DS 6040 HW 3

July 22, 2023

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2 DS 6040 HW 3

Honor Pledge: I have neither given nor received any aid on this assignment.

3 Part 1: Changepoint detection and samplers (50 points)

With the above information, complete the Gibbs sampler in the accompanying notebook. You should only need to complete the update steps for the and (called lambdap in the notebook) parameters. Run the Gibbs sampler, plot the posterior densities and calculate the EAP estimates with 95% (equal tailed) credible intervals for and . Provide the top 5 most probable values of k. Then do the the following:

(a) Describe your findings. What do these EAP and credible intervals imply? And what was the most likely year of the changepoint?

(b) Why is an EAP or credible interval not necessarily the most appropriate thing to report for the year of the changepoint?

[117]:
```
from scipy.stats import gamma, norm, poisson, multinomial
from scipy.special import logsumexp
import numpy as np
import matplotlib.pyplot as plt
import seaborn as sns
import pandas as pd
import mpmath as mp
mp.dps = 100
```

[118]:
```
#Import dataset
coal_dat = pd.read_csv("coaldisasters-ds6040.csv")
```

[119]:
```
coal_dat
```

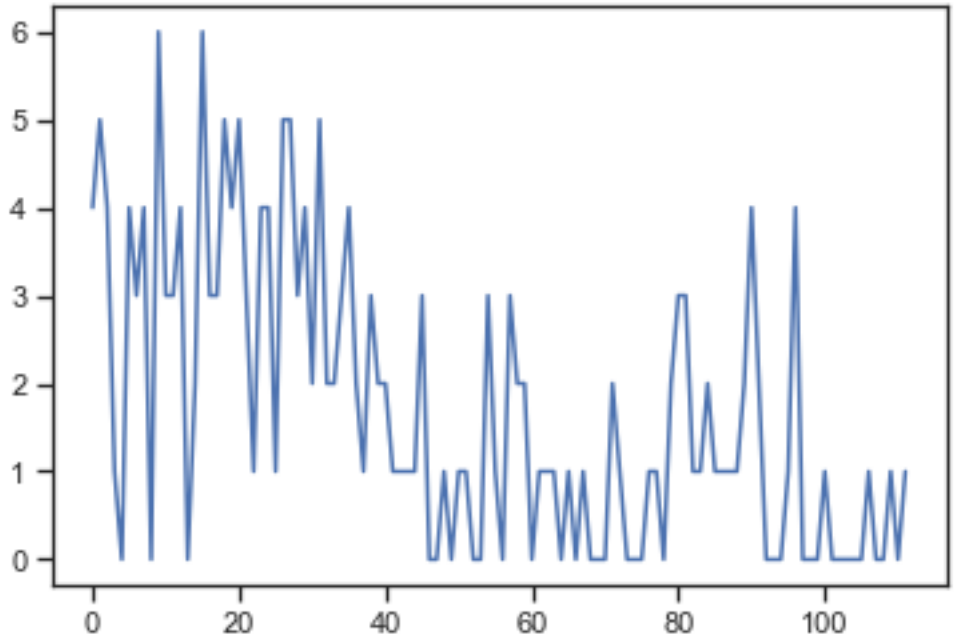
[119]:

	Year	Count
0	1851	4
1	1852	5
2	1853	4

```
3    1854      1
4    1855      0
..    …    …
107  1958      0
108  1959      0
109  1960      1
110  1961      0
111  1962      1

[112 rows x 2 columns]
```

[120]:
```
coal_dat['Count'].plot()
```

[120]:
```
<AxesSubplot:>
```



[121]:
```
class CoalDisasterModel():
    def __init__(self, data, a_mu, b_mu, a_lambda, b_lambda, start_mu = 5,␣
 ↪start_lambda = .1, start_k = 64, iter_num = 1000, burnin = 500):

        #Read in data and priors, and make them contained class variables
        self.data = data
        self.a_mu = a_mu
        self.b_mu = b_mu
        self.a_lambda = a_lambda
        self.b_lambda = b_lambda
```

```
        self.iter_num = iter_num
        self.burnin = burnin
        #Initalize sampling containers
        self.mu = np.zeros(iter_num+burnin+1)
        self.lambdap = np.zeros(iter_num+burnin+1)
        self.k = np.zeros(iter_num+burnin+1)

        #Put in starting values
        self.mu[0] = start_mu
        self.lambdap[0] = start_lambda
        self.k[0] = start_k


        for i in np.arange(iter_num+burnin):
            if i % 100 == 0:
                print("Iteration " + str(i))


            # This is where you modify the sampler
            self.mu[i+1] = gamma.rvs(a_mu + np.sum(data[0:int(self.k[i])]),␣
↪scale=1 / (self.k[i] + b_mu))
            self.lambdap[i+1] = gamma.rvs(a_lambda + np.sum(data[int(self.k[i]):
↪]), scale=1 / (len(data) - self.k[i] + b_lambda))

            # ------------------This is the changepoint update block
            likelihood_list = [] #Initialize an empty list

            # Iterate from 0 to the length of the data (the last timepoint␣
↪cannot be the changepoint)
            for k_hat in range(len(data)):
                # Probabilities get very small, so I am using the mp package to␣
↪get arbitrarily fine-grained precision.
                # I am also computing the probabilities in log form because␣
↪summing log probabilities is much easier (from a precision standpoint) than␣
↪multiplying regular probabilities.
                # This is likely overkill here
                temp = mp.mpf(np.sum(np.log(poisson.pmf(data[0:k_hat], self.
↪mu[i+1]))) + np.sum(np.log(poisson.pmf(data[k_hat:], self.lambdap[i+1]))))
                likelihood_list.append(temp)

            # Convert likelihood_list to probabilities (with arbitrary␣
↪precision) and normalize
            k_probs = [mp.exp(x) for x in likelihood_list]
            k_probs = np.asarray(k_probs).astype('float64')
```

