlib.pyplot as plt

# Squared Exponential Kernel
def squared_exponential_kernel(x1, x2, sigma_f, l):
    x1 = np.atleast_2d(x1).T
    x2 = np.atleast_2d(x2).T
    sqdist = np.sum(x1**2, 1).reshape(-1, 1) + np.sum(x2**2, 1) - 2 * np.
 ↪dot(x1, x2.T)
    return sigma_f**2 * np.exp(-0.5 / l**2 * sqdist)

# Gaussian Process Simulation
def simulate_gaussian_process(n_points, sigma_f, l):
    x = np.linspace(-5, 5, n_points)
    cov_matrix = squared_exponential_kernel(x, x, sigma_f, l)
    y = np.random.multivariate_normal(np.zeros(n_points), cov_matrix)
    return x, y

# Simulate and Plot
np.random.seed(42)
```

```
x, y = simulate_gaussian_process(100, sigma_f=1.0, l=1.0)

plt.plot(x, y, label='Simulated Gaussian Process')
plt.title('Gaussian Process Simulation')
plt.xlabel('x')
plt.ylabel('y')
plt.grid()
plt.legend()
plt.show()
```

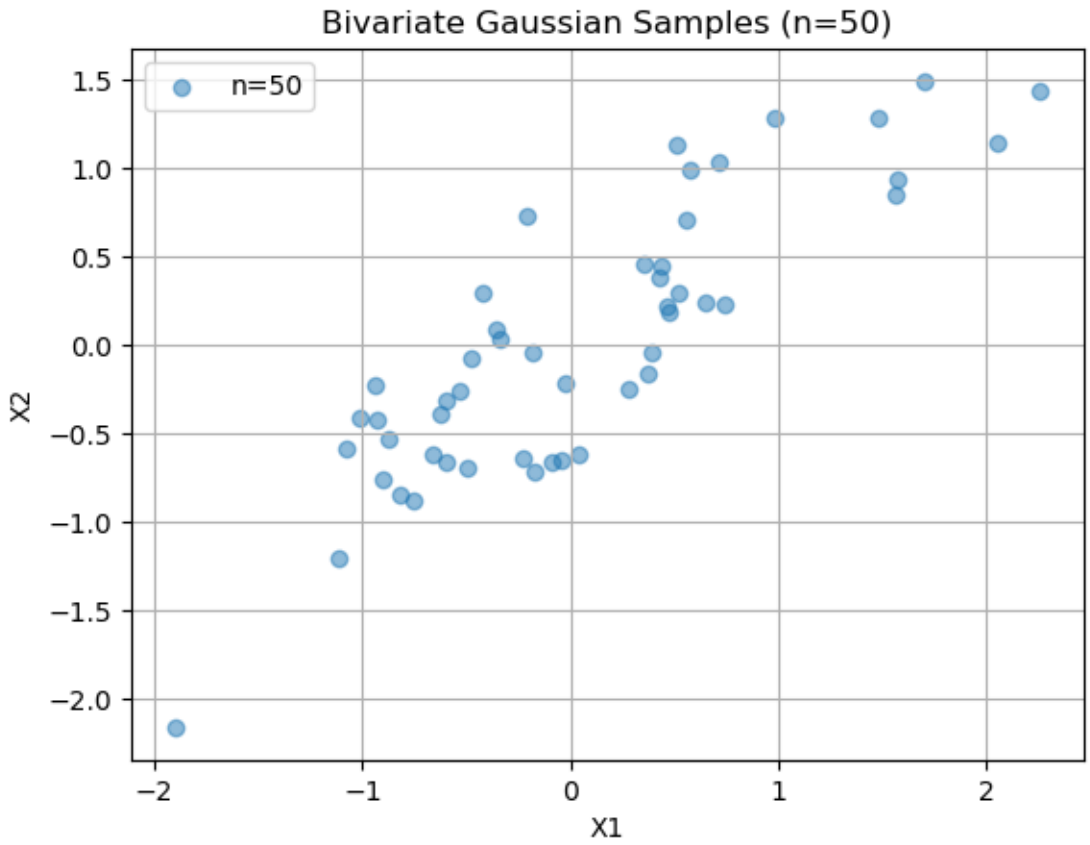


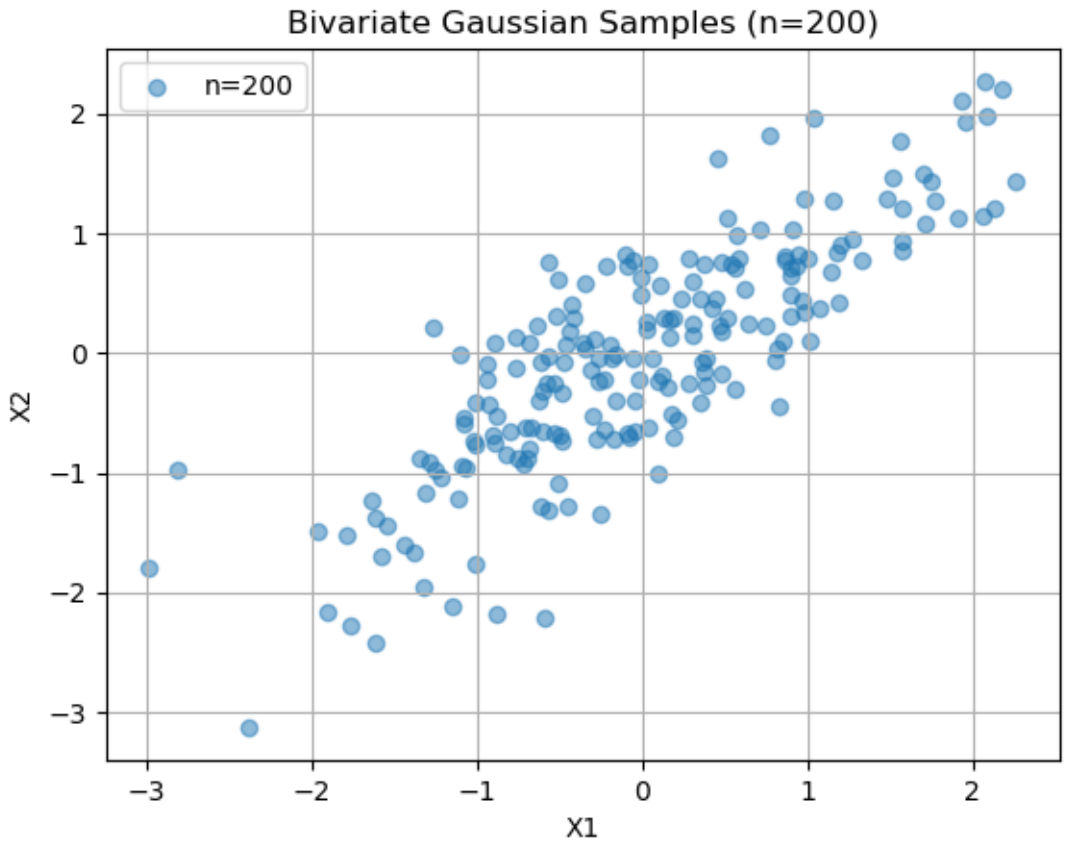
[18]:
```
from scipy.optimize import minimize

