lab03

September 22, 2021

1 Lab 3: Bayesian Estimation in Hierarchical Graphical Models

Welcome to the third Data 102 lab!

The goal of this lab is to go over Bayesian Estimation and provide an introduction to Hierarchial Graphical Models.

The code and responses you need to write are commented out with a message **"TODO: fill ..."**. There is additional documentation for each part as you go along.

1.1 Collaboration Policy

Data science is a collaborative activity. While you may talk with others about the labs, we ask that you **write your solutions individually**. If you do discuss the assignments with others please **include their names** in the cell below.

1.2 Gradescope Submission

To submit this assignment, rerun the notebook from scratch (by selecting Kernel > Restart & Run all), and then print as a pdf (File > download as > pdf) and submit it to Gradescope.

For full credit, this assignment should be completed and submitted before Wednesday, Sep 22, 2021 at 11:59 PM. PST

1.3 Collaborators

Write the names of your collaborators in this cell.

Riya Berry: 18rberry@berkeley.edu

Razi Mahmood: razi_mahmood@berkeley.edu

[1]:
```
import matplotlib.pyplot as plt
import numpy as np
import pandas as pd
import seaborn as sns
from scipy.stats import beta, binom
import itertools
from ipywidgets import interact, interactive

import hashlib
```

```
%matplotlib inline

sns.set(style="dark")
plt.style.use("ggplot")

def get_hash(num, significance = 4):
    num = round(num, significance)
    """Helper function for assessing correctness"""
    return hashlib.md5(str(num).encode()).hexdigest()
```

1.4 Question 1: Beta-Binomial Graphical Model

In this question we will look at the COVID modeling example. Here's the summary of what you need to know:

In this problem we are trying to estimate the COVID infection risk in households. To do that we curate a list of K studies. Each study has an associated pair (N_i, X_i) where N_i denotes the number of susceptible individuals considered and X_i is the number of them that became infected. In our modeling assumptions we assume that each susceptible person gets infected with probability θ_i. In epidemiology, this quantity is known as Secondary Attack Rate, or SAR for short.

We're trying to do two things: 1. We want to *combine* the information from all the studies, so we can get a better estimate of SAR than we would with any individual study on its own. 2. We want to understand why the studies got different results: specifically, we'd like to figure out the regions with the *lowest* SAR, so that we can investigate what contributed to their relative success. In the other direction, we want to know which regions had the *highest* SAR, since they're likely the ones most urgently in need of intervention measures to help slow the spread.

[2]:
```
# Read out a dataset
study_df = pd.read_csv("study_df.csv", header=0)
study_df
```

[2]:

	Name	X	N
0	Study 0	3	8
1	Study 1	2	11
2	Study 2	6	12
3	Study 3	9	27
4	Study 4	11	38
5	Study 5	21	59
6	Study 6	27	79
7	Study 7	23	82
8	Study 8	26	120
9	Study 9	57	145
10	Study 10	118	262
11	Study 11	122	341

1.4.1 1.a Compute the trivial estimate of SAR

The most straightforward way to estimate the probability of infection (SAR) is to divide the number of infected cases by the number of susceptible cases.

Compute this quantity in the cell below.

[3]:
```
# TODO: Complete the function
def trivial_theta_estimate(N_value, X_value):
    """
    Computes the trivial estimate of the Secondary Attack Rate

    Inputs:
        N_value : int, number of susceptible individuals
        X_value : int, number of infected individuals

    Output:
        theta_est : float, estimate of probability of infection (SAR)
    """
    theta_est = X_value/N_value
    return theta_est
```

[4]:
```
# Validation tests
n_test_array = [10, 100, 1000]
x_test_array = [10, 34, 852]
res_array = [trivial_theta_estimate(n, x_test_array[i]) for i,n in␣
 ↪enumerate(n_test_array)]
hash_list=['e4c2e8edac362acab7123654b9e73432','149dd5056939405870c9bb50cbc8691c','83659da620f4
for i,res in enumerate(res_array):
    assert get_hash(res) == hash_list[i]
print('Test passed!')
```

```
Test passed!
```

[5]:
```
# Apply  'trivial_theta_estimate' to each row of the dataframe and add a new␣
 ↪column to hold the result
study_df['Trivial estimate'] = study_df.apply(lambda row:␣
 ↪trivial_theta_estimate(row['N'], row['X']), axis =1)
study_df.sort_values('Trivial estimate')
```

[5]:

	Name	X	N	Trivial estimate
1	Study 1	2	11	0.181818
8	Study 8	26	120	0.216667
7	Study 7	23	82	0.280488
4	Study 4	11	38	0.289474
3	Study 3	9	27	0.333333
6	Study 6	27	79	0.341772
5	Study 5	21	59	0.355932

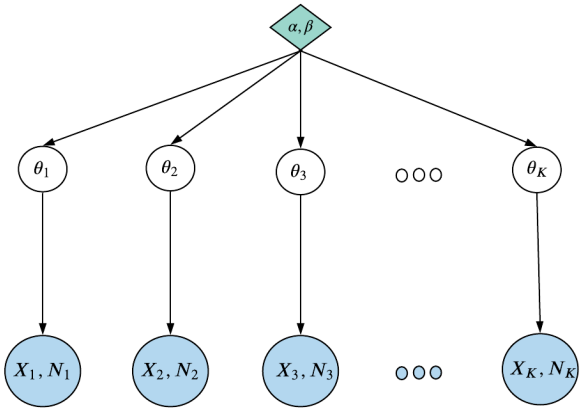
```
11  Study 11  122  341          0.357771
0    Study 0    3    8          0.375000
9    Study 9   57  145          0.393103
10  Study 10  118  262          0.450382
2    Study 2    6   12          0.500000
```

Trivial estimates suggest that both minimum and maximum probabilities of infection correspond to small studies.

	Min	Max
Name	Study 1	Study 2
X	2	8
N	11	12
θ	0.18	0.50

Intuitively, we probably shouldn't be making policy decision based on such small studies alone, especially when this dataset has other studies with tens or even hundreds of people. We would like to balance between strong evidence from the small studies and high confidence in estimates from larger studies.

Bayesian inference provides a flexible framework to balance our a priori beliefs with new evidence. Consider the following graphical model:



The circles represent random variables, and shaded circles represent observed random variables. The diamond at the top represents fixed, unknown parameters . You'll also see people draw dots or squares for these: there isn't really one consistent notation.

Here are a few important quantities in Bayesian inference. This lingo will be used at length in this course and in anything you'll learn in the future about Bayesian inference, so make sure you get familiar with it.

