Evaluating the Usage of a Bayesian Logistic Regression Framework for Predicting Stroke

H. Ko, G. McCauley, E. Tria

In [1]:
```
import numpy as np
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.metrics import plot_confusion_matrix
import pymc as pm
import arviz as az
import seaborn as sns
import matplotlib.pyplot as plt
import os
import sklearn.metrics as metrics
import warnings
warnings.filterwarnings("ignore")
```

In [2]:
```
# load and clean the data

stroke = pd.read_csv('stroke.csv')

# drop id column and rows with NaNs (bmi has 201 NaNs)
stroke.drop('id', axis=1, inplace=True)
stroke.dropna(inplace=True)
stroke = stroke[stroke['gender'] != 'Other'] # remove 1 instance of 'Other'

# convert two-level categorical predictors into binary variables
stroke['gender'] = (stroke['gender'] == 'Male').astype(int) # Male = 1, Female = 0
stroke['ever_married'] = (stroke['ever_married'] == 'Yes').astype(int) # Married = 1, Single = 0
stroke['Residence_type'] = (stroke['Residence_type'] == 'Urban').astype(int) # Urban = 1, Rural = 0

# drop multilevel categorical predictors
strokes = stroke.drop(['work_type', 'smoking_status'], axis = 1)

# cleaned data (note that the numeric predictors have not been normalized since there is evidence that this is superflu
strokes
```

Out[2]:

	gender	age	hypertension	heart_disease	ever_married	Residence_type	avg_glucose_level	bmi	stroke
0	1	67.0	0	1	1	1	228.69	36.6	1
2	1	80.0	0	1	1	0	105.92	32.5	1
3	0	49.0	0	0	1	1	171.23	34.4	1
4	0	79.0	1	0	1	0	174.12	24.0	1
5	1	81.0	0	0	1	1	186.21	29.0	1
...	...	...	...	...	...	...	...	...	...
5104	0	13.0	0	0	0	0	103.08	18.6	0
5106	0	81.0	0	0	1	1	125.20	40.0	0
5107	0	35.0	0	0	1	0	82.99	30.6	0
5108	1	51.0	0	0	1	0	166.29	25.6	0
5109	0	44.0	0	0	1	1	85.28	26.2	0

4908 rows × 9 columns

The cleaned dataset contains 4908 rows and 9 columns.

In [3]:
```
# split the data into training and test sets

train, test = train_test_split(strokes, test_size=0.2, random_state=6040)
X_train = train.loc[:, train.columns != 'stroke']
y_train = train.loc[:, 'stroke']
X_test = test.loc[:, test.columns != 'stroke']
y_test = test.loc[:, 'stroke']
```

In [4]:
```
discrete_columns = ['gender', 'hypertension', 'heart_disease', 'ever_married', 'Residence_type']
continuous_columns = ['age', 'avg_glucose_level', 'bmi']
```

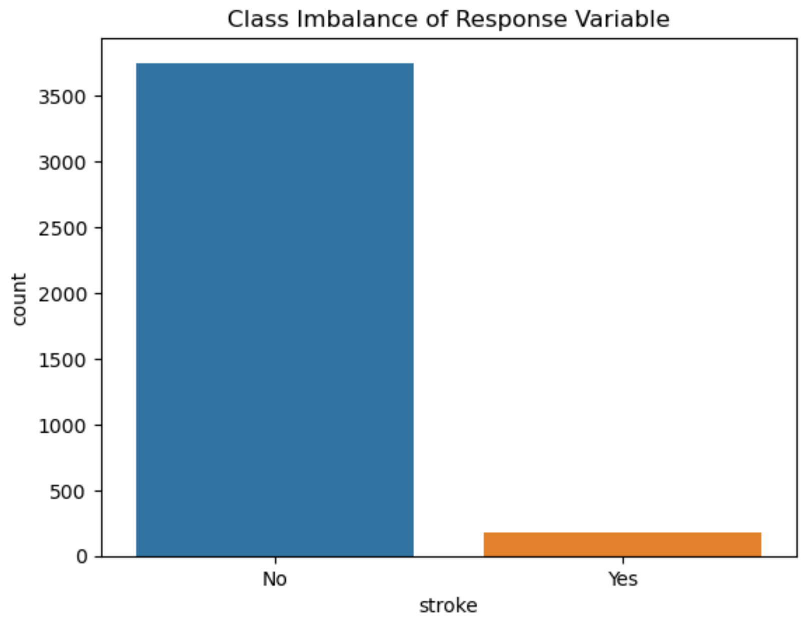
In [5]:
```
X_train_tf = X_train.copy()[discrete_columns]
X_train_tf['gender'] = X_train_tf['gender'].replace(0,"Female")
X_train_tf['gender'] = X_train_tf['gender'].replace(1,"Male")
X_train_tf = X_train_tf.replace(0,"No")
X_train_tf = X_train_tf.replace(1,"Yes")
```

```
y_train_tf = y_train.copy()
y_train_tf = y_train_tf.replace(0, "No")
y_train_tf = y_train_tf.replace(1, "Yes")
y_train_tf.value_counts()
```

Out[5]:
```
No      3752
Yes      174
Name: stroke, dtype: int64
```

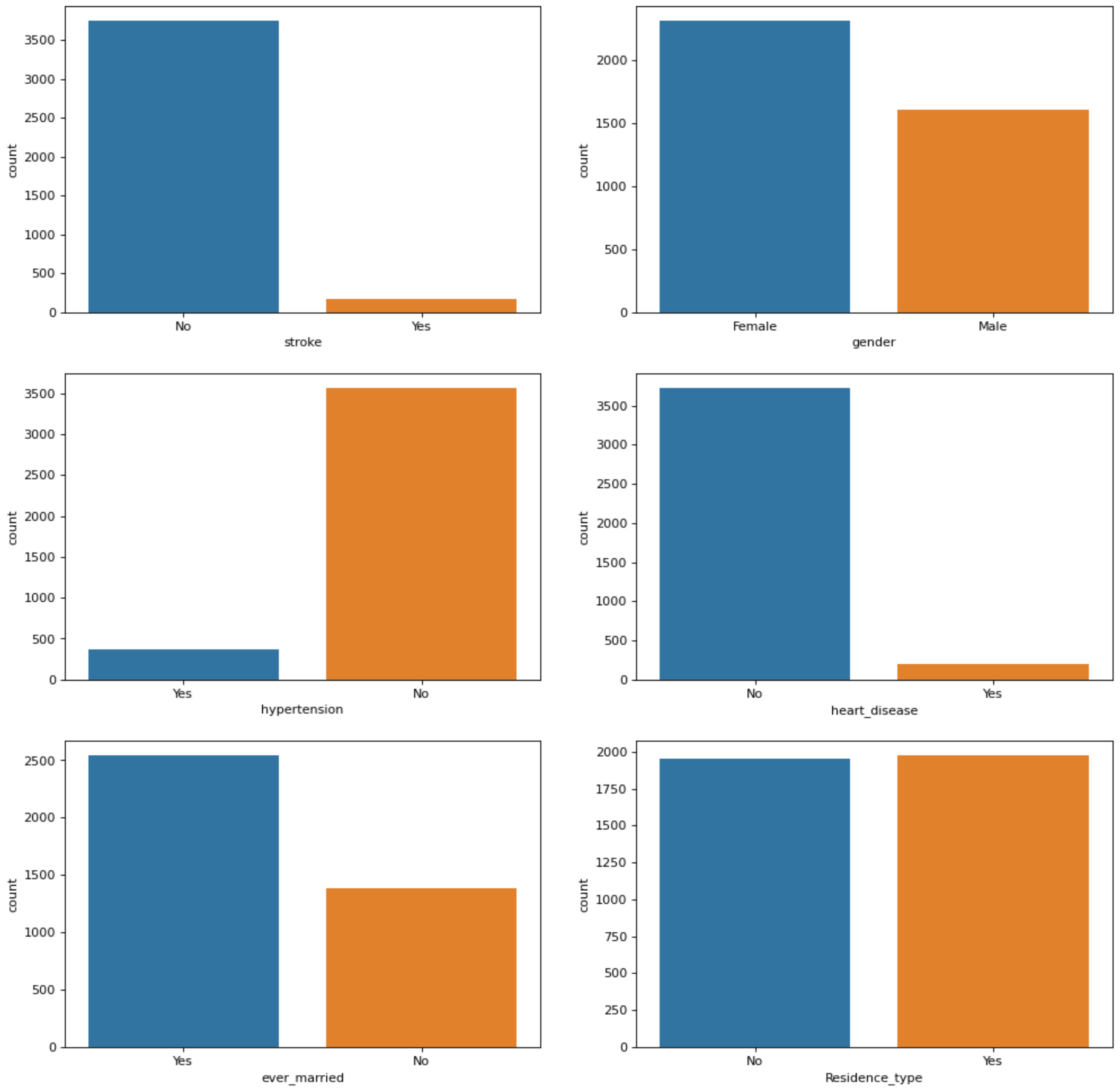
In [6]:
```
sns.countplot(y_train_tf)
plt.title("Class Imbalance of Response Variable")
```

Out[6]:
```
Text(0.5, 1.0, 'Class Imbalance of Response Variable')
```



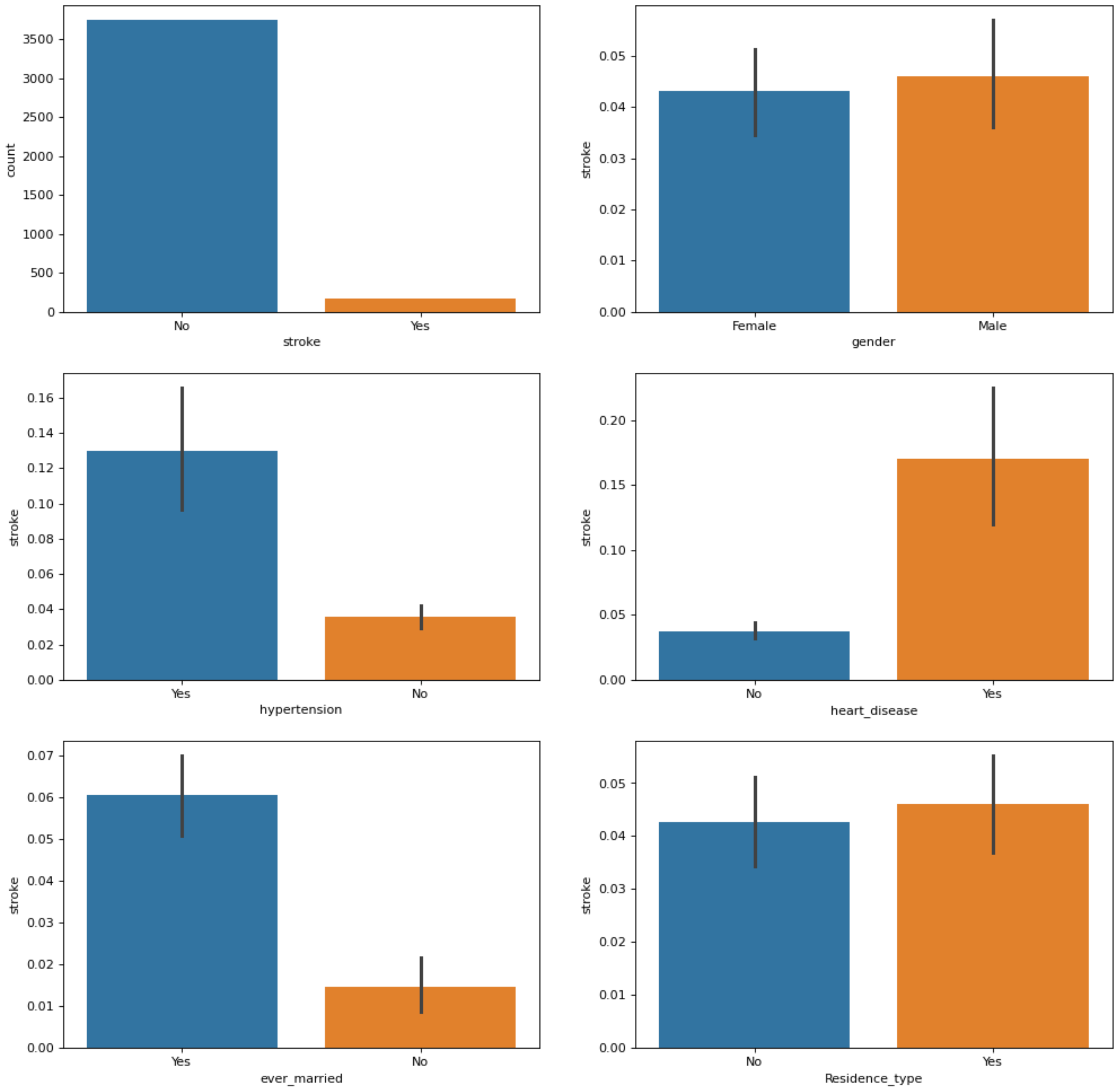
This plot shows the class imabalance for the response variable with a majority being patients without stroke.

