In [ ]:
```
import random
import numpy as np
import matplotlib.pyplot as plt
from functools import partial
import math
```

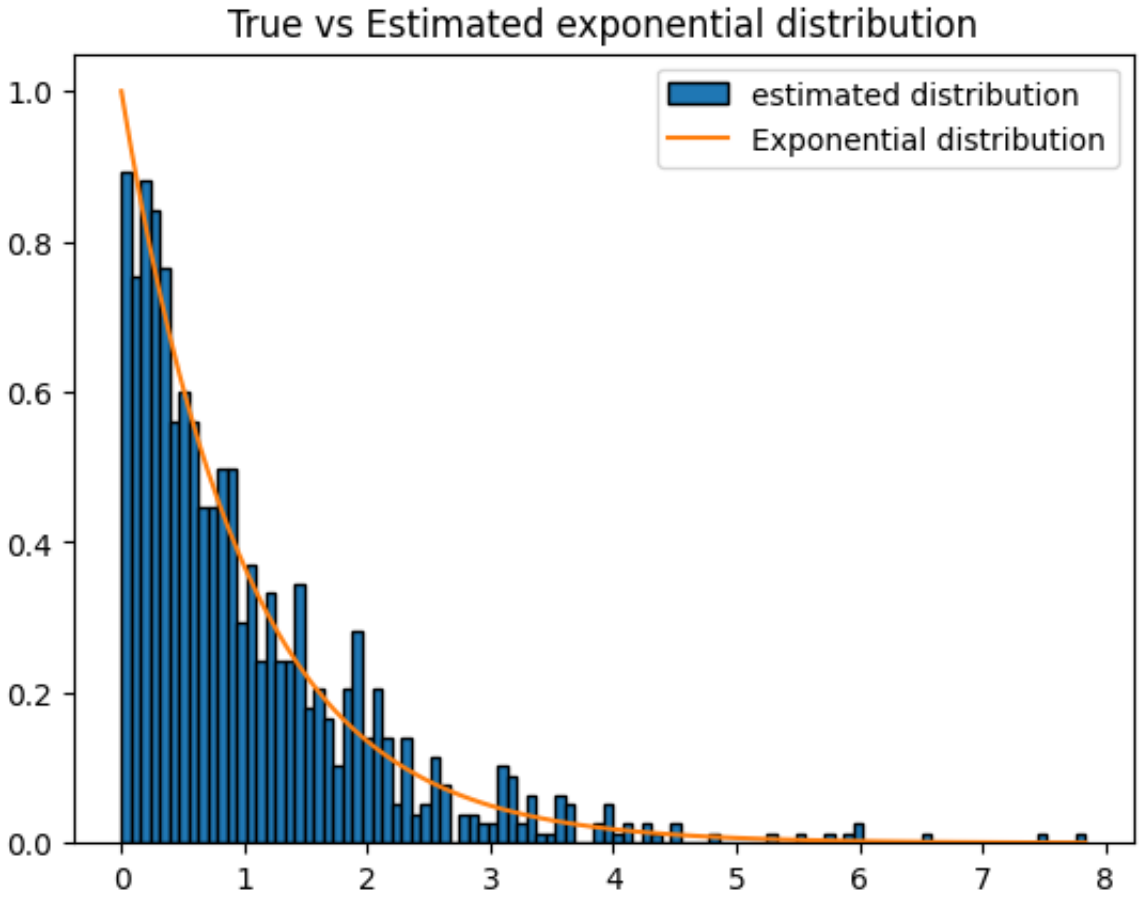
1.

- Derive and implement the inverse CDF for an exponential distribution with rate parameter $\lambda = 1$.

In [ ]:
```
def exponential_distribution(x, lamb):
    return lamb * np.exp(-lamb * x)

def inverse_exponetial_CDF(y, lamb):
    return -np.log(1 - y) / lamb
```

- Generate 1000 random variables using this inverse CDF and create a histogram of the results.
- Overlay the theoretical probability density function of the exponential distribution on the histogram.

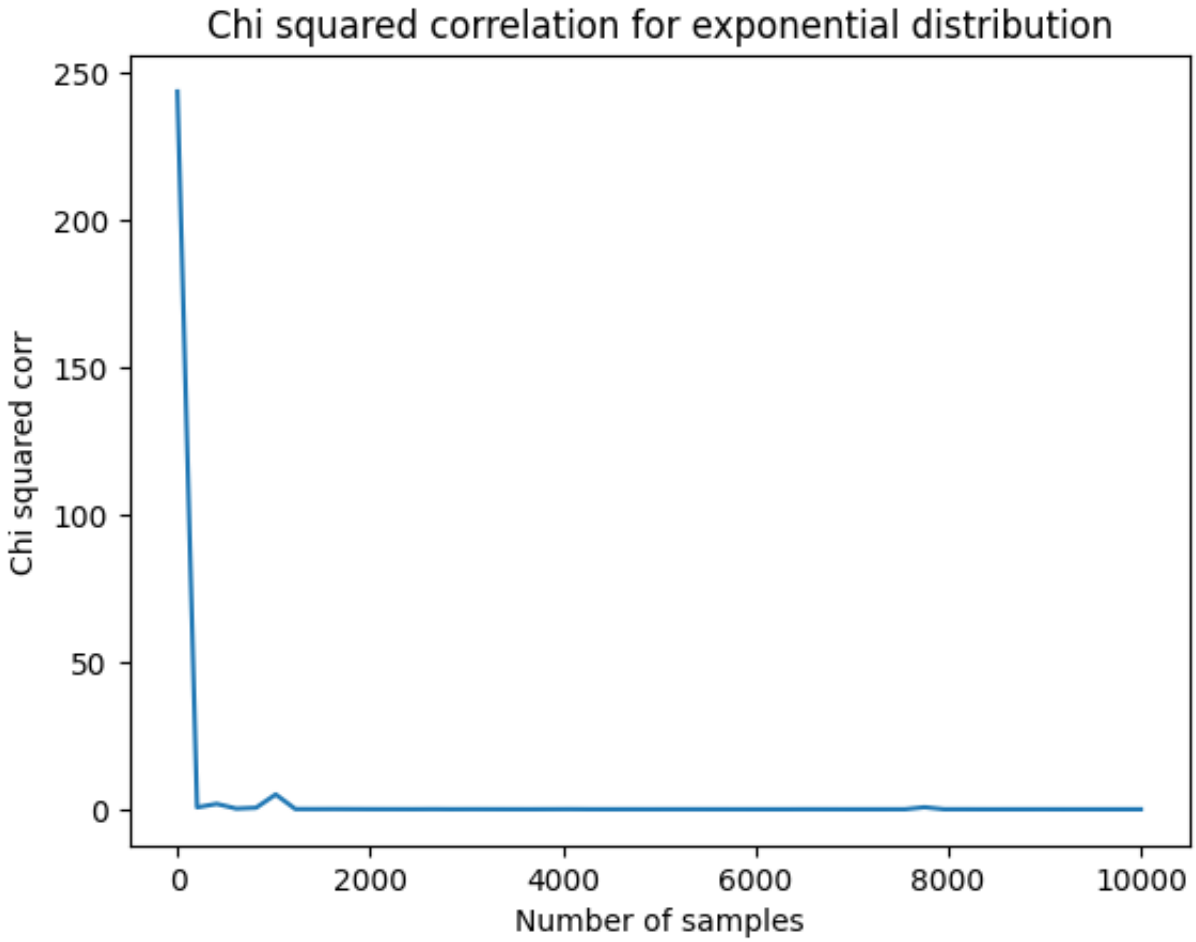
In [ ]:
```
Y = np.random.uniform(0, 1, 1000)
X = inverse_exponetial_CDF(Y, 1)
plt.hist(X, bins=100, density=True, label='estimated distribution', edgec
X2 = np.linspace(min(X), max(X), 100)
plt.plot(X2, exponential_distribution(X2, 1), label='Exponential distribu
plt.title('True vs Estimated exponential distribution')
plt.legend()
plt.show()
```



- Compare the effectiveness of the inverse transform sampling method to direct sampling methods available in NumPy. Discuss the findings in your report.