1.4.2 Joint Density / Joint Distribution:

The structure of the graphical model specified the full joint density of the parameters and data in the model. For this example the join density is:

$$p(\theta_1, \theta_2, \ldots, \theta_K, X_1, \ldots, X_K) = \prod_{\text{vertex } V \text{ in graph}} p(V|\text{parent of } V) = \prod_{i=1}^{K} \underbrace{p(\theta_i|\alpha, \beta)}_{\text{prior of } \theta_i} \prod_{i=1}^{K} \underbrace{p(X_i|\theta_i)}_{\text{likelihood of data } X_i}$$

The factorization of the joint density into products of priors and likelihoods is the key feature of Hierarchical Models. It allows to take a complex $2K$-dimensional joint probability and factorize it into products of 1-dimensional probabilities. This factorization is useful because it lets us simplify the distribution and control the amount of computation we have to do.

1.4.3 Prior: $\theta_i \sim Beta(\alpha, \beta)$

We have the prior distribution:

$$p(\theta_i) = \theta_i^{\alpha-1}(1-\theta_i)^{\beta-1}\frac{\Gamma(\alpha+\beta)}{\Gamma(\alpha)\Gamma(\beta)} \tag{1}$$

$$\propto_{\theta_i} \theta_i^{\alpha-1}(1-\theta_i)^{\beta-1} \tag{2}$$

where Γ is the gamma function. Since $\frac{\Gamma(\alpha+\beta)}{\Gamma(\alpha)\Gamma(\beta)}$ does not depend on the value of θ. It is a scaling factor that ensures that $p(\theta_i)$ is a valid probability function. This leads to a common notation in practice: $p(\theta_i) \propto_{\theta_i} \theta_i^{\alpha-1}(1-\theta_i)^{\beta-1}$. The symbol $\propto_{\theta_i}$ means *proportional in* θ_i. This is a little more explicit than the $\propto$ notation that you usually see.

1.4.4 Likelihood: $X_i|\theta \sim Binomial(N_i, \theta_i)$

We'll use the notation $p(X_i|\theta)$ for the likelihood function, which represents our belief about the distribution of the data if we know what the parameter θ is (in other words, if we condition on θ).

$$p(X_i|\theta_i) = \binom{N_i}{X_i}\theta_i^{X_i}(1-\theta_i)^{N_i-X_i}$$

1.4.5 Marginal: Unconditional distribution of X_i:

$$p(X_i) = \int_{\theta_i} \overbrace{p(X_i, \theta_i)}^{\text{joint distribution}} \tag{3}$$

$$= \int_0^1 \underbrace{p(X_i|\theta_i)}_{\text{likelihood}} \underbrace{p(\theta_i)}_{\text{prior}} d\theta_i \tag{4}$$

This is the marginal distribution over the data: we can plug in a particular set of X_i values and get out the probability that our model assigns to those values, averaged over all possible values of θ.

When formulating a model, we usually choose the prior and the likelihood based on what we know about the problem. This means that computing this marginal distribution over X_i requires *marginalizing* over the parameter θ: that involves either a summation or an integral (in this case it's an integral because θ is continuous).

1.4.6 Posterior: $\theta_i|X_i$

The goal of many estimation problems is to obtain the posterior distribution of the parameter of interest θ_i conditioned on the data X_i.

$$p(\theta_i|X_i) = \frac{p(X_i|\theta_i)p(\theta_i)}{p(X_i)} \quad \text{(by Bayes Rule)} \tag{5}$$

$$\propto_\theta p(X_i|\theta_i)p(\theta_i) \quad \text{(the data marginal } p(X_i) \text{ does not depend on } \theta) \tag{6}$$

$$\propto_\theta \underbrace{\theta_i^{X_i}(1-\theta_i)^{N_i-X_i}}_{\text{likelihood}} \underbrace{\theta^{\alpha-1}(1-\theta)^{\beta-1}}_{\text{prior}} \tag{7}$$

$$\propto_\theta \theta_i^{\alpha+X_i-1}(1-\theta_i)^{\beta+N_i-X_i-1} \quad \text{unnormalized Beta density} \tag{8}$$

$$\tag{9}$$

1.4.7 Hence $\theta_i|X_i \sim Beta(\alpha + X_i, \beta + N_i - X_i)$

The fact that the posterior probability comes from the same distribution family is known as *conjugacy*. It is a very useful property because it allows us to compute the posteriors in close form.

1.4.8 1.b Conceptual

1.b (i) When specifying a Bayesian model, we use our domain knowledge to establish certain distributions, and then we use computation to find other ones. Which of the following do we establish using our domain knowledge? Pick all that apply.

(a) Prior

(b) Likelihood

(c) Marginal distribution of the data

(d) Posterior

We establish (a) and (b) using domain knowledge.

(a) is established using domain knowledge because it is the probability before any data is available.

(b) is established using domain knowledge because it is an estimation of parameters.

`TODO: fill in with the relevant letters above`

1.4.9 1.c Examine the prior distribution

[6]:
```
def plot_beta(alpha_value, beta_value):
    x = np.arange(0, 1.01, 0.01)
    y = beta.pdf(x, alpha_value, beta_value)
    fig = plt.figure()
    plt.plot(x, y)
```

```
    plt.xlabel(r'$\theta_i$')
    plt.ylabel(r'$p(\theta_i)$')
    plt.title(r'Beta distribution with parameters $\alpha$ and $\beta$')
    plt.ylim(0, 10)
    plt.show()
```

[7]:
```
interactive_plot = interactive(plot_beta, alpha_value=(1, 20, 0.5),␣
↪beta_value=(1,20, 0.5))
interactive_plot
```

```
interactive(children=(FloatSlider(value=10.0, description='alpha_value', max=20.
↪0, min=1.0, step=0.5), FloatSl…
```

1.c (i) Fix `alpha_value = 5`, and experiment with different values of `beta_value`. Write 1 sentence of your observations.

The higher the beta value, the more up and left the "peak" aka the mode of the distribution is.

`TODO:` fill in

1.c (ii) Fix `beta_value = 5`, and experiment with different values of `alpha_value`. Write 1 sentence of your observations.

The higher the alpha value, the more up and right the "peak" aka the mode of the distribution is.

`TODO:` fill in

1.c (iii) Set `alpha_value = beta_value = 1`, increase their value such that `alpha_value=beta_value`. Write 1 sentence of your observations.

When `alpha_value` = `beta_value`, then the distribution is always symmetrical looking i.e. not left skewed or right skewed. However, when we increase `alpha_value` and `beta_value`, the peak becomes higher and sharper around 0.5 i.e. the plot becomes less wide.

`TODO:` fill in

1.4.10 1.d Compute Posterior Mean Estimates for SAR

In Problem 1 of Discussion 3 we showed that the **posterior mean** minimizes the **Bayes Risk** for the **Squared Error Loss**.