In [7]:
```
fig, axs = plt.subplots(nrows = 3, ncols = 2, figsize=(15,15), dpi = 80)
count = 0
for i in range (0,3):
    for j in range(0,2):
        if i == 0 and j == 0:
            # first plot uses the count of response variable
            sns.countplot(y_train_tf, ax = axs[i,j])

        else:
            col = discrete_columns[count]
            sns.countplot(X_train_tf[col], ax = axs[i,j])
            count += 1
```



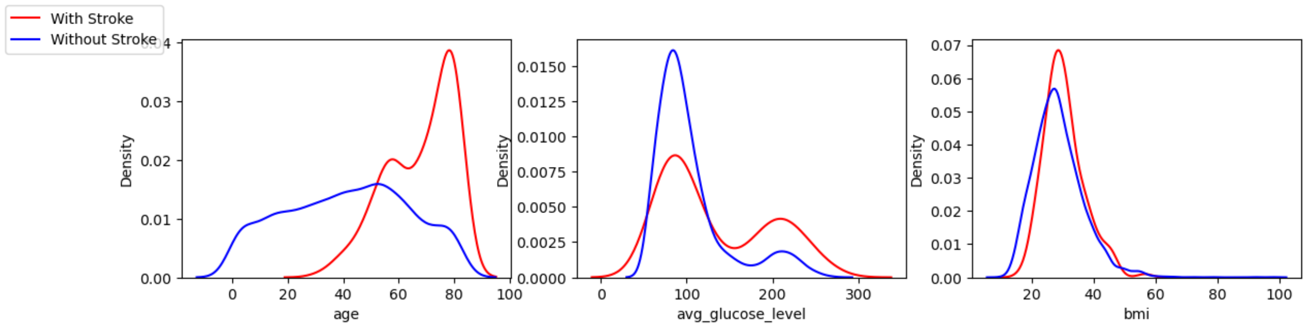
There is a noteable difference for the *hypertension* and *heart_disease* columns in terms of count.

In [8]:
```
fig, axs = plt.subplots(nrows = 3, ncols = 2, figsize=(15,15), dpi = 80)
count = 0
for i in range (0,3):
    for j in range(0,2):
        if i == 0 and j == 0:
            # first plot uses the count of response variable
            sns.countplot(y_train_tf, ax = axs[i,j])
        else:
            col = discrete_columns[count]
            sns.barplot(X_train_tf[col], y_train, ax = axs[i,j])
            count += 1
```



```
In [9]: fig, axs = plt.subplots(nrows = 1, ncols = 3, figsize=(14,3))
        count = 0
        for i in range (0,3):
            col = continuous_columns[i]
            sns.kdeplot(train[train['stroke'] == 1][col], ax = axs[i], color = 'red')
            sns.kdeplot(train[train['stroke'] == 0][col], ax = axs[i], color = 'blue')
        fig.legend(loc='upper left', labels= ['With Stroke', 'Without Stroke'])
```

```
Out[9]: <matplotlib.legend.Legend at 0x7ff501020cd0>
```



The plots above show the distribution of the continuous variables split up for patients with stroke and without stroke.

In [10]:
```
# create a dictionary to access the feature names

beta_dict = dict()
count = 0
for col in X_train.columns:
    beta_dict[str(count)] = col
    count += 1

beta_dict['1']
```

Out[10]:
```
'age'
```

In [11]:
```
# function to get the precision, accuracy, and recall given a confusion matrix

def get_rates(A):
    TN = A[0,0]
    FN = A[1,0]
    FP = A[0,1]
    TP = A[1,1]

    rates = dict()
    rates['Precision'] = round(TP / (TP + FP), 3)
    rates['Accuracy'] = round((TP + TN) / (TP + TN + FP + FN),3)
    rates['Recall'] = round(TP / (TP + FN), 3)
    return rates
```

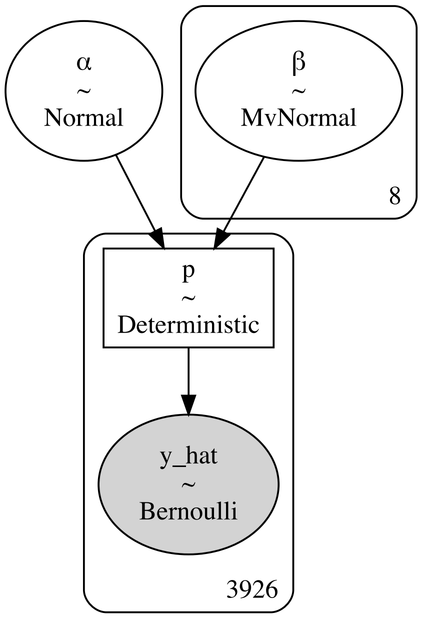
In [12]:
```
def get_cost(A, fp_cost=1, fn_cost=50):
    FN = A[0,1]
    FP = A[1,0]
    return fp_cost * FP + fn_cost * FN
```

Model 1: Full Sampling Model (8 predictors)

- Result: {'Precision': 0.105, 'Accuracy': 0.713, 'Recall': 0.943}

In [13]:
```
# build the full Bayesian logistic regression model

with pm.Model() as logistic_regression:

    k = X_train.shape[1]

    # Gaussian priors for random intercepts and slopes
    α = pm.Normal('α', mu=0., sigma=100)
    β = pm.MvNormal('β', mu=np.zeros(k), cov=100*np.eye(k), shape=k)

    # Calculate the logit
    μ = α + pm.math.dot(np.array(X_train),β)
    p = pm.Deterministic('p',  pm.invlogit(μ))

    # Pass the logits to a Bernoulli outcome, with the observed data
    y_hat = pm.Bernoulli('y_hat', p=p, observed=y_train)

# the graphical model
fig1 = pm.model_to_graphviz(logistic_regression)
fig1
```

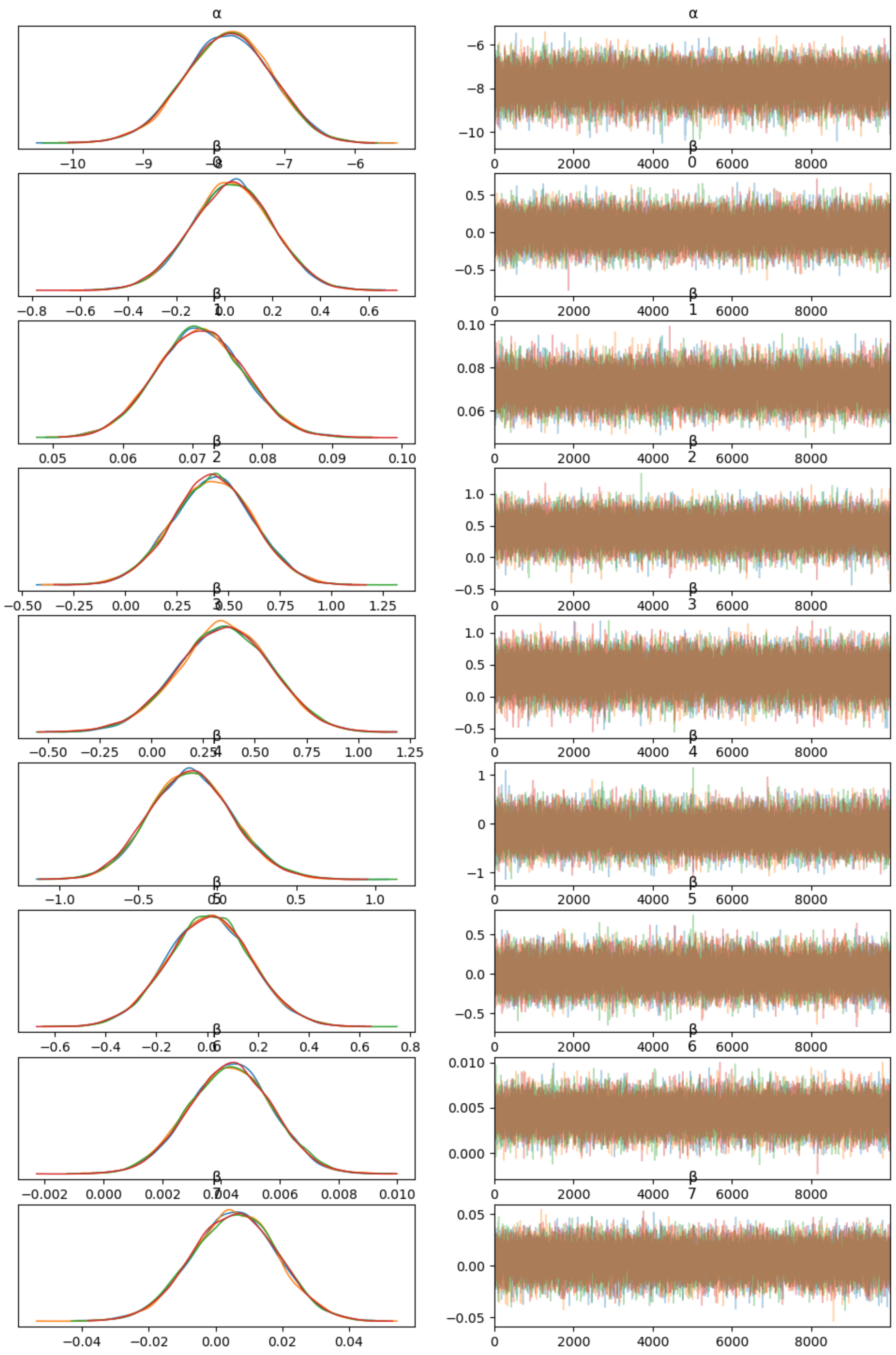
Out[13]:



In [14]:
```
# run HMC sampling for the full model

with logistic_regression:
    full_trace = pm.sample(10000, cores = 4, random_seed = 6040)
```

In [15]:
```
# saving and reading trace results

# full_trace_fpath = 'full_trace.nc'
# full_trace.to_netcdf(full_trace_fpath)

# uncomment to read trace from file:
# full_trace = az.from_netcdf(full_trace_fpath)
```

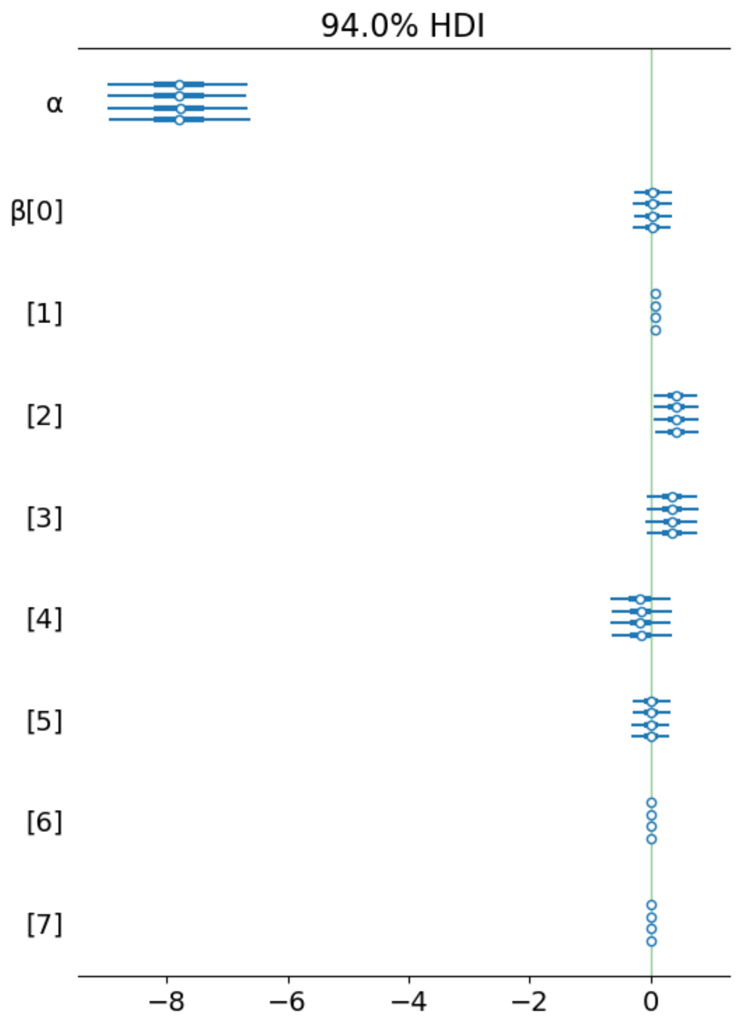
In [16]:
```
# trace plots

fig2 = az.plot_trace(full_trace, compact = False, var_names = ['α','β']);
```


α
β
0
β
1
β
2
β
3
β
4
β
5
β
6
β
7

The trace plots for the full model show good convergence.

In [17]:
```
# forest plots

az.plot_forest(full_trace, var_names = ['α','β'], rope=(0,0))
```

Out[17]:
```
array([<AxesSubplot:title={'center':'94.0% HDI'}>], dtype=object)
```



The forest plot shows that a majority of the predictors include 0 in their 94% HDI intervals, which menas they are possibly statistically insignificant.

In [18]:
```
# summary table

az.summary(full_trace, var_names = ['α','β'], round_to=2)
```

Out[18]:

	mean	sd	hdi_3%	hdi_97%	mcse_mean	mcse_sd	ess_bulk	ess_tail	r_hat
α	-7.81	0.62	-8.96	-6.64	0.0	0.0	28421.10	28019.40	1.0
β[0]	0.03	0.17	-0.28	0.35	0.0	0.0	48045.93	28547.77	1.0
β[1]	0.07	0.01	0.06	0.08	0.0	0.0	34592.09	28630.74	1.0
β[2]	0.42	0.20	0.06	0.79	0.0	0.0	55406.40	27643.87	1.0
β[3]	0.35	0.23	-0.07	0.78	0.0	0.0	48196.08	29012.39	1.0
β[4]	-0.16	0.27	-0.66	0.34	0.0	0.0	45985.07	27618.89	1.0
β[5]	0.01	0.17	-0.31	0.32	0.0	0.0	49788.86	27040.43	1.0
β[6]	0.00	0.00	0.00	0.01	0.0	0.0	53658.69	28785.46	1.0
β[7]	0.01	0.01	-0.02	0.03	0.0	0.0	37327.25	29522.74	1.0

In [19]:
```
print(beta_dict['1'])
print(beta_dict['2'])
```

```
age
hypertension
```

The two statistically significant parameters are β_0 and β_1, which are *age* and *hypertension* respectively.

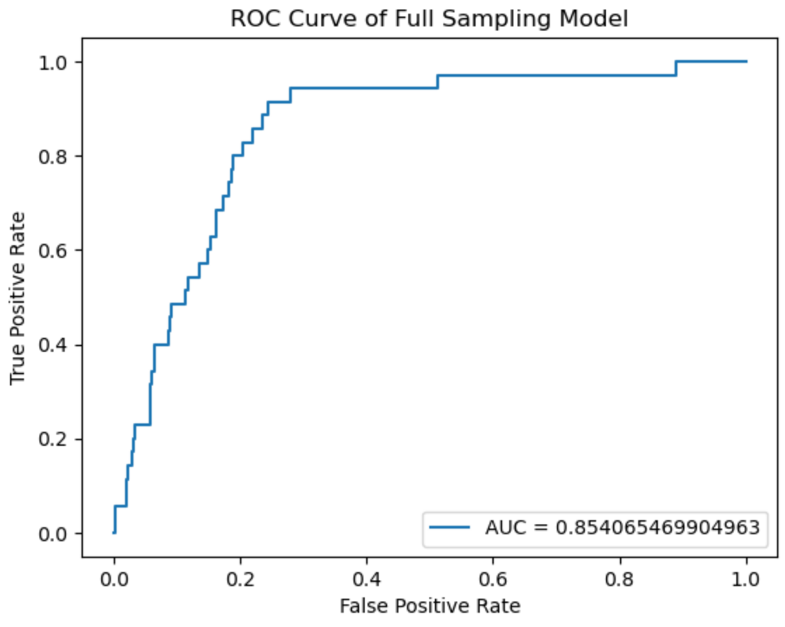
In [20]:
```
def inv_logit(p):
    return np.exp(p) / (1 + np.exp(p))

def calculate_tstar(p, y_hat, y_test):
    t = np.linspace(0,1,101)
    accuracies = np.full(len(t), None)
    TPs = np.full(len(t), None)
    FPs = np.full(len(t), None)
    TNs = np.full(len(t), None)
    FNs = np.full(len(t), None)
    for i in range(len(t)):
        y_hat = (p>=t[i]).astype(int)
        accuracies[i] = sum(y_hat == y_test)/len(y_test)
        TPs[i] = sum(np.all([y_hat == 1, y_test == 1], axis=0))
        FPs[i] = sum(np.all([y_hat == 1, y_test == 0], axis=0))
        TNs[i] = sum(np.all([y_hat == 0, y_test == 0], axis=0))
        FNs[i] = sum(np.all([y_hat == 0, y_test == 1], axis=0))

    # Using 50 as the cost of misclassification
    t_star = t[np.argmin(FPs + 50*FNs)]
    return t_star
```

In [21]:
```
a = full_trace.posterior['α'].mean(axis=1).mean(axis=0).to_numpy()
b = full_trace.posterior['β'].mean(axis=1).mean(axis=0).to_numpy()

m = a + X_test.dot(b)
p = inv_logit(m)

t_star_full = calculate_tstar(p, y_hat, y_test)
print('Optimal Threshold:', t_star_full)
sum((p>=t_star_full).astype(int) == y_test)/len(y_test)
```

```
Optimal Threshold: 0.04
```

Out[21]:
```
0.7128309572301426
```

In [22]:
```
# ROC Curve

fpr, tpr, _ = metrics.roc_curve(y_test,  p)
auc = metrics.roc_auc_score(y_test, p)

plt.plot(fpr, tpr, label = "AUC = "+str(auc))
plt.ylabel('True Positive Rate')
plt.xlabel('False Positive Rate')
plt.legend(loc=4)
plt.title("ROC Curve of Full Sampling Model")
plt.savefig("full_roc.png")
plt.show()
```



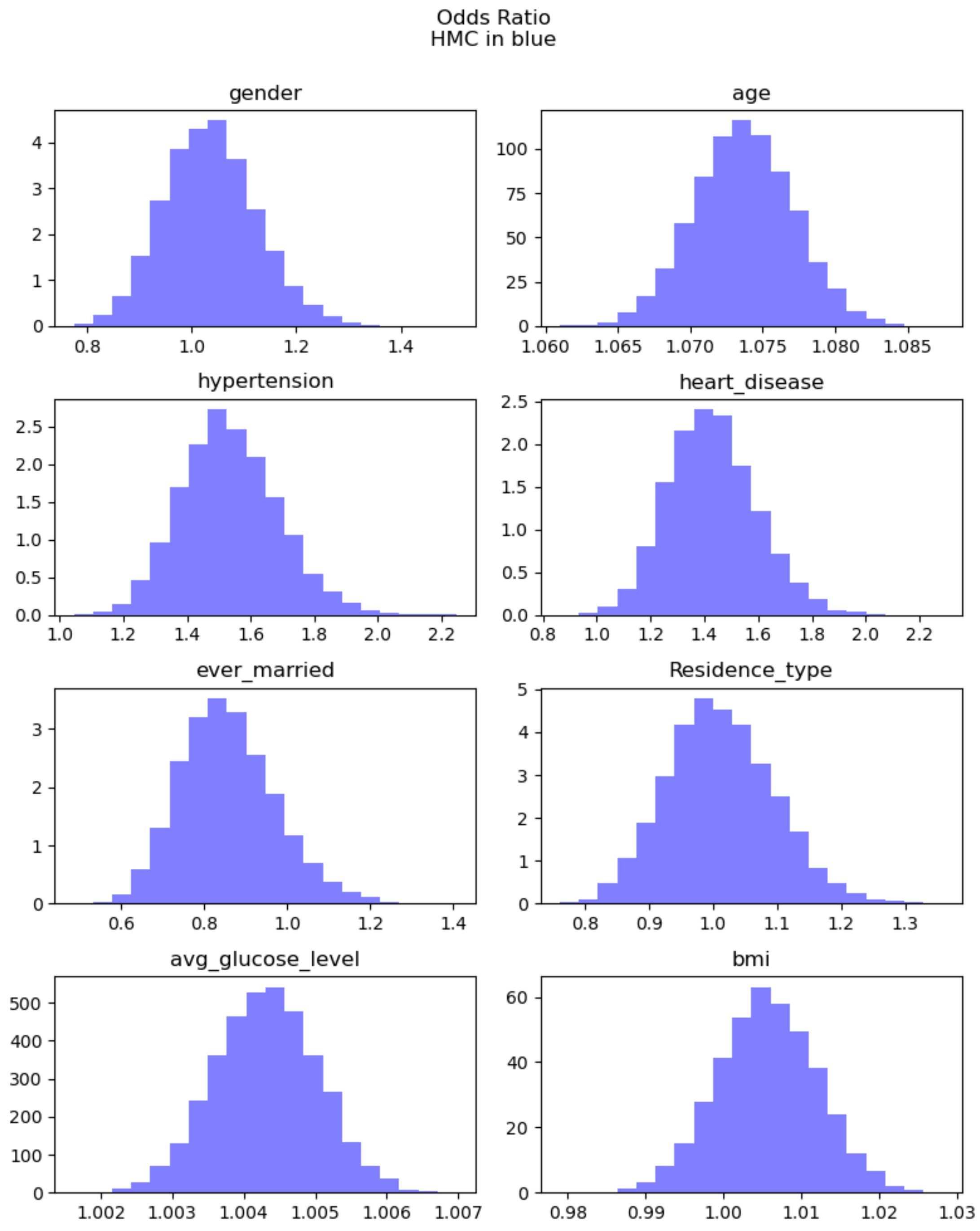
The full model has an Area Under the Curve (AUC) value of 0.854.

In [23]:
```
# Confusion Matrix

cm = metrics.confusion_matrix(y_test, (p>=t_star_full).astype(int))
print(cm)

get_rates(cm)
```

```
[[667 280]
 [  2  33]]
```

Out[23]:
```
{'Precision': 0.105, 'Accuracy': 0.713, 'Recall': 0.943}
```

In [24]:
```
# Odds ratio for all parameters (Full model)
# Odds ratio = pr() / 1 - pr()

full_betas = full_trace.posterior['β']
full_predictor_cols = list(X_train.columns)
k = len(full_predictor_cols)

fig, axes = plt.subplots(nrows = 4, ncols = 2, figsize = (8, 10), dpi = 100, constrained_layout = False)

for ax, estimate_sample, title, xlabel in zip(
    axes.ravel(),
    [full_betas[:,:,i] for i in range(k)],
    full_predictor_cols,
    full_predictor_cols):

    OR_sample = np.mean(estimate_sample, axis=0)
    ax.hist(np.exp(OR_sample), bins=20, density=True, color = 'blue', alpha = 0.5)
    ax.set_title(title, fontsize=12)

plt.suptitle('Odds Ratio\nHMC in blue')
plt.tight_layout()
plt.subplots_adjust(top = 0.9)
plt.show()
```



The plot above shows the odds ratio for the different parameters for the full HMC sampling model.

Model 2: Full ADVI Model (8 predictors)

- Result: {'Precision': 0.096, 'Accuracy': 0.733, 'Recall': 0.771}

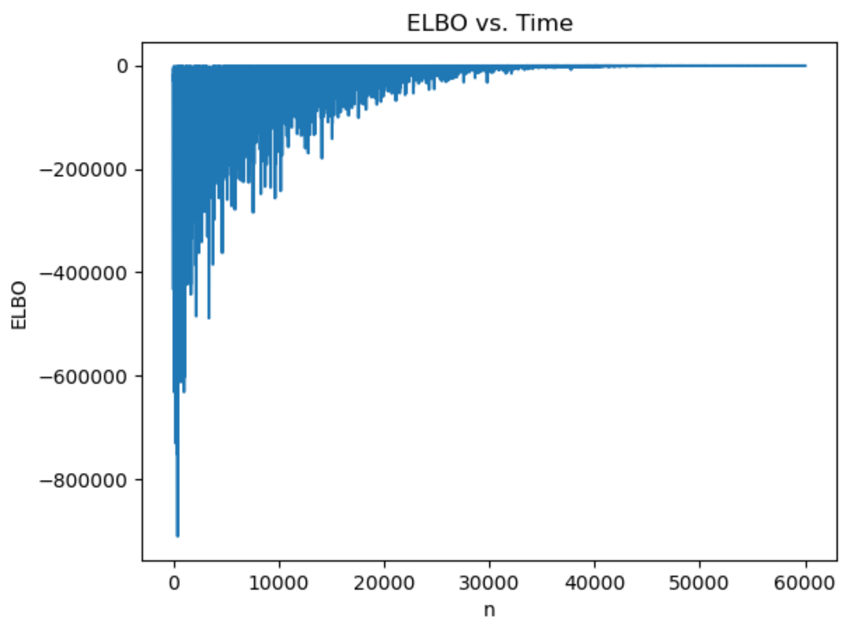
In [25]:
```
# Variational inference with ADVI optimization

advi_fit = pm.fit(60000, method = 'advi', model = logistic_regression, random_seed=6040)
```

100.00% [60000/60000 00:21<00:00 Average Loss = 666.31]

```
Finished [100%]: Average Loss = 666.31
```

In [26]:
```
# plot the ELBO over time

advi_elbo = pd.DataFrame(
    {'ELBO': -advi_fit.hist,
     'n': np.arange(advi_fit.hist.shape[0])})
```

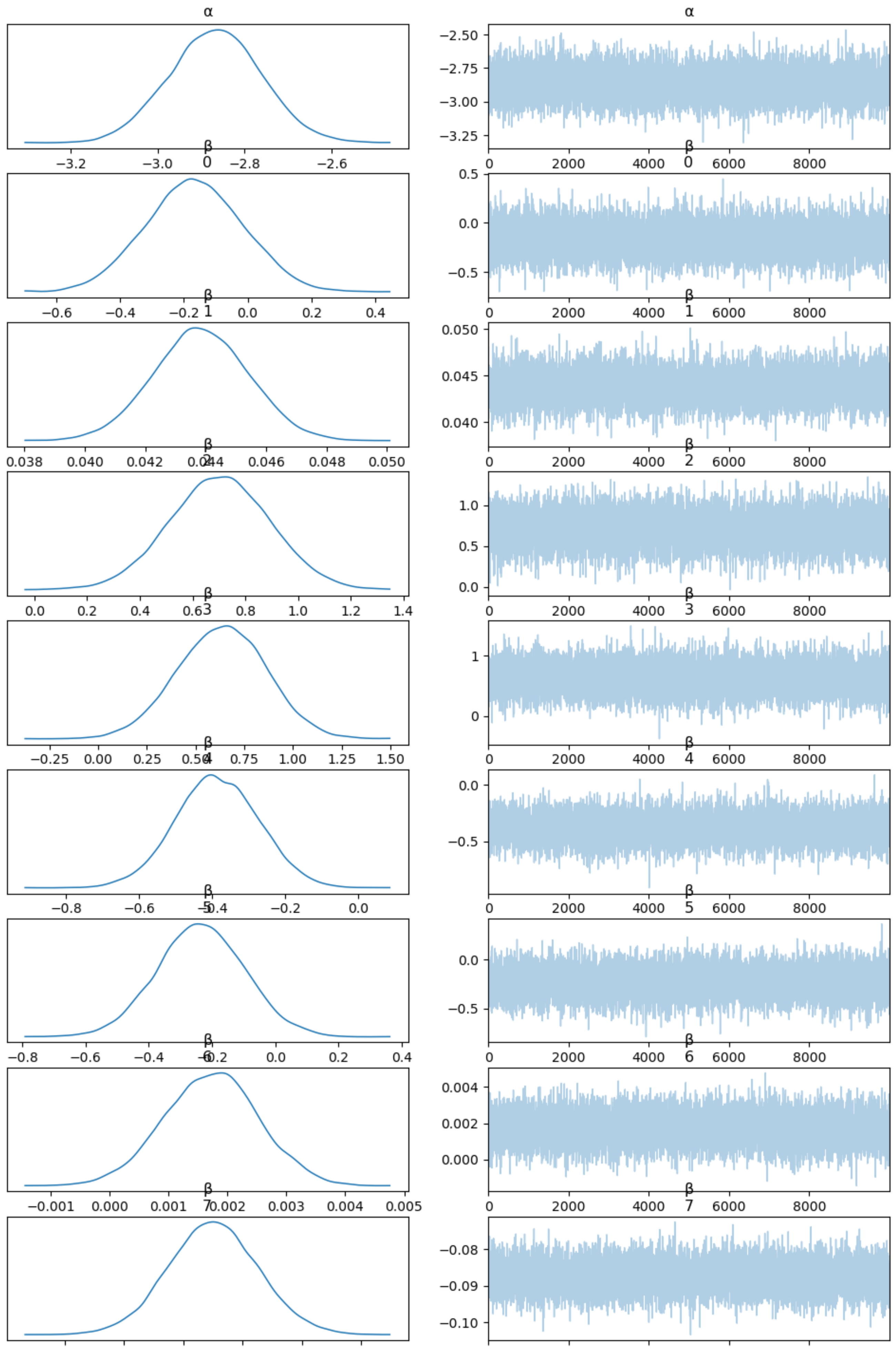
```
_ = sns.lineplot(y='ELBO', x='n', data=advi_elbo)
_.set_title('ELBO vs. Time');
```



The plot of the ELBO shows that as n increases, convergence occurs as expected. The average loss is at 666.31

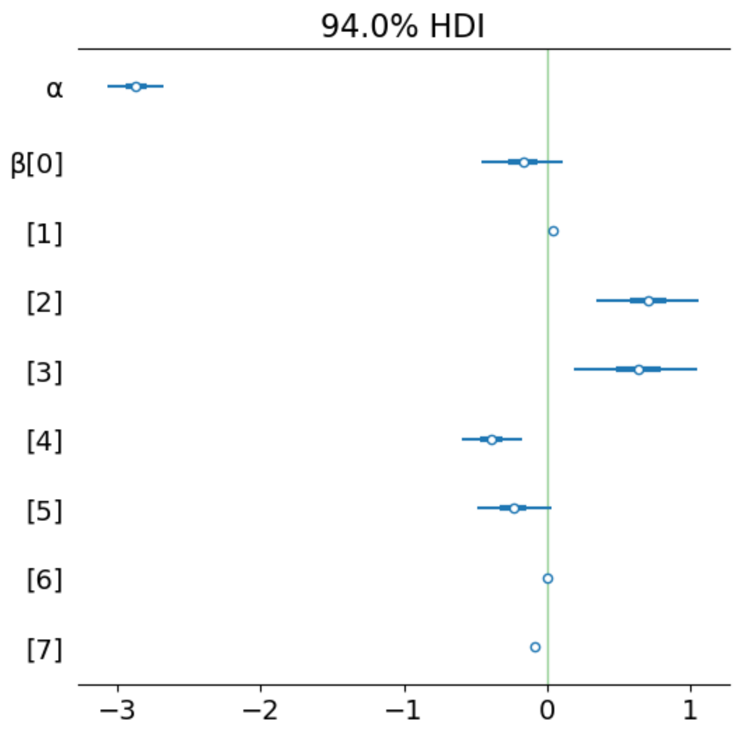
In [27]:
```
# sample from the variational posterior distribution

full_advi_trace = advi_fit.sample(10000, random_seed = 6040)
```

In [28]:
```
# trace plots

az.plot_trace(full_advi_trace, compact = False, var_names = ['α','β']);
```


α
−3.2 −3.0 −2.8 −2.6
−2.50 −2.75 −3.00 −3.25
β 0
−0.6 −0.4 −0.2 0.0 0.2 0.4
0.5 0.0 −0.5
β 1
0.038 0.040 0.042 0.044 0.046 0.048 0.050
0.050 0.045 0.040
β 2
0.0 0.2 0.4 0.6 0.8 1.0 1.2 1.4
1.0 0.5 0.0
β 3
−0.25 0.00 0.25 0.50 0.75 1.00 1.25 1.50
1 0
β 4
−0.8 −0.6 −0.4 −0.2 0.0
0.0 −0.5
β 5
−0.8 −0.6 −0.4 −0.2 0.0 0.2 0.4
0.0 −0.5
β 6
−0.001 0.000 0.001 0.002 0.003 0.004 0.005
0.004 0.002 0.000
β 7
−0.08 −0.09 −0.10
0 2000 4000 6000 8000

The trace plots for the full ADVI model show good convergence.

In [29]:
```
# forest plots

az.plot_forest(full_advi_trace, var_names = ['α','β'], rope=(0,0));
```



The forest plot for the ADVI model is similar to the one for the full HMC model although there are additional predictors that do not have 0 in their 94% HDI interval.

In [30]:
```
# summary table

az.summary(full_advi_trace, var_names = ['α','β'], round_to=2)
```

```
arviz - WARNING - Shape validation failed: input_shape: (1, 10000), minimum_shape: (chains=2, draws=4)
```

Out[30]:

	mean	sd	hdi_3%	hdi_97%	mcse_mean	mcse_sd	ess_bulk	ess_tail	r_hat
α	-2.87	0.11	-3.07	-2.67	0.0	0.0	9837.03	9636.59	NaN
β[0]	-0.17	0.15	-0.45	0.11	0.0	0.0	9620.83	9342.89	NaN
β[1]	0.04	0.00	0.04	0.05	0.0	0.0	8548.56	9378.23	NaN
β[2]	0.70	0.19	0.34	1.06	0.0	0.0	10149.82	9883.38	NaN
β[3]	0.63	0.23	0.19	1.04	0.0	0.0	9735.82	9581.93	NaN
β[4]	-0.39	0.11	-0.60	-0.17	0.0	0.0	9766.66	9370.84	NaN
β[5]	-0.24	0.14	-0.49	0.03	0.0	0.0	9892.28	9876.61	NaN
β[6]	0.00	0.00	0.00	0.00	0.0	0.0	9882.37	9351.07	NaN
β[7]	-0.09	0.00	-0.09	-0.08	0.0	0.0	9985.12	9756.59	NaN

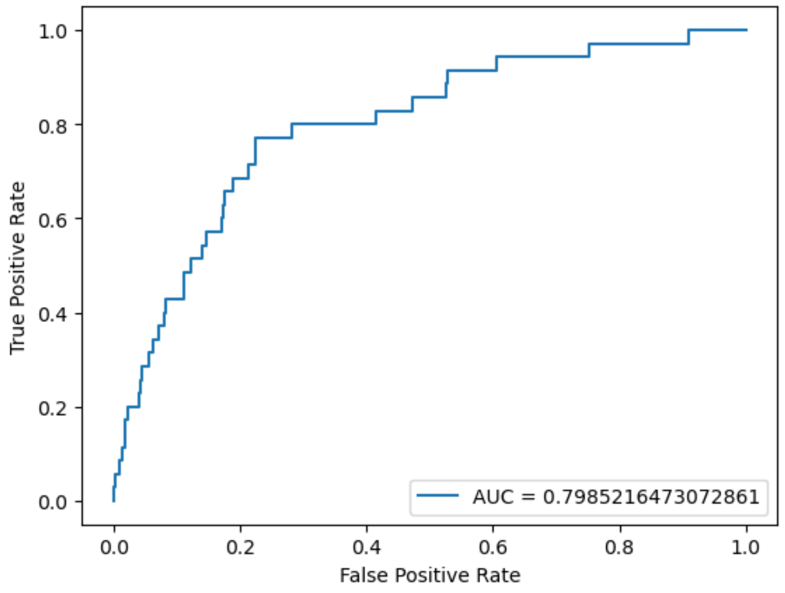
The summary table for the ADVI trace indicates that more of the variables are statistically significant than just *age* and *hypertension* as the HMC sampling trace suggests.

In [31]:
```
a = full_advi_trace.posterior['α'].mean(axis=1).mean(axis=0).to_numpy()
b = full_advi_trace.posterior['β'].mean(axis=1).mean(axis=0).to_numpy()

m = a + X_test.dot(b)
p = inv_logit(m)

t_star_full_advi = calculate_tstar(p, y_hat, y_test)
print('Optimal Threshold:', t_star_full_advi)
sum((p>=t_star_full_advi).astype(int) == y_test)/len(y_test)
```

```
Optimal Threshold: 0.04
```

Out[31]:
```
0.7331975560081466
```

In [32]:
```python
# ROC Curve

fpr, tpr, _ = metrics.roc_curve(y_test,  p)
auc = metrics.roc_auc_score(y_test, p)

plt.plot(fpr, tpr, label = "AUC = "+str(auc))
plt.ylabel('True Positive Rate')
plt.xlabel('False Positive Rate')
plt.legend(loc=4)
plt.show()
```

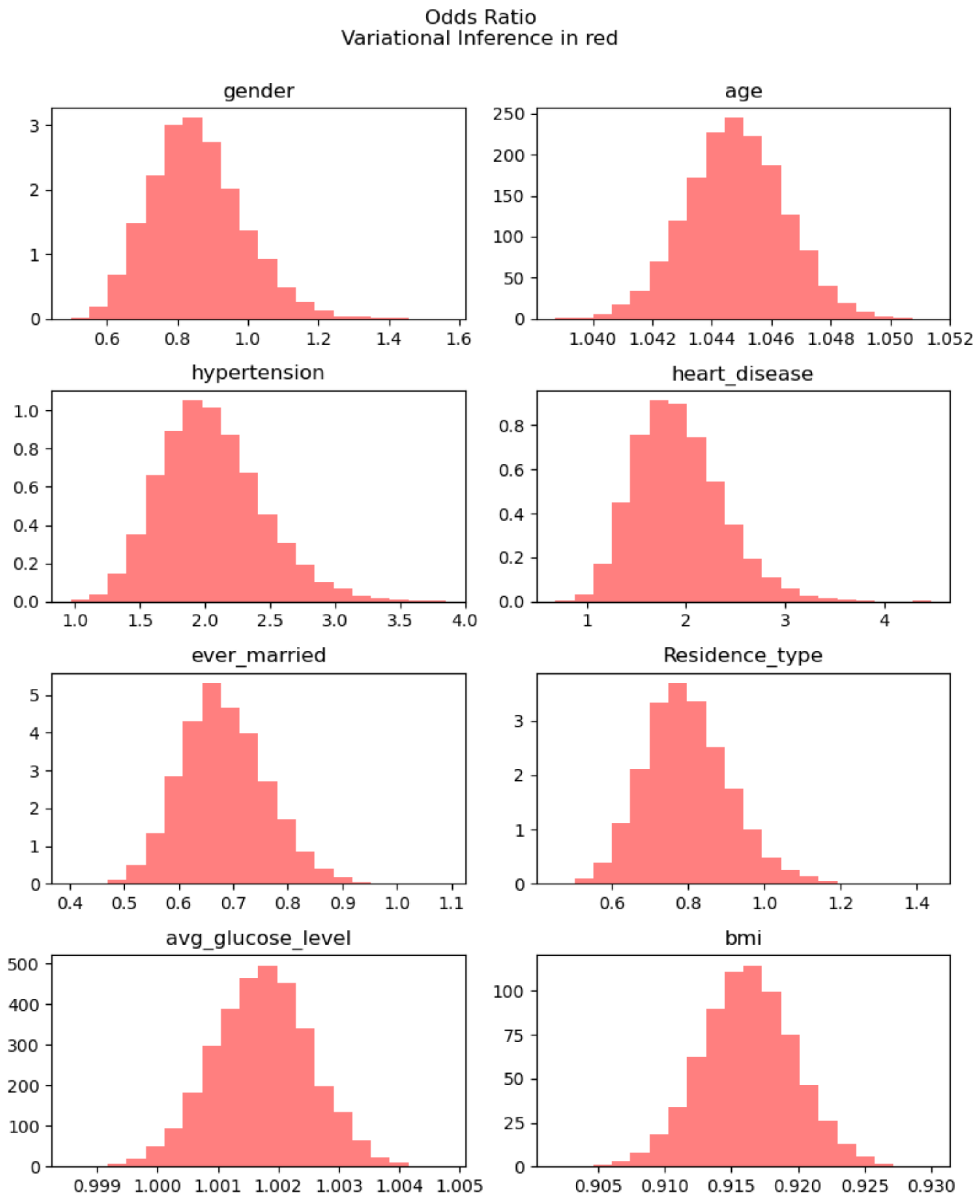


The full ADVI model has an Area Under the Curve (AUC) value of 0.798

In [33]:
```python
# Confusion Matrix

cm = metrics.confusion_matrix(y_test, (p>=t_star_full_advi).astype(int))
print(cm)

get_rates(cm)
```

```
[[693 254]
 [  8  27]]
```
Out[33]:
```
{'Precision': 0.096, 'Accuracy': 0.733, 'Recall': 0.771}
```

In [34]:
```python
# Odds ratio for all parameters (Full Model ADVI)
# Odds ratio = pr() / 1 - pr()

full_advi_betas = full_advi_trace.posterior['β']
full_predictor_cols = list(X_train.columns)
k = len(full_predictor_cols)

fig, axes = plt.subplots(nrows = 4, ncols = 2, figsize = (8, 10), dpi = 100, constrained_layout = False)

for ax, estimate_advi, title, xlabel in zip(
    axes.ravel(),
    [full_advi_betas[:,:,i] for i in range(k)],
    full_predictor_cols,
    full_predictor_cols):

    OR_advi = np.mean(estimate_advi, axis=0)
    ax.hist(np.exp(OR_advi), bins=20, density=True, color = 'red', alpha = 0.5)
    ax.set_title(title, fontsize=12)

plt.suptitle('Odds Ratio\nVariational Inference in red')
plt.tight_layout()
plt.subplots_adjust(top = 0.9)
plt.show()
```



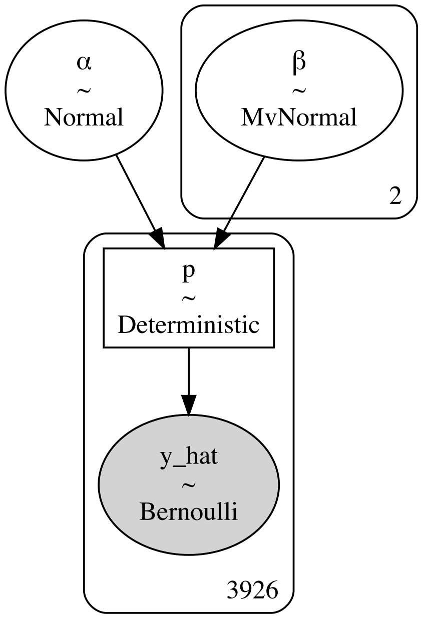
The plot above shows the odds ratio for the different parameters for the full ADVI model.

Model 3: Reduced Sampling Model (Age & Hypertension)

- Result: {'Precision': 0.097, 'Accuracy': 0.686, 'Recall': 0.943}

In [35]:
```
# build the reduced Bayesian logistic regression model

X_train_reduced = X_train[["age", "hypertension"]]

with pm.Model() as logistic_regression_reduced:

    k = X_train_reduced.shape[1]

    # Gaussian priors for random intercepts and slopes
    α = pm.Normal('α', mu=0., sigma=100)
    β = pm.MvNormal('β', mu=np.zeros(k), cov=100*np.eye(k), shape=k)

    # Calculate the logit
    μ = α + pm.math.dot(np.array(X_train_reduced),β)
    p = pm.Deterministic('p',  pm.invlogit(μ))
    # Pass the logits to a Bernoulli outcome, with the observed data
    y_hat = pm.Bernoulli('y_hat', p=p, observed=y_train)

# the graphical model
pm.model_to_graphviz(logistic_regression_reduced)
```

Out[35]:



In [36]:

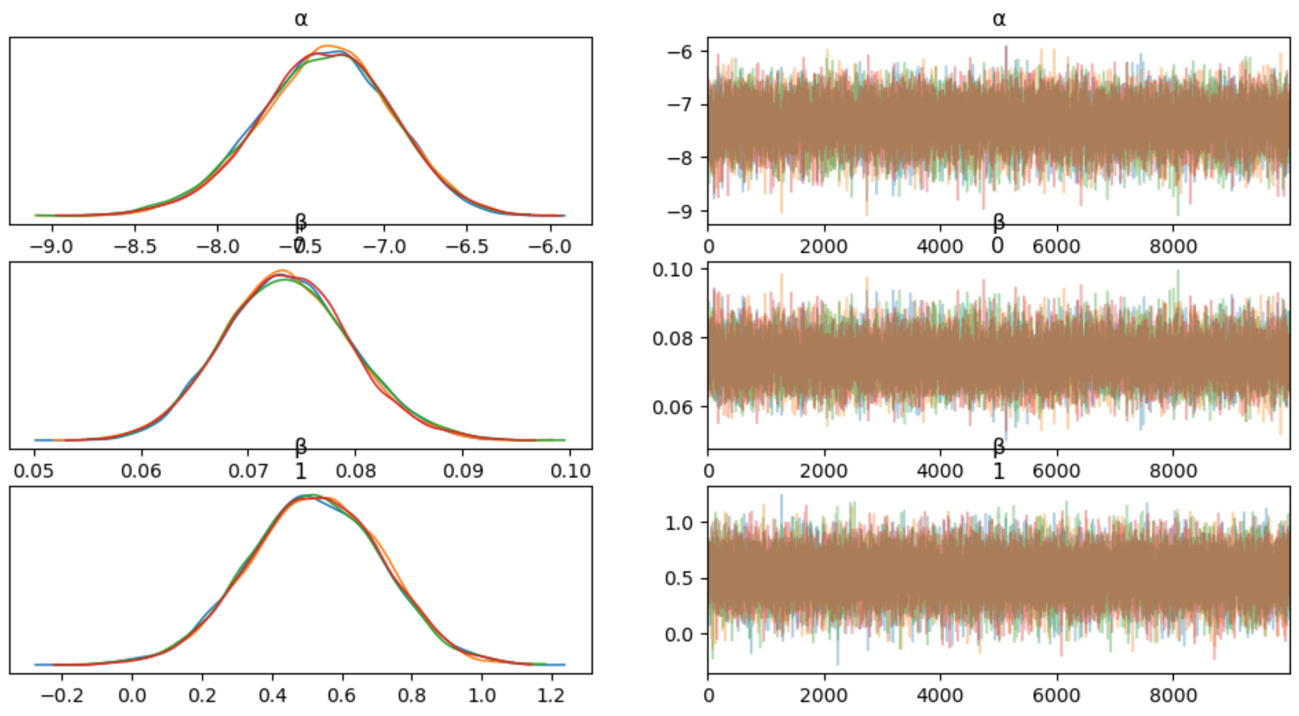
```
# HMC sampling for the reduced model

with logistic_regression_reduced:
    reduced_trace = pm.sample(10000, cores = 4, random_seed = 6040)
```

In [37]:

```
# save and read trace data

# reduced_trace_fpath = 'reduced_trace.nc'
# reduced_trace.to_netcdf(reduced_trace_fpath)

# uncomment to read trace from file:
# reduced_trace = az.from_netcdf(reduced_trace_fpath)
```

In [38]:

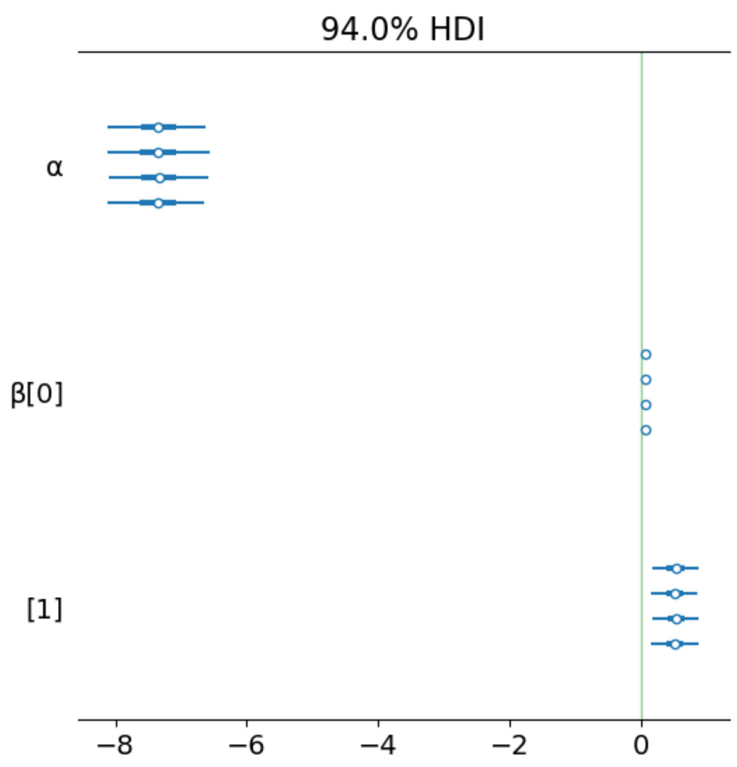
```
az.plot_trace(reduced_trace, compact = False, var_names = ['α','β']);
```



The trace plots for the reduced sampling model shows good convergence.

In [39]:
```
# forest plots

az.plot_forest(reduced_trace, var_names = ['α','β'], rope=(0,0))
```

Out[39]:
```
array([<AxesSubplot:title={'center':'94.0% HDI'}>], dtype=object)
```



The forest plots show that the parameters in the reduced sampling model are all statistically significant.

In [40]:
```
# summary table

az.summary(reduced_trace, var_names = ['α','β'], round_to=2)
```

Out[40]:

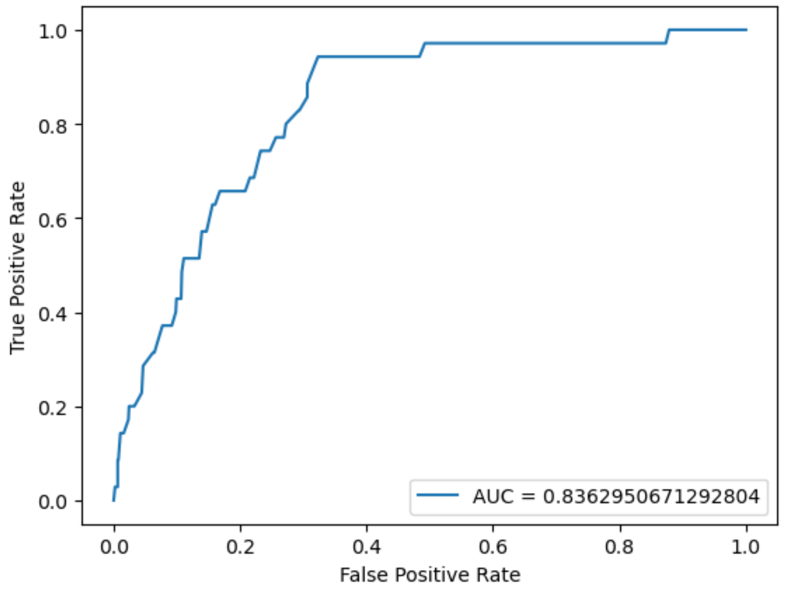
	mean	sd	hdi_3%	hdi_97%	mcse_mean	mcse_sd	ess_bulk	ess_tail	r_hat
α	-7.36	0.40	-8.10	-6.59	0.0	0.0	12899.91	14098.87	1.0
β[0]	0.07	0.01	0.06	0.08	0.0	0.0	12727.58	14233.31	1.0
β[1]	0.52	0.19	0.16	0.87	0.0	0.0	19028.53	18754.93	1.0

In [41]:
```
a = reduced_trace.posterior['α'].mean(axis=1).mean(axis=0).to_numpy()
b = reduced_trace.posterior['β'].mean(axis=1).mean(axis=0).to_numpy()

X_test_reduced = X_test[["age", "hypertension"]]

m = a + X_test_reduced.dot(b)
p = inv_logit(m)

t_star_reduced = calculate_tstar(p, y_hat, y_test)
print('Optimal Threshold:', t_star_reduced)
sum((p>=t_star_reduced).astype(int) == y_test)/len(y_test)
```

```
Optimal Threshold: 0.04
```

Out[41]:
```
0.6863543788187373
```

In [42]:
```
# ROC Curve

fpr, tpr, _ = metrics.roc_curve(y_test,  p)
auc = metrics.roc_auc_score(y_test, p)

plt.plot(fpr, tpr, label = "AUC = "+str(auc))
plt.ylabel('True Positive Rate')
plt.xlabel('False Positive Rate')
plt.legend(loc=4)
plt.show()
```



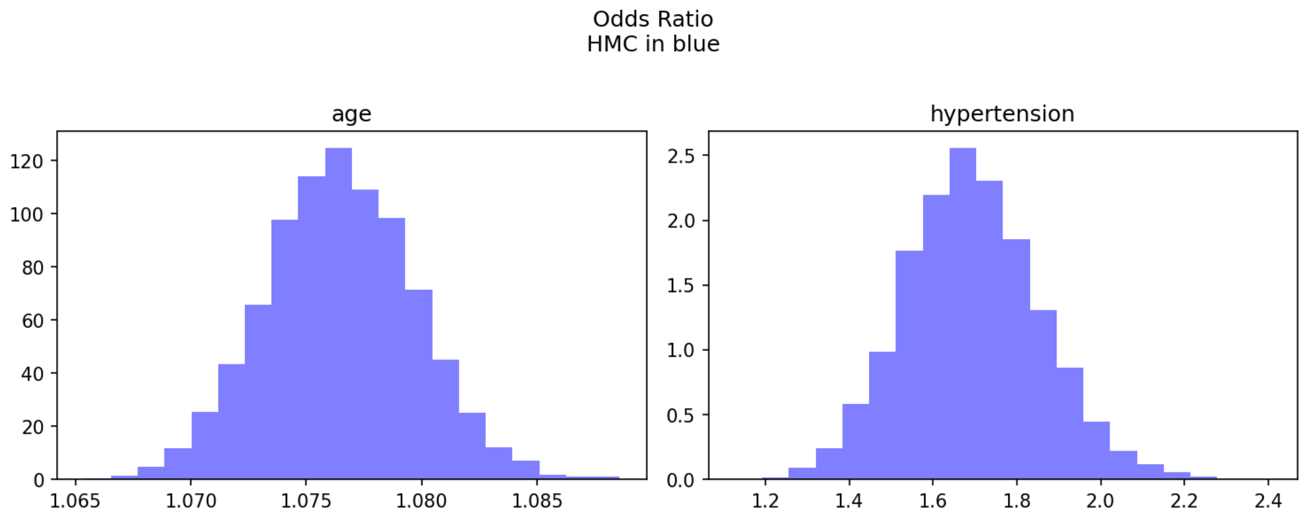
The reduced sampling model has an Area Under the Curve (AUC) value of 0.836

In [43]:
```
# Confusion Matrix

cm = metrics.confusion_matrix(y_test, (p>=t_star_reduced).astype(int))
print(cm)

get_rates(cm)
```

```
[[641 306]
 [  2  33]]
```

Out[43]:
```
{'Precision': 0.097, 'Accuracy': 0.686, 'Recall': 0.943}
```

In [44]:
```
# Odds ratio for reduced parameters (Reduced Model HMC)
# Odds ratio = pr() / 1 - pr()

reduced_betas = reduced_trace.posterior['β']
reduced_predictor_cols = list(X_train_reduced.columns)
k = len(reduced_predictor_cols)

fig, axes = plt.subplots(nrows = 1, ncols = 2, figsize = (10, 4), dpi = 150, constrained_layout = False)

for ax, estimate_sample, title, xlabel in zip(
    axes.ravel(),
    [reduced_betas[:,:,i] for i in range(k)],
    reduced_predictor_cols,
    reduced_predictor_cols):

    OR_sample = np.mean(estimate_sample, axis=0)
    ax.hist(np.exp(OR_sample), bins=20, density=True, color = 'blue', alpha = 0.5)
    ax.set_title(title, fontsize=12)

plt.suptitle('Odds Ratio\nHMC in blue')
plt.tight_layout()
plt.subplots_adjust(top = 0.75)
plt.show()
```



The plot above shows the odds ratio for the different parameters for the reduced HMC sampling model.

In [45]:
```
# WAIC

cmp_waic = az.compare({'model_full':full_trace, 'model_reduced':reduced_trace}, ic='waic')
cmp_waic
```

Out[45]:

	rank	waic	p_waic	d_waic	weight	se	dse	warning	waic_scale
model_full	0	-573.887623	8.938357	0.000000	0.55937	32.610260	0.000000	False	log
model_reduced	1	-575.013870	2.891536	1.126247	0.44063	32.295276	4.011291	False	log

Based on WAIC rankings, the full sampling model is ranked higher but only due to a small difference in WAIC.

Model 4: Bayesian Averaging (Full Sampling & Reduced Sampling)

- Result: {'Precision': 0.102, 'Accuracy': 0.701, 'Recall': 0.943}

In [46]:
```
# Model function

def lm_full(trace, intercept = 0, hypertension = 0):
    shape = trace['α'].shape
    x = np.linspace(min(X_train['age']), max(X_train['age']), shape[1])
    x = np.array(x)
    z = np.broadcast_to(x, shape)

    return (1 / (
      1
      + np.exp(
          -(
              trace['α']*intercept
              + trace["β"][:,:,1] * z
              + trace["β"][:,:,2] * hypertension
              + trace["β"][:,:,6] * np.mean(X_train['avg_glucose_level'])
              + trace["β"][:,:,7] * np.mean(X_train['bmi'])
          )
      )
    ))
```

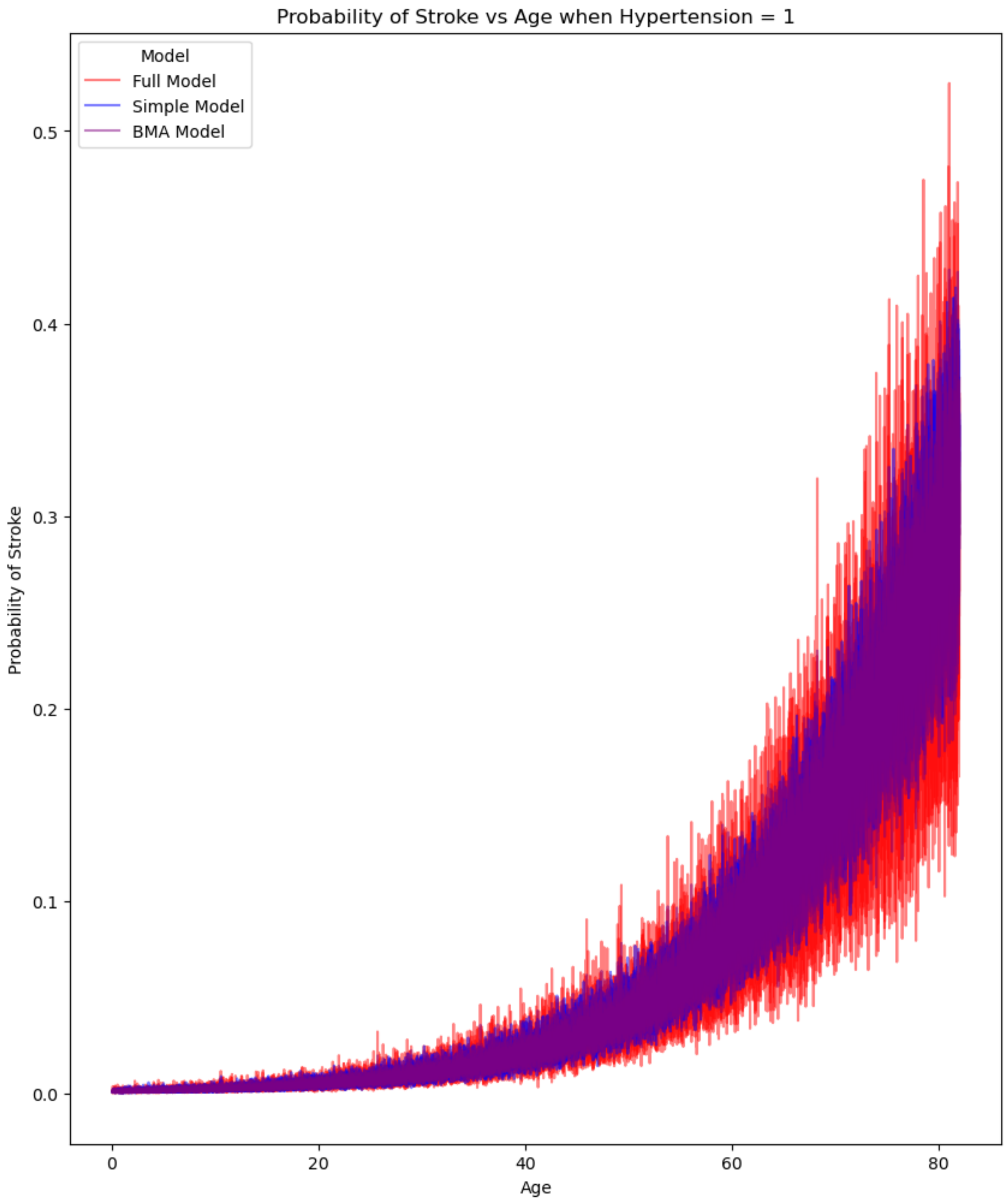
In [47]:
```
# Model function

def lm_reduced(trace, intercept = 0, hypertension = 0):
    shape = trace['α'].shape
    x = np.linspace(min(X_train['age']), max(X_train['age']), shape[1])
    x = np.array(x)
    z = np.broadcast_to(x, shape)

    return (1 / (
      1
      + np.exp(
          -(
              trace['α']*intercept
              + trace["β"][:,:,0] * z
              + trace["β"][:,:,1] * hypertension
          )
      )
    ))
```

In [48]:
```
def plot_posterior_predictive(weights, full_trace, reduced_trace, hypertension_value, plot_title):
    plt.figure(figsize = (10,12))

    shape = full_trace.posterior['α'].shape
    x = np.linspace(min(X_train['age']), max(X_train['age']), shape[1])
    for j in range(3):
        out =[]
        for i in range(4):
            if i == 0:
                if j == 0:
                    out.append(lm_full(full_trace.posterior, intercept=1, hypertension = hypertension_value)[i,:])
                    plt.plot(x,out[i], color = 'red', alpha = 0.5, label = 'Full Model')
                elif j == 1:
                    out.append(lm_reduced(reduced_trace.posterior, intercept=1, hypertension = hypertension_value)[i,:]
                    plt.plot(x,out[i], color = 'blue', alpha = 0.5, label = 'Simple Model')
                else:
                    out.append(weights[0]*lm_full(full_trace.posterior, intercept=1, hypertension = hypertension_value)
                               + weights[1]*lm_reduced(reduced_trace.posterior, intercept=1, hypertension = hypertensio
                    plt.plot(x,out[i], color = 'purple', alpha = 0.5, label = 'BMA Model')
            else:
                if j == 0:
                    out.append(lm_full(full_trace.posterior, intercept=1, hypertension = hypertension_value)[i,:])
                    plt.plot(x,out[i], color = 'red', alpha = 0.5)
                elif j == 1:
                    out.append(lm_reduced(reduced_trace.posterior, intercept=1, hypertension = hypertension_value)[i,:]
                    plt.plot(x,out[i], color = 'blue', alpha = 0.5)
                else:
                    out.append(weights[0]*lm_full(full_trace.posterior, intercept=1, hypertension = hypertension_value)
                               + weights[1]*lm_reduced(reduced_trace.posterior, intercept=1, hypertension = hypertensio
                    plt.plot(x,out[i], color = 'purple', alpha = 0.5)
    plt.title(plot_title)
    plt.xlabel('Age')
    plt.ylabel('Probability of Stroke')
    plt.legend(title = 'Model')

def plot_posterior_precitive_using_mean(weights, full_trace, reduced_trace, hypertension_value, plot_title):
    x_new = np.linspace(min(X_train['age']), max(X_train['age']), 100)
    α_l_post = full_trace.posterior['α'].mean(axis=1).mean(axis=0).to_numpy()
    β_l_post = full_trace.posterior['β'].mean(axis=1).mean(axis=0).to_numpy()
    y_l_post = α_l_post + β_l_post[1] * x_new + (β_l_post[2] * hypertension_value) + \
               β_l_post[6]*np.mean(X_train['avg_glucose_level']) + \
               β_l_post[7]*np.mean(X_train['bmi'])
    y_l_post = (1 / (1 + np.exp(-(y_l_post))))
    plt.figure(figsize = (10,10))
    plt.plot(x_new, y_l_post, 'C1', label='Full Model')
    α_p_post = reduced_trace.posterior['α'].mean(axis=1).mean(axis=0).to_numpy()
    β_p_post = reduced_trace.posterior['β'].mean(axis=1).mean(axis=0).to_numpy()
    y_p_post = α_p_post + β_p_post[0] * x_new + (β_l_post[1] * hypertension_value)
    y_p_post = (1 / (1 + np.exp(-(y_p_post))))
    plt.plot(x_new, y_p_post, 'C2', label='Simple Model')
    y_bma_post = (1-w)*y_p_post+w*y_l_post

    plt.plot(x_new, y_bma_post, 'C3', label='BMA Model')
    plt.title(plot_title)
    plt.xlabel('Age')
    plt.ylabel('Probability of Stroke vs Age')
    plt.legend(title = 'Model')
```

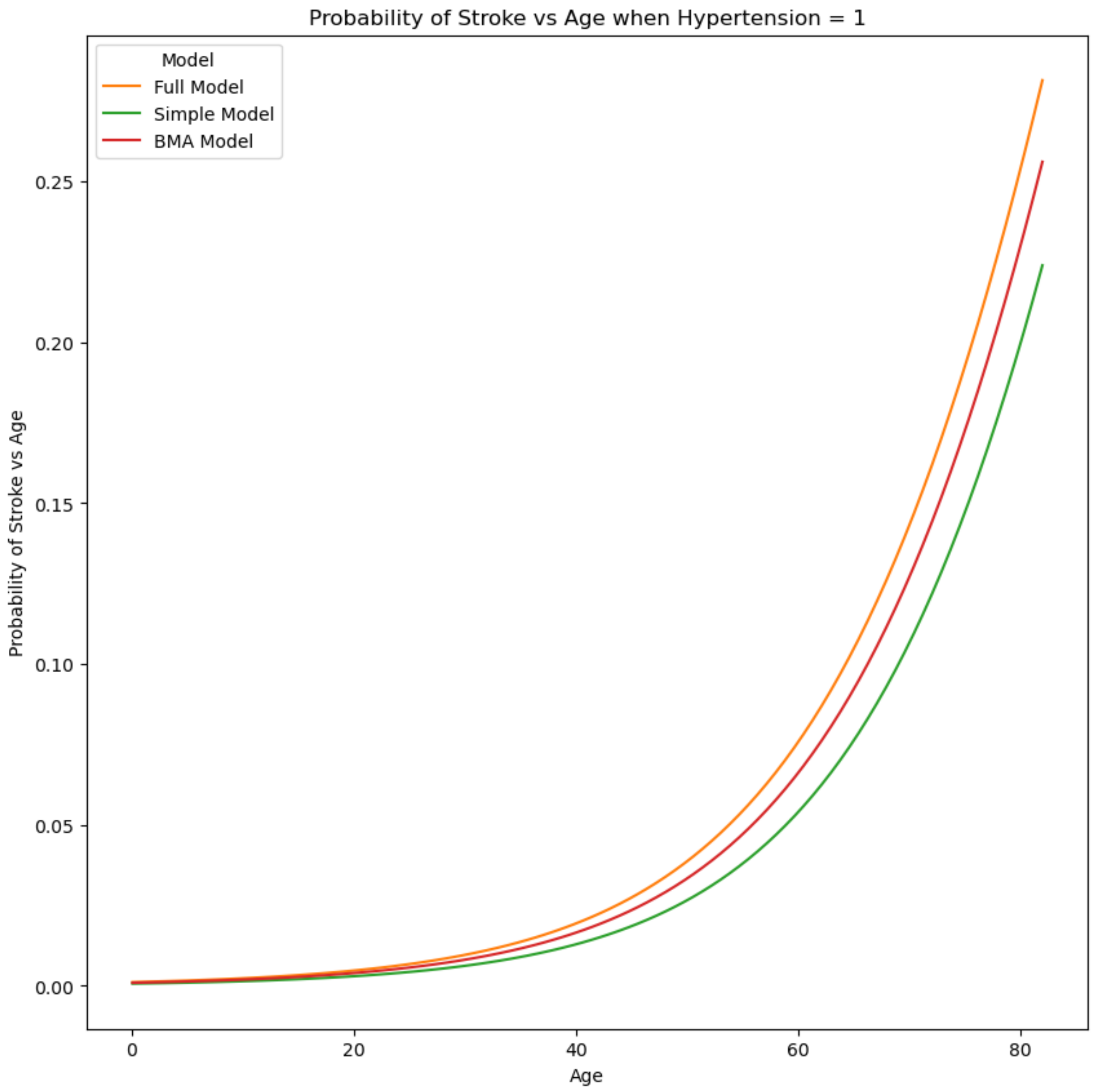
In [49]:
```
def plot_full_posterior_predictive(ax, hypertension_value):
    shape = full_trace.posterior['α'].shape
    x = np.linspace(min(X_train['age']), max(X_train['age']), shape[1])
    out =[]
    for i in range(4):
        out.append(lm_full(full_trace.posterior, intercept = 1, hypertension = hypertension_value)[i,:])
        ax.plot(x,out[i], color = 'red', alpha = 0.5)
    ax.title.set_text('Full Model')


def plot_reduced_posterior_predictive(ax, hypertension_value):
    shape = reduced_trace.posterior['α'].shape
    x = np.linspace(min(X_train_reduced['age']), max(X_train_reduced['age']), shape[1])
    out =[]
    for i in range(4):
        out.append(lm_reduced(reduced_trace.posterior, intercept = 1, hypertension = hypertension_value)[i,:])
        ax.plot(x,out[i], color = 'blue', alpha = 0.5)
    ax.title.set_text('Reduced Model')

def plot_bma_posterior_predictive(ax, hypertension_value):
    shape = full_trace.posterior['α'].shape
    x = np.linspace(min(X_train['age']), max(X_train['age']), shape[1])
    out =[]
    for i in range(4):
        out.append(weights[0]*lm_full(full_trace.posterior, intercept = 1, hypertension = hypertension_value)[i,:]
                   + weights[1]*lm_reduced(reduced_trace.posterior, intercept = 1, hypertension = hypertension_value)[i
        ax.plot(x,out[i], color = 'purple', alpha = 0.5)
    ax.title.set_text('BMA Model')
```

The following plots depict the probability of stroke vs. age, fixing hypertension as 1:

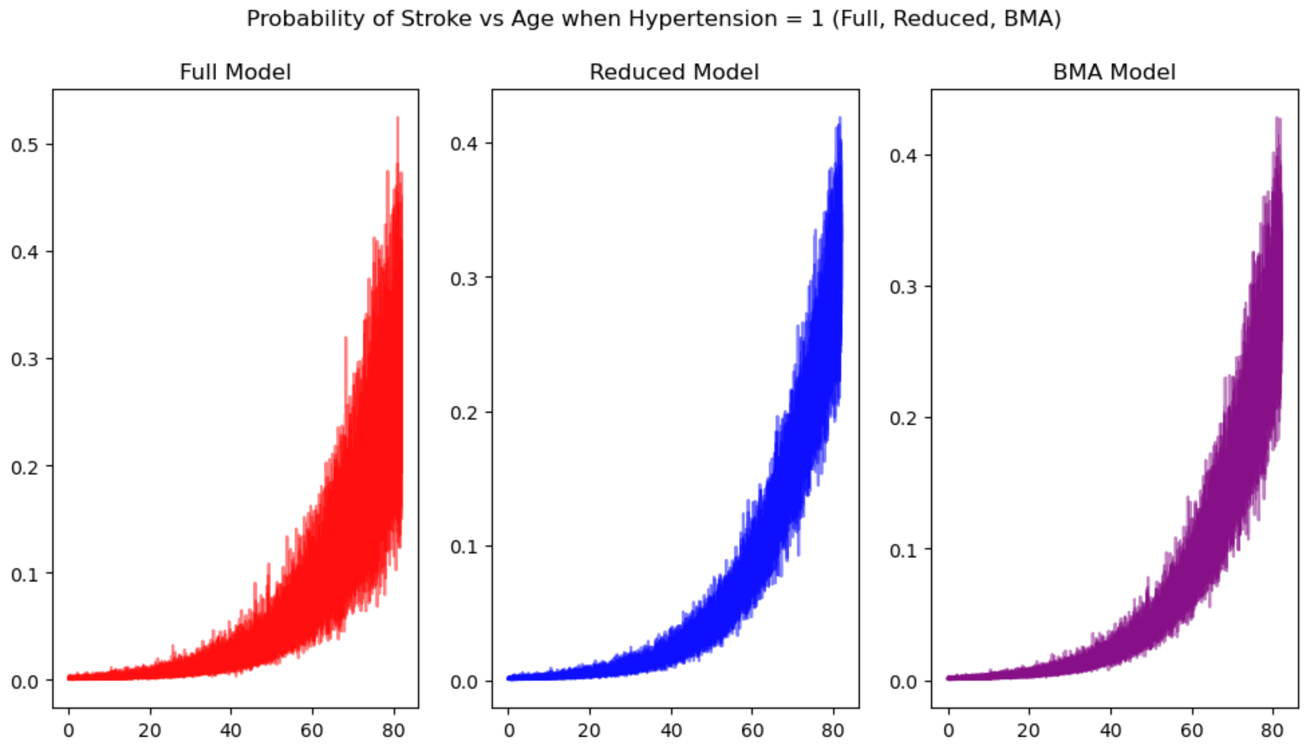
In [50]:
```
# use WAIC values as weights for BMA
weights = cmp_waic['weight']

# plot of the probability of stroke vs. age for the Bayesian model average
plot_posterior_predictive(weights, full_trace, reduced_trace, 1, 'Probability of Stroke vs Age when Hypertension = 1')
```



In [51]:
```
# Computing predictions by combining the models using the WAIC weights
w = cmp_waic.loc['model_full','weight']
weights = [w, 1-w]

# plot of models with bma
plot_posterior_precitive_using_mean(weights, full_trace, reduced_trace, 1, 'Probability of Stroke vs Age when Hypertens
```



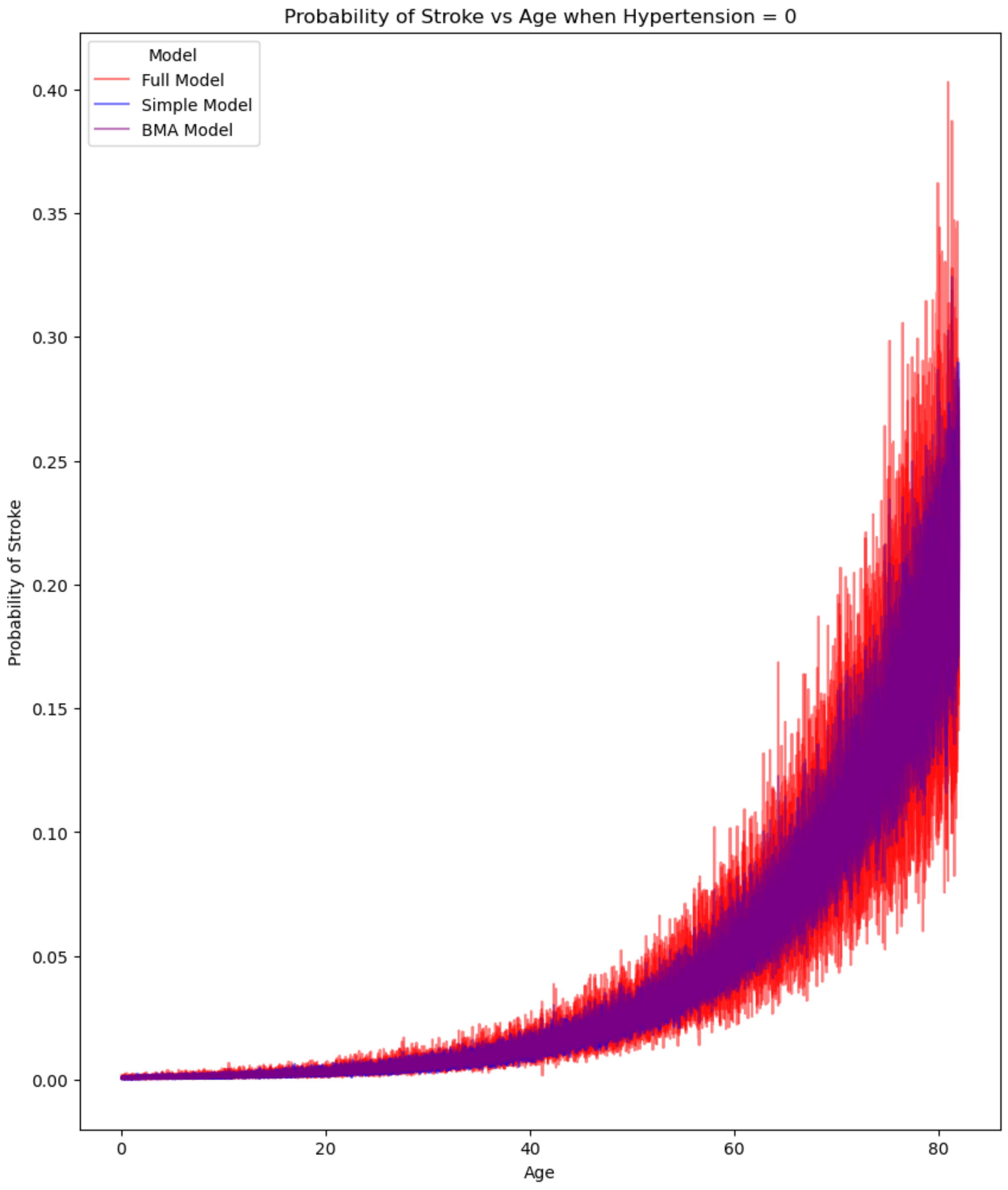
In [52]:
```
fig, ax = plt.subplots(nrows = 1, ncols = 3, figsize = (12, 6))

i = 0
for col in ax:
    if i == 0:
        plot_full_posterior_predictive(
            ax = col,
            hypertension_value = 1
        )
    elif i == 1:
        plot_reduced_posterior_predictive(
            ax = col,
            hypertension_value = 1
        )
    else:
        plot_bma_posterior_predictive(
            ax = col,
            hypertension_value = 1
        )

    i += 1

plt.suptitle('Probability of Stroke vs Age when Hypertension = 1 (Full, Reduced, BMA)')
plt.show()
```



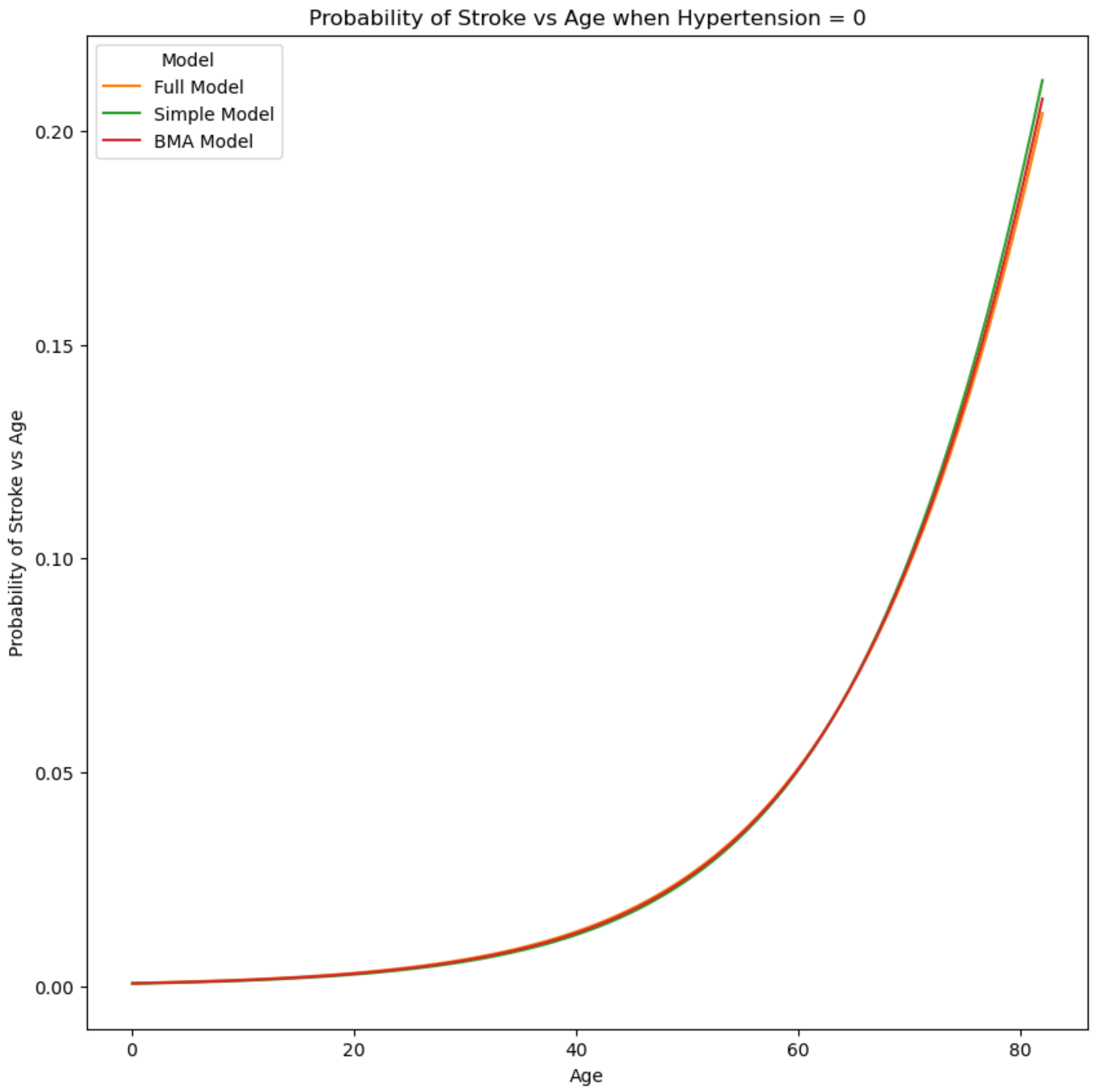
The plots above show that the full model has more variability than the reduced one when hypertension is 1.

The following plots depict the probability of stroke vs. age, fixing hypertension as 0:

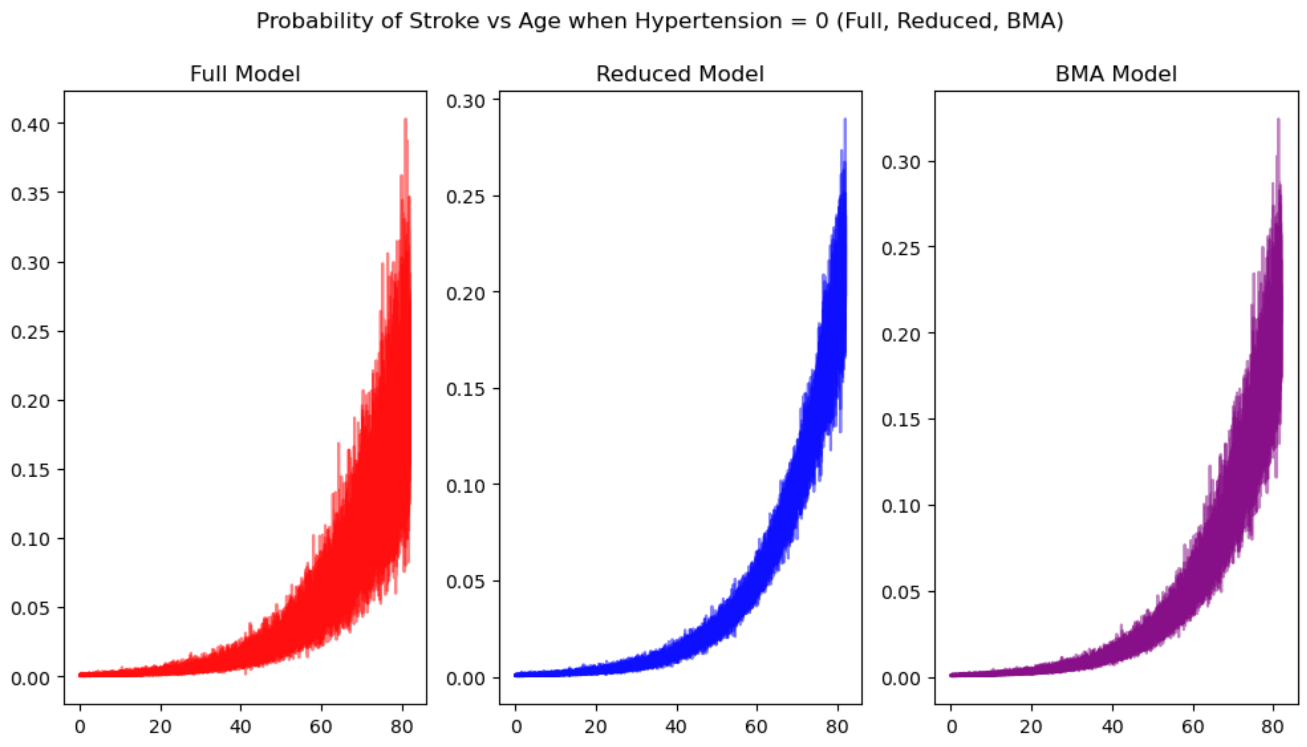
In [53]:
```
# use WAIC values as weights for BMA
weights = cmp_waic['weight']

# plot of the probability of stroke vs. age for the Bayesian model average

plot_posterior_predictive(weights, full_trace, reduced_trace, 0, 'Probability of Stroke vs Age when Hypertension = 0')
```



In [54]:
```
# Computing predictions by combining the models using the WAIC weights
w = cmp_waic.loc['model_full','weight']
weights = [w, 1-w]
# Plot of models with bma
plot_posterior_precitive_using_mean(weights, full_trace, reduced_trace, 0, 'Probability of Stroke vs Age when Hypertens
```



In [55]:
```
fig, ax = plt.subplots(nrows = 1, ncols = 3, figsize = (12, 6))

i = 0
for col in ax:
    if i == 0:
        plot_full_posterior_predictive(
            ax = col,
            hypertension_value = 0
        )
    elif i == 1:
        plot_reduced_posterior_predictive(
            ax = col,
            hypertension_value = 0
        )
    else:
        plot_bma_posterior_predictive(
            ax = col,
            hypertension_value = 0
        )

    i += 1

plt.suptitle('Probability of Stroke vs Age when Hypertension = 0 (Full, Reduced, BMA)')
plt.show()
```

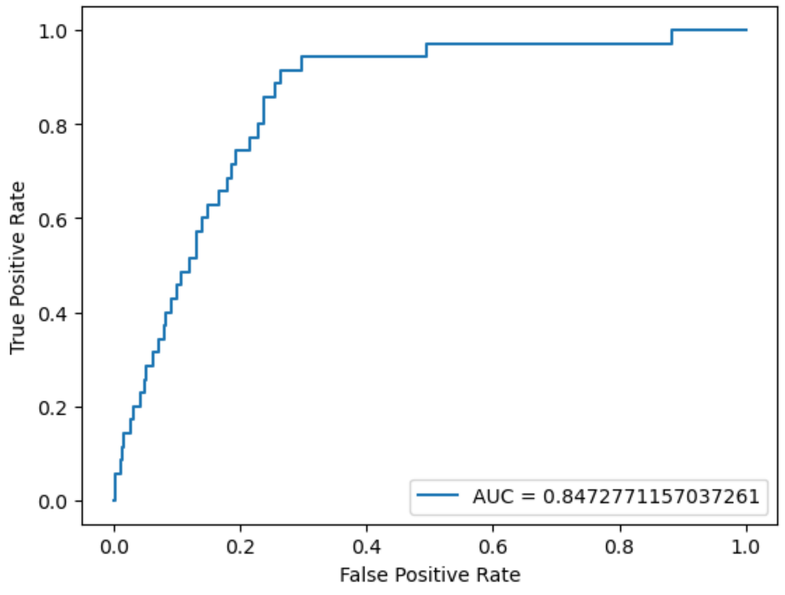


The plots above show that the full model has more variability than the reduced one when hypertension is 0.

In [56]:
```python
a = reduced_trace.posterior['α'].mean(axis=1).mean(axis=0).to_numpy()
b = reduced_trace.posterior['β'].mean(axis=1).mean(axis=0).to_numpy()

X_test_reduced = X_test[["age", "hypertension"]]

m = a + X_test_reduced.dot(b)
p_reduced = inv_logit(m)

a = full_trace.posterior['α'].mean(axis=1).mean(axis=0).to_numpy()
b = full_trace.posterior['β'].mean(axis=1).mean(axis=0).to_numpy()

m = a + X_test.dot(b)
p_full = inv_logit(m)

p_bma = w*p_full + (1-w)*p_reduced

t_star_bma = calculate_tstar(p_bma, y_hat, y_test)
print('Optimal Threshold:', t_star_bma)
sum((p>=t_star_bma).astype(int) == y_test)/len(y_test)
```

```
Optimal Threshold: 0.04
```
Out[56]:
```
0.6863543788187373
```

In [57]:
```python
# ROC Curve

fpr, tpr, _ = metrics.roc_curve(y_test,  p_bma)
auc = metrics.roc_auc_score(y_test, p_bma)

plt.plot(fpr, tpr, label = "AUC = "+str(auc))
plt.ylabel('True Positive Rate')
plt.xlabel('False Positive Rate')
plt.legend(loc=4)
plt.show()
```



The BMA model has an Area Under the Curve (AUC) value of 0.847

In [58]:
```
# Confusion Matrix

cm = metrics.confusion_matrix(y_test, (p_bma>=t_star_bma).astype(int))
print(cm)

get_rates(cm)
```

```
[[655 292]
 [  2  33]]
```

Out[58]:
```
{'Precision': 0.102, 'Accuracy': 0.701, 'Recall': 0.943}
```

Final Result

- Full Sampling: {'Precision': 0.105, 'Accuracy': 0.713, 'Recall': 0.943, 'AUC': 0.854}
- Reduced Sampling: {'Precision': 0.097, 'Accuracy': 0.686, 'Recall': 0.943, 'AUC': 0.836}
- BMA: {'Precision': 0.102, 'Accuracy': 0.701, 'Recall': 0.943, 'AUC': 0.847}

In [59]:
```
model_results = [
    {
        'precision': 0.105,
        'accuracy': 0.713,
        'recall': 0.943,
        'AUC': 0.854
    },
    {
        'precision': 0.097,
        'accuracy': 0.686,
        'recall': 0.943,
        'AUC': 0.836
    },
    {
        'precision': 0.102,
        'accuracy': 0.701,
        'recall': 0.943,
        'AUC': 0.847
    }
]
result_df = pd.DataFrame(model_results)
result_df.index = ['Full Sampling', 'Reduced Sampling', 'BMA']
result_df
```

Out[59]:

	precision	accuracy	recall	AUC
Full Sampling	0.105	0.713	0.943	0.854
Reduced Sampling	0.097	0.686	0.943	0.836
BMA	0.102	0.701	0.943	0.847

The BMA model is able to balance variability with good accuracy, recall, and AUC values.

```
In [ ]:
```