In [ ]:
```
def monte_carlo_integral_approximation(func, a, b, N):
    x = np.random.uniform(a, b, N)
    y = func(x)
    return (b-a)*np.sum(y)/N

def chi_squared_corr(O, E):
    O = O if isinstance(O, np.ndarray) else np.array(O)
    E = E if isinstance(E, np.ndarray) else np.array(E)
    return np.sum((O-E)**2 / np.array(E))

def get_exp_chi2_corr(number_samples, number_bins, lamb):
    Y = np.random.uniform(0, 1, number_samples)
    X = inverse_exponetial_CDF(Y, lamb)
    hist, bins = np.histogram(X, bins=number_bins, density=True)

    O = []
    E = []

    for i in range(len(bins)-1):
        O.append(hist[i]*(bins[i+1] - bins[i]))
        func = partial(exponential_distribution, lamb=lamb)
        E.append(monte_carlo_integral_approximation(func, bins[i], bins[i
```

```
    O = np.array(O)
    E = np.array(E)

    return chi_squared_corr(O, E)

X = np.linspace(1, 10000, 50).astype(int)
Y = np.array([get_exp_chi2_corr(i, 100, 1) for i in X])
plt.plot(X, Y)
plt.title('Chi squared correlation for exponential distribution')
plt.xlabel('Number of samples')
plt.ylabel('Chi squared corr')
plt.show()
```

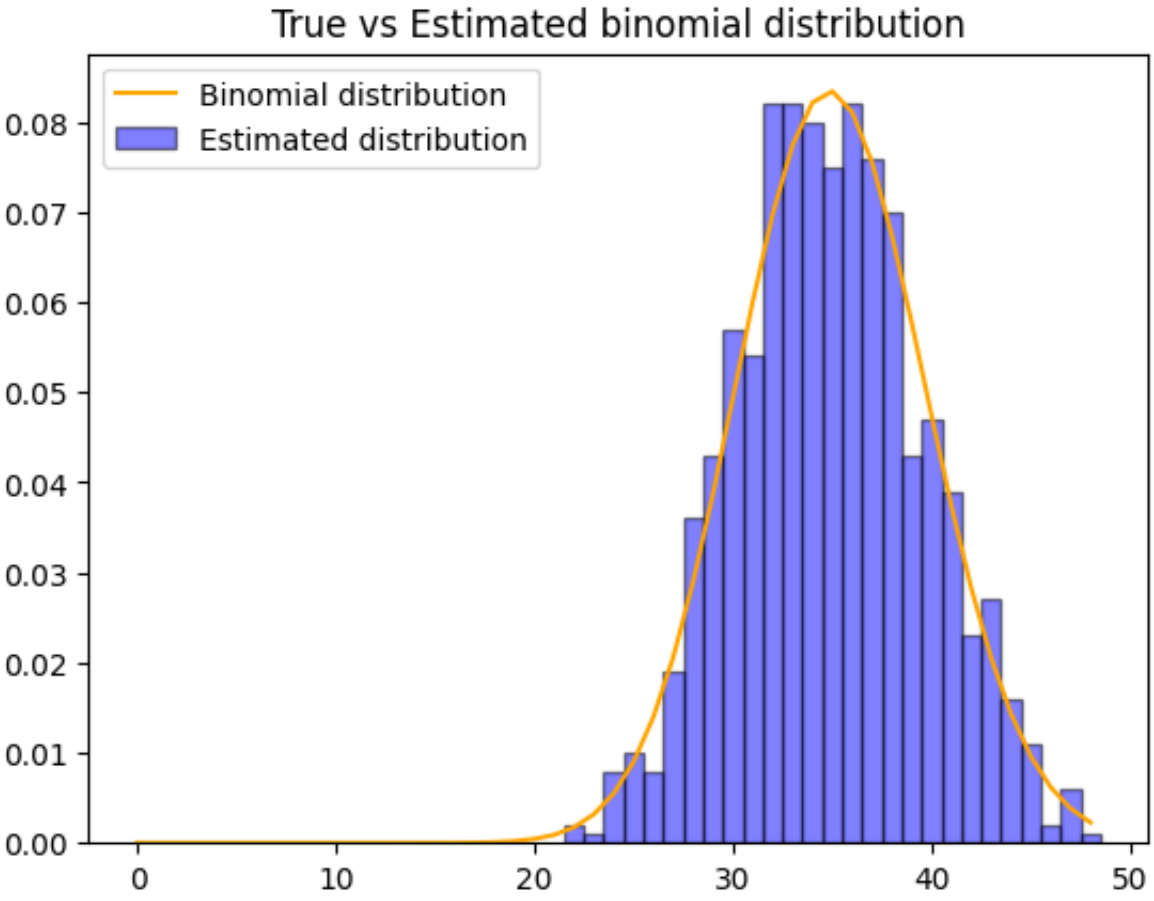


We can see by doing a chi squared correlation plot that with higher values of number of samples that the error between the real and simulated distribution goes to zero, which is a strong indicative that the simulation is correct and on point with Monte-Carlo sampling strategy.

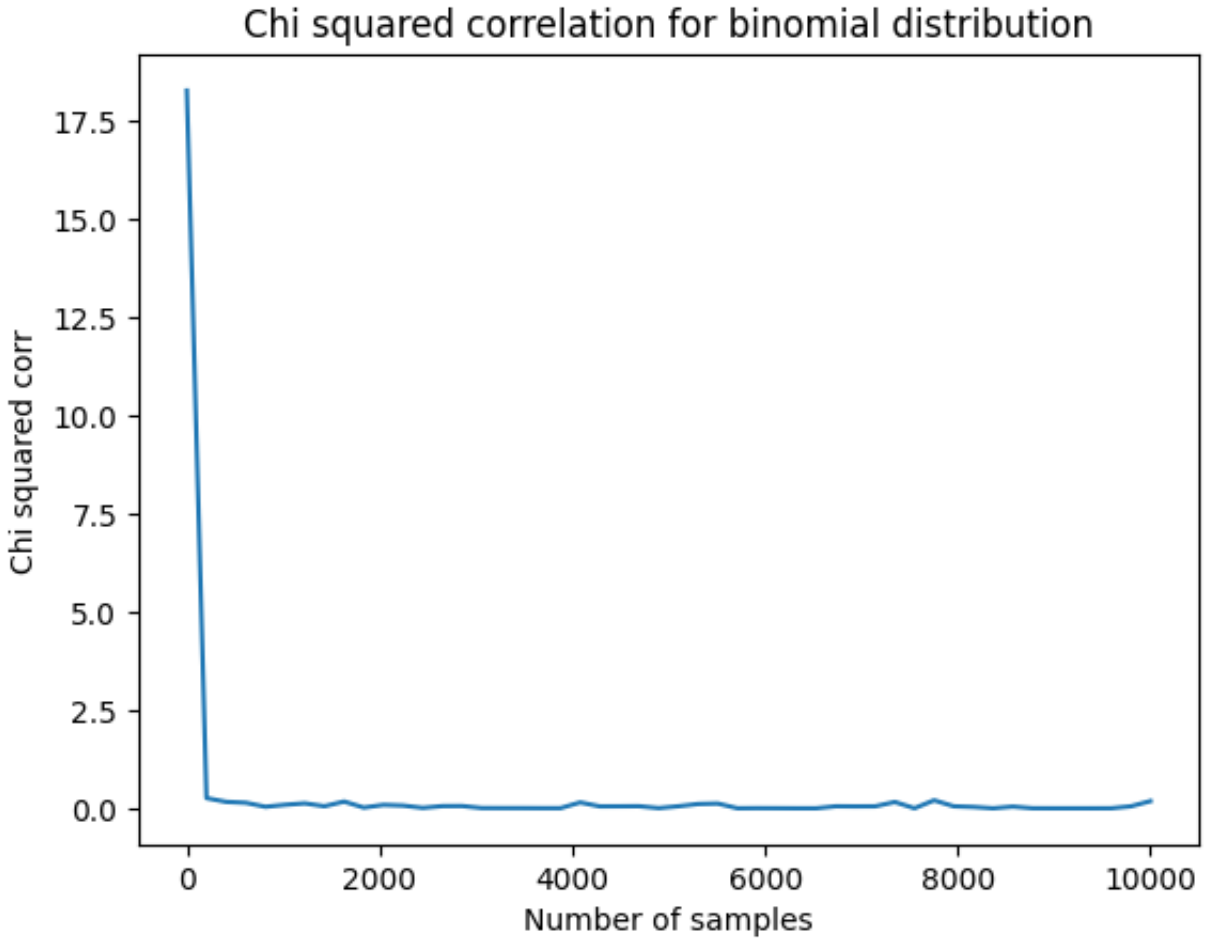
- Do the same as previous analysis but now with another distribution instead of exponential.