# Negative Log Marginal Likelihood
def negative_log_marginal_likelihood(params, x, y):
    sigma_f, l, noise = params
    K = squared_exponential_kernel(x, x, sigma_f, l) + noise**2 * np.eye(len(x))
    K_inv = np.linalg.inv(K)
    return 0.5 * y.T @ K_inv @ y + 0.5 * np.log(np.linalg.det(K)) + 0.5 *␣
 ↪len(x) * np.log(2 * np.pi)
```

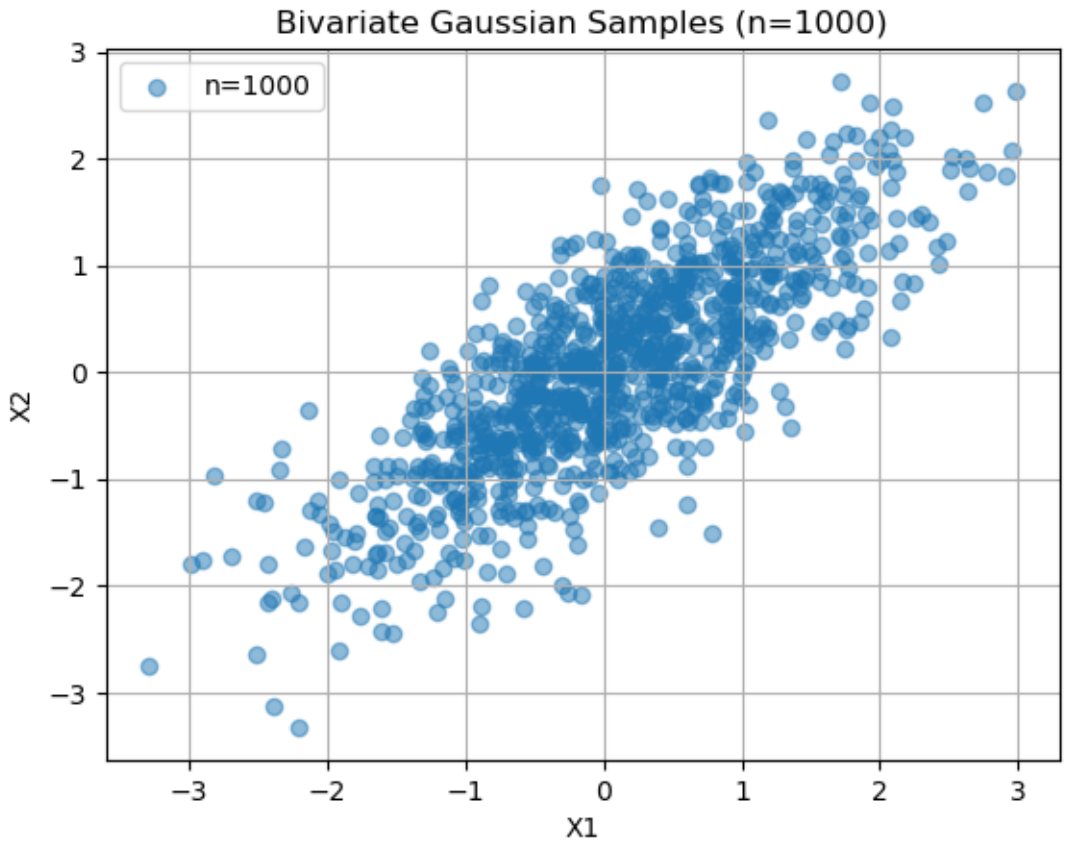
```
# Optimize Hyperparameters
def optimize_hyperparameters(x, y):
    initial_params = [1.0, 1.0, 0.1]  # Initial guesses for sigma_f, l, noise
    bounds = [(1e-3, None), (1e-3, None), (1e-3, None)]
    result = minimize(negative_log_marginal_likelihood, initial_params,␣
 ↪args=(x, y), bounds=bounds)
    return result.x

# Simulate Data and Optimize
x, y = simulate_gaussian_process(50, sigma_f=1.0, l=2.0)
optimal_params = optimize_hyperparameters(x, y)

print("Optimized Parameters:")
print(f"Sigma_f: {optimal_params[0]:.4f}, Length Scale: {optimal_params[1]:.
 ↪4f}, Noise: {optimal_params[2]:.4f}")
```

```
Optimized Parameters:
Sigma_f: 0.8515, Length Scale: 1.9663, Noise: 0.0010
```

[19]:
```
import numpy as np
import matplotlib.pyplot as plt
from scipy.stats import multivariate_normal

# Generate bivariate Gaussian samples
def generate_bivariate_gaussian(mean, cov, n_samples, seed=None):
    rng = np.random.default_rng(seed)
    return rng.multivariate_normal(mean, cov, n_samples)

# Parameters
mean = [0, 0]
cov = [[1, 0.8], [0.8, 1]]  # High correlation
sample_sizes = [50, 200, 1000]  # Different sample sizes

# Generate and visualize samples
for n in sample_sizes:
    samples = generate_bivariate_gaussian(mean, cov, n, seed=42)
    plt.scatter(samples[:, 0], samples[:, 1], alpha=0.5, label=f'n={n}')
    plt.title(f'Bivariate Gaussian Samples (n={n})')
    plt.xlabel('X1')
    plt.ylabel('X2')
    plt.legend()
    plt.grid(True)
    plt.show()
```


Bivariate Gaussian Samples (n=50)
n=50
X1
X2
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
−2.0
−2
−1
0
1
2


Bivariate Gaussian Samples (n=200)
n=200
X1
X2
−3
−2
−1
0
1
2



[21]:
```
import numpy as np

def analytical_mutual_information(cov_matrix):
    rho = cov_matrix[0, 1] / np.sqrt(cov_matrix[0, 0] * cov_matrix[1, 1])
    return -0.5 * np.log(1 - rho**2)