In the cell below write a function that computes the posterior mean corresponding to $\theta_i|X_i$**.** *Hint: If you need to look up facts about certain well-known distributions, you can always (a) go to textbooks from classes you've taken before, (b) look on Wikipedia, or (c) do a simple web search.*

[8]:
```
# TODO: complete the function
def posterior_mean_estimate(N_value, X_value, alpha_value, beta_value):
    """
    Computes the posterior E[theta_i|X_i] when we consider a prior theta_i ~␣
↪Beta(alpha, beta)

```

```
    Inputs:
        N_value : int, total number of susceptible individuals
        X_value : int, number of individuals that became infected
        alpha_value, beta_value : floats, parameters of the prior Beta␣
↪Distribution
    """
    posterior_mean = (alpha_value + X_value) / (alpha_value + beta_value +␣
↪N_value)
    return posterior_mean
```

[9]:
```
# Validation tests
N_test = 100
X_test = 20
alpha_test_array = [1, 10, 100]
beta_test_array = [1, 10, 100]
inputs = list(itertools.product(alpha_test_array, beta_test_array))
hash_list =␣
↪['8ae3cf8f9366cbdea2ccf7706546ba4a','f8ddc3234c0a54e55b01384bcfb23f90','82589ee1f18a2e0b9fe
            ␣
↪'08cf5a2033e7e21ec90b6707c24facaf','70da82175ec8a195a3d8b0fa8f69681d','ced20bed08ecfba035cb
            ␣
↪'c8a7feeaced214c662a999d9bf075e8c','790abc5c38e7c740420b03c24fabb05b','54fbf38cf649866815e0
for i,inp in enumerate(inputs):
    assert hash_list[i] == get_hash(posterior_mean_estimate(N_test, X_test,␣
↪*inp))
print('Test passed!')
```

```
Test passed!
```

1.4.11 1.e Examine the posterior mean estimate

Let's assume that from domain knowledge, we think that the probability of infection (SAR) is close to $\frac{1}{3}$. We pick a prior distribution for θ_is that has mean $\frac{1}{3}$. Any distribution of the form $\theta_i \sim Beta(k, 2k)$ has this property. The value of k determines the 'strength' of the prior. Low values of k correspond to 'flatter' priors, while larger values of k correspond to 'peakier' priors. Play with the sliders in **1.b** to convince yourself.

Examine the plotting function below and answer the qualitative questions in the next cells.

[10]:
```
study_df
```

[10]:

	Name	X	N	Trivial estimate
0	Study 0	3	8	0.375000
1	Study 1	2	11	0.181818
2	Study 2	6	12	0.500000
3	Study 3	9	27	0.333333

```
4     Study 4   11   38          0.289474
5     Study 5   21   59          0.355932
6     Study 6   27   79          0.341772
7     Study 7   23   82          0.280488
8     Study 8   26  120          0.216667
9     Study 9   57  145          0.393103
10  Study 10  118  262          0.450382
11  Study 11  122  341          0.357771
```

[11]:
```python
# Do not modify: Examine the code
def plot_thetas(k):

    study_df["bayesian_theta"] = study_df.apply(
        lambda row: posterior_mean_estimate(row['N'], row['X'], k, 2*k),
        axis=1
    )
    study_df["trivial_theta"] = study_df.apply(
        lambda row: trivial_theta_estimate(row['N'], row['X']),
        axis=1
    )
    fig = plt.figure(figsize=(14, 6))
    plt.subplot(1, 2, 1)
    graph = sns.scatterplot(
        x="trivial_theta", y="bayesian_theta",
        data=study_df, size="N", sizes=(50, 300), alpha=.8
    )
    sns.lineplot(
        x='trivial_theta', y='trivial_theta',
        data= study_df, ls="--", color='black', lw=1
    )
    plt.ylim(0.16, 0.52)
    graph.axhline(
        1/3, color='black',
        label = "$\frac{1}{3}$ Prior Expectation"
    )
    plt.xlabel('Trivial Estimate')
    plt.ylabel('Posterior Mean Estimate')

    plt.subplot(1, 2, 2)
    x = np.arange(0,1.01,0.01)
    y = beta.pdf(x, k, 2*k)
    plt.plot(x, y)
    plt.xlabel(r'$\theta_i$')
    plt.ylabel(r'$p(\theta_i)$')
    plt.title(rf'Prior: $Beta(\alpha={k}, \beta={2*k})$')
    plt.ylim(0, 10)
    plt.show()
```

[12]:
```
interactive_plot = interactive(plot_thetas, k=(0, 50, 2))
interactive_plot
```

```
interactive(children=(IntSlider(value=24, description='k', max=50, step=2),␣
↪Output()), _dom_classes=('widget-i…
```

In the plot above the horizontal dashed line represents the prior mean estimate $\mathbb{E}[\theta_i] = \frac{k}{k+2k} = 1/3$. The diagonal solid line marks $x = y$. Each data-point corresponds to a study, the size of the marker denotes the number of susceptible individuals in each study. Such that larger markers correspond to larger studies.

Answer the following questions with 1-2 sentences each.

1.e (i) Set $k = 0$, what do you notice about the data points? Increase steadily the value of k. What happens with the points above the solid horizontal line? What about the points below it?

When k=0, all the data points lie on the straight diagonal line (since this line is x=y, this means that the posterior mean estimate is equal to the trivial estimate). As k increases, the points above the solid horizontal line move down towards the horizontal line at 1/3 and the points below the solid horizontal line move up towards the horizontal line. At this point, the peak of the prior is at its highest and sharpest i.e. the prior is heavily concentrated upon a value.

`TODO:` fill in

1.e (ii) As you increase k, which points move faster, larger or slower ones? How can you explain this?

As you increase k, the smaller points (i.e. smaller circles, with less data) move way faster than the big points (i.e. bigger circles, with more data). This is because bigger circles mean there is a lot of data to support that particular point, so changing it to the posterior mean estimate will require more effort (data).

`TODO:` fill in

1.e (iii) Imagine that we let $k \to \infty$. How do you think the two graphs above will look in the limit $k \to \infty$?

If we let k go to infinity, all the data points on the plot on the left will lie on the horizontal line at 1/3. For the right plot, it will be a vertical line at 1/3, indicating that we are very concentrated (sure) of our prior.

`TODO:` fill in

1.e (iv) Fill in the blank in this sentence with either "small" or "large", and explain your answer:

If we're very sure that the true SAR is close to $\frac{1}{3}$, we should choose a _____ *value of k.*

Large. This is because as k goes to infinity, the peak will become taller and sharper, having less room for uncertainty.

`TODO:` fill in

1.5 Question 2: Computational Approximate Inference

In the previous question we looked at a Beta-Binomial Graphical model. We took advantage of the conjugacy properties of the model and were able to compute closed form solutions for the posterior mean estimates.

However, as we introduce more complexity to the model, the conjugacy property quickly breaks and we have to resort to approximate inference. In this class, we'll focus primarily on *sampling* for approximate inference: this will be the topic of the next few lectures and next week's labs. In sampling-based approaches, we don't even try to get the exact posterior: instead, we generate a bunch of samples from it, and use those to approximate the distribution.