In [ ]:
```
def binomial_distribution(n, k, p):
```

```
    return math.comb(n,k)*(p**k)*((1-p)**(n-k))

def bernoulli(p):
    return 1 if random.random() < p else 0

def inverse_binomial_CDF(n, p):
    sum = 0
    for i in range(n):
        sum += bernoulli(p)
    return sum

n = 100
p = 0.35

X = np.array([inverse_binomial_CDF(n, p) for _ in range(1000)])
unique = np.unique(X)
hist, bins = np.histogram(X, bins=len(unique), density=True)
hist=hist/np.sum(hist)

for i in range(len(bins)-2):
    plt.bar(bins[i], hist[i], width=bins[i+1]-bins[i], color='blue', alph
plt.bar(bins[-2], hist[-1], width=bins[-1]-bins[-2], color='blue', alpha=

K = list(range(0,max(X),1))
Y = np.array([binomial_distribution(n, k, p) for k in K])

plt.plot(K, Y, label='Binomial distribution', color='orange')
plt.title('True vs Estimated binomial distribution')
plt.legend()
plt.show()
```



In [ ]:
```
def get_binomial_chi2_corr(number_samples, n, p):

    X = np.array([inverse_binomial_CDF(n, p) for _ in range(number_sample
    unique = np.unique(X)
    hist, bins = np.histogram(X, bins=len(unique), density=True)
    hist=hist/np.sum(hist)

    O = hist
    E = []
    for e in unique:
        E.append(binomial_distribution(n, e, p))
    E = np.array(E)

    return chi_squared_corr(O, E)

n = 100
p = 0.35

X = np.linspace(1, 10000, 50).astype(int)
Y = np.array([get_binomial_chi2_corr(i, n, p) for i in X])
plt.plot(X, Y)
plt.title('Chi squared correlation for binomial distribution')
plt.xlabel('Number of samples')
plt.ylabel('Chi squared corr')
plt.show()
```



2.

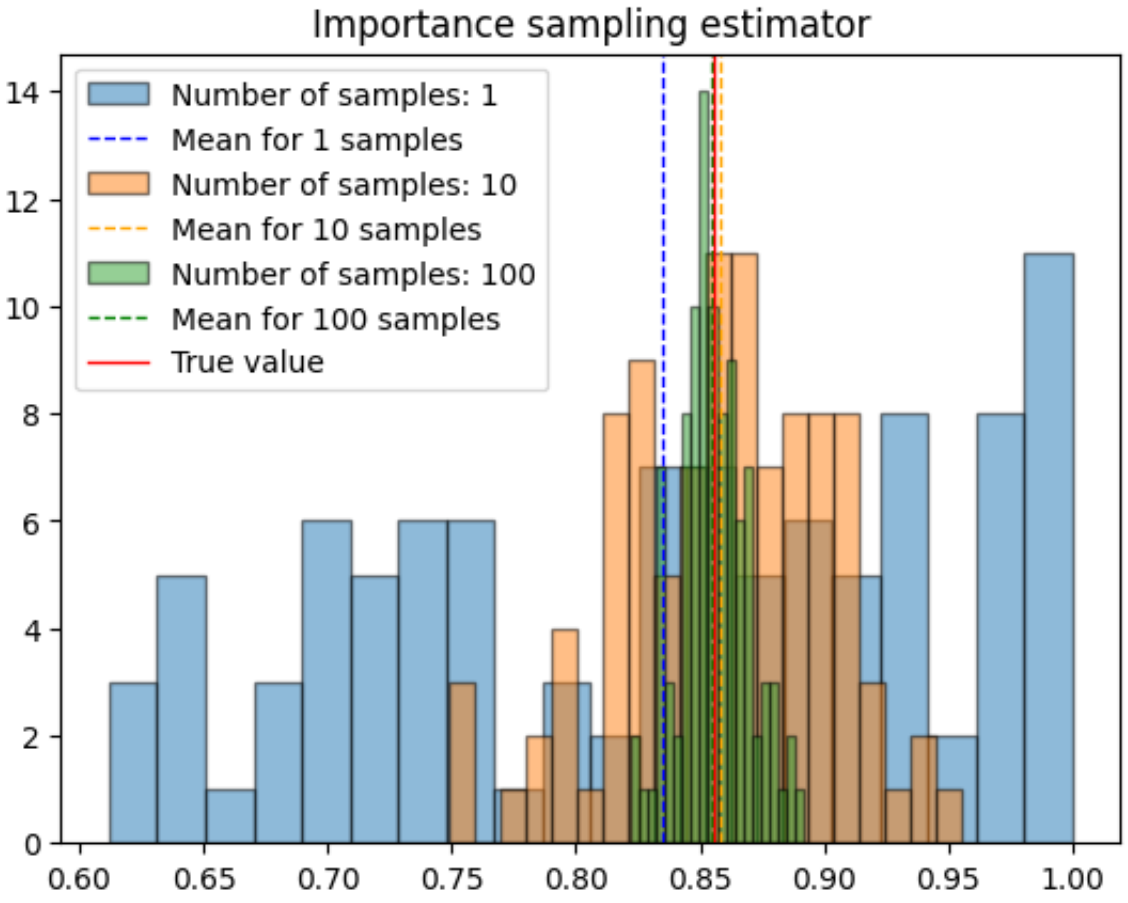
- Write a function to generate n random samples from the uniform distribution over [0, 1], compute $g(Xi)$, and apply the importance sampling estimator to estimate the integral.

In [ ]:
```
g = lambda x: np.exp(-x**2/2)
f = lambda x: 1

def importance_sampling_estimator(g, f, number_samples):
    X = np.random.uniform(0, 1, number_samples)
    Y = g(X)/f(X)
    return np.mean(Y)
```

- Evaluate this function for n = 1, 10, and 100, and repeat each experiment 100 times. Store the estimates.

In [ ]:
```
times = 100
num_samples = [1,10,100]
results = {}
```

```
for n in num_samples:
    results[n] = [importance_sampling_estimator(g, f, n) for _ in range(t
```



- Plot a histogram of the estimates for each n and mark the true integral value with a vertical line next to a vertical line with the mean of the estimates.

In [ ]:
```
colors = ['blue', 'orange', 'green']

for k,v in results.items():
    plt.hist(v, bins=20, edgecolor='black', alpha=0.5, label=f'Number of
    plt.axvline(np.mean(v), color=colors.pop(0), linestyle='dashed', line
plt.axvline(0.855624, color='red', linewidth=1, label='True value')


plt.title('Importance sampling estimator')
plt.legend()
plt.show()
```

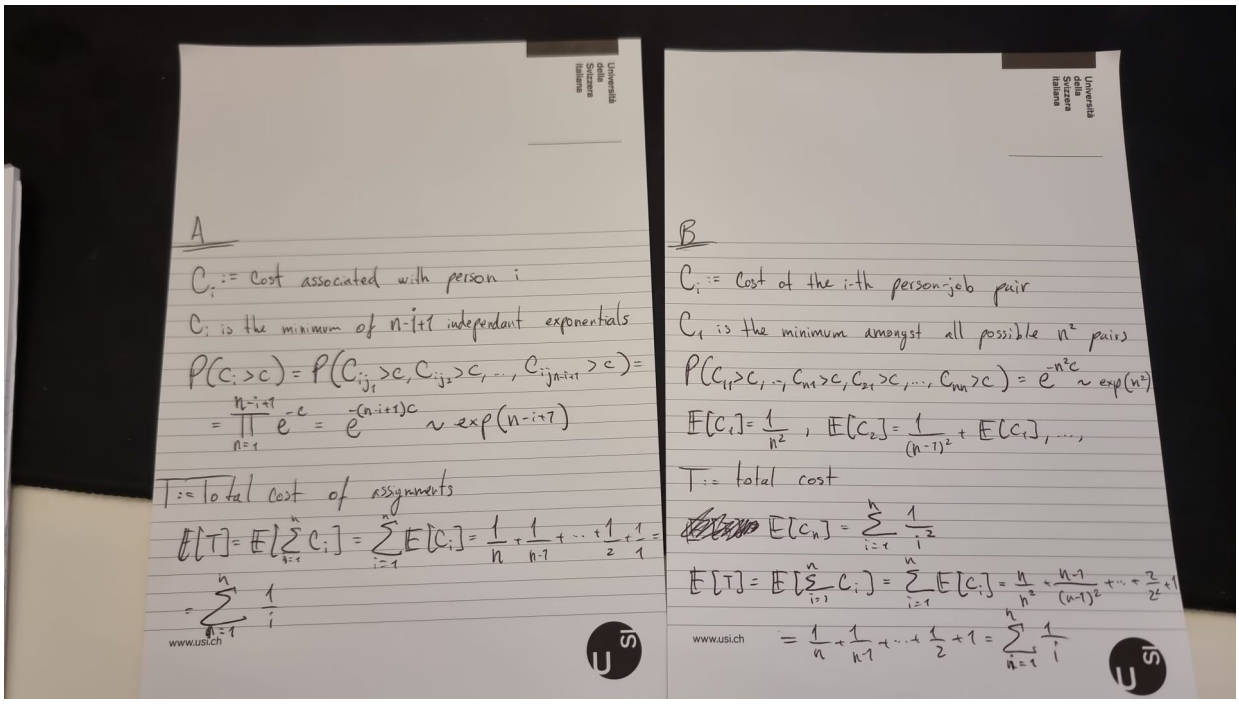
- Analyze the distribution of the estimates and the effect of the number of samples on the accuracy and precision.

As before, we can see that higher number of samples gives us better approximation of the true value. The means of each sampling number distribution also tends to be really close to the true expected value as a function from the number of samples.

3.

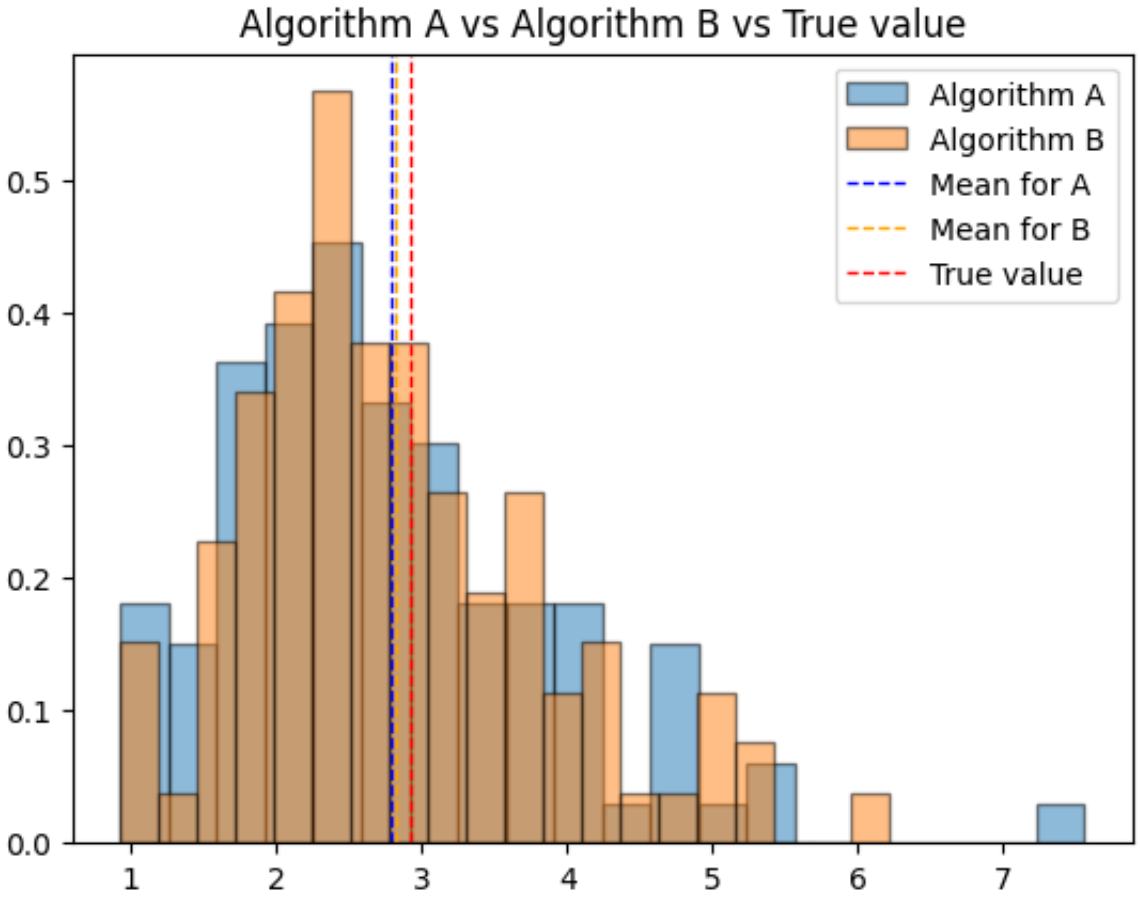
In [ ]:
```
from IPython import display
display.Image("ex3.jpeg")
```

Out[ ]:



In [ ]:
```
def get_person_job_cost(number_persons_jobs):
    person_job_cost = []

    for i in range(number_persons_jobs):
        for j,c in enumerate(inverse_exponetial_CDF(np.random.uniform(0,1
            person_job_cost.append((i,j,c))

    return person_job_cost

def algo_A(person_job_cost):
    total_cost = 0
    persons = set([x[0] for x in person_job_cost])

    for p in persons:
        job,cost = min([(x[1],x[2]) for x in person_job_cost if x[0] == p
        total_cost += cost
        person_job_cost = [x for x in person_job_cost if x[0] != p and x[

    return total_cost

def algo_B(person_job_cost):
    cost = 0

    while len(person_job_cost) > 0:
        min_cost_tuple = min(person_job_cost, key=lambda x: x[2])
```

```
        cost += min_cost_tuple[2]
        person_job_cost = [x for x in person_job_cost if x[0] != min_cost

    return cost

def harmonic_sum(n=10):
    return sum([1/i for i in range(1,n+1)])


A = []
B = []

for _ in range(100):
    person_job_cost = get_person_job_cost(10)
    A.append(algo_A(person_job_cost))
    B.append(algo_B(person_job_cost))

true_val = harmonic_sum(10)


#histogram
plt.hist(A, bins=20, edgecolor='black', density=True, alpha=0.5, label='A
plt.hist(B, bins=20, edgecolor='black', density=True, alpha=0.5, label='A
plt.axvline(np.mean(A), color='blue', linestyle='dashed', linewidth=1, la
plt.axvline(np.mean(B), color='orange', linestyle='dashed', linewidth=1,
plt.axvline(true_val, color='red', linestyle='dashed', linewidth=1, label
plt.title('Algorithm A vs Algorithm B vs True value')
plt.legend()
plt.show()
```



- Discuss which of the two algorithms is likely to result in a smaller expected total cost. Provide a justification for your answer based on the theoretical and numerical results.

We can see that both algorithms converge to the same average expected value, which is congruent with the theoretical analysis.

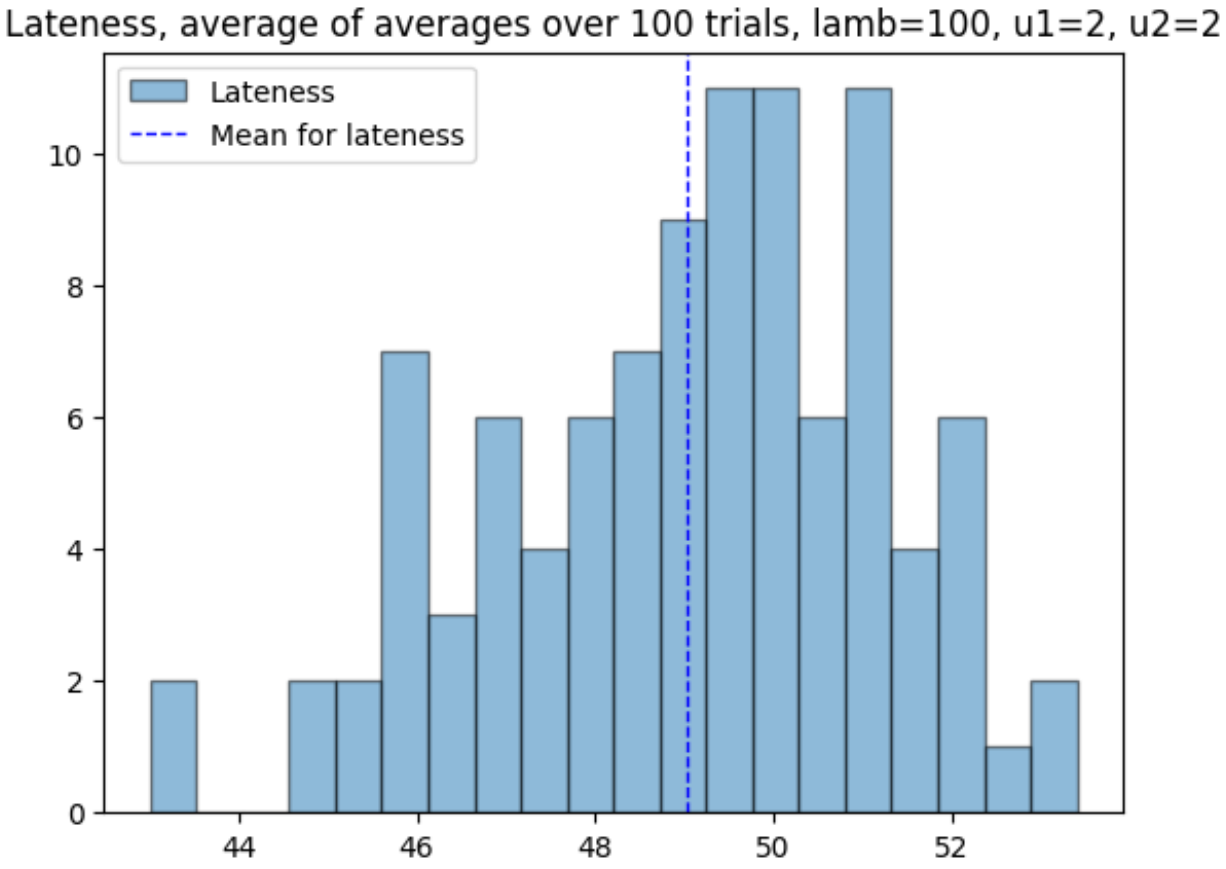
5.

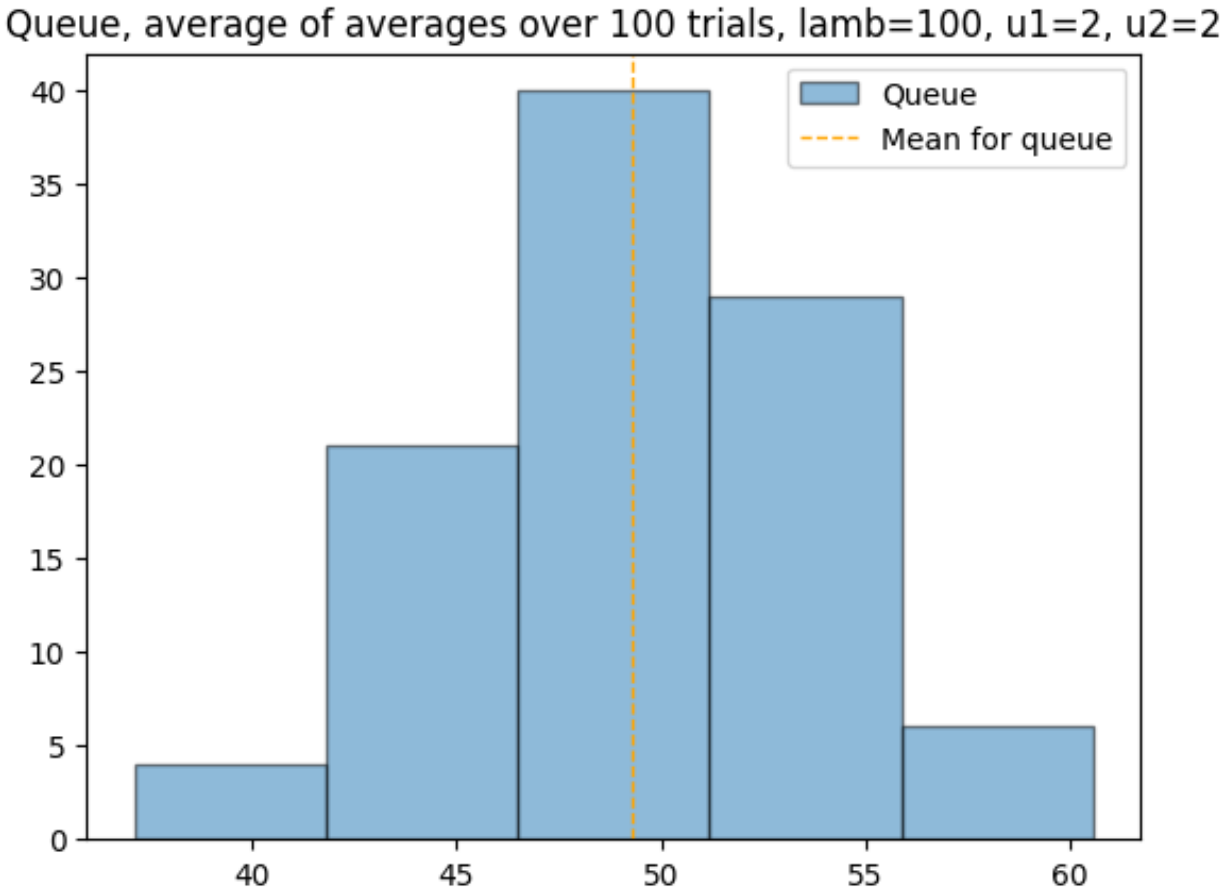
In [ ]:
```
def exercise4_cmtc(lamb, u1, u2, number_events):

    time_between_arrivals = inverse_exponetial_CDF(np.random.uniform(0,1,
    arrivals = np.cumsum(time_between_arrivals).tolist()
    process_1_times = inverse_exponetial_CDF(np.random.uniform(0,1,number
    process_2_times = inverse_exponetial_CDF(np.random.uniform(0,1,number

    current_time = 0

    task_in_out_times = {}
    for j,a in enumerate(arrivals):
        task_in_out_times[j] = {}
        task_in_out_times[j]['arrival'] = a
```

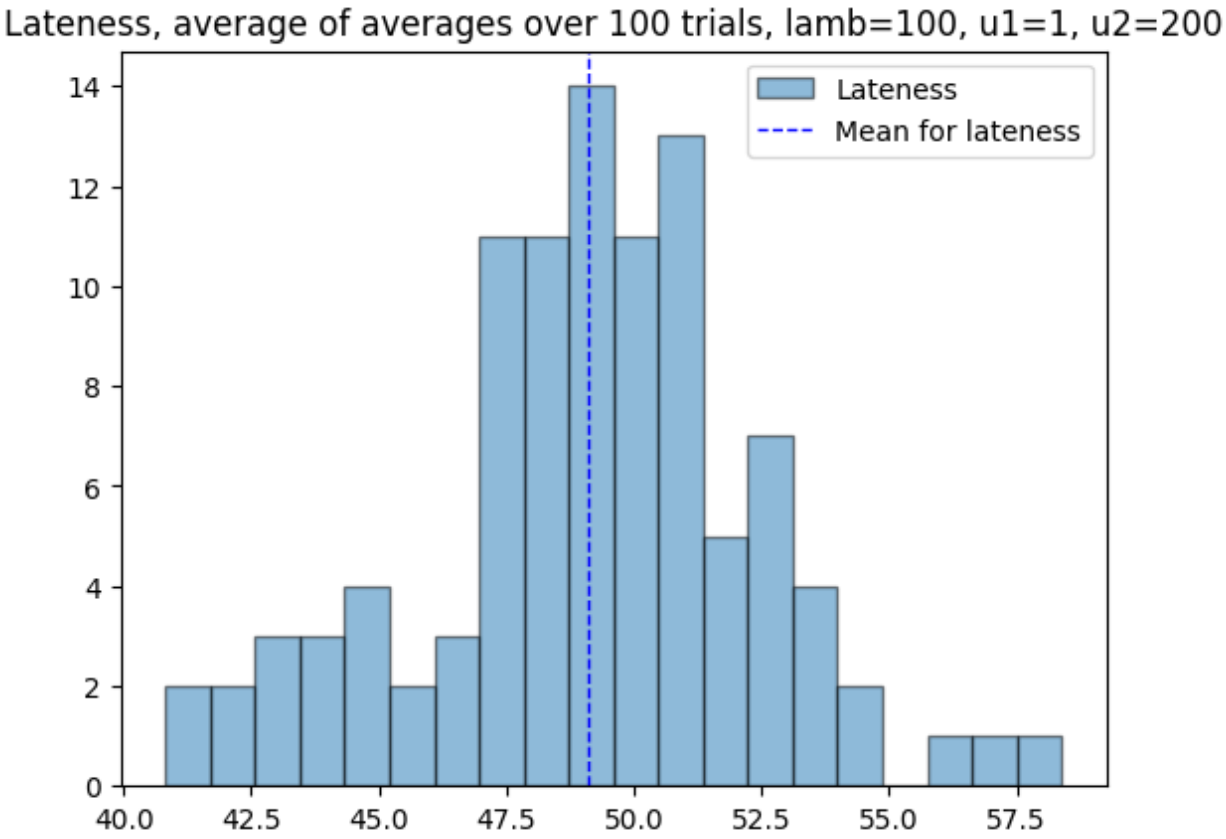
```
    for i in range(number_events):
        elements_in_queue = sorted([j for j,v in enumerate(arrivals) if v

        if len(elements_in_queue) == 0:
            current_time = arrivals[i]

        task_in_out_times[i]['start'] = current_time
        current_time += process_1_times[i] + process_2_times[i]
        task_in_out_times[i]['end'] = current_time

    lateness = []
    queue_status = []
    for k,v in task_in_out_times.items():
        queue_status.append((k,v['arrival']))
        queue_status.append((k,v['start']))
        if v['arrival'] == v['start']:
            lateness.append(0)
        else:
            lateness.append(v['start'] - v['arrival'])

    seen = []
    current_count = 0
    queue_time_accum = [(0,0)]
    queue_status = sorted(queue_status, key=lambda x: x[1])
    for (k,v) in queue_status:
        if k not in seen:
            seen.append(k)
            current_count += 1
            queue_time_accum.append((current_count, v))
        else:
            current_count -= 1
            queue_time_accum.append((current_count, v))

    total_time = max([v['end'] for k,v in task_in_out_times.items()])
    average_element_queue = 0
    for j in range(0,len(queue_time_accum)-1):
        average_element_queue += queue_time_accum[j][0]*(queue_time_accum

    average_element_queue /= total_time
    average_lateness = np.mean(lateness)

    return average_element_queue, average_lateness



def exercise4_trials(num_trials, lamb, u1, u2, number_events):
    late_avgs = []
    queue_avgs = []

    for _ in range(num_trials):
        average_lateness, average_element_queue = exercise4_cmtc(lamb,u1,
        late_avgs.append(average_lateness)
        queue_avgs.append(average_element_queue)
```

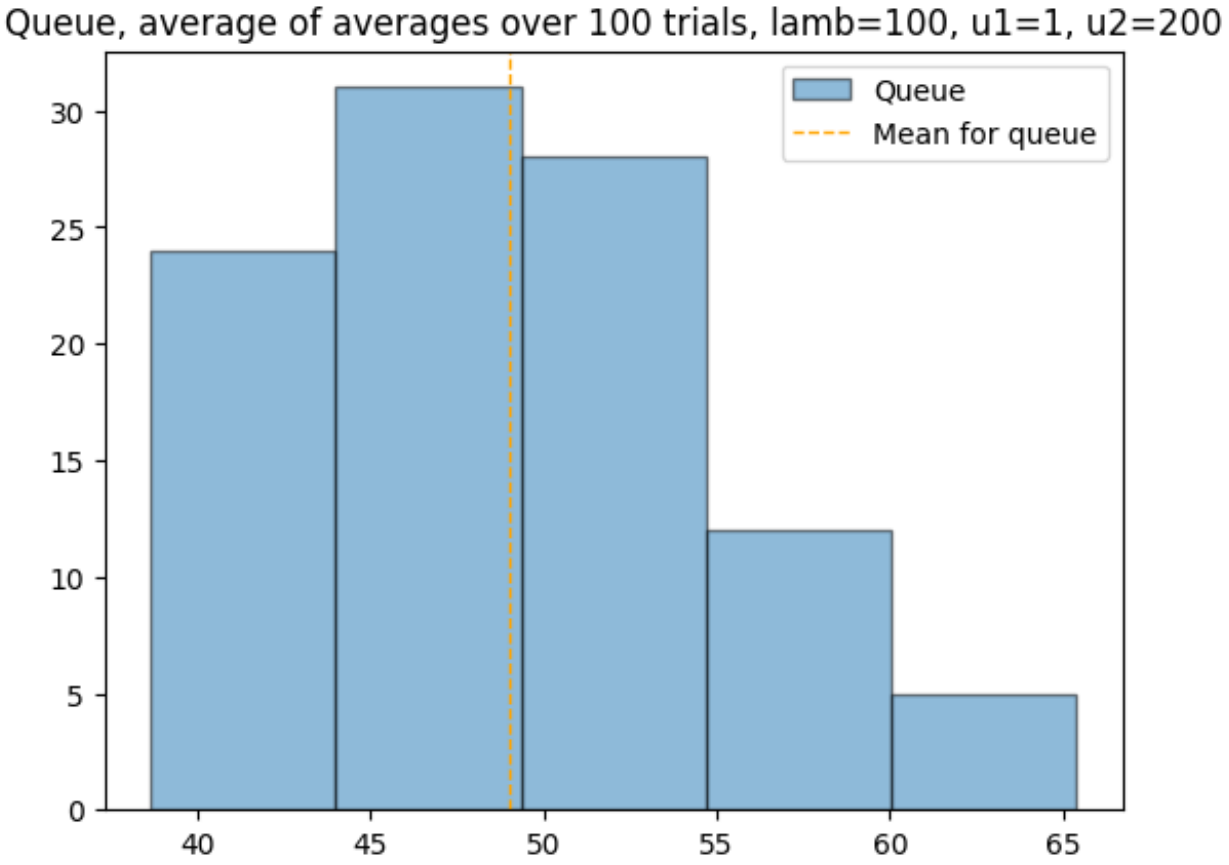
```
    plt.hist(late_avgs, bins=20, edgecolor='black', alpha=0.5, label='Lat
    plt.axvline(np.mean(late_avgs), color='blue', linestyle='dashed', lin
    plt.legend()
    plt.title(f'Lateness, average of averages over {num_trials} trials, l
    plt.show()

    plt.hist(queue_avgs, bins=5, edgecolor='black', alpha=0.5, label='Que
    plt.axvline(np.mean(queue_avgs), color='orange', linestyle='dashed',
    plt.title(f'Queue, average of averages over {num_trials} trials, lamb
    plt.legend()
    plt.show()
```

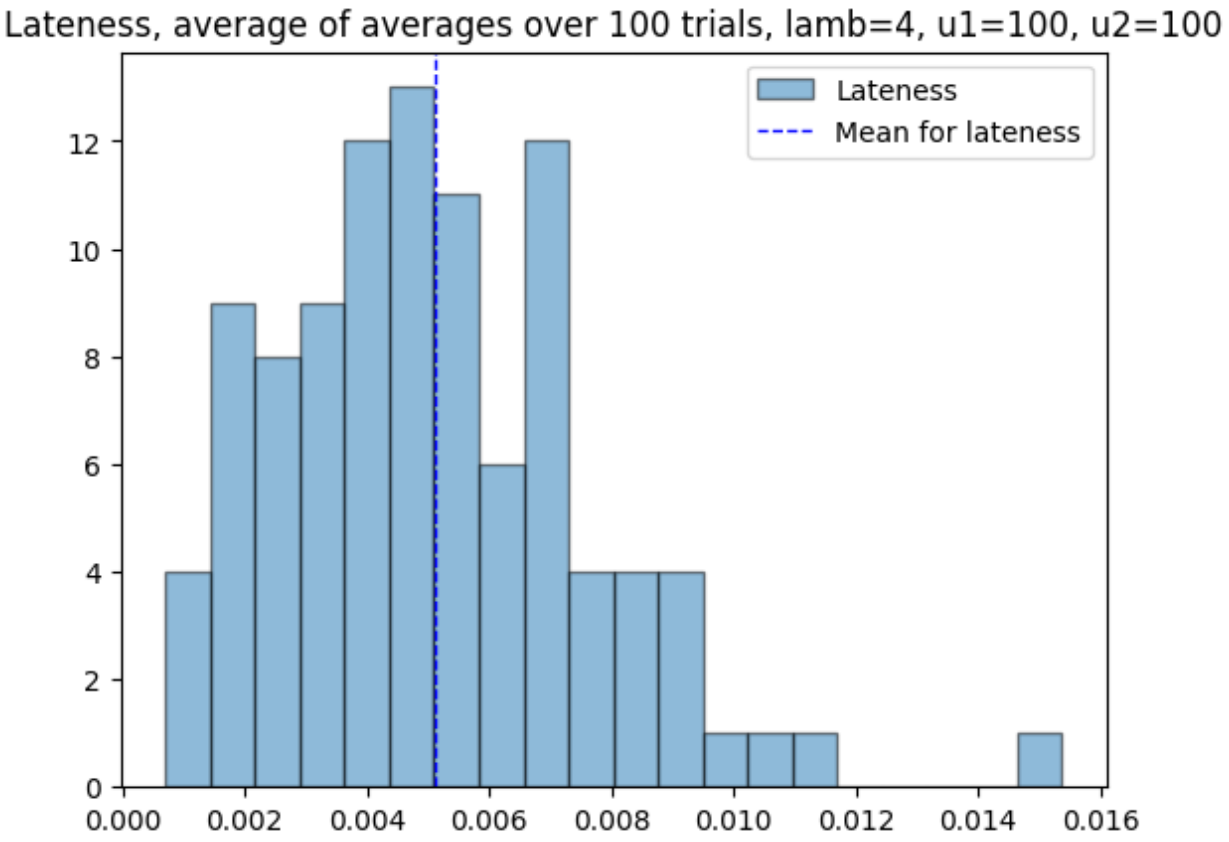
In [ ]:
```
exercise4_trials(num_trials = 100, lamb = 100, u1 = 2, u2 = 2, number_eve
exercise4_trials(num_trials = 100, lamb = 100, u1 = 1, u2 = 200, number_e
exercise4_trials(num_trials = 100, lamb = 4, u1 = 100, u2 = 100, number_e
```

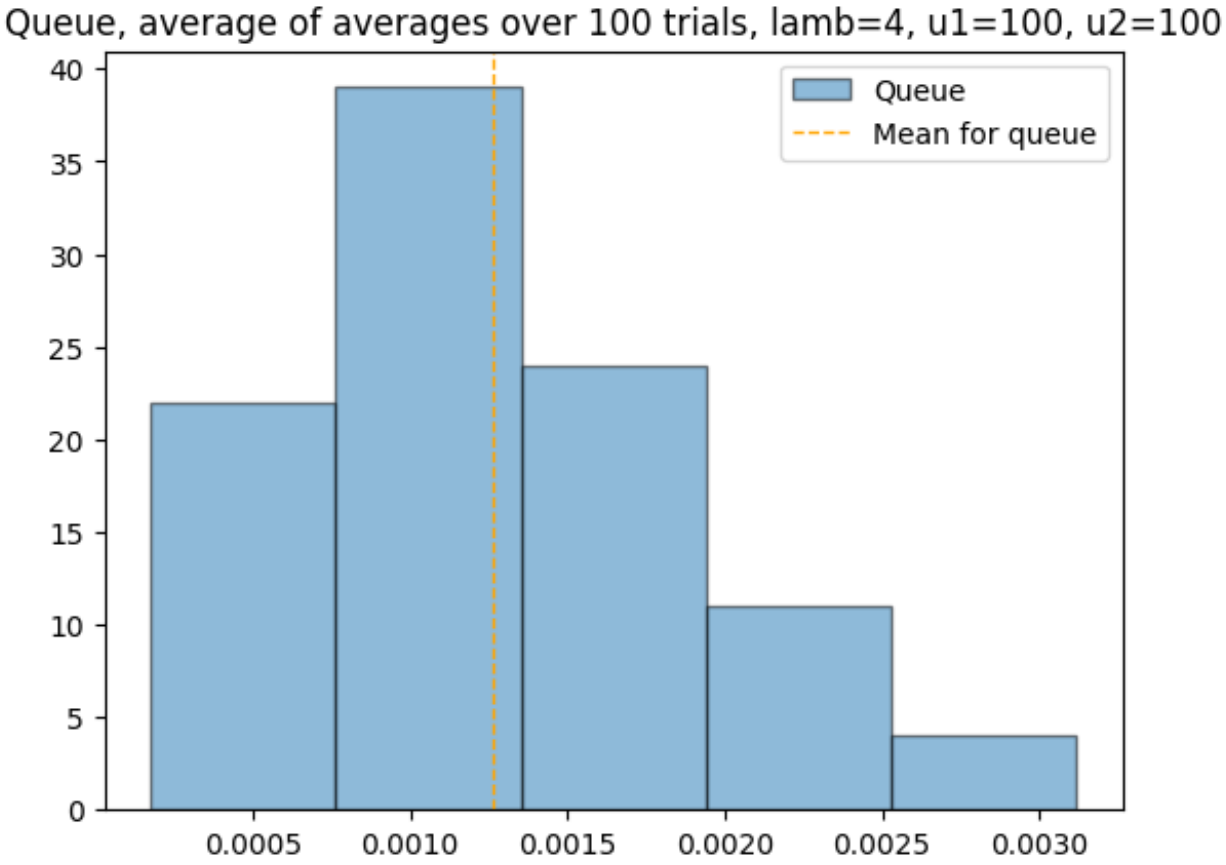



Queue, average of averages over 100 trials, lamb=100, u1=2, u2=2
Queue
Mean for queue
0
5
10
15
20
25
30
35
40
40
45
50
55
60


Lateness, average of averages over 100 trials, lamb=100, u1=1, u2=200
Lateness
Mean for lateness
0
2
4
6
8
10
12
14
40.0
42.5
45.0
47.5
50.0
52.5
55.0
57.5


Queue, average of averages over 100 trials, lamb=100, u1=1, u2=200
Queue
Mean for queue
0
5
10
15
20
25
30
40
45
50
55
60
65


Lateness, average of averages over 100 trials, lamb=4, u1=100, u2=100
Lateness
Mean for lateness
0
2
4
6
8
10
12
0.000
0.002
0.004
0.006
0.008
0.010
0.012
0.014
0.016



The plots above show the histogram and the average of the averages of the time in queue (lateness) and the number of elements in queue. We can see that for higher rates of lambda than the sum of the mnius, there tends to be more lateness and elements in queue, which is expected. On the other hand, when we have small values of lambda but high values of mnius then processed are quicker than the rate of income of the tasks, thus we have less elements in queue and waiting times in averages.

5.

In [ ]:
```
from IPython import display
display.Image("ex5_1.jpg")
```

Out[ ]:

Let $M(t) = \mathbb{E}[N(t)]$,

$$M(t+h) = \mathbb{E}[N(t+h)] = \mathbb{E}\left[\mathbb{E}[N(t+h) \mid N(t)]\right]$$

$$N(t+h) = \begin{cases} N(t)+1, & p = N(t)\lambda h + o(h) \\ N(t)-1, & p = N(t)\mu h + o(h) \\ N(t), & p = 1 - N(t)h(\lambda+\mu) + o(h) \end{cases}$$

Then

$$\mathbb{E}[N(t+h) \mid N(t)] = N(t) + hN(t)(\lambda - \mu) + o(h)$$

and

$$\mathbb{E}\left[\mathbb{E}[N(t+h) \mid N(t)]\right] =$$

$$= \mathbb{E}[N(t) + hN(t)(\lambda-\mu) + o(h)] =$$

$$= \mathbb{E}[N(t)] + h(\lambda-\mu)\mathbb{E}[N(t)] + o(h)$$

$$= M(t) + h(\lambda-\mu)M(t) + o(h)$$

$$\Leftrightarrow M(t+h) = M(t) + h(\lambda-\mu)M(t) + o(h)$$

$$\Leftrightarrow \underbrace{\frac{M(t+h) - M(t)}{h}}_{M'(t)} = (\lambda-\mu)M(t) + \underbrace{\frac{o(h)}{h}}_{h\to 0 \Rightarrow \frac{o(h)}{h} \to 0}$$

In [ ]:
```
display.Image("ex5_2.jpg")
```

Out[ ]:

take the limit $h \to 0$

$$\underbrace{M'(t) = (\lambda - \mu) M(t)}_{\checkmark}$$

Let $h(t) = (\lambda - \mu) M(t)$

$$h'(t) = (\lambda - \mu) M'(t)$$

$$\Leftrightarrow M'(t) = \frac{h'(t)}{\lambda - \mu}$$

Then we have

$$\frac{h'(t)}{\lambda - \mu} = M'(t) = (\lambda - \mu) M(t) = h(t) \Leftrightarrow$$

$$\Leftrightarrow \frac{h'(t)}{\lambda - \mu} = \lambda(t) \Leftrightarrow \frac{h'(t)}{h(t)} = \lambda - \mu$$

$$\int_t \frac{h'(t)}{h(t)} \, dt = \int_t \lambda - \mu \, dt = (\lambda - \mu) t + c$$

but also

$$\int_t \frac{h'(t)}{h(t)} \, dt = \log(h(t))$$

In [ ]:
```
display.Image("ex5_3.jpg")
```

Out[ ]:

Then:

$$\log(h(t)) = (\lambda-\mu)t + c \quad , \text{ let } e^c = K \text{ constant!!}$$

$$\Leftrightarrow h(t) = K e^{(\lambda-\mu)t}$$

Remember $h(t) = (\lambda-\mu)M(t)$, then

$$(\lambda-\mu)M(t) = K e^{(\lambda-\mu)t}$$

$$\Leftrightarrow M(t) = \frac{K e^{(\lambda-\mu)t}}{\lambda-\mu}$$

To determine K we know

$$M(0) = \mathbb{E}[N(0)] = N(0)$$

Then $N(0) = \frac{K e^0}{\lambda-\mu} \Leftrightarrow K = N(0)(\lambda-\mu)$

Hence:

$$M(t) = N(0)(\lambda-\mu)\frac{e^{(\lambda-\mu)t}}{\lambda-\mu} =$$

$$= N(0)\, e^{(\lambda-\mu)t}$$

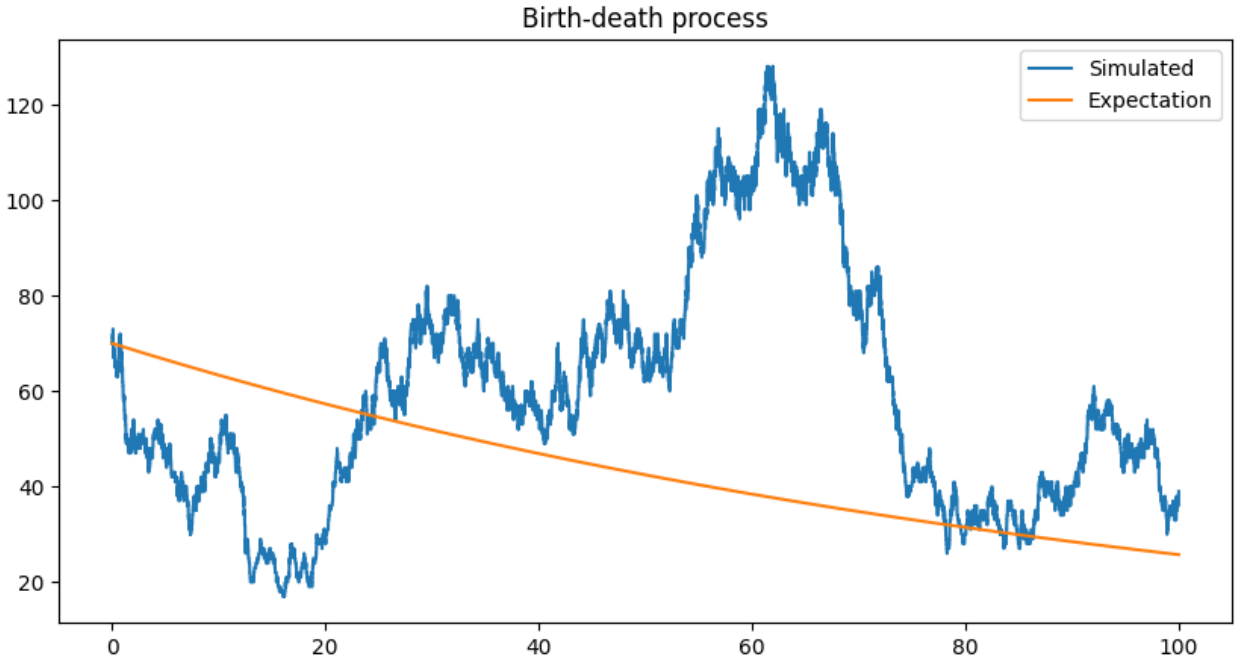
In [ ]:

```
def expected_birth_death_individuals(n0, dt, lamb, mniu):
    return n0*np.exp((lamb-mniu)*dt)

def incremental_birth_death_individuals(T, n0, lamb, mniu, dt):
```

```
    times = np.arange(0,T+dt,dt)
    persons = np.zeros_like(times)
    persons[0] = n0

    for i in range(1,len(times)):
        born = np.random.poisson(lamb*dt*persons[i-1])
        dead = np.random.poisson(mniu*dt*persons[i-1])
        persons[i] = persons[i-1] + born - dead

    return times, persons
```

In [ ]:
```
n0 = 70
lamb = 0.5
mniu = 0.51
T = 100
dt = 0.001

times, persons = incremental_birth_death_individuals(T, n0, lamb, mniu, d
true_values = expected_birth_death_individuals(n0, times, lamb, mniu)
```

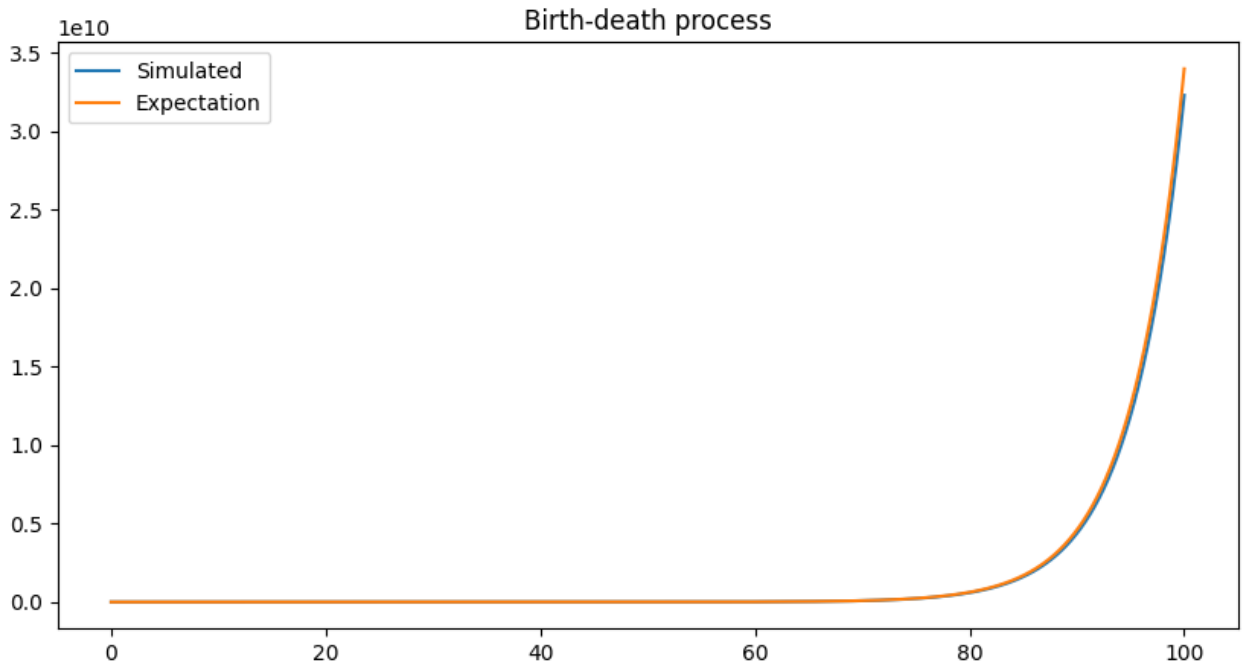
In [ ]:
```
plt.figure(figsize=(10,5))
plt.plot(times, persons, label='Simulated')
plt.plot(times, true_values, label='Expectation')
plt.title('Birth-death process')
plt.legend()
plt.show()
```



In [ ]:
```
n0 = 70
lamb = 0.6
mniu = 0.4
T = 100
dt = 0.001
```

```
times, persons = incremental_birth_death_individuals(T, n0, lamb, mniu, d
true_values = expected_birth_death_individuals(n0, times, lamb, mniu)
```

In [ ]:
```
plt.figure(figsize=(10,5))
plt.plot(times, persons, label='Simulated')
plt.plot(times, true_values, label='Expectation')
plt.title('Birth-death process')
plt.legend()
plt.show()
```



We can see in the aboce images that values for lamb = mniu there tends to be more oscilations, which is expected, whereas if one rate is bigger than the other then the tendency follows the given rate category (more or less individuals, respective to lamb>mniu and lamb<mniu)