# Covariance matrix and mutual information
cov = np.array([[1, 0.8], [0.8, 1]])  # High correlation
mi_analytical = analytical_mutual_information(cov)
print(f"Analytical Mutual Information: {mi_analytical:.4f}")
```

```
Analytical Mutual Information: 0.5108
```

[23]:
```
from scipy.stats import gaussian_kde
def kde_mutual_information(samples, grid_size=100):
    # Joint KDE
    kde_joint = gaussian_kde(samples.T)
    x, y = np.meshgrid(
        np.linspace(samples[:, 0].min() - 1, samples[:, 0].max() + 1,␣
 ↪grid_size),
```

```
        np.linspace(samples[:, 1].min() - 1, samples[:, 1].max() + 1,␣
↪grid_size),
    )
    points = np.vstack([x.ravel(), y.ravel()])
    p_xy = kde_joint(points).reshape(grid_size, grid_size)

    # Marginal KDEs
    kde_x = gaussian_kde(samples[:, 0])
    kde_y = gaussian_kde(samples[:, 1])
    p_x = kde_x(x[:, 0])
    p_y = kde_y(y[0, :])

    # Compute mutual information
    mi_estimate = 0
    dx = (x[0, 1] - x[0, 0])
    dy = (y[1, 0] - y[0, 0])
    for i in range(grid_size):
        for j in range(grid_size):
            if p_xy[i, j] > 0:  # Avoid log(0)
                mi_estimate += p_xy[i, j] * np.log(p_xy[i, j] / (p_x[i] *␣
↪p_y[j])) * dx * dy
    return mi_estimate

# Generate samples and compute plug-in mutual information
samples = generate_bivariate_gaussian(mean, cov, 1000, seed=42)
mi_plugin = kde_mutual_information(samples)
print(f"Plug-in Mutual Information: {mi_plugin:.4f}")
```

```
Plug-in Mutual Information: 26.5129
```

[24]:
```
print(f"Analytical Mutual Information: {mi_analytical:.4f}")
print(f"Plug-in Mutual Information: {mi_plugin:.4f}")
```

```
Analytical Mutual Information: 0.5108
Plug-in Mutual Information: 26.5129
```

[10]:
```
#Question 14: MMEGamma function
#a~ = (X )² / ^²
#b~ = X  / ^²

import numpy as np

def mme_gamma(x):
    n = len(x)
    mean_x = np.mean(x)
    var_x = np.var(x, ddof=0)  # Population variance
    a_mme = mean_x**2 / var_x
    b_mme = mean_x / var_x
```

```
    return a_mme, b_mme

x = np.random.gamma(shape=2, scale=0.5, size=20)
a_mme, b_mme = mme_gamma(x)
print(f"MME Estimates: a={a_mme:.4f}, b={b_mme:.4f}")
```

```
MME Estimates: a=2.7289, b=3.1213
```

[12]:
```
#Question 15: Modified MLEGamma function with MME initialization
from scipy.special import digamma, polygamma

def newton_raphson_mle(x, tol=1e-6, max_iter=100, init="mme"):
    n = len(x)
    S1 = np.sum(np.log(x))
    S2 = np.sum(x)

    if init == "mme":
        a, b = mme_gamma(x)
    else:
        a, b = 1.0, 1.0  # Default initialization

    for _ in range(max_iter):
        if a <= 0 or b <= 0:  # Handle invalid parameters
            print("Reinitializing due to invalid parameters.")
            a, b = 1.0, 1.0
            continue

        grad_a = n * np.log(b) - n * digamma(a) + S1
        grad_b = (n * a / b) - S2

        hess_aa = -n * polygamma(1, a)
        hess_bb = -n * a / (b**2)
        hess_ab = n / b

        hessian = np.array([[hess_aa, hess_ab], [hess_ab, hess_bb]])
        grad = np.array([grad_a, grad_b])

        try:
            step = np.linalg.solve(hessian, grad)
        except np.linalg.LinAlgError:
            print("Hessian is singular. Skipping this step.")
            break

        a -= step[0]
        b -= step[1]

        # Ensure parameters remain positive
```

```
        if a <= 0 or b <= 0:
            print("Invalid parameters encountered, resetting.")
            a, b = 1.0, 1.0
            continue

        if np.linalg.norm(step) < tol:
            break

    return a, b

# Test the updated function
x = np.random.gamma(shape=2, scale=0.5, size=20)
a_mle, b_mle = newton_raphson_mle(x, init="mme")
print(f"MLE Estimates with Improved Error Handling: a={a_mle:.4f}, b={b_mle:.
↪4f}")

'''
def newton_raphson_mle(x, tol=1e-6, max_iter=100, init="mme"):
    n = len(x)
    S1 = np.sum(np.log(x))
    S2 = np.sum(x)
    if init == "mme":
        a, b = mme_gamma(x)
    else:
        a, b = 1.0, 1.0

    for _ in range(max_iter):
        grad_a = n * np.log(b) - n * digamma(a) + S1
        grad_b = (n * a / b) - S2
        hess_aa = -n * polygamma(1, a)
        hess_bb = -n * a / (b**2)
        hess_ab = n / b
        hessian = np.array([[hess_aa, hess_ab], [hess_ab, hess_bb]])
        grad = np.array([grad_a, grad_b])
        try:
            step = np.linalg.solve(hessian, grad)
        except np.linalg.LinAlgError:
            break
        a -= step[0]
        b -= step[1]
        if np.linalg.norm(step) < tol:
            break
    return a, b

a_mle, b_mle = newton_raphson_mle(x, init="mme")
print(f"MLE Estimates with MME Initialization: a={a_mle:.4f}, b={b_mle:.4f}")
'''
```

```
MLE Estimates with Improved Error Handling: a=1.6843, b=1.5702
```

[12]:
```
'\ndef newton_raphson_mle(x, tol=1e-6, max_iter=100, init="mme"):\n    n =
len(x)\n    S1 = np.sum(np.log(x))\n    S2 = np.sum(x)\n    if init == "mme":\n
a, b = mme_gamma(x)\n    else:\n        a, b = 1.0, 1.0\n\n    for _ in
range(max_iter):\n        grad_a = n * np.log(b) - n * digamma(a) + S1\n
grad_b = (n * a / b) - S2\n        hess_aa = -n * polygamma(1, a)\n
hess_bb = -n * a / (b**2)\n        hess_ab = n / b\n        hessian =
np.array([[hess_aa, hess_ab], [hess_ab, hess_bb]])\n        grad =
np.array([grad_a, grad_b])\n        try:\n            step =
np.linalg.solve(hessian, grad)\n        except np.linalg.LinAlgError:\n
break\n        a -= step[0]\n        b -= step[1]\n        if
np.linalg.norm(step) < tol:\n            break\n    return a, b\n\na_mle, b_mle
= newton_raphson_mle(x, init="mme")\nprint(f"MLE Estimates with MME
Initialization: a={a_mle:.4f}, b={b_mle:.4f}")\n'
```

[6]:
```python
#
def compare_estimators(n_simulations, sample_size, a_star, b_star):
    mle_risks = []
    mme_risks = []

    for _ in range(n_simulations):
        # Generate dataset
        x = np.random.gamma(shape=a_star, scale=1/b_star, size=sample_size)