In this question you will get a taste for probabilistic programming using `PyMC3`. Spend some time perusing the documentation, but don't worry if it doesn't fully make sense just yet. We'll be using PyMC3 to run an algorithm called Markov Chain Monte Carlo (MCMC), which you'll learn about this week. We'll start by using the same model from Q.1, and compare the results from MCMC with the exact solutions we calculated above. Then, we'll add an extra parameter to the model and make things more complex: even though we can no longer compute our posterior in closed form, MCMC will still generate samples that we can use to estimate the θ_is.

[13]:
```
# Import PyMC3, and create a dummy model so that one-time initialization
# happens while you're reading over the code in the next cell.

# Note: this and the following cells may take a while to run

# You can ignore the output of this cell.

import pymc3 as pm

with pm.Model() as model:
    dummy = pm.Beta('dummy', alpha=1, beta=1)
    pm.sample(1)
```

```
/tmp/ipykernel_23/3897985474.py:12: FutureWarning: In v4.0, pm.sample will
return an `arviz.InferenceData` object instead of a `MultiTrace` by default. You
can pass return_inferencedata=True or return_inferencedata=False to be safe and
silence this warning.
  pm.sample(1)
Only 1 samples in chain.
Auto-assigning NUTS sampler…
Initializing NUTS using jitter+adapt_diag…
Multiprocess sampling (4 chains in 4 jobs)
NUTS: [dummy]
```

```
<IPython.core.display.HTML object>
```

```
Sampling 4 chains for 1_000 tune and 1 draw iterations (4_000 + 4 draws total)
took 5 seconds.
/opt/conda/lib/python3.9/site-packages/arviz/data/base.py:169: UserWarning: More
chains (4) than draws (1). Passed array should have shape (chains, draws,
```

```
*shape)
  warnings.warn(
/opt/conda/lib/python3.9/site-packages/pymc3/sampling.py:643: UserWarning: The
number of samples is too small to check convergence reliably.
  warnings.warn("The number of samples is too small to check convergence
reliably.")
```

[14]:
```python
# Do not modify: Spend some time examining the code
def approximate_inference_MCMC(
    alpha_value, beta_value, study_df = study_df
):
    """
    Creates and generates samples from a PyMC3 model of
    the posterior distribution that corresponds to the
    graphical model in Q.1, using Markov Chain Monte Carlo (MCMC)

    Inputs:
        alpha_value, beta_value : floats, parameters of
        the prior Beta Distribution
        study_df : DataFrame containing study data

    Outputs: (model, trace)
        model is a PyMC3 model object, which represents the graphical model
        trace is a PyMC3 trace object, which represents 2000 samples
            of everything from the posterior
    """
    # Defines the graphical model
    with pm.Model() as model:
        # The prior for theta is a Beta distribution with parameters
        # alpha and beta, and there's one for each study.
        theta = pm.Beta('theta', alpha=alpha_value, beta=beta_value,␣
↪shape=len(study_df)
        )

        # The likelihood for X is binomial, with parameter p=theta,
        # observed counts in study_df['X'], and observed N similarly
        X = pm.Binomial(
            'X', p=theta, observed=study_df['X'], n=study_df['N']
        )

        # Generate samples from the posterior distribution using : run 4
        # Markov chains of sampling in parallel, generating 500 samples
        # each.
        trace = pm.sample(500, chains=4, tune=1000, target_accept=0.95)

    return (model, trace)
```

Try running the following cell.

[15]:
```
# Run approximate inference
model, trace = approximate_inference_MCMC(10, 20)

# Get posterior samples of theta
thetas = trace['theta']
thetas
```

```
/tmp/ipykernel_23/2997294687.py:36: FutureWarning: In v4.0, pm.sample will
return an `arviz.InferenceData` object instead of a `MultiTrace` by default. You
can pass return_inferencedata=True or return_inferencedata=False to be safe and
silence this warning.
  trace = pm.sample(500, chains=4, tune=1000, target_accept=0.95)
Auto-assigning NUTS sampler…
Initializing NUTS using jitter+adapt_diag…
Multiprocess sampling (4 chains in 4 jobs)
NUTS: [theta]
```

```
<IPython.core.display.HTML object>
```

```
Sampling 4 chains for 1_000 tune and 500 draw iterations (4_000 + 2_000 draws
total) took 8 seconds.
```

[15]:
```
array([[0.32212383, 0.31859754, 0.3053673 , …, 0.38184229, 0.5005448 ,
        0.3656524 ],
       [0.339641  , 0.25877898, 0.4161113 , …, 0.38322067, 0.35385333,
        0.34943113],
       [0.23757142, 0.30014398, 0.29519237, …, 0.41641295, 0.416184  ,
        0.35284506],
       …,
       [0.32020668, 0.31766257, 0.40247153, …, 0.39154861, 0.38738383,
        0.36318786],
       [0.32496907, 0.22909974, 0.39876247, …, 0.43528373, 0.49800645,
        0.34960758],
       [0.33268925, 0.32121269, 0.3569503 , …, 0.40814822, 0.43385547,
        0.31013853]])
```

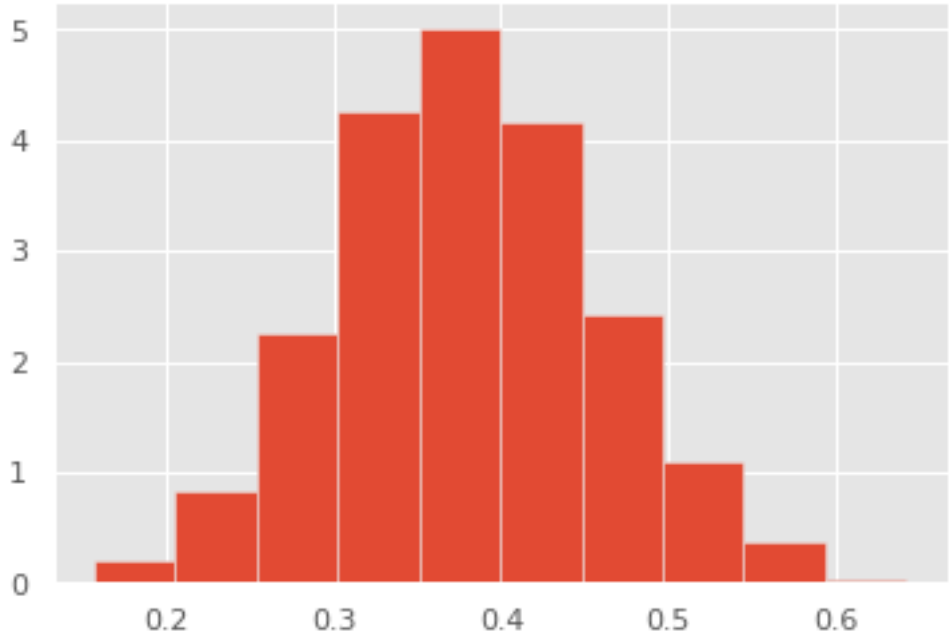
1.5.1 2.a Using the output of PyMC3

Generate a histogram of all 2,000 posterior samples for θ_2 (the SAR for Study 2). How do the samples compare to the two different estimates you saw in Question 1?

[16]:
```
# TODO: fill in
plt.hist(thetas[:, 2], density=True)
```

[16]:
```
(array([0.20636777, 0.82547107, 2.24940867, 4.25117602, 5.00441837,
        4.15831052, 2.43513966, 1.10406756, 0.36114359, 0.04127355]),
 array([0.15716732, 0.2056245 , 0.25408168, 0.30253886, 0.35099604,
        0.39945322, 0.4479104 , 0.49636758, 0.54482476, 0.59328194,
```

```
       0.64173912]),
<BarContainer object of 10 artists>)
```



The estimates in Q1 have a much smoother graph than what we have here. The reason for this is because this data (theta_2) focuses specifically on one study, and hence, finite samples. Since we know all the samples for an existing study, and this data is finite, this data represents a posterior histogram. Hence, the new distribution is more normal.

`TODO:` fill in

1.5.2 2.b Compute Posterior Mean Estimates from Samples

Fill in the function that computes posterior mean estimates for θ_is for different parameters α, β of the prior distribution.

[17]:
```
# TODO: complete the function
def empirical_posterior_mean_estimates(alpha_value, beta_value, study_df =␣
↪study_df):
    """
    Computes posterior mean estimates of theta_i by performing approximate␣
↪inference
    and then sampling from the posterior distribution:

    Inputs:
        alpha_value, beta_value : floats, parameters of the prior Beta␣
↪Distribution
```

```
        study_df : DataFrame containing study data

    Output:
        posterior_estimates : (num_studies,) 1-D array of the same length as␣
↪the
            number of studies. posterior_estimates[i] contains the
            mean estimate for theta_i based on running MCMC

    """

    model, trace = approximate_inference_MCMC(alpha_value, beta_value,␣
↪study_df=study_df)

    posterior_estimates = trace['theta']
    return np.mean(posterior_estimates, axis=0)
```

[18]:
```
# Validation tests: Do not modify
posterior_estimates_test = empirical_posterior_mean_estimates(10,25)
hash_list = [["e85b79abfd76b7c13b1334d8d8c194a5"],
             ["261943f3a93b683ceeac658927f3923f"],
             ["149dd5056939405870c9bb50cbc8691c"],
             ["ba6197788db60f5e2cb45cd403fa6559"],
             ["246c0903b5a64b2a854ec1e7865f174f"],
             ["ffa243f771800363714f6055d9236fd6"],
             ["ffa243f771800363714f6055d9236fd6",␣
↪"9f4721cf71c0ed18cd60356036b953cc"],
             ["45efc23f34e05a9ea4f5024988047dd6"],
             ["8f11bfb91ec29936603314c7cbc46119"],
             ["a3f2a910685f5b07f5f45a5fc1fdb389"],
             ["91afec64e32d6bf957e441df2ab638bb"],
             ["8ce3fac7e23a02ab4e00cf0f1e03310a"]]
print()

for i, est in enumerate(posterior_estimates_test):
    print("Study {}: {:.3f} ".format(i, est))

for i, est in enumerate(posterior_estimates_test):
    assert get_hash(est, 2) in hash_list[i]

print("Test passed!")
```

```
/tmp/ipykernel_23/2997294687.py:36: FutureWarning: In v4.0, pm.sample will
return an `arviz.InferenceData` object instead of a `MultiTrace` by default. You
can pass return_inferencedata=True or return_inferencedata=False to be safe and
silence this warning.
  trace = pm.sample(500, chains=4, tune=1000, target_accept=0.95)
Auto-assigning NUTS sampler…
```

```
Initializing NUTS using jitter+adapt_diag…
Multiprocess sampling (4 chains in 4 jobs)
NUTS: [theta]
```

```
<IPython.core.display.HTML object>
```

```
Sampling 4 chains for 1_000 tune and 500 draw iterations (4_000 + 2_000 draws
total) took 3 seconds.
```

```
Study 0: 0.300
Study 1: 0.260
Study 2: 0.341
Study 3: 0.307
Study 4: 0.289
Study 5: 0.329
Study 6: 0.323
Study 7: 0.282
Study 8: 0.233
Study 9: 0.371
Study 10: 0.431
Study 11: 0.352
Test passed!
```

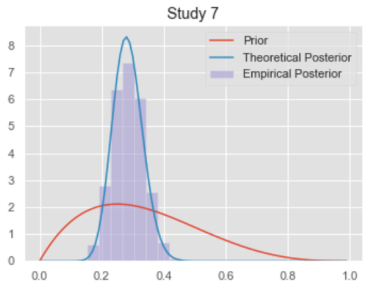
1.5.3 2.c Plot the theoretical distribution of the posterior from Question 1 and the empirical distribution of the posterior from Question 2.

Make a 4x3 plot such that each subplot corresponds to a study.

Each subplot should contain 2 curves and a frequency histogram: - The PDF of the prior distribution of θ_i - The PDF of the true posterior distribution $\theta_i|X_i$ computed in closed form, as in Q.1 - The histogram of posterior samples of $\theta_i|X_i$ computed in Q.2

Make sure that you properly label each curve and histogram and give each subplot a meaningful title.

To give you a mental image of what we have in mind here is a sample subplot. Don't worry if the colors in yours are different.



[19]:
```
# TODO: write the plotting function
def plot_densities(alpha_value, beta_value, study_df = study_df):
    """
    Plots for each study the prior distribution, true posterior,
```

```
    and histogram of posterior samples using MCMC

    Inputs:
        alpha_value, beta_value : floats, parameters of the prior Beta␣
↪Distribution
        study_df : DataFrame containing study data

    Outputs:
        fig : Figure with 12 subplots
    """
    fig, axs = plt.subplots(4, 3)
    fig.set_figheight(15)
    fig.set_figwidth(15)


    theta = np.arange(0, 1.01, 0.01)
    prior = beta.pdf(theta, alpha_value, beta_value)

    model, trace = approximate_inference_MCMC(alpha_value, beta_value,␣
↪study_df=study_df) #TODO: Fill in
    samples = trace['theta'] #TODO: Fill in

    for i in range(4):
        for j in range(3):
            idx = 3*i+ j
            X_i = study_df.loc[idx, 'X']
            N_i = study_df.loc[idx, 'N']
            study_name = f'Study {idx}'
            true_posterior = beta.pdf(theta, alpha_value + X_i, beta_value +␣
↪N_i - X_i) #TODO: Fill in

            ax = axs[i, j]
            ax.plot(theta, prior, label = 'Prior')
            ax.plot(theta, true_posterior, label = "Theoretical Posterior")
            ax.hist(samples[:,idx], label = "Empirical Posterior",␣
↪density=True, alpha = 0.7)
            ax.set_title(study_name)
            ax.legend()

    plt.tight_layout()
    plt.show()
    return fig
```