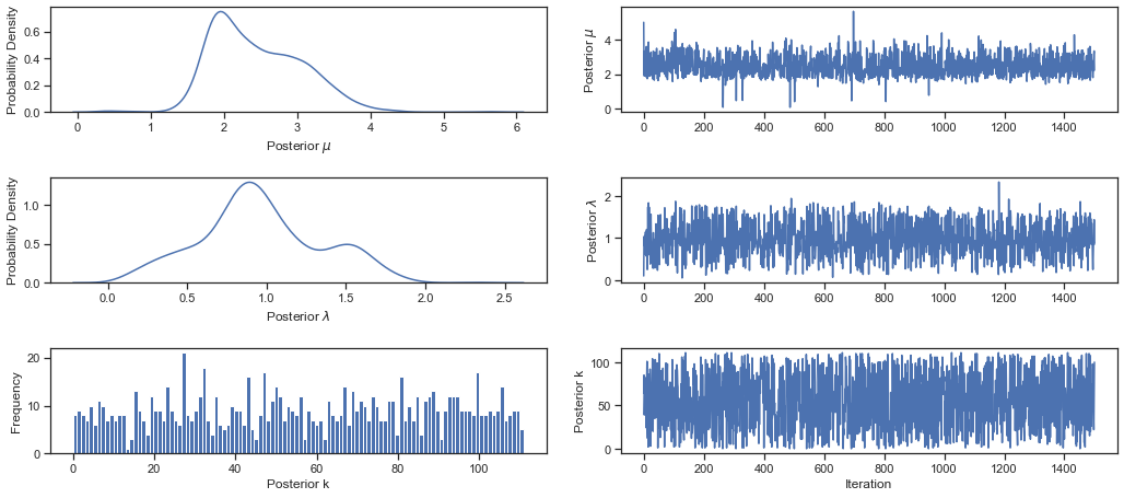
```
            # Ensure the probabilities sum to 1 and avoid potential NaN values␣
↪in k_probs due to floating-point precision
            if np.sum(k_probs) != 1.0 or np.isnan(np.sum(k_probs)):
                # If the probabilities don't sum to 1 or contain NaN values,␣
↪set all probabilities to be equal
                k_probs = np.ones(len(k_probs)) / len(k_probs)

            # Finally, sample from the multinomial distribution
            self.k[i+1] = np.where(multinomial.rvs(n=1, p=k_probs) == 1)[0][0]

            #------------------End changepoint block

    def plot_posteriors(self):
        f, axs = plt.subplots(3,2, figsize = (15, 7))
        f.tight_layout(pad = 3)
        sns.kdeplot(self.mu[self.burnin:],ax =axs[0,0])
        axs[0,0].set_xlabel(r'Posterior $\mu$')
        axs[0,0].set_ylabel('Probability Density')
        sns.kdeplot(self.lambdap[self.burnin:], ax =axs[1,0])
        axs[1,0].set_xlabel(r'Posterior $\lambda$')
        axs[1,0].set_ylabel('Probability Density')
        axs[2,0].hist(self.k[self.burnin:], bins = 112)
        axs[2,0].set_xlabel(r'Posterior k')
        axs[2,0].set_ylabel('Frequency')
        axs[0,1].plot(np.arange(self.iter_num+self.burnin+1),self.mu, '-')
        axs[0,1].set_xlabel('')
        axs[0,1].set_ylabel(r'Posterior $\mu$')
        axs[1,1].plot(np.arange(self.iter_num+self.burnin+1),self.lambdap,'-')
        axs[1,1].set_xlabel('')
        axs[1,1].set_ylabel(r'Posterior $\lambda$')
        axs[2,1].plot(np.arange(self.iter_num+self.burnin+1),self.k,'-')
        axs[2,1].set_xlabel('Iteration')
        axs[2,1].set_ylabel('Posterior k')

    def get_rate_estimates(self):
        to_return =pd.DataFrame(columns = ['Posterior EAP', 'Posterior Cred␣
↪Interval Lower', 'Posterior Cred Interval Upper'])
        to_return.loc[r'mu', 'Posterior EAP'] = self.mu[self.burnin:].mean()
        to_return.loc[r'lambda', 'Posterior EAP'] = self.lambdap[self.burnin:].
↪mean()
        to_return.loc[r'mu', 'Posterior Cred Interval Lower'] = np.
↪quantile(self.mu[self.burnin:],.025)
        to_return.loc[r'lambda', 'Posterior Cred Interval Lower'] = np.
↪quantile(self.lambdap[self.burnin:],.025)
        to_return.loc[r'mu', 'Posterior Cred Interval Upper'] = np.
↪quantile(self.mu[self.burnin:],.975)
```

```
        to_return.loc[r'lambda', 'Posterior Cred Interval Upper'] = np.
↪quantile(self.lambdap[self.burnin:],.975)
        return to_return

    def get_k_probs(self):
        freq = np.bincount(abs(self.k.astype('int'))[self.burnin:])
        ii = np.nonzero(freq)[0]
        freq = np.vstack((ii,freq[ii])).T
        freq = freq.astype("float16")
        freq[:,1] = freq[:,1]/(freq[:,1].sum())
        freq = pd.DataFrame(freq, columns=['k', 'Probability of k'])

        return freq
```

[82]:
```
count_data = coal_dat['Count'].to_numpy()
test = CoalDisasterModel(count_data, 1, 1, 1, 1)
```

```
Iteration 0
Iteration 100
Iteration 200
Iteration 300
Iteration 400
Iteration 500
Iteration 600
Iteration 700
Iteration 800
Iteration 900
Iteration 1000
Iteration 1100
Iteration 1200
Iteration 1300
Iteration 1400
```

[83]:
```
test.plot_posteriors()
```



[84]:
```
test.get_rate_estimates()
```

[84]:
```
        Posterior EAP Posterior Cred Interval Lower  \
mu           2.458481                       1.586641
lambda       0.963927                       0.238079

        Posterior Cred Interval Upper
mu                           3.718927
lambda                         1.7047
```

4 Top 5 Most Probable Values of k:

[129]:
```
most_prob_k = test.get_k_probs()
most_prob_k.sort_values(by = ["Probability of k"], ascending = False).head(5)
most_prob_k['year'] = [int(y + 1851) for y in most_prob_k['k']]
most_prob_k.sort_values(by = ["Probability of k"], ascending = False).head(5)
```

[129]:
```
          k  Probability of k  year
27    27.0          0.020981  1878
32    32.0          0.017975  1883
47    47.0          0.016983  1898
100  100.0          0.016983  1951
81    81.0          0.015991  1932
```

5 (a) Describe your findings. What do these EAP and credible intervals imply? And what was the most likely year of the changepoint?