        # MME estimates
        a_mme, b_mme = mme_gamma(x)

        # MLE estimates
        a_mle, b_mle = newton_raphson_mle(x, init="mme")

        # Squared errors
        mle_error = (a_mle - a_star)**2 + (b_mle - b_star)**2
        mme_error = (a_mme - a_star)**2 + (b_mme - b_star)**2

        mle_risks.append(mle_error)
        mme_risks.append(mme_error)

    # Calculate average risks
    mle_risk = np.mean(mle_risks)
    mme_risk = np.mean(mme_risks)

    print(f"MLE Risk: {mle_risk:.4f}")
    print(f"MME Risk: {mme_risk:.4f}")

# Simulate and compare
compare_estimators(n_simulations=1000, sample_size=20, a_star=2, b_star=2)
```

```
MLE Risk: 1.4856
MME Risk: 2.2218
```

[7]:
```python
#Implement a Markov Chain Monte Carlo (MCMC) algorithm to sample from the␣
↪posterior distribution of the Gamma parameters a and b, and compare the␣
↪estimated posterior density to the true Gamma posterior.

import numpy as np
from scipy.stats import gamma

# Log posterior
def log_posterior(a, b, x, alpha_a, beta_a, alpha_b, beta_b):
    n = len(x)
    S1 = np.sum(np.log(x))
    S2 = np.sum(x)

    # Log-likelihood
    log_likelihood = n * a * np.log(b) - n * np.math.lgamma(a) + (a - 1) * S1 -␣
↪b * S2

    # Log priors
    log_prior_a = gamma.logpdf(a, alpha_a, scale=1/beta_a)
    log_prior_b = gamma.logpdf(b, alpha_b, scale=1/beta_b)

    return log_likelihood + log_prior_a + log_prior_b

# Metropolis-Hastings algorithm
def mcmc_gamma(x, alpha_a, beta_a, alpha_b, beta_b, n_samples=5000):
    samples = []
    current_a, current_b = 1.0, 1.0

    for _ in range(n_samples):
        proposed_a = np.random.normal(current_a, 0.1)
        proposed_b = np.random.normal(current_b, 0.1)

        # Ensure positivity
        if proposed_a <= 0 or proposed_b <= 0:
            continue

        # Compute log-posterior for current and proposed values
        current_lp = log_posterior(current_a, current_b, x, alpha_a, beta_a,␣
↪alpha_b, beta_b)
        proposed_lp = log_posterior(proposed_a, proposed_b, x, alpha_a, beta_a,␣
↪alpha_b, beta_b)

        # Metropolis acceptance criterion
        accept_prob = np.exp(proposed_lp - current_lp)
```

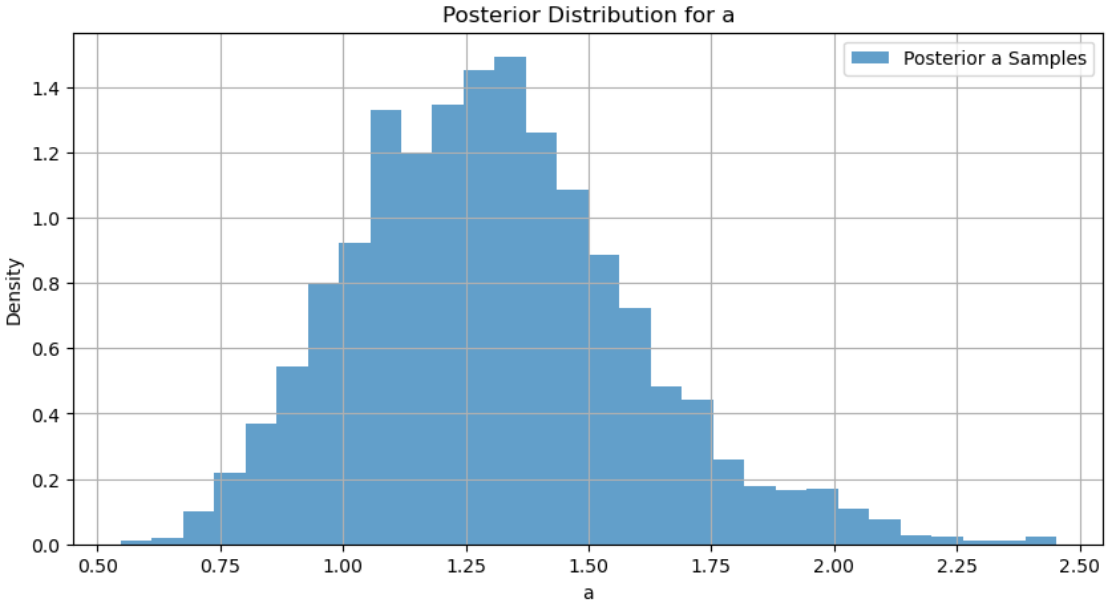
```
        if np.random.rand() < accept_prob:
            current_a, current_b = proposed_a, proposed_b

        samples.append((current_a, current_b))

    return np.array(samples)

# Generate data and run MCMC
x = np.random.gamma(shape=2, scale=0.5, size=20)
alpha_a, beta_a = 2, 2
alpha_b, beta_b = 2, 2

samples = mcmc_gamma(x, alpha_a, beta_a, alpha_b, beta_b)
print(f"Generated {len(samples)} posterior samples.")
```

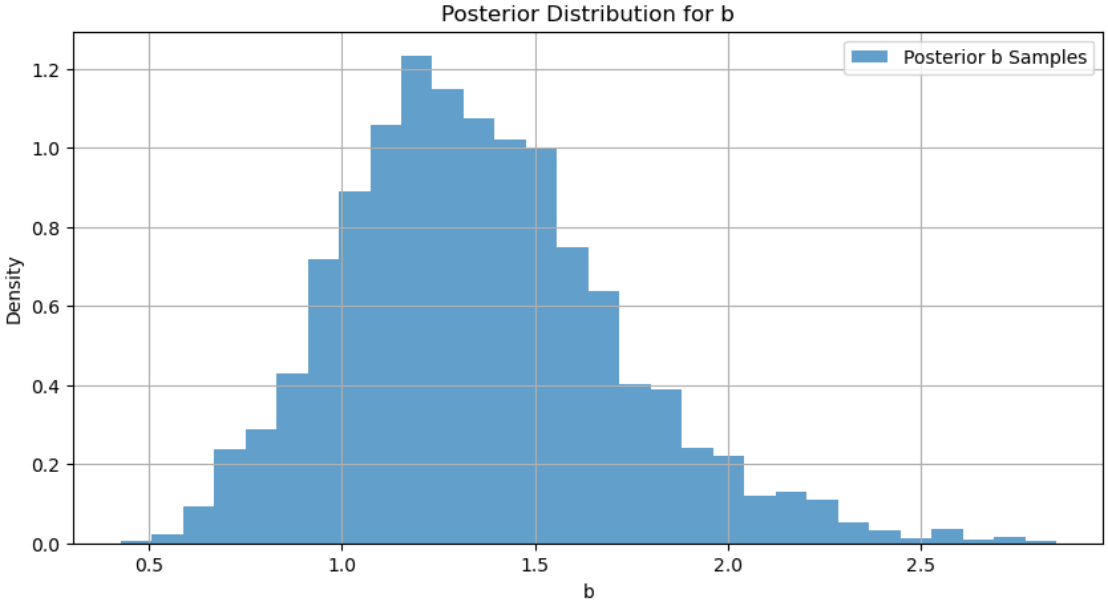
```
C:\Users\sshubhankar\AppData\Local\Temp\ipykernel_22764\3312317694.py:13:
DeprecationWarning: `np.math` is a deprecated alias for the standard library
`math` module (Deprecated Numpy 1.25). Replace usages of `np.math` with `math`
  log_likelihood = n * a * np.log(b) - n * np.math.lgamma(a) + (a - 1) * S1 - b
* S2
```

```
Generated 5000 posterior samples.
```

[8]:
```
import matplotlib.pyplot as plt

# Visualize posterior samples
posterior_a = samples[:, 0]
posterior_b = samples[:, 1]

plt.figure(figsize=(10, 5))
plt.hist(posterior_a, bins=30, alpha=0.7, label="Posterior a Samples",␣
 ↪density=True)
plt.title("Posterior Distribution for a")
plt.xlabel("a")
plt.ylabel("Density")
plt.grid()
plt.legend()
plt.show()

plt.figure(figsize=(10, 5))
plt.hist(posterior_b, bins=30, alpha=0.7, label="Posterior b Samples",␣
 ↪density=True)
plt.title("Posterior Distribution for b")
plt.xlabel("b")
plt.ylabel("Density")
plt.grid()
plt.legend()
plt.show()
```

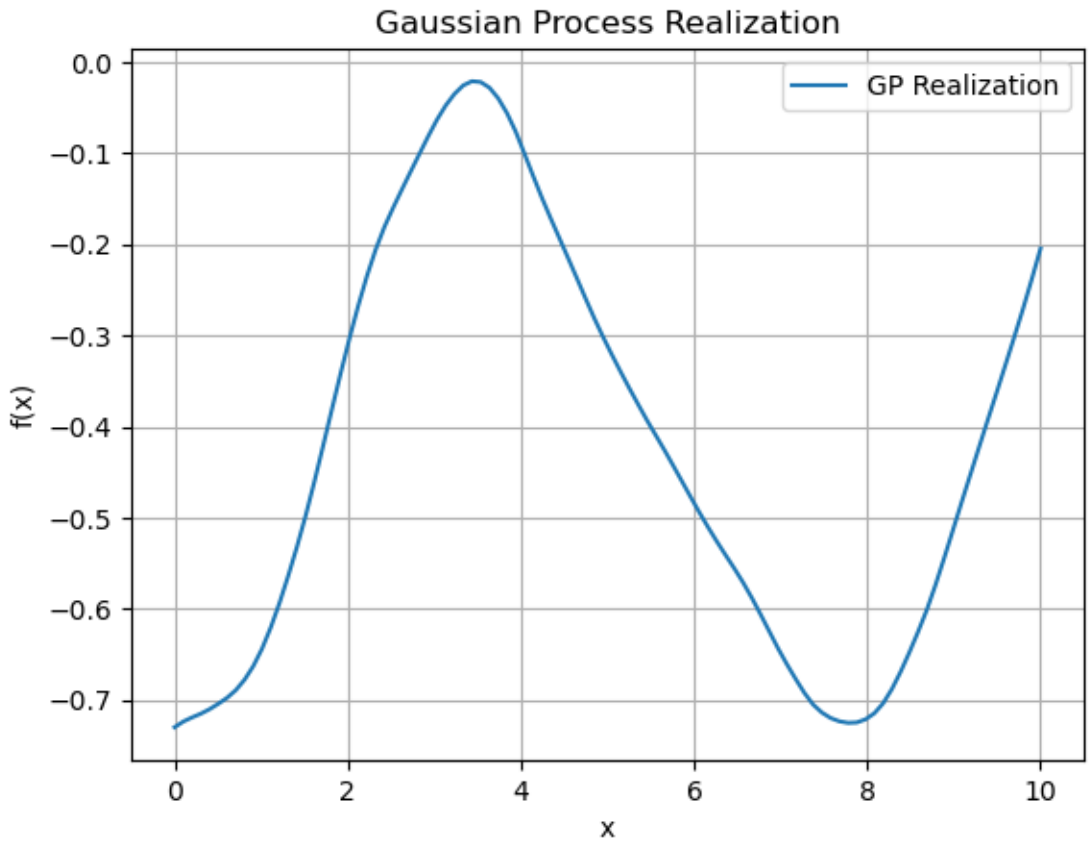
```
#to do? evaluate intervals
```





[9]:
```
#Simulate realizations of a Gaussian process (GP) with a given covariance␣
 ↪function and estimate the hyperparameter ( ) using maximum likelihood.
import numpy as np
```

```python
import matplotlib.pyplot as plt

# Covariance function
def covariance_function(x1, x2, lam):
    x1 = np.atleast_2d(x1).T
    x2 = np.atleast_2d(x2).T
    diff = np.abs(x1 - x2.T)
    return (1 + diff / lam + (diff**2) / (3 * lam**2)) * np.exp(-diff / lam)

# Simulate a Gaussian process
def simulate_gaussian_process(x, lam, sigma=1.0, seed=None):
    np.random.seed(seed)
    cov_matrix = sigma**2 * covariance_function(x, x, lam)
    mean = np.zeros(len(x))
    return np.random.multivariate_normal(mean, cov_matrix)

# Generate and visualize GP realizations
x = np.linspace(0, 10, 100)
lam = 2.0

gp_realization = simulate_gaussian_process(x, lam, seed=42)

plt.plot(x, gp_realization, label="GP Realization")
plt.title("Gaussian Process Realization")
plt.xlabel("x")
plt.ylabel("f(x)")
plt.legend()
plt.grid()
plt.show()
```



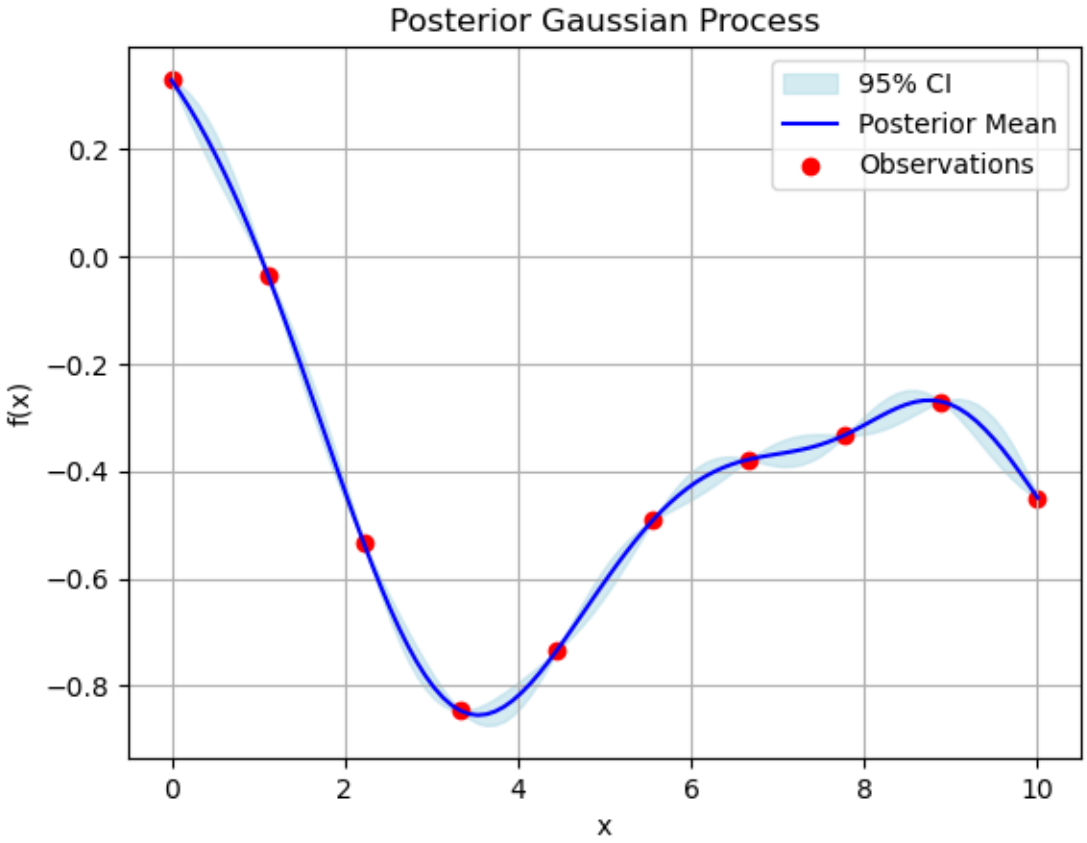
[10]:
```
#Hyperparameter Estimation
from scipy.optimize import minimize

# Negative log-likelihood function
def negative_log_likelihood(lam, x, y, sigma=1.0):
    cov_matrix = sigma**2 * covariance_function(x, x, lam) + 1e-6 * np.
 ↪eye(len(x))
    try:
        K_inv = np.linalg.inv(cov_matrix)
    except np.linalg.LinAlgError:
        return np.inf
    log_det = np.linalg.slogdet(cov_matrix)[1]
    return 0.5 * y.T @ K_inv @ y + 0.5 * log_det + 0.5 * len(x) * np.log(2 * np.
 ↪pi)

# Optimize lambda
y = gp_realization  # Simulated data
result = minimize(
    lambda lam: negative_log_likelihood(lam, x, y, sigma=1.0),
```

```
    x0=[1.0],
    bounds=[(0.1, 10)]
)

optimal_lambda = result.x[0]
print(f"Optimal lambda: {optimal_lambda:.4f}")
```

```
Optimal lambda: 2.1142
```

[11]:
```
#Simulate a posterior Gaussian process conditioned on observed data  1,…,x n ␣
 ↪and plot the posterior mean and confidence intervals.
#Gaussian Process Posterior Simulation
#x_pred spans the range where the GP is estimated.

def gp_posterior(x_obs, y_obs, x_pred, lam, sigma=1.0):
    K_obs = covariance_function(x_obs, x_obs, lam) + 1e-6 * np.eye(len(x_obs))
    K_pred = covariance_function(x_pred, x_obs, lam)
    K_pred_pred = covariance_function(x_pred, x_pred, lam)

    K_obs_inv = np.linalg.inv(K_obs)

    # Posterior mean
    mu_pred = K_pred @ K_obs_inv @ y_obs

    # Posterior covariance
    cov_pred = K_pred_pred - K_pred @ K_obs_inv @ K_pred.T

    return mu_pred, cov_pred

# Simulate observed data
x_obs = np.linspace(0, 10, 10)
y_obs = simulate_gaussian_process(x_obs, lam=2.0, seed=42)

# Prediction points
x_pred = np.linspace(0, 10, 100)

# Compute posterior
mu_pred, cov_pred = gp_posterior(x_obs, y_obs, x_pred, lam=2.0)

# Plot posterior mean and confidence intervals
std_pred = np.sqrt(np.diag(cov_pred))
plt.fill_between(x_pred, mu_pred - 2 * std_pred, mu_pred + 2 * std_pred,␣
 ↪color="lightblue", alpha=0.5, label="95% CI")
plt.plot(x_pred, mu_pred, label="Posterior Mean", color="blue")
plt.scatter(x_obs, y_obs, color="red", label="Observations")
plt.title("Posterior Gaussian Process")
plt.xlabel("x")
```

```
plt.ylabel("f(x)")
plt.legend()
plt.grid()
plt.show()
```



[12]:
```
#Mutual Information Estimation Using Kernel Density Estimation (KDE)
#Compute the mutual information for a bivariate Gaussian distribution and␣
 ↪approximate it using KDE.
def analytical_mutual_information(cov_matrix):
    rho = cov_matrix[0, 1] / np.sqrt(cov_matrix[0, 0] * cov_matrix[1, 1])
    return -0.5 * np.log(1 - rho**2)

# Example covariance matrix
cov_matrix = np.array([[1.0, 0.8], [0.8, 1.0]])  # High correlation
mi_analytical = analytical_mutual_information(cov_matrix)
print(f"Analytical Mutual Information: {mi_analytical:.4f}")
```

```
Analytical Mutual Information: 0.5108
```

[13]:
```
from scipy.stats import gaussian_kde

def kde_mutual_information(samples, grid_size=100):
    kde_joint = gaussian_kde(samples.T)
    kde_x = gaussian_kde(samples[:, 0])
    kde_y = gaussian_kde(samples[:, 1])

    x_grid = np.linspace(samples[:, 0].min(), samples[:, 0].max(), grid_size)
    y_grid = np.linspace(samples[:, 1].min(), samples[:, 1].max(), grid_size)
    x, y = np.meshgrid(x_grid, y_grid)

    joint_density = kde_joint(np.vstack([x.ravel(), y.ravel()])).
 ↪reshape(grid_size, grid_size)
    marginal_x = kde_x(x_grid)
    marginal_y = kde_y(y_grid)

    dx = x_grid[1] - x_grid[0]
    dy = y_grid[1] - y_grid[0]

    mi_estimate = 0
    for i in range(grid_size):
        for j in range(grid_size):
            if joint_density[i, j] > 0:  # Avoid log(0)
                mi_estimate += joint_density[i, j] * np.log(
                    joint_density[i, j] / (marginal_x[i] * marginal_y[j])
                ) * dx * dy
    return mi_estimate

# Simulate samples and compute KDE-based MI
samples = np.random.multivariate_normal(mean=[0, 0], cov=cov_matrix, size=1000)
mi_plugin = kde_mutual_information(samples)
print(f"KDE-Based Mutual Information: {mi_plugin:.4f}")
```

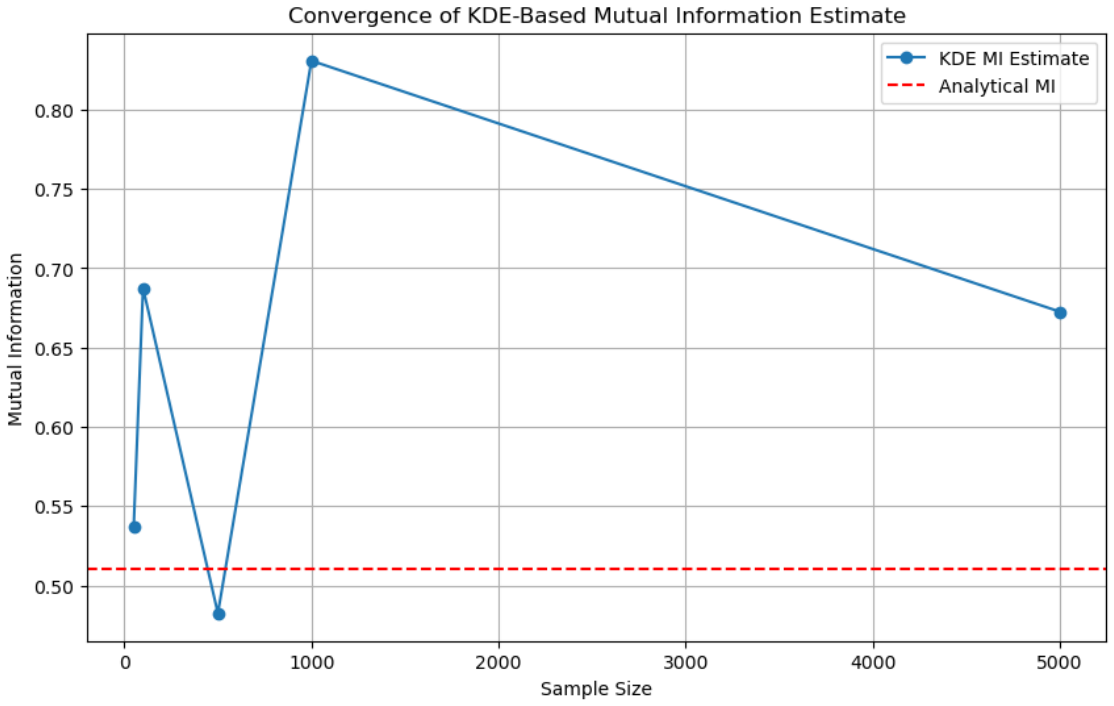
```
KDE-Based Mutual Information: 0.4921
```

[14]:
```
print(f"Analytical Mutual Information: {mi_analytical:.4f}")
print(f"KDE-Based Mutual Information: {mi_plugin:.4f}")
```

```
Analytical Mutual Information: 0.5108
KDE-Based Mutual Information: 0.4921
```

[15]:
```
def evaluate_convergence(cov_matrix, sample_sizes, grid_size=100):
    analytical_mi = analytical_mutual_information(cov_matrix)
    kde_estimates = []

    for n in sample_sizes:
        samples = np.random.multivariate_normal(mean=[0, 0], cov=cov_matrix,␣
 ↪size=n)
```

```
        kde_mi = kde_mutual_information(samples, grid_size=grid_size)
        kde_estimates.append(kde_mi)

    return analytical_mi, kde_estimates

# Sample sizes to test
sample_sizes = [50, 100, 500, 1000, 5000]

# Evaluate convergence
cov_matrix = np.array([[1.0, 0.8], [0.8, 1.0]])
analytical_mi, kde_estimates = evaluate_convergence(cov_matrix, sample_sizes)

# Plot convergence
plt.figure(figsize=(10, 6))
plt.plot(sample_sizes, kde_estimates, label="KDE MI Estimate", marker="o")
plt.axhline(analytical_mi, color="red", linestyle="--", label="Analytical MI")
plt.title("Convergence of KDE-Based Mutual Information Estimate")
plt.xlabel("Sample Size")
plt.ylabel("Mutual Information")
plt.legend()
plt.grid()
plt.show()

# robustness of KDE-based methods for estimating mutual information
```



[18]:
```
#16. Compare the performance of the Maximum Likelihood Estimator (MLE), Method␣
↪of Moments Estimator (MME), and Bayesian Estimator using quadratic risk.

def compare_risks(n_simulations, sample_size, a_star, b_star, alpha_a, beta_a,␣
↪alpha_b, beta_b):
    mle_risks = []
    mme_risks = []
    bayes_risks = []

    for _ in range(n_simulations):
        x = np.random.gamma(shape=a_star, scale=1/b_star, size=sample_size)

        # MME
        a_mme, b_mme = mme_gamma(x)
        mme_error = (a_mme - a_star)**2 + (b_mme - b_star)**2

        # MLE
        a_mle, b_mle = newton_raphson_mle(x, init="mme")
        mle_error = (a_mle - a_star)**2 + (b_mle - b_star)**2

        # Bayesian Estimator
        samples = mcmc_gamma(x, alpha_a, beta_a, alpha_b, beta_b, n_samples=500)
        bayes_mean_a = np.mean(samples[:, 0])
        bayes_mean_b = np.mean(samples[:, 1])
        bayes_error = (bayes_mean_a - a_star)**2 + (bayes_mean_b - b_star)**2

        mle_risks.append(mle_error)
        mme_risks.append(mme_error)
        bayes_risks.append(bayes_error)

    # Average risks
    mle_risk = np.mean(mle_risks)
    mme_risk = np.mean(mme_risks)
    bayes_risk = np.mean(bayes_risks)

    return mle_risk, mme_risk, bayes_risk

# Compare risks
sample_size = 20
n_simulations = 100
a_star, b_star = 2, 2
alpha_a, beta_a = 2, 2
alpha_b, beta_b = 2, 2

mle_risk, mme_risk, bayes_risk = compare_risks(
    n_simulations, sample_size, a_star, b_star, alpha_a, beta_a, alpha_b, beta_b
)
```

```
print(f"MLE Risk: {mle_risk:.4f}")
print(f"MME Risk: {mme_risk:.4f}")
print(f"Bayesian Risk: {bayes_risk:.4f}")
```

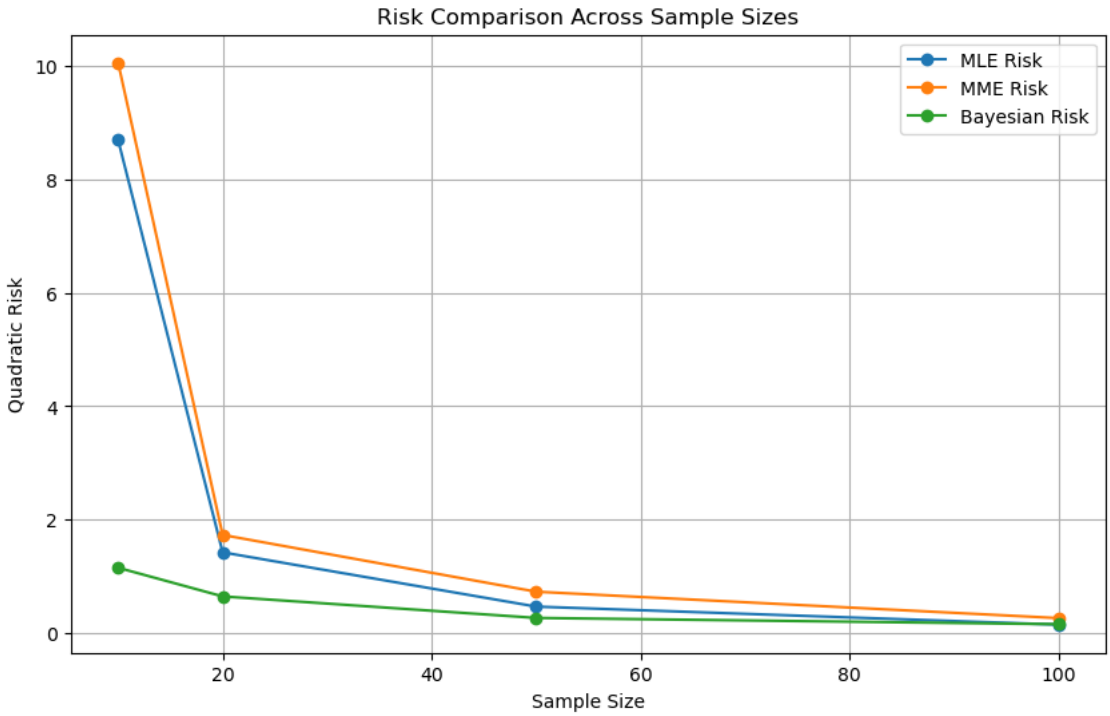
```
C:\Users\sshubhankar\AppData\Local\Temp\ipykernel_22764\3312317694.py:13:
DeprecationWarning: `np.math` is a deprecated alias for the standard library
`math` module (Deprecated Numpy 1.25). Replace usages of `np.math` with `math`
  log_likelihood = n * a * np.log(b) - n * np.math.lgamma(a) + (a - 1) * S1 - b
* S2
```

```
MLE Risk: 1.2294
MME Risk: 2.5194
Bayesian Risk: 0.7145
```

[20]:
```
sample_sizes = [10, 20, 50, 100]
risks = []

for n in sample_sizes:
    risks.append(
        compare_risks(n_simulations, n, a_star, b_star, alpha_a, beta_a,␣
 ↪alpha_b, beta_b)
    )

mle_risks, mme_risks, bayes_risks = zip(*risks)

# Plot risks
plt.figure(figsize=(10, 6))
plt.plot(sample_sizes, mle_risks, label="MLE Risk", marker="o")
plt.plot(sample_sizes, mme_risks, label="MME Risk", marker="o")
plt.plot(sample_sizes, bayes_risks, label="Bayesian Risk", marker="o")
plt.title("Risk Comparison Across Sample Sizes")
plt.xlabel("Sample Size")
plt.ylabel("Quadratic Risk")
plt.legend()
plt.grid()
plt.show()
```

```
C:\Users\sshubhankar\AppData\Local\Temp\ipykernel_22764\3312317694.py:13:
DeprecationWarning: `np.math` is a deprecated alias for the standard library
`math` module (Deprecated Numpy 1.25). Replace usages of `np.math` with `math`
  log_likelihood = n * a * np.log(b) - n * np.math.lgamma(a) + (a - 1) * S1 - b
* S2
```

```
Invalid parameters encountered, resetting.
```


Risk Comparison Across Sample Sizes
MLE Risk
MME Risk
Bayesian Risk
Quadratic Risk
Sample Size
0
2
4
6
8
10
20
40
60
80
100

[ ]:

[ ]: