# Assignment1

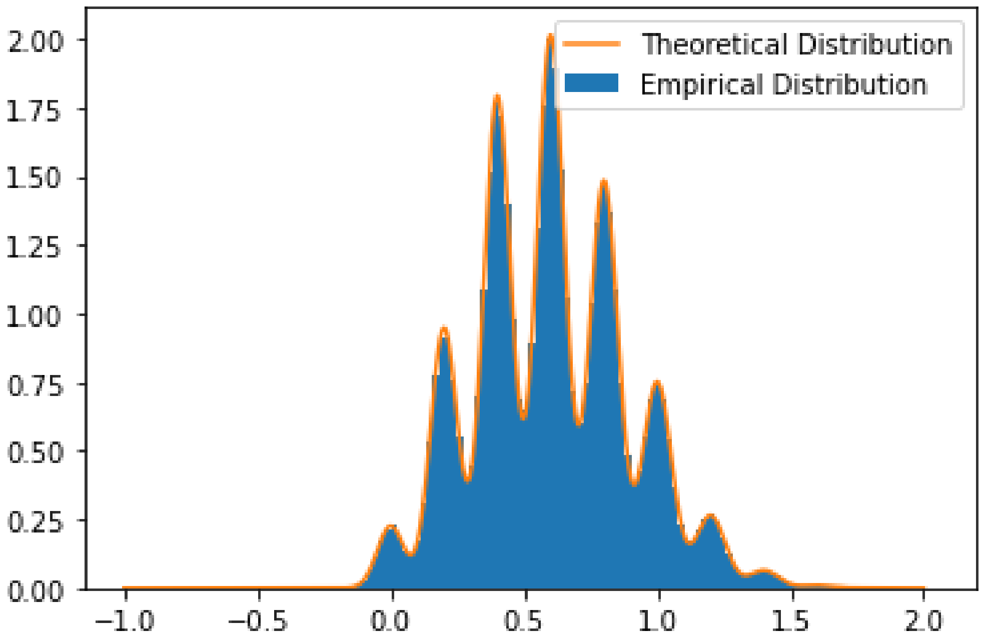
November 24, 2021

[1]:
```
import numpy as np
import matplotlib.pyplot as plt
from scipy.stats import binom, norm, chi2
```

## 0.1 Q4(ii)

[2]:
```
n = 10
p = 0.3
a = 0.2
sigma = 0.01
s = 0.05

m = int(1e6)

V = np.random.normal(0, s, size=(m,))
V += np.sum((np.random.rand(n, m) < p) * np.random.normal(a, sigma, size=(n,␣
 ↪m)), axis=0)

fig, ax = plt.subplots()
ax.hist(V, label="Empirical Distribution", density=True, bins=100)

P_V = 0
for K in range(n+1):
    P_V += norm.pdf(np.linspace(-1, 2, 1000), loc=K * a, scale=np.
 ↪sqrt(K*sigma**2 + s**2)) * binom.pmf(K, n, p)
ax.plot(np.linspace(-1, 2, 1000), P_V, label="Theoretical Distribution")
ax.legend()
```

[2]:
```
<matplotlib.legend.Legend at 0x7f7250405fa0>
```

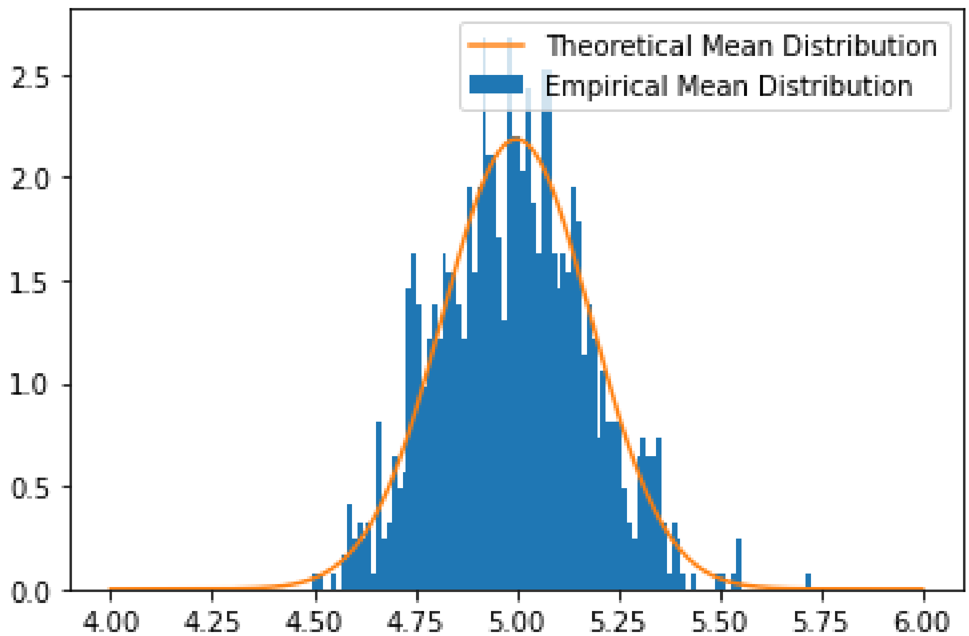


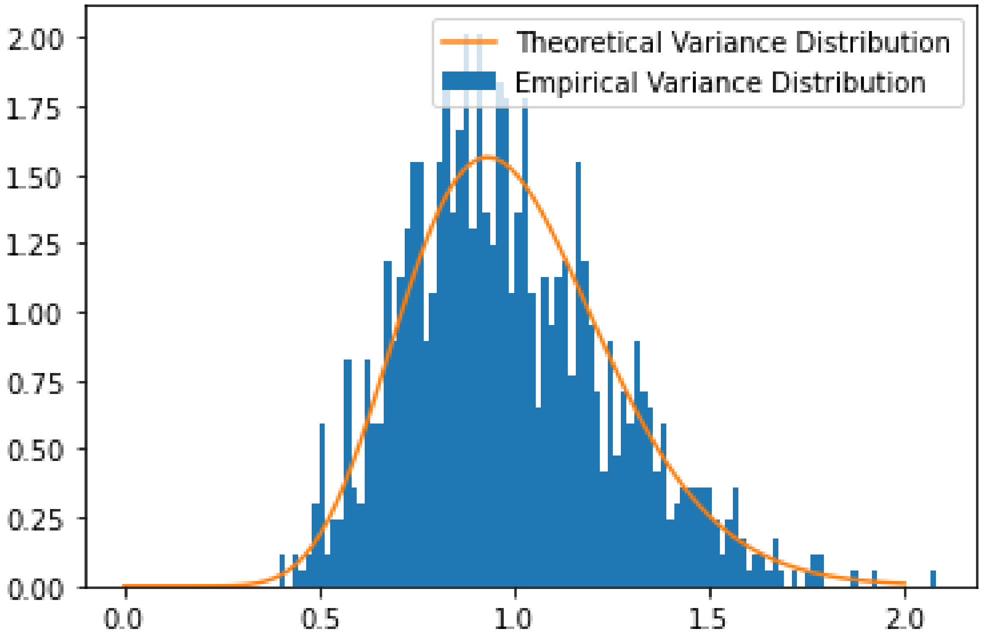

## 0.2 Q6

[3]:
```
n = 30
mu = 5
sigma = 1

m = 1000

X = np.random.normal(mu, sigma, size=(n, m))
means = np.mean(X, axis=0)
variances = np.sum((X - means) ** 2, axis=0) / (n-1)

fig, ax = plt.subplots()
ax.hist(means, label="Empirical Mean Distribution", density=True, bins=100)

# Central Limit Theorem tells us that the mean has distribution N(mu, sigma^2 /␣
↪n)
# Where mu and sigma are the popuplation statistics
P_means = norm.pdf(np.linspace(4, 6, 1000), loc=mu, scale=np.sqrt(sigma**2 / n))
ax.plot(np.linspace(4, 6, 1000), P_means, label="Theoretical Mean Distribution")
ax.legend()

fig, ax = plt.subplots()
ax.hist(variances, label="Empirical Variance Distribution", density=True,␣
↪bins=100)
```

```
# The sum of squares of a standard normal has a Chi squared distribution
# If we transform the variance by dividing through by n-1 and the population␣
↪variance,
# then the sample variance is the same as just a sum of squares of standard␣
↪normals
P_variances = chi2.pdf(np.linspace(0, 2 * (n - 1) / sigma ** 2, 100), n-1)
ax.plot(np.linspace(0, 2, 100), P_variances * (n - 1) * sigma ** 2,␣
↪label="Theoretical Variance Distribution")
ax.legend()
```

[3]: <matplotlib.legend.Legend at 0x7f7199d1e7c0>






### 0.3 Q7

[4]:
```
a = np.array([65, 73, 51, 67, 48, 80, 69, 83, 89, 62, 71, 67, 64, 78, 85, 49,␣
 ↪80, 60, 51, 70])
b = np.array([63, 72, 47, 63, 44, 78, 67, 52, 54, 58, 68, 65, 63, 77, 62, 46,␣
 ↪78, 56, 49, 65])

n_a = a.shape[0]
n_b = b.shape[0]

a_mean = np.mean(a)
b_mean = np.mean(b)

a_var = n / (n - 1) * np.var(a)
b_var = n / (n - 1) * np.var(b)

Z = (a_mean - b_mean) / np.sqrt((a_var / n_a + b_var / n_b))
print("Calculated Z statistic: ", Z)

p = 1 - norm.cdf(Z) + norm.cdf(-Z)
print("Calculated P Value (2 Tailed): ", p)
```

```
Calculated Z statistic:  1.8868698069325487
Calculated P Value (2 Tailed):  0.05917783903576096
```

Hence, we would reject the null hypothesis at the 10% significance, but we would fail to reject the null hypothesis at the 5% signficiance level.

For this dataset, there are only around 20 samples. This is a bit less than is suitable for a 2 tailed Z test. A 2 tailed t-test with the student's t distribution (with 19 degrees of freedom) would be more suitable.

## 0.4 Q8

[5]:
```
n = 100
p = 0.7

X = np.random.randn(n) < p
print(X[:10])
```

```
[ True  True  True  True False False  True  True  True  True]
```

Clearly, the likelihood of getting a single head is $p$ and a single tail is $(1-p)$. Hence the likelihood of getting an exact sequence with $k = \sum_{i=1}^{n} X_i$ heads and $n-k$ tails is $p^k(1-p)^{n-k}$

By Bayes rule, the posterior

$$P(p|X) = \frac{P(X|p)P(p)}{P(X)}$$

For a uniform prior, $P(p) = 1$. Hence $P(p|X) \propto p^k(1-p)^{n-k}$

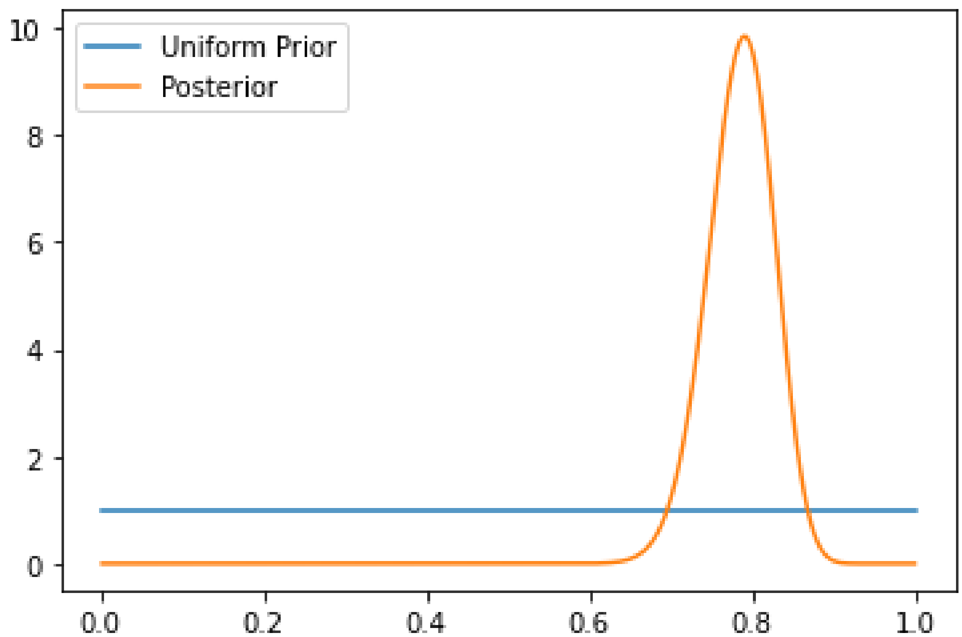
For the prior $P(p) \propto (1-p^4)$
$P(p|X) \propto p^{k+1}(1-p)^{n-k}(1-p^4)$

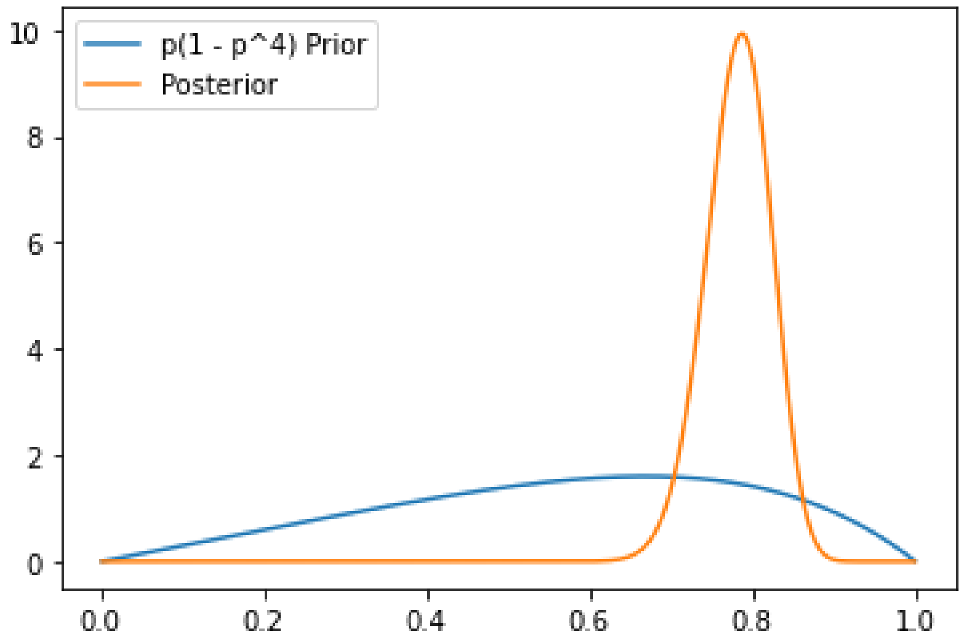
We can work out the normalising coefficient later with some numerical integration (since these priors are certainly not conjugate as the conjugate prior is a Beta distribution).

[6]:
```
k = np.sum(X)

dp = 1/1000
p_space = np.linspace(dp, 1 - dp, 1000)

# We'll do things in log space for numerical stability's sake
log_likelihood = lambda p: k * np.log(p) + (n - k) * np.log(1 - p)

# For a uniform prior, the posterior and the prior have the same distribution
# Since the prior has density 1 everywhere
posterior = np.exp(log_likelihood(p_space))

# numerical integration via trapezium rule
norm_posterior = np.sum(0.5 * dp * (posterior[1:] + posterior[:-1]))

posterior = np.exp(np.log(posterior) - np.log(norm_posterior))

fig, ax = plt.subplots()
ax.plot(p_space, np.ones(p_space.shape), label='Uniform Prior')
ax.plot(p_space, posterior, label='Posterior')
```

```python
plt.legend()

# For prior proportional to p (1 - p^4)
# We'll stay in log space again to keep things numerically stable
log_prior = np.log(p_space) + np.log(1 - p_space**4)
posterior = np.exp(log_likelihood(p_space) + log_prior)

# numerical integration via trapezium rule
norm_posterior = np.sum(0.5 * dp * (posterior[1:] + posterior[:-1]))
posterior = np.exp(np.log(posterior) - np.log(norm_posterior))

prior = np.exp(log_prior)
norm_prior = np.sum(0.5 * dp * (prior[1:] + prior[:-1]))
prior = np.exp(log_prior - np.log(norm_prior))

fig, ax = plt.subplots()
ax.plot(p_space, prior, label='p(1 - p^4) Prior')
ax.plot(p_space, posterior, label='Posterior')
plt.legend()
```

[6]: <matplotlib.legend.Legend at 0x7f7199b20940>






The 90% credible interval can be found numerically by starting at the centre of the unimodal distrbution, and numerically integrating outwards until 90% is reached. This obtains the 90% central credible interval.

Alternatively, the highest density credible interval can be computed by integrating numerically the probability mass above a given threshold, and then moving the threshold down until 90% of the probability mass is obtained.

The integration can be done in a number of different ways, though my preferred method is the trapezium rule as a fast and accurate way of integrating.

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[ ]:
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