Considering the assumption of a changepoint for the counts of coal mining disasters (k = 27), we can compare the posterior Expected A Posteriori (EAP) values of mu and lambda with the initial count plot. In the count plot, we notice that leading up to around k = 30, the mean of disasters was generally higher than after k = 30. By analyzing our EAP estimates and credible intervals, we observe a slight overlap between the two intervals (from approx. ~1.5 to ~1.7). This suggests the presence of a noticeable change in the behavior of coal mining disasters, indicating the existence of two separate distributions.

Interestingly, the top 3 most probable k values (27, 32, and 47) as shown above closely align with the patterns initially observed from the counts plots andf are grouped relatively close together, but the next 2 most probable seem a bit more random.

Accoridng to the k probability results, the most likely year of the changepoint was 1878. (1883 also seems to be a likely candidate for the year of the changepoint.)

6 (b) Why is an EAP or credible interval not necessarily the most appropriate thing to report for the year of the changepoint?

The EAP represents the expected value, but it may not be the most suitable measure in this context because our primary interest lies in understanding the overall distribution shape and identifying the moment of change. While the EAP analysis is valuable for interpreting the nature of Bayesian statistics, it is essential to acknowledge the inherent flexibility of Bayesian methods. Alternatively, this analysis could have been conducted using Maximum A Posteriori (MAP) estimation, leading to potentially different conclusions. Also, altering the prior information could significantly impact the EAP and credible intervals, emphasizing the vulnerability of the EAP approach to manipulation.

7 Part 2: Bayesian Logistic Regression with PyMC3

1. Load the data from whitewine-training-ds6040.csv and create a new 0/1 quality variable, where the new quality of the wine is 0 if the wine received a C or F, and 1 if the wine received an A.

[91]:
```
wine_2 = pd.read_csv("whitewine-training-ds6040.csv")
wine_2.head()
```

[91]:

	fixed.acidity	volatile.acidity	citric.acid	residual.sugar	chlorides	\
0	0.183032	-0.088263	0.223977	2.798612	-0.038083	
1	-0.640290	0.206999	0.056475	-0.946679	0.142355	
2	1.476825	0.010158	0.558982	0.092590	0.187465	
3	-0.757907	0.403840	-1.451043	0.112199	-0.038083	
4	0.183032	-0.088263	0.223977	2.798612	-0.038083	

	free.sulfur.dioxide	total.sulfur.dioxide	density	pH	sulphates	\

```
0             0.549032              0.744783  2.293274 -1.231221  -0.336441
1            -1.246502             -0.149673 -0.008274  0.711107   0.011581
2            -0.319775             -0.973515  0.353398  0.452130  -0.423446
3            -0.319775             -0.055520  0.287640 -0.065824  -0.162430
4             0.549032              0.744783  2.293274 -1.231221  -0.336441

    alcohol wine_quality
0 -1.395289            C
1 -0.831034            C
2 -0.347387            C
3 -0.750426            C
4 -1.395289            C
```

[110]:
```
new_wine = {'C':0,
            'F':0,
            'A':1}
wine_2["wine_class"] = wine_2["wine_quality"].map(new_wine)
wine_2.head()
```

[110]:
```
   fixed_acidity  volatile_acidity  citric_acid  residual_sugar  chlorides  \
0       0.183032         -0.088263     0.223977        2.798612  -0.038083
1      -0.640290          0.206999     0.056475       -0.946679   0.142355
2       1.476825          0.010158     0.558982        0.092590   0.187465
3      -0.757907          0.403840    -1.451043        0.112199  -0.038083
4       0.183032         -0.088263     0.223977        2.798612  -0.038083

   free_sulfur_dioxide  total_sulfur_dioxide   density        pH  sulphates  \
0             0.549032              0.744783  2.293274 -1.231221  -0.336441
1            -1.246502             -0.149673 -0.008274  0.711107   0.011581
2            -0.319775             -0.973515  0.353398  0.452130  -0.423446
3            -0.319775             -0.055520  0.287640 -0.065824  -0.162430
4             0.549032              0.744783  2.293274 -1.231221  -0.336441

    alcohol wine_quality  wine_class
0 -1.395289            C           0
1 -0.831034            C           0
2 -0.347387            C           0
3 -0.750426            C           0
4 -1.395289            C           0
```

[111]:
```
wine_2.columns = [x.replace('.','_') if '.' in x else x for x in wine_2.columns]
wine_2.head()
```

[111]:
```
   fixed_acidity  volatile_acidity  citric_acid  residual_sugar  chlorides  \
0       0.183032         -0.088263     0.223977        2.798612  -0.038083
1      -0.640290          0.206999     0.056475       -0.946679   0.142355
2       1.476825          0.010158     0.558982        0.092590   0.187465
```

```
3      -0.757907          0.403840    -1.451043         0.112199  -0.038083
4       0.183032         -0.088263     0.223977         2.798612  -0.038083

   free_sulfur_dioxide  total_sulfur_dioxide   density        pH  sulphates  \
0             0.549032              0.744783  2.293274 -1.231221  -0.336441
1            -1.246502             -0.149673 -0.008274  0.711107   0.011581
2            -0.319775             -0.973515  0.353398  0.452130  -0.423446
3            -0.319775             -0.055520  0.287640 -0.065824  -0.162430
4             0.549032              0.744783  2.293274 -1.231221  -0.336441

    alcohol wine_quality  wine_class
0 -1.395289            C           0
1 -0.831034            C           0
2 -0.347387            C           0
3 -0.750426            C           0
4 -1.395289            C           0
```

2. Using the notebook BayesLogisticRegression.ipynb as an implementation guide, fit two logistic regression models chosen as follows (Note: you won't be penalized if you, for example, did something in the HW2 incorrectly and are presenting models I don't expect):

   • Choose the set of 3 variables that in HW2 gave you the best classification rate overall within the training data.

   • Choose the set of 3 variables that gave you the best classification rates of A grade wines in the training dataset (you will have to look back into HW2, and make some slight modifications to your code to obtain this information. Hint, you need to use the cross-tab information).

Once you have fit your two models, plot both traceplots and forestplots using code from the BayesLogisticRegression notebook.

Discuss your findings. Note that I am not asking you to calculate miss-classification rates, rather to examine your parameter distributions and explain what those estimates mean, and how they compare to one another. Don't forget to interpret the intercept as well.

[94]:
```
import pymc3 as pm
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
```

8 Choose the set of 3 variables that in HW2 gave you the best classification rate overall within the training data.

[95]:
```
###The following code is heavily based or taken directly from: https://www.
 ↪kaggle.com/billbasener/pymc3-bayesian-logistic-regression-classification

def plot_traces(traces, retain=0):
```

```
    '''
    Convenience function:
    Plot traces with overlaid means and values
    '''

    ax = pm.traceplot(traces[-retain:],
                      lines=tuple([(k, {}, v['mean'])
                                   for k, v in pm.summary(traces[-retain:]).
 ↪iterrows()]))

    for i, mn in enumerate(pm.summary(traces[-retain:])['mean']):
        ax[i,0].annotate('{:.2f}'.format(mn), xy=(mn,0), xycoords='data'
                    ,xytext=(5,10), textcoords='offset points', rotation=90
                    ,va='bottom', fontsize='large', color='#AA0022')
```

Best set of 3 variables from HW 2: ['volatile.acidity', 'density', 'alcohol', 'wine_quality'] 0.4877906976744186

[96]:
```
#This is the general form for the logistic. You will need to change the model␣
 ↪formula to match the white wine data.
with pm.Model() as model:
    pm.glm.GLM.from_formula(formula = 'wine_class ~ volatile_acidity + density␣
 ↪+ alcohol',
                            data = wine_2,
                            family = pm.glm.families.Binomial())

    trace = pm.sample(1000)


#You can obtain forest plots with:
pm.plots.forestplot(trace, figsize = (12,5))

#You can get a table of summary statistics out using:
pm.summary(trace)
```

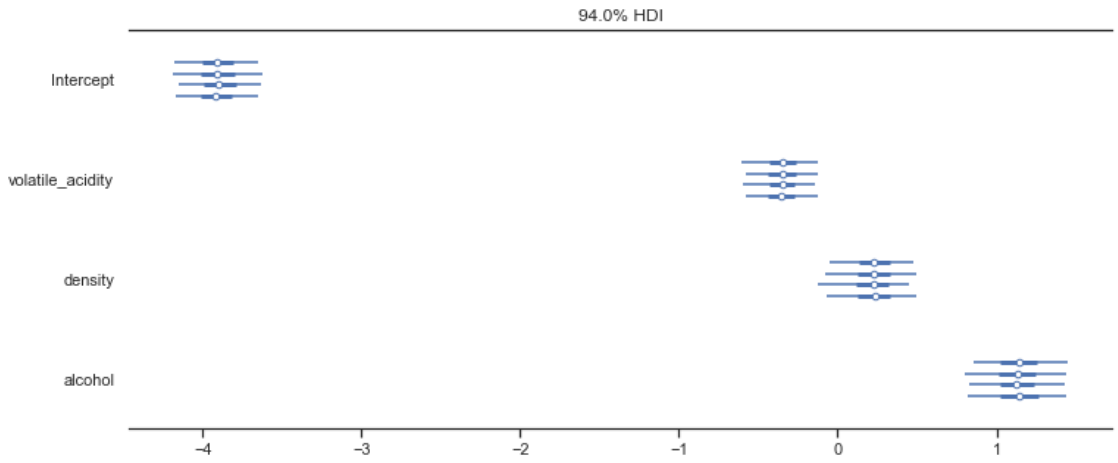
```
The glm module is deprecated and will be removed in version 4.0
We recommend to instead use Bambi https://bambinos.github.io/bambi/
/Users/matthewscheffel/opt/anaconda3/lib/python3.9/site-
packages/deprecat/classic.py:215: FutureWarning: In v4.0, pm.sample will return
an `arviz.InferenceData` object instead of a `MultiTrace` by default. You can
pass return_inferencedata=True or return_inferencedata=False to be safe and
silence this warning.
  return wrapped_(*args_, **kwargs_)
Auto-assigning NUTS sampler…
Initializing NUTS using jitter+adapt_diag…
Multiprocess sampling (4 chains in 4 jobs)
NUTS: [alcohol, density, volatile_acidity, Intercept]
```

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

<IPython.core.display.HTML object>

/Users/matthewscheffel/opt/anaconda3/lib/python3.9/site-
packages/scipy/stats/_continuous_distns.py:624: RuntimeWarning: overflow
encountered in _beta_ppf
  return _boost._beta_ppf(q, a, b)
/Users/matthewscheffel/opt/anaconda3/lib/python3.9/site-
packages/scipy/stats/_continuous_distns.py:624: RuntimeWarning: overflow
encountered in _beta_ppf
  return _boost._beta_ppf(q, a, b)
/Users/matthewscheffel/opt/anaconda3/lib/python3.9/site-
packages/scipy/stats/_continuous_distns.py:624: RuntimeWarning: overflow
encountered in _beta_ppf
  return _boost._beta_ppf(q, a, b)
/Users/matthewscheffel/opt/anaconda3/lib/python3.9/site-
packages/scipy/stats/_continuous_distns.py:624: RuntimeWarning: overflow
encountered in _beta_ppf
  return _boost._beta_ppf(q, a, b)
Sampling 4 chains for 1_000 tune and 1_000 draw iterations (4_000 + 4_000 draws
total) took 31 seconds.
/var/folders/9s/pz872p91741110p_4gz6llzc0000gn/T/ipykernel_94255/845273577.py:11
: DeprecationWarning: The function `forestplot` from PyMC3 is just an alias for
`plot_forest` from ArviZ. Please switch to `pymc3.plot_forest` or
`arviz.plot_forest`.
  pm.plots.forestplot(trace, figsize = (12,5))
Got error No model on context stack. trying to find log_likelihood in
translation.
/Users/matthewscheffel/opt/anaconda3/lib/python3.9/site-
packages/arviz/data/io_pymc3_3x.py:98: FutureWarning: Using `from_pymc3` without
the model will be deprecated in a future release. Not using the model will
return less accurate and less useful results. Make sure you use the model
argument or call from_pymc3 within a model context.
  warnings.warn(
Got error No model on context stack. trying to find log_likelihood in
translation.
/Users/matthewscheffel/opt/anaconda3/lib/python3.9/site-
packages/arviz/data/io_pymc3_3x.py:98: FutureWarning: Using `from_pymc3` without
the model will be deprecated in a future release. Not using the model will
return less accurate and less useful results. Make sure you use the model
argument or call from_pymc3 within a model context.
  warnings.warn(
```

[96]:

```
                    mean     sd  hdi_3%  hdi_97%  mcse_mean  mcse_sd  ess_bulk  \
Intercept         -3.907  0.146  -4.164   -3.627      0.003    0.002    2268.0
volatile_acidity -0.352  0.125  -0.588   -0.124      0.003    0.002    2454.0
density            0.220  0.153  -0.069    0.501      0.003    0.002    2017.0
```

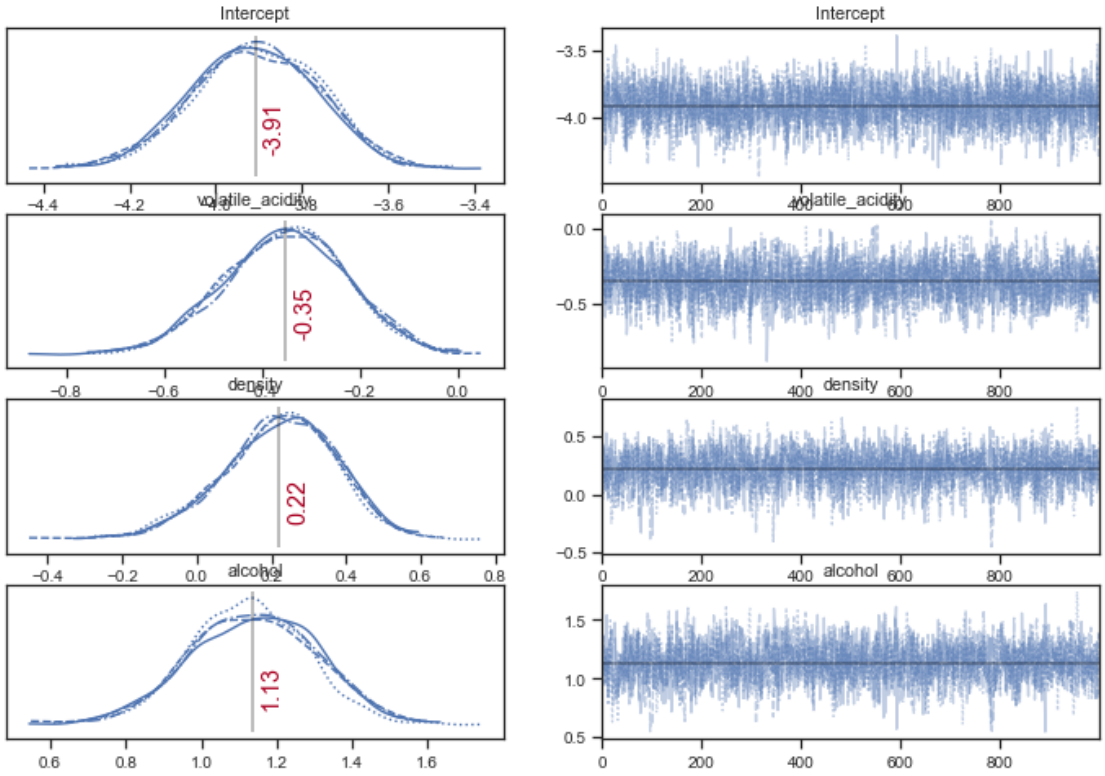
```
alcohol           1.134  0.167   0.829    1.449      0.004    0.003     1583.0

                 ess_tail  r_hat
Intercept          2714.0    1.0
volatile_acidity   2420.0    1.0
density            1833.0    1.0
alcohol            1695.0    1.0
```



[97]:
```
plot_traces(trace)
```

```
Got error No model on context stack. trying to find log_likelihood in
translation.
/Users/matthewscheffel/opt/anaconda3/lib/python3.9/site-
packages/arviz/data/io_pymc3_3x.py:98: FutureWarning: Using `from_pymc3` without
the model will be deprecated in a future release. Not using the model will
return less accurate and less useful results. Make sure you use the model
argument or call from_pymc3 within a model context.
  warnings.warn(
/var/folders/9s/pz872p91741110p_4gz6llzc0000gn/T/ipykernel_94255/2855945336.py:9
: DeprecationWarning: The function `traceplot` from PyMC3 is just an alias for
`plot_trace` from ArviZ. Please switch to `pymc3.plot_trace` or
`arviz.plot_trace`.
  ax = pm.traceplot(traces[-retain:],
Got error No model on context stack. trying to find log_likelihood in
translation.
/Users/matthewscheffel/opt/anaconda3/lib/python3.9/site-
packages/arviz/data/io_pymc3_3x.py:98: FutureWarning: Using `from_pymc3` without
the model will be deprecated in a future release. Not using the model will
return less accurate and less useful results. Make sure you use the model
argument or call from_pymc3 within a model context.
  warnings.warn(
```

```
Got error No model on context stack. trying to find log_likelihood in
translation.
Got error No model on context stack. trying to find log_likelihood in
translation.
/Users/matthewscheffel/opt/anaconda3/lib/python3.9/site-
packages/arviz/data/io_pymc3_3x.py:98: FutureWarning: Using `from_pymc3` without
the model will be deprecated in a future release. Not using the model will
return less accurate and less useful results. Make sure you use the model
argument or call from_pymc3 within a model context.
  warnings.warn(
```



9 Choose the set of 3 variables that gave you the best classification rates of A grade wines in the training dataset (you will have to look back into HW2, and make some slight modifications to your code to obtain this information. Hint, you need to use the cross-tab information).

[103]:
```
# rerun LDA from HW2
```

[104]:
```
# import libraries

import itertools
import pandas as pd
import numpy as np
from scipy.stats import multivariate_normal
import matplotlib.pyplot as plt
import seaborn as sns
sns.set_theme(style = "ticks")
from itertools import combinations
```

[105]:
```
# LDA Class (code given in example from Professor)

class LDA():
    def __init__(self, dataset, class_var, priors = None):
        n_class = len(dataset[class_var].unique())
        if priors is None:
            priors = np.repeat(1/n_class, n_class)
        self.priors =  np.asarray(priors)
        self.means = dataset.groupby(class_var).mean()
        self.sigma = dataset.cov()
        self.class_var = class_var
        self.training_data = dataset
    def predict_probs(self, data = None):
        if data is None:
            data = self.training_data
        data_temp = data.drop(self.class_var, axis = 1)
        dens_list = []
        col_names = []
        for ind, row in self.means.iterrows():
            col_names.append(ind)
            dens_list.append(multivariate_normal.pdf(data_temp, mean = np.
 ↪asarray(row), cov = self.sigma))
        dens_list = pd.DataFrame(np.transpose(np.vstack(dens_list)),columns=␣
 ↪col_names)
        dens_list = dens_list.mul(self.priors, axis=1)
        dens_list = dens_list.div(dens_list.sum(axis=1), axis=0)
        dens_list['True Class'] = data[self.class_var]
        return dens_list
    def predict_MAP(self, data = None):
        if data is None:
            data = self.training_data
        dens_list = self.predict_probs(data).drop('True Class', axis = 1)
        map_list = dens_list.idxmax(axis = 1)
        maps = {'MAP Class': map_list}
        maps = pd.DataFrame(maps)
        maps['True Class'] = data[self.class_var]
```

```
        return maps
    def misclass_rate(self, data = None):
        if data is None:
            data = self.training_data
        maps = self.predict_MAP(data = data)


        maps['Mis_class'] = maps['MAP Class']  == maps['True Class']

        mis_class =  1 - maps['Mis_class'].mean()

        return mis_class
    def misclass_xtabs(self, data = None):
        if data is None:
            data = self.training_data
        maps = self.predict_MAP(data = data)

        xtabs = pd.crosstab(maps['MAP Class'], maps['True Class'])
        return xtabs
    def misclass_pairplot(self, data = None):
        if data is None:
            data = self.training_data
        maps = self.predict_MAP(data = data)
        temp_dat = data.copy(deep = True)
        temp_dat['Mis-Classified'] = maps['MAP Class']  != maps['True Class']
        plot = sns.pairplot(temp_dat,hue="Mis-Classified", height = 1.5, aspect␣
 ↪= 1.5)
        return plot
```

[106]:
```
# find best wines from Class A

wine_A = pd.read_csv("whitewine-training-ds6040.csv")
e_rates_list = []

for i in itertools.combinations(wine_A.columns[:-1], 3):
    combination = list(i) + ["wine_quality"]
    flat_priors_lda = LDA(wine_A[combination], 'wine_quality')
    A_error = flat_priors_lda.misclass_xtabs()["A"][0] / sum(flat_priors_lda.
 ↪misclass_xtabs()["A"])
    e_rates_list.append([",".join(combination[:-1]), A_error])

e_rates_df = pd.DataFrame(e_rates_list)

e_rates_df.columns = ["combinations",\
                                    "class_A_correct"]
```

[107]:
```
e_rates_df.sort_values("class_A_correct", ascending = False)
```

[107]:

	combinations	class_A_correct
140	chlorides,density,sulphates	0.72
79	volatile.acidity,pH,alcohol	0.72
159	total.sulfur.dioxide,pH,alcohol	0.72
135	chlorides,total.sulfur.dioxide,density	0.72
107	citric.acid,pH,alcohol	0.72
..	…	…
97	citric.acid,free.sulfur.dioxide,sulphates	0.30
47	volatile.acidity,citric.acid,free.sulfur.dioxide	0.30
7	fixed.acidity,volatile.acidity,sulphates	0.29
69	volatile.acidity,free.sulfur.dioxide,sulphates	0.28
51	volatile.acidity,citric.acid,sulphates	0.21

[165 rows x 2 columns]

10 We get that chlorides, density, and sulphates are the best combination from the Class A wines.

[75]:
```
with pm.Model() as model2:
    pm.glm.GLM.from_formula(formula = 'wine_class ~ chlorides + density +␣
 ↪sulphates',
                            data = wine_data,
                            family = pm.glm.families.Binomial())

    trace2 = pm.sample(1000)


#You can obtain forest plots with:
pm.plots.forestplot(trace2, figsize = (12,5))

#You can get a table of summary statistics out using:
pm.summary(trace2)
```

```
The glm module is deprecated and will be removed in version 4.0
We recommend to instead use Bambi https://bambinos.github.io/bambi/
/Users/matthewscheffel/opt/anaconda3/lib/python3.9/site-
packages/deprecat/classic.py:215: 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.
  return wrapped_(*args_, **kwargs_)
Auto-assigning NUTS sampler…
Initializing NUTS using jitter+adapt_diag…
Multiprocess sampling (4 chains in 4 jobs)
NUTS: [sulphates, density, chlorides, Intercept]
```

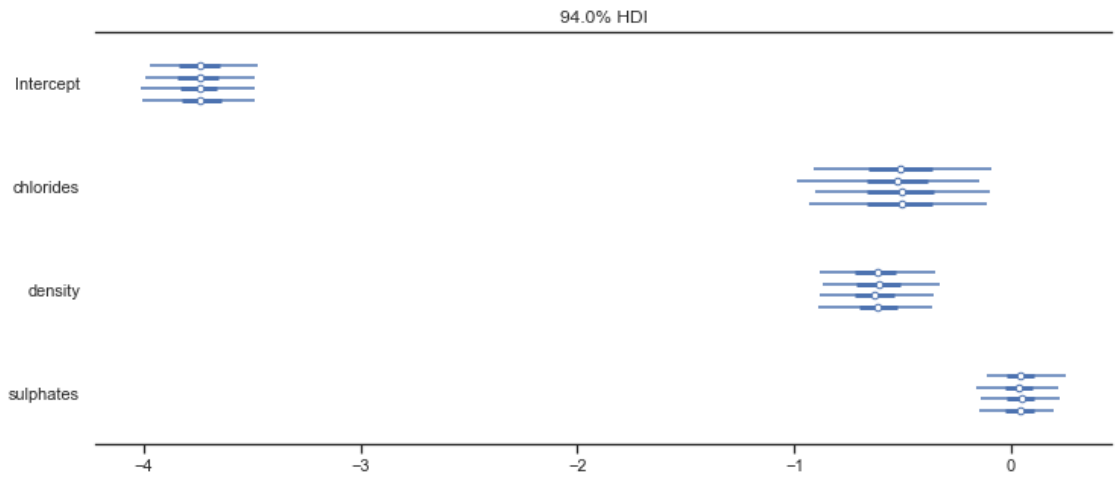
```
<IPython.core.display.HTML object>
```

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

```
/Users/matthewscheffel/opt/anaconda3/lib/python3.9/site-
packages/scipy/stats/_continuous_distns.py:624: RuntimeWarning: overflow
encountered in _beta_ppf
  return _boost._beta_ppf(q, a, b)
/Users/matthewscheffel/opt/anaconda3/lib/python3.9/site-
packages/scipy/stats/_continuous_distns.py:624: RuntimeWarning: overflow
encountered in _beta_ppf
  return _boost._beta_ppf(q, a, b)
Sampling 4 chains for 1_000 tune and 1_000 draw iterations (4_000 + 4_000 draws
total) took 29 seconds.
/var/folders/9s/pz872p91741110p_4gz6llzc0000gn/T/ipykernel_94255/345171114.py:10
: DeprecationWarning: The function `forestplot` from PyMC3 is just an alias for
`plot_forest` from ArviZ. Please switch to `pymc3.plot_forest` or
`arviz.plot_forest`.
  pm.plots.forestplot(trace2, figsize = (12,5))
Got error No model on context stack. trying to find log_likelihood in
translation.
/Users/matthewscheffel/opt/anaconda3/lib/python3.9/site-
packages/arviz/data/io_pymc3_3x.py:98: FutureWarning: Using `from_pymc3` without
the model will be deprecated in a future release. Not using the model will
return less accurate and less useful results. Make sure you use the model
argument or call from_pymc3 within a model context.
  warnings.warn(
Got error No model on context stack. trying to find log_likelihood in
translation.
/Users/matthewscheffel/opt/anaconda3/lib/python3.9/site-
packages/arviz/data/io_pymc3_3x.py:98: FutureWarning: Using `from_pymc3` without
the model will be deprecated in a future release. Not using the model will
return less accurate and less useful results. Make sure you use the model
argument or call from_pymc3 within a model context.
  warnings.warn(
```

[75]:

	mean	sd	hdi_3%	hdi_97%	mcse_mean	mcse_sd	ess_bulk	ess_tail	r_hat
Intercept	-3.744	0.138	-4.009	-3.494	0.002	0.002	3088.0	2855.0	1.0
chlorides	-0.523	0.225	-0.946	-0.117	0.004	0.003	3004.0	2262.0	1.0
density	-0.620	0.142	-0.883	-0.350	0.003	0.002	2643.0	2337.0	1.0
sulphates	0.038	0.096	-0.146	0.219	0.002	0.001	3357.0	2313.0	1.0



[76]:
```
plot_traces(trace2)
```

```
Got error No model on context stack. trying to find log_likelihood in
translation.
/Users/matthewscheffel/opt/anaconda3/lib/python3.9/site-
packages/arviz/data/io_pymc3_3x.py:98: FutureWarning: Using `from_pymc3` without
the model will be deprecated in a future release. Not using the model will
return less accurate and less useful results. Make sure you use the model
argument or call from_pymc3 within a model context.
  warnings.warn(
/var/folders/9s/pz872p91741110p_4gz6llzc0000gn/T/ipykernel_94255/2855945336.py:9
: DeprecationWarning: The function `traceplot` from PyMC3 is just an alias for
`plot_trace` from ArviZ. Please switch to `pymc3.plot_trace` or
`arviz.plot_trace`.
  ax = pm.traceplot(traces[-retain:],
Got error No model on context stack. trying to find log_likelihood in
translation.
/Users/matthewscheffel/opt/anaconda3/lib/python3.9/site-
packages/arviz/data/io_pymc3_3x.py:98: FutureWarning: Using `from_pymc3` without
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translation.
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/Users/matthewscheffel/opt/anaconda3/lib/python3.9/site-
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the model will be deprecated in a future release. Not using the model will
return less accurate and less useful results. Make sure you use the model
```
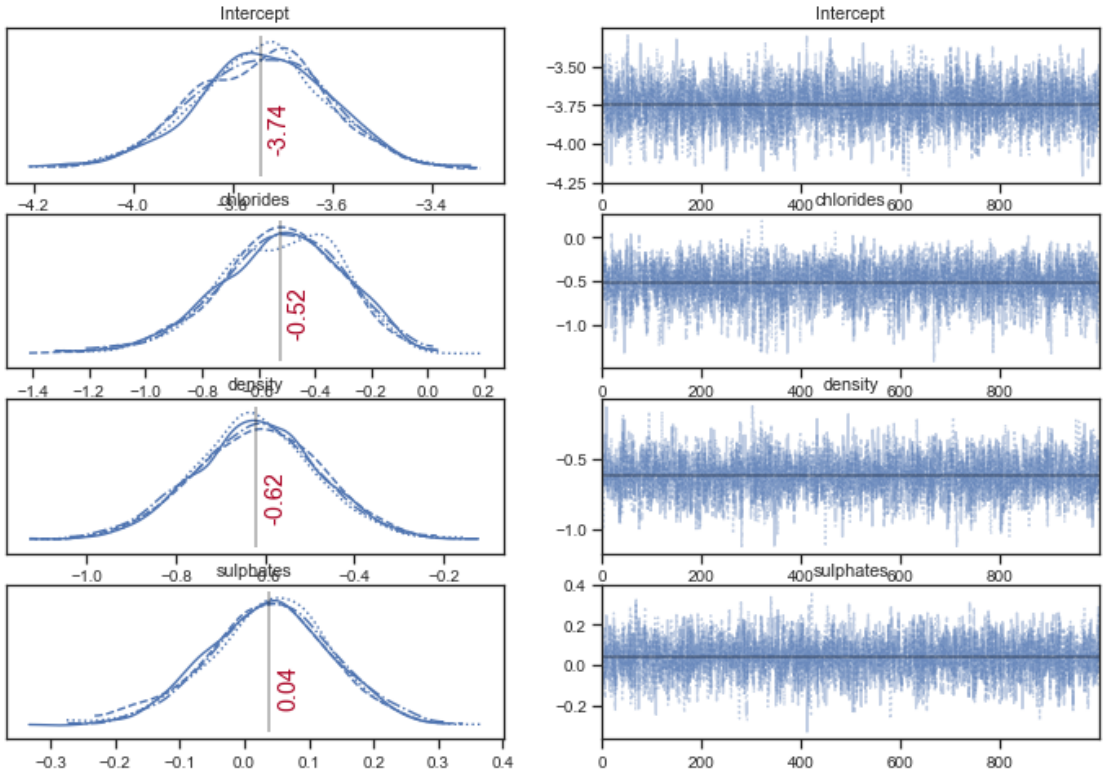

```
argument or call from_pymc3 within a model context.
  warnings.warn(
```



[108]:
```
pm.summary(trace)
```

```
Got error No model on context stack. trying to find log_likelihood in
translation.
/Users/matthewscheffel/opt/anaconda3/lib/python3.9/site-
packages/arviz/data/io_pymc3_3x.py:98: FutureWarning: Using `from_pymc3` without
the model will be deprecated in a future release. Not using the model will
return less accurate and less useful results. Make sure you use the model
argument or call from_pymc3 within a model context.
  warnings.warn(
```

[108]:

	mean	sd	hdi_3%	hdi_97%	mcse_mean	mcse_sd	ess_bulk	ess_tail	r_hat
Intercept	-3.907	0.146	-4.164	-3.627	0.003	0.002	2268.0	2714.0	1.0
volatile_acidity	-0.352	0.125	-0.588	-0.124	0.003	0.002	2454.0	2420.0	1.0
density	0.220	0.153	-0.069	0.501	0.003	0.002	2017.0		
alcohol	1.134	0.167	0.829	1.449	0.004	0.003	1583.0		

```
density              1833.0    1.0
alcohol              1695.0    1.0
```

[109]:
```
pm.summary(trace2)
```

```
Got error No model on context stack. trying to find log_likelihood in
translation.
/Users/matthewscheffel/opt/anaconda3/lib/python3.9/site-
packages/arviz/data/io_pymc3_3x.py:98: FutureWarning: Using `from_pymc3` without
the model will be deprecated in a future release. Not using the model will
return less accurate and less useful results. Make sure you use the model
argument or call from_pymc3 within a model context.
  warnings.warn(
```

[109]:

	mean	sd	hdi_3%	hdi_97%	mcse_mean	mcse_sd	ess_bulk	ess_tail	r_hat
Intercept	-3.744	0.138	-4.009	-3.494	0.002	0.002	3088.0	2855.0	1.0
chlorides	-0.523	0.225	-0.946	-0.117	0.004	0.003	3004.0	2262.0	1.0
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sulphates	0.038	0.096	-0.146	0.219	0.002	0.001	3357.0	2313.0	1.0

11 Discuss your findings. Note that I am not asking you to calculate miss-classification rates, rather to examine your parameter distributions and explain what those estimates mean, and how they compare to one another. Don't forget to interpret the intercept as well.

The summaries reveal that both the first and second models have negative intercepts. This implies that when volatile_acidity, density, and alcohol are set to 0 in the first model, the prediction will tend towards 0, corresponding to wine types C and F in the context of the problem. This reasoning aligns with our understanding that a wine lacking density, alcohol, and volatile acidity is unlikely to be of high quality. The same principle applies to the second model, where a wine with no chlorides, density, and sulphates will not be classified as a good wine.

We see from the analysis of the first model that notably the predictor "volatile_acidity" displayed a negative slope. This indicates that as the volatile acidity in a wine increases, the likelihood of it being classified as a bad wine also rises. Regarding the "density" predictor, the mean was positive, but the Highest Density Interval (HDI) contained 0. On average, higher density in a wine seems to be associated with a higher probability of being classified as type A. However, since the interval contains 0, further investigation is required to establish this relationship more definitively. For the "alcohol" parameter, the mean was positive, and the HDI did not include 0. Consequently, we can

assert that the more alcohol a wine contains, the better it is likely to be classified as wine type A. However, it's essential to approach the conclusion cautiously and not interpret it as an indication that increasing alcohol content will always lead to a better wine. Most likely the alcohol volume would reach a "tippiing point" or level that would make the wine quality worse if the alcohol content was too high.

The second model, which focused on identifying the best predictors for distinguishing the finest wines rather than the overall wine classifications, identified three distinct predictors: chlorides, density, and sulphates. Notably, the density predictor was the only one that overlapped with the first model. In this case, density displayed a negative slope, and the HDI did not contain 0. This suggests that denser wines are more likely to be classified as lower quality wines. This aligns well with real-world intuition, since a wine's excessive density might result in a less smooth-tasting wine experience. Similarly, chlorides exhibited behavior similar to density, with the interpretation being akin to more chlorides in a wine type being associated with a higher likelihood of it being classified as a bad (C or F) wine. On the other hand, the only predictor with a positive slope in the second model was sulphates. However, it's important to note that the HDI interval contained 0, implying that sulphates may not significantly influence the prediction of wine quality according to this model. Despite knowing that sulphates are beneficial for better tasting wine and extended shelf life in the real world, the model's results don't definitively support the notion that more sulphates lead to better wine quality.