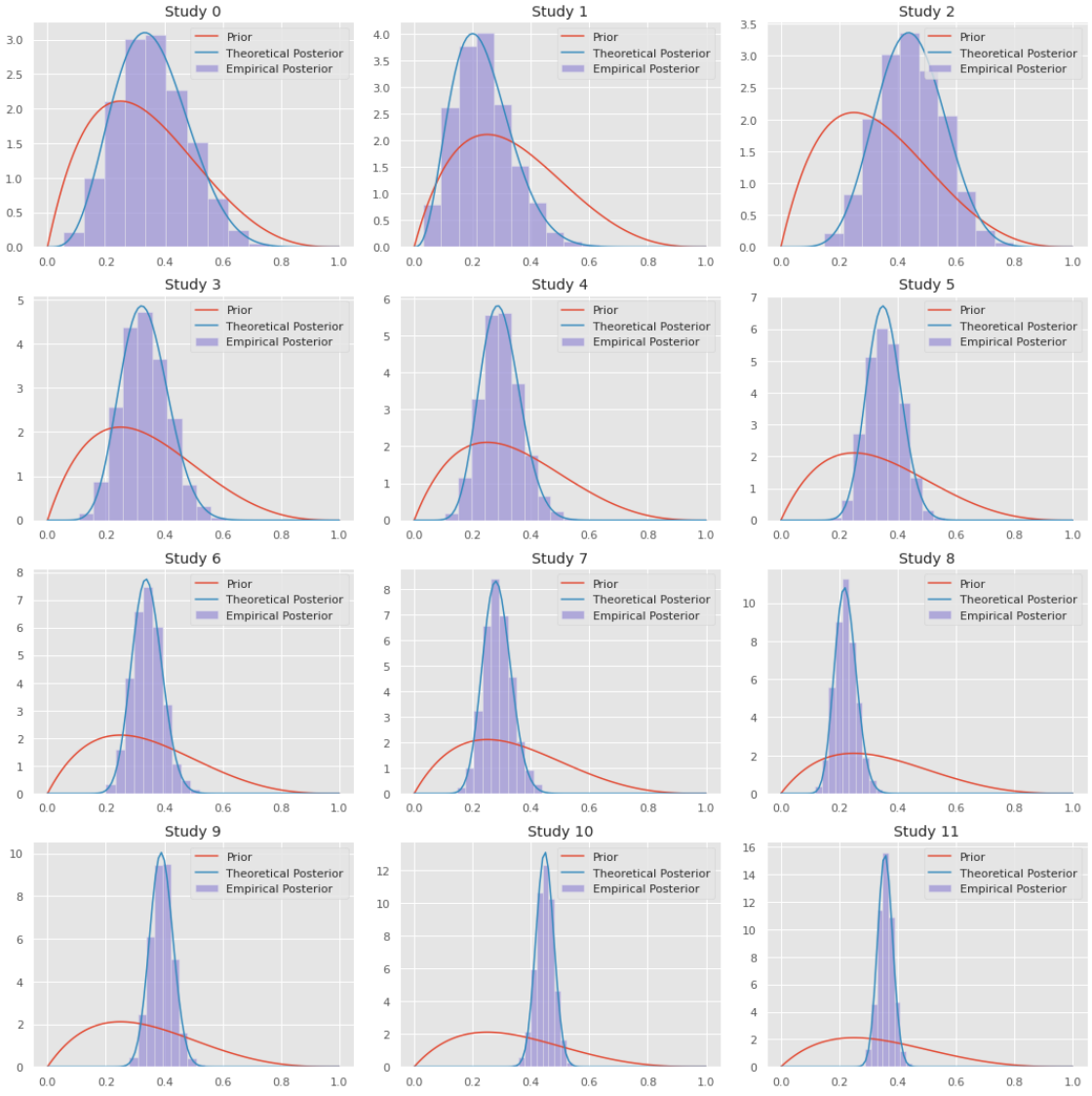
[20]:
```
# Plot the resulting densities for a weak prior
fig1 = plot_densities(2, 4, study_df = study_df)
```

```
/tmp/ipykernel_23/2997294687.py:36: FutureWarning: In v4.0, pm.sample will
```

```
return an `arviz.InferenceData` object instead of a `MultiTrace` by default. You
can pass return_inferencedata=True or return_inferencedata=False to be safe and
silence this warning.
  trace = pm.sample(500, chains=4, tune=1000, target_accept=0.95)
Auto-assigning NUTS sampler…
Initializing NUTS using jitter+adapt_diag…
Multiprocess sampling (4 chains in 4 jobs)
NUTS: [theta]
```

```
<IPython.core.display.HTML object>
```

```
Sampling 4 chains for 1_000 tune and 500 draw iterations (4_000 + 2_000 draws
total) took 3 seconds.
```

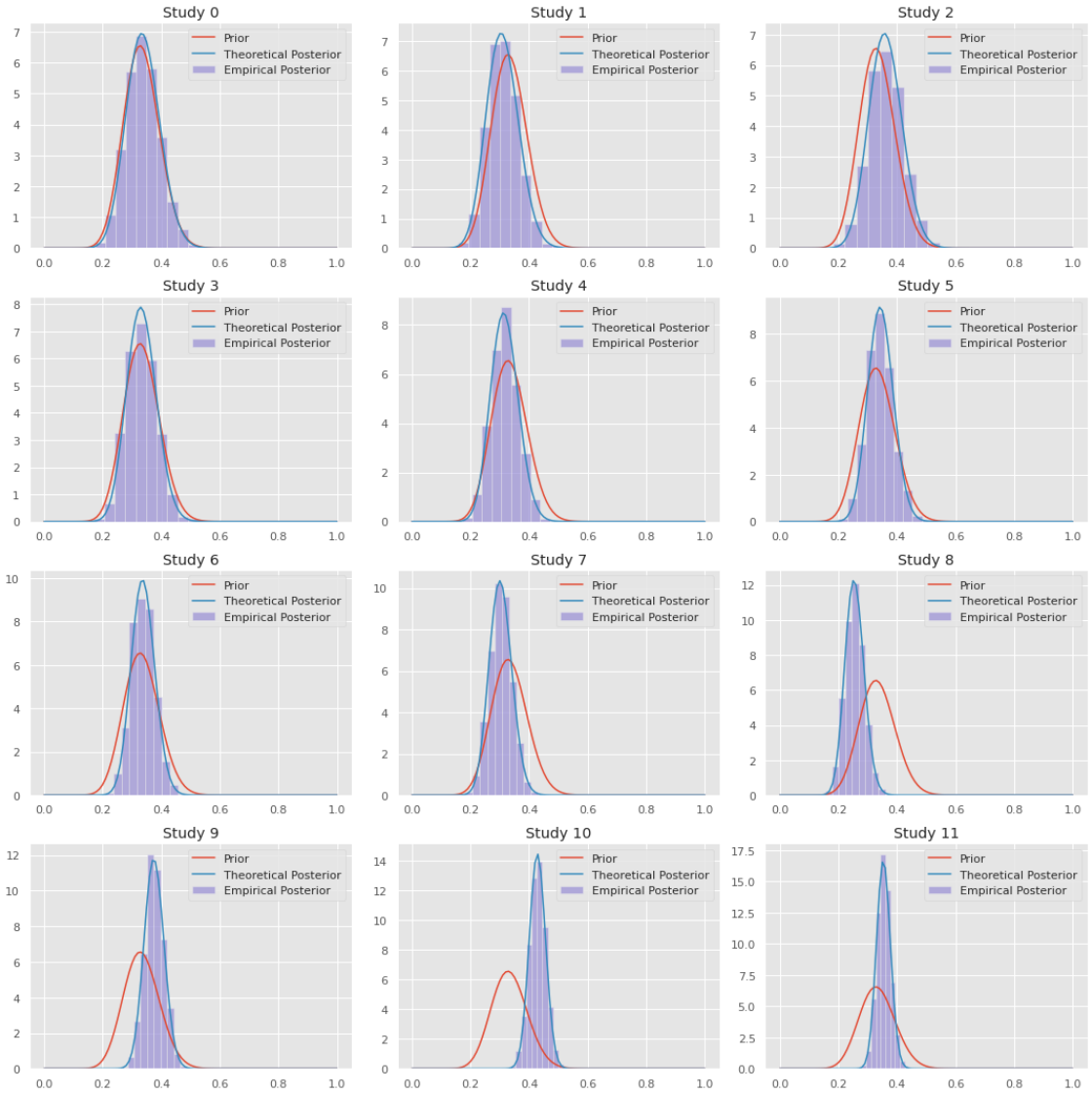


[21]:
```
# Plot the resulting densities for a strong prior
fig2 = plot_densities(20, 40, study_df = study_df)
```

```
/tmp/ipykernel_23/2997294687.py:36: FutureWarning: In v4.0, pm.sample will
return an `arviz.InferenceData` object instead of a `MultiTrace` by default. You
can pass return_inferencedata=True or return_inferencedata=False to be safe and
silence this warning.
  trace = pm.sample(500, chains=4, tune=1000, target_accept=0.95)
Auto-assigning NUTS sampler…
Initializing NUTS using jitter+adapt_diag…
Multiprocess sampling (4 chains in 4 jobs)
NUTS: [theta]
```

```
<IPython.core.display.HTML object>
```

```
Sampling 4 chains for 1_000 tune and 500 draw iterations (4_000 + 2_000 draws
total) took 3 seconds.
```



2.c (i) Compare the curve of the theoretical distribution with the histogram of samples from the empirical posterior. Are they similar or different? Explain why.

In both cases, the theoretical posterior is pretty close to the empirical posterior. This is because both the empirical posterior and theoretical posterior depend on the fact that as you obtain more data, you become more concentrated on specific values.

`TODO:` fill in

2.c (ii) Compare the two figures corresponding to 'weak' prior $\theta_i \sim Beta(2, 4)$ and 'strong' prior $\theta_i \sim Beta(20, 40)$. How are they different? Explain why.

In the strong prior, the histogram starts off pretty narrow compared to the weak prior. At each step, it becomes narrow faster and faster in the weak prior since there is less evidence for specific points, so the peak changes quickly. However, the histogram ends up converging to the same level

of "sharpness" at the end.

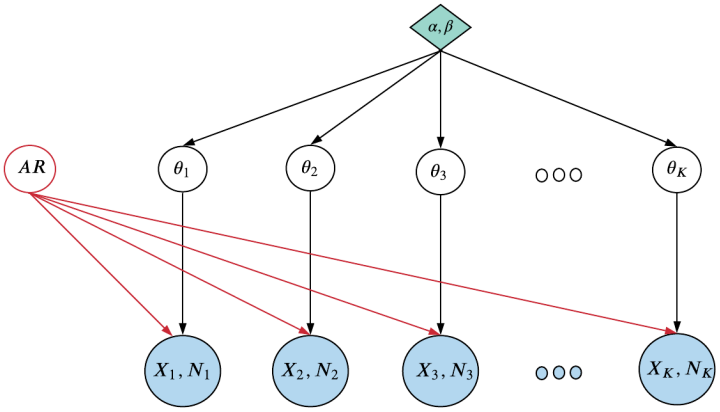
This happens because we are pretty sure about our mode value in the strong prior, so our graph is more sharp and concentrated.

`TODO:` fill in

1.5.4 2.d Approximate Inference for a More Complex Model

The previous 2 parts served as a sanity check that the approximate inference techniques used by PyMC3 can approximate the theoretical posterior. The usefulness of such packages becomes apparent when we are dealing with more complex models that don't have conjugacy properties.

Consider the following graphical model:



Recent studies have shown that a large fraction of COVID cases do not show symptoms, but all of the studies considered here tested only symptomatic cases. This means that the probability of testing positive (which what we observe) isn't the same as the SAR θ_i!

The estimates of the asymptomatic rate fall in the range $[0.18, 0.43]$. We assume a prior $A \sim Uniform(0.18, 0.43)$. This means that the probability that a person in a study tests positive is really $\theta_i * (1 - A)$. Hence:

$$X_i|\theta_i, A \sim Binomial(N_i, \theta_i \cdot (1 - A))$$

Complete the `approximate_inference_asympotmatic_MCMC` function to add dependence on the asymptomatic rate: *Hint: You may need to do a search to find the right distribution to use (instead of `pm.Binomial`, etc. above).*

[22]:
```
# TODO: complete the function
def approximate_inference_asympotmatic_MCMC(alpha_value, beta_value, study_df =␣
↪study_df):
    """
    Creates and fits a PyMC3 model corresponding to the graphical model above

    Inputs:
```

```
        alpha_value, beta_value : floats, parameters of the prior Beta␣
↪Distribution
        study_df : DataFrame containing study data

    Outputs: (model, trace)
    """
    with pm.Model() as model:
        theta = pm.Beta('theta', alpha = alpha_value, beta = beta_value,␣
↪shape=len(study_df))
        A = pm.Uniform('A', lower=0.18, upper=0.43)
        X = pm.Binomial('X', p=theta*(1-A), observed=study_df['X'],␣
↪n=study_df['N'])

        trace = pm.sample(500, tune=1000, target_accept=0.95)
    return (model, trace)
```

Notice that the `trace` now contains samples for both `theta` and `A`!

Plot a histogram of the posterior estimates for A if $\alpha = 5$ and $\beta = 10$. Assuming the model we defined is correct, what can you conclude about the asymptomatic rate A based on the studies and the model?

[23]:
```
model, trace = approximate_inference_asympotmatic_MCMC(5, 10)
```

```
/tmp/ipykernel_23/2098793016.py:17: FutureWarning: In v4.0, pm.sample will
return an `arviz.InferenceData` object instead of a `MultiTrace` by default. You
can pass return_inferencedata=True or return_inferencedata=False to be safe and
silence this warning.
  trace = pm.sample(500, tune=1000, target_accept=0.95)
Auto-assigning NUTS sampler…
Initializing NUTS using jitter+adapt_diag…
Multiprocess sampling (4 chains in 4 jobs)
NUTS: [A, theta]
```

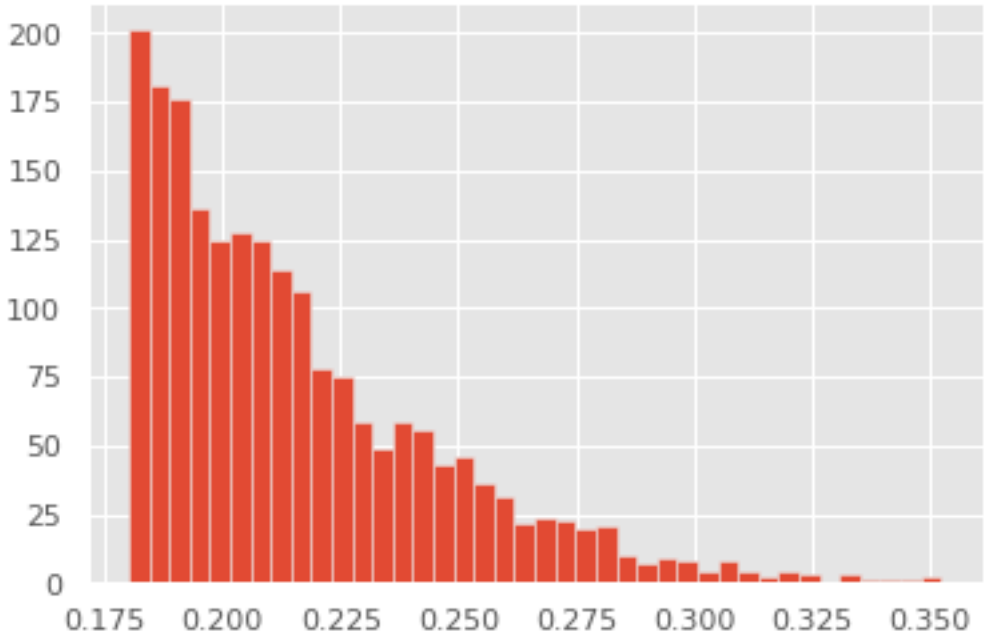
```
<IPython.core.display.HTML object>
```

```
Sampling 4 chains for 1_000 tune and 500 draw iterations (4_000 + 2_000 draws
total) took 5 seconds.
```

[24]:
```
# TODO: fill in
plt.hist(trace['A'], bins=40)
```

[24]:
```
(array([201., 181., 176., 136., 125., 127., 125., 114., 106.,  78.,  75.,
         59.,  49.,  59.,  56.,  43.,  46.,  36.,  31.,  22.,  24.,  23.,
         20.,  21.,  10.,   7.,   9.,   8.,   4.,   8.,   4.,   2.,   4.,
          3.,   0.,   3.,   1.,   1.,   1.,   2.]),
 array([0.18000764, 0.18431731, 0.18862699, 0.19293666, 0.19724633,
        0.201556  , 0.20586567, 0.21017535, 0.21448502, 0.21879469,
        0.22310436, 0.22741403, 0.23172371, 0.23603338, 0.24034305,
```

```
        0.24465272, 0.2489624 , 0.25327207, 0.25758174, 0.26189141,
        0.26620108, 0.27051076, 0.27482043, 0.2791301 , 0.28343977,
        0.28774944, 0.29205912, 0.29636879, 0.30067846, 0.30498813,
        0.3092978 , 0.31360748, 0.31791715, 0.32222682, 0.32653649,
        0.33084616, 0.33515584, 0.33946551, 0.34377518, 0.34808485,
        0.35239453]),
 <BarContainer object of 40 artists>)
```



We can conclude that this distribution is heavily right skewed. This means that there are many more samples with a smaller asymptomatic rate.

TODO: fill in

[25]:
```
# Validation tests: Do not modify
model_test, trace_test = approximate_inference_asympotmatic_MCMC(5, 10)
post_samples_test = trace_test['theta']
estimates = np.mean(post_samples_test, axis = 0)
rounded_estimates = np.round(estimates / 2, 2) * 2

hash_list = ['afbc48a7ca8d716f9efa7cc993316668',
             'e85b79abfd76b7c13b1334d8d8c194a5',
             '0bd1ed7e9617a4ed139b2f4014c7aa23',
             'afbc48a7ca8d716f9efa7cc993316668',
             '4a42799b212019a2db0b77644e33790c',
             '964e2b882801bd4ba988904454316d76',
             '964e2b882801bd4ba988904454316d76',
```

```
            '4a42799b212019a2db0b77644e33790c',
            '45efc23f34e05a9ea4f5024988047dd6',
            '451d13a5be2581a451c2284dcecddd4e',
            '2363c78ab7dba59b8443d958b47cfa2b',
            '0bd1ed7e9617a4ed139b2f4014c7aa23']

print()

for i, est in enumerate(estimates):
    print("Study {}: {:.3f} ".format(i, est))

for hash_val, est in zip(hash_list, rounded_estimates):
    assert hash_val == get_hash(est, 2)

print("Test passed! You are awesome!")
```

```
/tmp/ipykernel_23/2098793016.py:17: FutureWarning: In v4.0, pm.sample will
return an `arviz.InferenceData` object instead of a `MultiTrace` by default. You
can pass return_inferencedata=True or return_inferencedata=False to be safe and
silence this warning.
  trace = pm.sample(500, tune=1000, target_accept=0.95)
Auto-assigning NUTS sampler…
Initializing NUTS using jitter+adapt_diag…
Multiprocess sampling (4 chains in 4 jobs)
NUTS: [A, theta]
```

```
<IPython.core.display.HTML object>
```

```
Sampling 4 chains for 1_000 tune and 500 draw iterations (4_000 + 2_000 draws
total) took 5 seconds.
```

```
Study 0: 0.372
Study 1: 0.300
Study 2: 0.441
Study 3: 0.385
Study 4: 0.355
Study 5: 0.423
Study 6: 0.414
Study 7: 0.354
Study 8: 0.286
Study 9: 0.479
Study 10: 0.555
Study 11: 0.449
Test passed! You are awesome!
```

[26]:
```
import matplotlib.image as mpimg
img = mpimg.imread('baby_donkey.jpg')
imgplot = plt.imshow(img)
```

```
imgplot.axes.get_xaxis().set_visible(False)
imgplot.axes.get_yaxis().set_visible(False)
plt.show()
```

[ ]: