farina_nomin_project_final

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[1]:
```
import numpy as np
import pandas as pd

import pymc as pm
from scipy.stats import halfnorm

import os

import seaborn as sns
import matplotlib.pyplot as plt
import arviz as az
```

1 Bayesian Data Analysis: USA College Completion Analysis

DS&AI: 3rd year's Semestral project

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1.1 Description of data and exploratory analysis

The chosen dataset contains records of various data related to USA colleges/universities. There are more than 60 columns present between categorical information and numerical statistics.

The required tasks to be done for the following project are as follows: - At least one hypothesis test for each student, discussing: - the choice of the prior and likelihood; - convergence diagnostics; - prior sensitivity (i.e., re-run with a different and reasonable prior); - posterior predictive checks; - conclusions based on the posterior, including a meaningful definition of rope.

- At least a hierarchical model presenting:
  - the choice of the prior and likelihood;
  - the **posterior distribution of the mean** for a specific group;
  - the **predictive distribution for the same group**, i.e., the probability distribution for a future measure for that group. The predictive distribution has to be computed by a cycle implemented by you, without using pymc3 functions such as sample_posterior_predictive
  - the posterior distribution of a novel group, for which there are currently not yet observation(for instance, a hospital not yet included in the trial).
- At least a regression model including:

  - choice of prior and likelihood
  - convergence diagnostics
  - predictive distribution for an observation of the test set.

What we decided to focus on from the dataset are the following two information: * Graduation rate: represented by two features, *grad_100_value* and *grad_150_value*, respectively containing the percentage of students that completed the institution within either 100% or 150% of "normal" graduation time. The one we decide to use is the 150 one. * SAT score connection to graduation rate: the dataset contains a column called *med_sat_value* which represents the median SAT score of the institution

[2]:
```python
df = pd.read_csv('cc_institution_details.csv').drop(columns=['index'])
df.head()
```

[2]:
```
   unitid                         chronname        city    state   level  \
0  100654               Alabama A&M University      Normal  Alabama  4-year
1  100663  University of Alabama at Birmingham  Birmingham  Alabama  4-year
2  100690                   Amridge University  Montgomery  Alabama  4-year
3  100706  University of Alabama at Huntsville  Huntsville  Alabama  4-year
4  100724             Alabama State University  Montgomery  Alabama  4-year

                  control                                            basic  \
0                  Public  Masters Colleges and Universities--larger prog…
1                  Public  Research Universities--very high research acti…
2  Private not-for-profit           Baccalaureate Colleges--Arts & Sciences
3                  Public  Research Universities--very high research acti…
4                  Public  Masters Colleges and Universities--larger prog…

  hbcu flagship     long_x  …  vsa_grad_after6_transfer  \
0    X      NaN -86.568502  …                      36.4
1  NaN      NaN -86.809170  …                       NaN
2  NaN      NaN -86.174010  …                       NaN
3  NaN      NaN -86.638420  …                       0.0
4    X      NaN -86.295677  …                       NaN

  vsa_grad_elsewhere_after6_transfer  vsa_enroll_after6_transfer  \
0                                5.6                        17.2
1                                NaN                         NaN
2                                NaN                         NaN
3                                0.0                         0.0
4                                NaN                         NaN

   vsa_enroll_elsewhere_after6_transfer  \
0                                  11.1
1                                   NaN
2                                   NaN
3                                   0.0
4                                   NaN
```

```
                                              similar  state_sector_ct  \
0  232937|100724|405997|113607|139533|144005|2285…               13
1  196060|180461|201885|145600|209542|236939|1268…               13
2  217925|441511|205124|247825|197647|221856|1353…               16
3  232186|133881|196103|196413|207388|171128|1900…               13
4  100654|232937|242617|243197|144005|241739|2354…               13

   carnegie_ct  counted_pct  nicknames  cohort_size
0          386      99.7|07        NaN        882.0
1          106      56.0|07        UAB       1376.0
2          252     100.0|07        NaN          3.0
3          106      43.1|07        UAH        759.0
4          386      88.0|07        ASU       1351.0

[5 rows x 62 columns]
```

[3]:
```python
df.shape
```

[3]:
```
(3798, 62)
```

As mentioned already, what we wanted to keep as information are the college's name, state, graduation rate and the median SAT score. For this reason we created another dataframe containing only the neccessary data.

[4]:
```python
partial_df = df[['chronname', 'state', 'grad_150_value',
                 'med_sat_value']]
partial_df.shape
```

[4]:
```
(3798, 4)
```

At first we checked the presence of null values. Since there are several tasks that require either one variable both, for tasks that require graduation rate, we will drop only those rows keeping also the ones where the median SAT value is null, whereas when the latter will be needed (for the regression model), we will also drop the rows having null values of SAT. We decided not to impute the data since it is real colleges data that we analyze, therefore imputing those data based on a variety of information that differ such as state, city and so on, we decided to just drop those rows (having also a substantial amount of rows even after elimination)

[5]:
```python
print(partial_df.isnull().sum())
print('-'*50)
print(round((partial_df.isnull().sum() / partial_df.shape[0])*100, 2))
```

```
chronname            0
state                0
grad_150_value     331
med_sat_value     2461
dtype: int64
--------------------------------------------------
```

```
chronname          0.00
state              0.00
grad_150_value     8.72
med_sat_value     64.80
dtype: float64
```

[6]:
```
grad_150_df = partial_df.dropna(subset=['grad_150_value'])
print("After removing null values of grad_150_value: ", grad_150_df.shape)

median_sat_values_df = grad_150_df.dropna(subset=['med_sat_value'])
print("After removing null values of both grad_150_value and med_sat_value: ",␣
  ↪median_sat_values_df.shape)
```

```
After removing null values of grad_150_value:  (3467, 4)
After removing null values of both grad_150_value and med_sat_value:  (1319, 4)
```

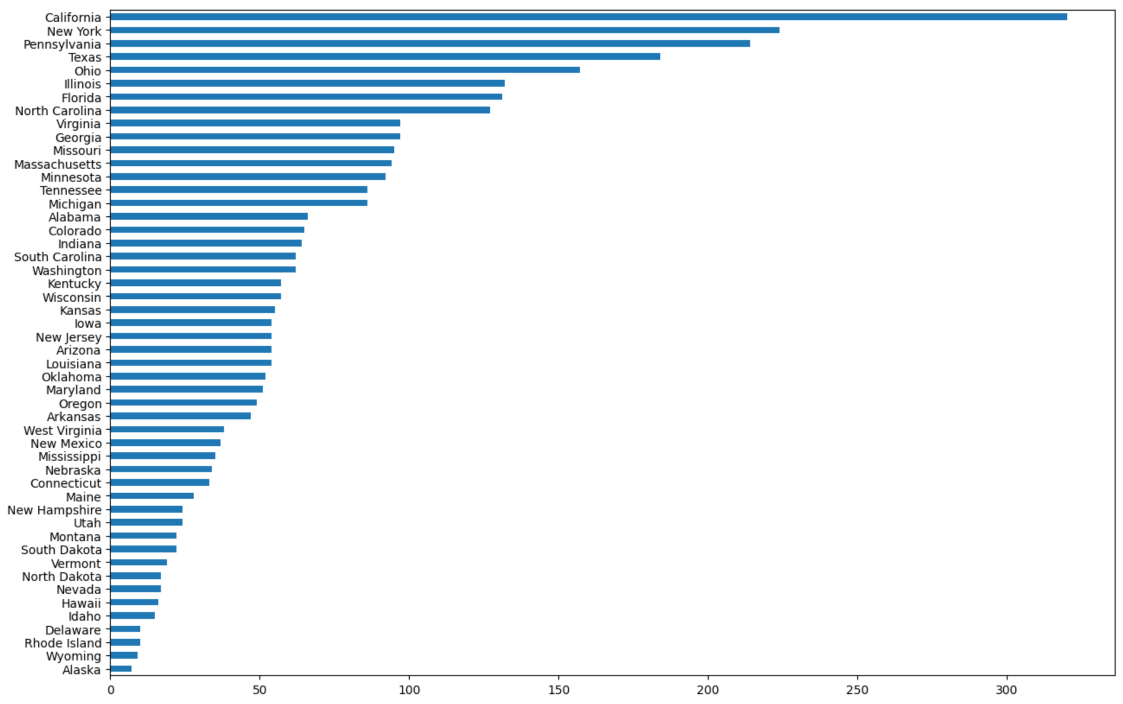
Since we want to analyze the states, we remove District of Columbia from the dataset and we'll consider only the records from the official states

[7]:
```
grad_150_df = grad_150_df[grad_150_df['state'] != 'District of Columbia']
```

Below the counts for each state, in order to understand for further analysis, how many samples are available for the Hierarchical modelling part. Except for a few, all the states have a sufficient amount of observable data which can be used for eventual sampling and so on.

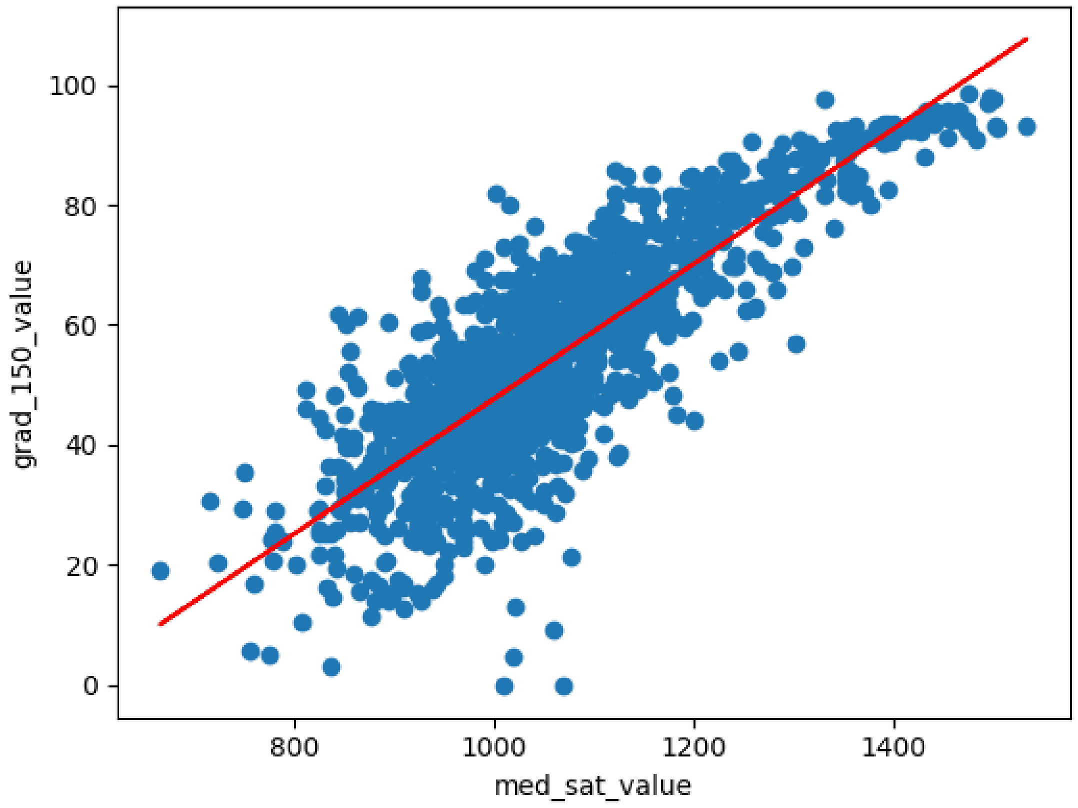
[8]:
```
plt.figure(figsize=(15, 10))
state_counts = grad_150_df['state'].value_counts().sort_values(ascending=True)
state_counts.plot(kind='barh')
```

[8]:
```
<Axes: >
```



For the same reasons as above, we decided to plot the scatter plot for the two numerical variables of graduation and median SAT score. It can be clearly seen that the correlation is pretty strong, therefore we expect to be able to model properly this relation and being able to predict well testing data.

[9]:
```python
med_sat_values = median_sat_values_df['med_sat_value'].values
grad_values = median_sat_values_df['grad_150_value'].values

plt.scatter(med_sat_values, grad_values)

m, b = np.polyfit(med_sat_values, grad_values, 1)
plt.plot(med_sat_values, m*med_sat_values + b, color='red')

plt.xlabel('med_sat_value')
plt.ylabel('grad_150_value')

plt.show()
```



1.2 Hypothesis test: Graduation rate between New York and California

During a brief exploratory analysis performed beforehand, we noticed that New York and California are the two states with the highest number of samples, therefore we decided that it would be a meaningful comparison considering that the model would be pretty robust. By means of a 2 sample hypothesis test, we want to compare if there is a significant difference between the graduation rate withing the two states. In order to do so, we perform a hypothesis t-test formulated as:

$$H_0 : \mu_{\text{new-york}} = \mu_{\text{california}}$$
$$H_1 : \mu_{\text{new-york}} \neq \mu_{\text{california}}$$

[10]:
```
newyork_data = grad_150_df[grad_150_df['state'] == 'New York']
california_data = grad_150_df[grad_150_df['state'] == 'California']
```

1.2.1 Choice of prior and likelihood

Prior for $\mu_{\text{new-york}}$ and $\mu_{\text{california}}$ As per national reports, we can assume the mean graduation rate in the USA to revolve around 55%, with standard deviation that can be chosen around 7.5 since there are states that get to just 40% and others that can get up to 70%. We will setup our prior believes on these data.

The mean graduation rate of the population lies in (40, 70); we interpret this as an interval of +-2σ. We will be assigning the same prior to both the states, so that neither one will be fabored over another

$$\mu_{\text{new-york}} \sim N(55, 7.5)$$
$$\mu_{\text{california}} \sim N(55, 7.5)$$

Prior for $\sigma_{\textbf{new-york}}$ and $\sigma_{\textbf{california}}$ Assuming the same standard deviation for both the states, we tune the half-normal prior in order to get a median close to the std value, being 7.5. The value we obtained is 11

$$\sigma_{\text{new-york}} \sim HN(11)$$
$$\sigma_{\text{california}} \sim HN(11)$$

[11]:
```
pd.DataFrame(halfnorm.rvs(scale=11, size=10000)).describe()
```

[11]:
```
                  0
count  10000.000000
mean       8.827791
std        6.695193
min        0.005882
25%        3.477595
50%        7.394744
75%       12.885716
max       43.506226
```

Likelihood

- Assuming a Gaussian distribution of the observations we have the following priors, where the parameters of the two distributions are the priors we defined above

$$\vec{y}_{new-york} \sim N(\mu_{\text{new-york}}, \sigma_{\text{new-york}})$$

$$\vec{y}_{california} \sim N(\mu_{\text{california}}, \sigma_{\text{california}})$$

* By means of this we already created the first layer of the hierarchy information sharing, where we model a lower level information with the knowledge about a higher level prior. * In this case vector notation is used to make it clear that there are array of measures, and not just one single observation. These vectors represent the data of New York and California

- With this, we can build the full probabilistic model by combining prior and likelihood in the following way:

$$\begin{aligned}
\mu_{\text{new-york}} &\sim N(55, 7.5)\\
\sigma_{\text{new-york}} &\sim HN(11)\\
\vec{y}_{\text{new-york}} &\sim N(\mu_{\text{new-york}}, \sigma_{\text{new-york}})\\
\\
\mu_{\text{california}} &\sim N(55, 7.5)\\
\sigma_{\text{california}} &\sim HN(11)\\
\vec{y}_{\text{california}} &\sim N(\mu_{\text{california}}, \sigma_{\text{california}})
\end{aligned}$$

1.2.2 Model

- Having now the complete information about how the data are assumed to be distributed and which distributions do they follow, we can implement the model using the pymc3 library.
- In order to see if there is proof of significant difference between the mean rates of the two states involved, the difference itself needs to be computed, which can be done on pymc using a *Deterministic* variable, because it can be considered as a deterministic function of two different variables/parameters.

$$\mu_{\text{new-york}} - \mu_{\text{california}}$$

- The information regarding this deterministic difference will be stored in the computed trace

[12]:
```
# Our defined priors
if os.path.exists('trace_ht_1_correct_prior.nc'):
    trace_ht_1_correct_prior = az.from_netcdf('trace_ht_1_correct_prior.nc')
else:
    with pm.Model() as model_ht_1_correct_prior:
        # Priors
        mu_newyork          = pm.Normal     ('mu_newyork',   mu = 55,   sigma = 7.
 ↪5)
        mu_california       = pm.Normal     ('mu_california', mu = 55,   sigma =␣
 ↪7.5)
        sigma_newyork       = pm.HalfNormal ('sigma_newyork',   sigma=11)
        sigma_california    = pm.HalfNormal ('sigma_california', sigma=11)

        # Likelihood
        y_newyork = pm.Normal  ('y_new_york',   mu=mu_newyork,          ␣
 ↪sigma=sigma_newyork,        observed=newyork_data['grad_150_value'])
        y_california = pm.Normal  ('y_california',   mu=mu_california,␣
 ↪sigma=sigma_california, observed= california_data['grad_150_value'])

        diff_of_means = pm.Deterministic ('diff_of_means', mu_newyork -␣
 ↪mu_california)


        trace_ht_1_correct_prior    = pm.sample(return_inferencedata=True)
        az.to_netcdf(trace_ht_1_correct_prior, 'trace_ht_1_correct_prior.nc')
```

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

<IPython.core.display.HTML object>

<IPython.core.display.HTML object>

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

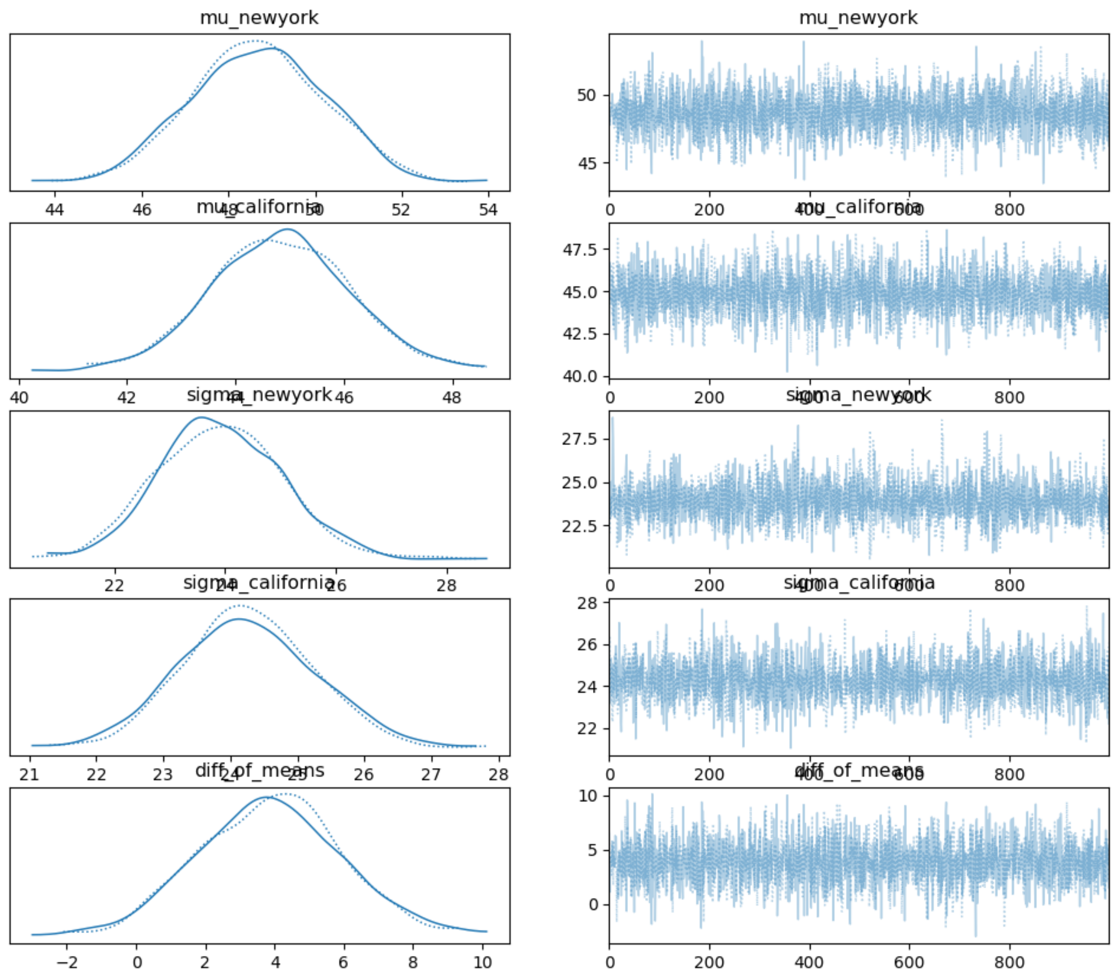
1.2.3 Convergence diagnostics

In order to understand the convergence of our model or a lack of, we can analyze some factors available from the trace such as: - Density plots: the various lines that can be seen from the leften side of the plot are smooth and converging towards the same bell-shaped distributions, indicating a good convergence - Trace plots: the righten side of the plot shows the values that were samples throughout the time. There is a good converence if these resemble "fuzzy caterpillars", which they do. If there were some predisposition towards oversampling some values and ignoring others, it woudl've been a problem, but here the situation seems to be adequate - r_hat: the closer they are to 1, the better the convergence is. In our case all the values are exactly 1, confirming convergence once again - ess_bulk / ess_tail: representing the effective sample size for the bulk and the tail of the distribution, these values can tell us about the chain exploration of the posterior space. If these two numbers are high, it means that the model was able to explore succesfully the whole posterior space, as is our case

The values for mean and standard deviation of the various parameters are pretty lower than expected, but that didn't influence much the finalr results.

```
[13]: az.plot_trace(trace_ht_1_correct_prior);
```

```
/usr/local/lib/python3.10/dist-packages/arviz/utils.py:184:
NumbaDeprecationWarning: The 'nopython' keyword argument was not supplied to the
'numba.jit' decorator. The implicit default value for this argument is currently
False, but it will be changed to True in Numba 0.59.0. See
https://numba.readthedocs.io/en/stable/reference/deprecation.html#deprecation-
of-object-mode-fall-back-behaviour-when-using-jit for details.
  numba_fn = numba.jit(**self.kwargs)(self.function)
```



[14]:
```
az.summary(trace_ht_1_correct_prior, hdi_prob=0.95)
```

```
/usr/local/lib/python3.10/dist-packages/arviz/utils.py:184:
NumbaDeprecationWarning: The 'nopython' keyword argument was not supplied to the
'numba.jit' decorator. The implicit default value for this argument is currently
False, but it will be changed to True in Numba 0.59.0. See
https://numba.readthedocs.io/en/stable/reference/deprecation.html#deprecation-
of-object-mode-fall-back-behaviour-when-using-jit for details.
  numba_fn = numba.jit(**self.kwargs)(self.function)
```

[14]:
```
                    mean     sd  hdi_2.5%  hdi_97.5%  mcse_mean  mcse_sd  \
mu_newyork        48.686  1.561    45.527     51.467      0.026    0.018
mu_california     44.826  1.287    42.115     47.180      0.022    0.016
sigma_newyork     23.926  1.138    21.731     26.099      0.019    0.014
sigma_california  24.259  1.001    22.289     26.138      0.017    0.012
diff_of_means      3.860  2.057     0.137      7.941      0.032    0.025
```

```
                   ess_bulk  ess_tail  r_hat
mu_newyork           3680.0    1660.0    1.0
mu_california        3405.0    1491.0    1.0
sigma_newyork        3646.0    1450.0    1.0
sigma_california     3301.0    1630.0    1.0
diff_of_means        4167.0    1640.0    1.0
```

1.2.4 Prior sensitivity

In Bayesian analysis the prior is an important part of the model, and choosing wrong priors can destabilize the model making it not converge, therefore weak. To understand the sensitivity of the model towards the prior choice, we decided to choose other values of the prior. These values have a higher mean for the two states, but also a higher sigma, allowing values of the mean to range from 40 to 80.

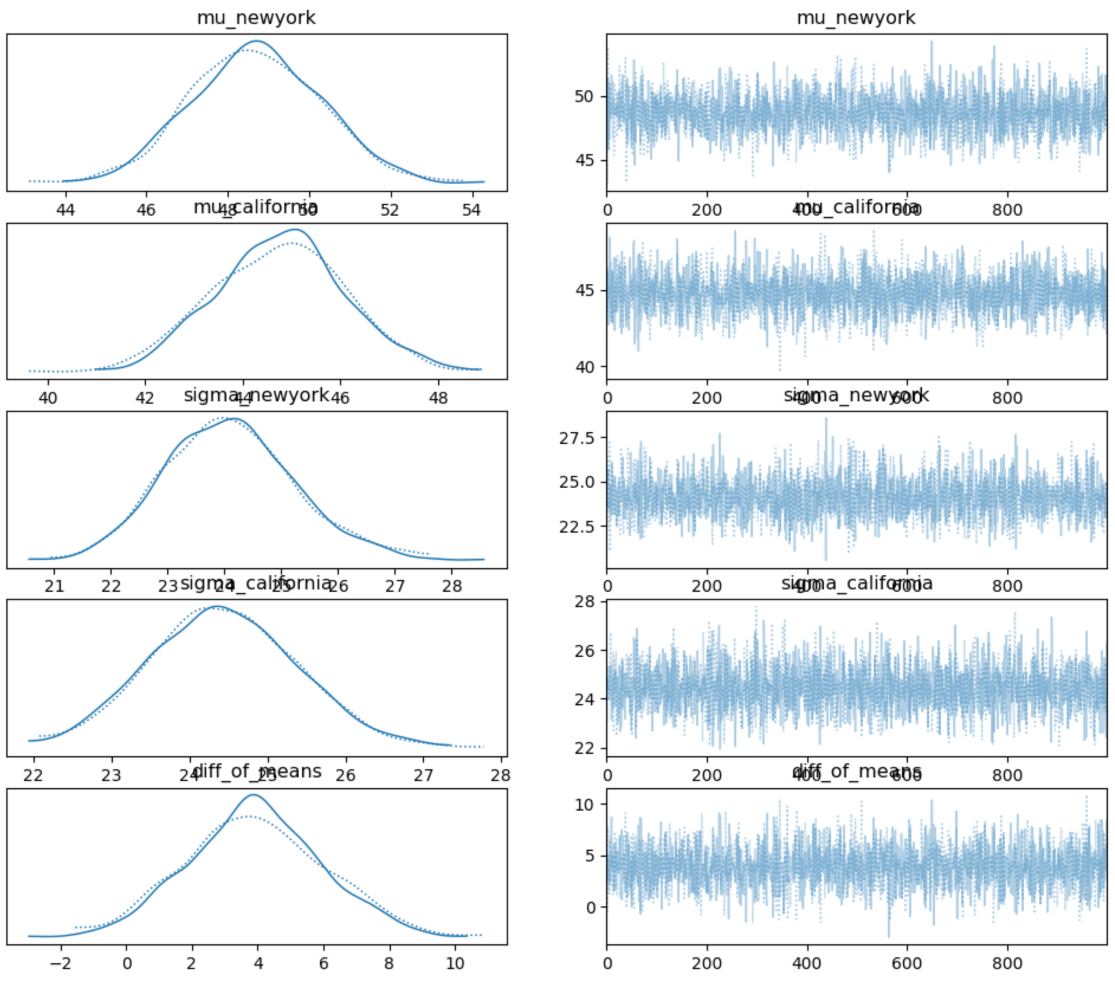
By doing so we confirmed the model's ability to converge, analyzing the plots of the trace and the summary dataframe. * Densities for the 5 parameters end up towards the same shape and mean values, with the different chains overlapping one on another * The traces show the homogeneous sampling of the same range of data, with no evident peaks or drifts * r_hat values are all equal to 1, as before * High values of ess_bulk and ess_tail are indicating good space exploration

```
[15]: # Checking for prior sensitivity by assuming a pretty different priors
      if os.path.exists('trace_ht_1_different_prior.nc'):
          trace_ht_1_different_prior = az.from_netcdf('trace_ht_1_different_prior.nc')
      else:
          with pm.Model() as model_ht_1_different_prior:
              mu_newyork          = pm.Normal     ('mu_newyork',  mu = 60,  sigma = 10)
              mu_california       = pm.Normal     ('mu_california', mu = 60,  sigma =␣
        ↪10)
              sigma_newyork       = pm.HalfNormal ('sigma_newyork',  sigma=25)
              sigma_california    = pm.HalfNormal ('sigma_california', sigma=25)


              y_newyork = pm.Normal  ('y_new_york',  mu=mu_newyork,      ␣
        ↪sigma=sigma_newyork,       observed=newyork_data['grad_150_value'])
              y_california = pm.Normal  ('y_california',  mu=mu_california,␣
        ↪sigma=sigma_california, observed= california_data['grad_150_value'])

              diff_of_means = pm.Deterministic ('diff_of_means', mu_newyork -␣
        ↪mu_california)

              trace_ht_1_different_prior   = pm.sample(return_inferencedata=True)
              az.to_netcdf(trace_ht_1_different_prior, 'trace_ht_1_different_prior.
        ↪nc')
```

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

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

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

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

[16]:
```
az.plot_trace(trace_ht_1_different_prior);
```



[17]:
```
az.summary(trace_ht_1_different_prior, hdi_prob=0.95)
```

[17]:
```
                    mean     sd  hdi_2.5%  hdi_97.5%  mcse_mean  mcse_sd  \
mu_newyork        48.680  1.599    45.623     51.867      0.029    0.021
mu_california     44.754  1.329    42.301     47.447      0.024    0.017
sigma_newyork     24.099  1.142    21.900     26.425      0.020    0.014
sigma_california  24.442  0.951    22.618     26.304      0.016    0.011
diff_of_means      3.926  2.072    -0.132      7.880      0.037    0.029

                  ess_bulk  ess_tail  r_hat
mu_newyork          2975.0    1601.0    1.0
```

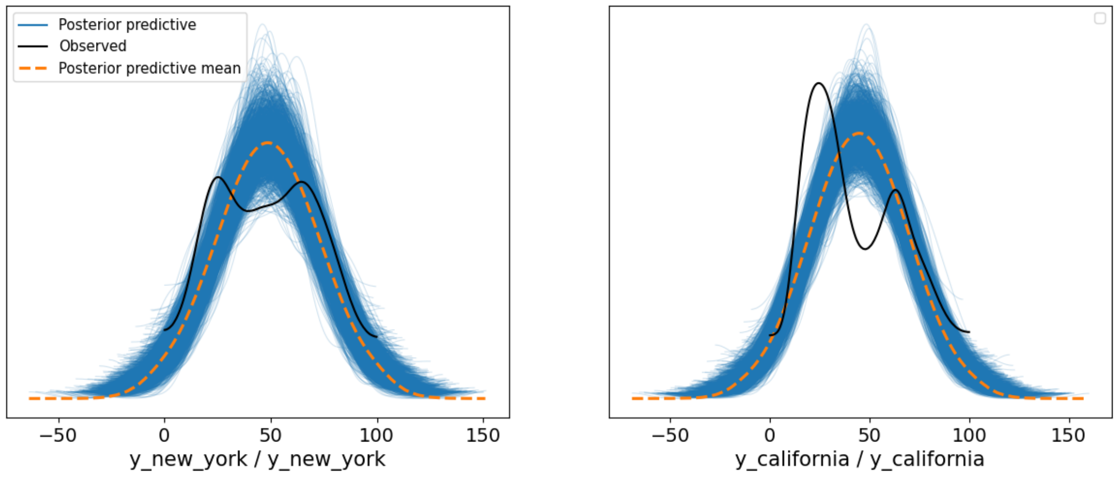
```
mu_california        3131.0    1417.0    1.0
sigma_newyork        3264.0    1585.0    1.0
sigma_california     3677.0    1746.0    1.0
diff_of_means        3134.0    1571.0    1.0
```

1.2.5 Posterior predictive check

To have a visual check of the posterior distribution with respect to the observed data, we can plot the together by sampling from the trace's posterior. In order to do this, we used the function given by PYMC called sample_posterior_predictive From the plots below, the following can be concluded: - The density in the bulk and tail region reflects the one shown by the observed data - The distributions of the observed data for both New York and California appear to be two modal in the center, New York a bit less and California a bit more. This doesn't impact though on the final results, being those distributions approximated pretty well - There is no need to take the Robust Likelihood approach, the one less sensitive to the outliers, since our outliers outside of the +-2σ range are still captured

[18]:
```
if not os.path.exists("trace_ht_1_correct_prior"):
  with model_ht_1_different_prior:
      ppc = pm.sample_posterior_predictive(trace_ht_1_correct_prior)
  az.plot_ppc(ppc);
```

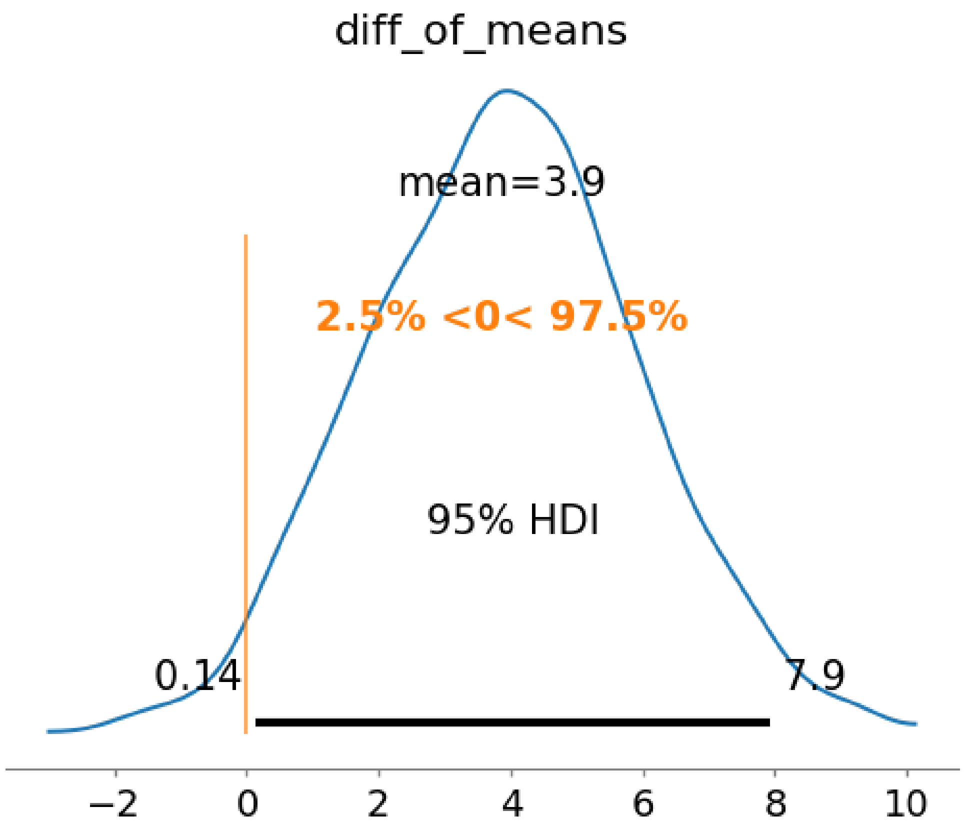
```
<IPython.core.display.HTML object>

<IPython.core.display.HTML object>

/usr/local/lib/python3.10/dist-packages/IPython/core/pylabtools.py:151:
UserWarning: Creating legend with loc="best" can be slow with large amounts of
data.
  fig.canvas.print_figure(bytes_io, **kw)
```



1.2.6 Conclusions based on posterior, including a meaningful definition of ROPE

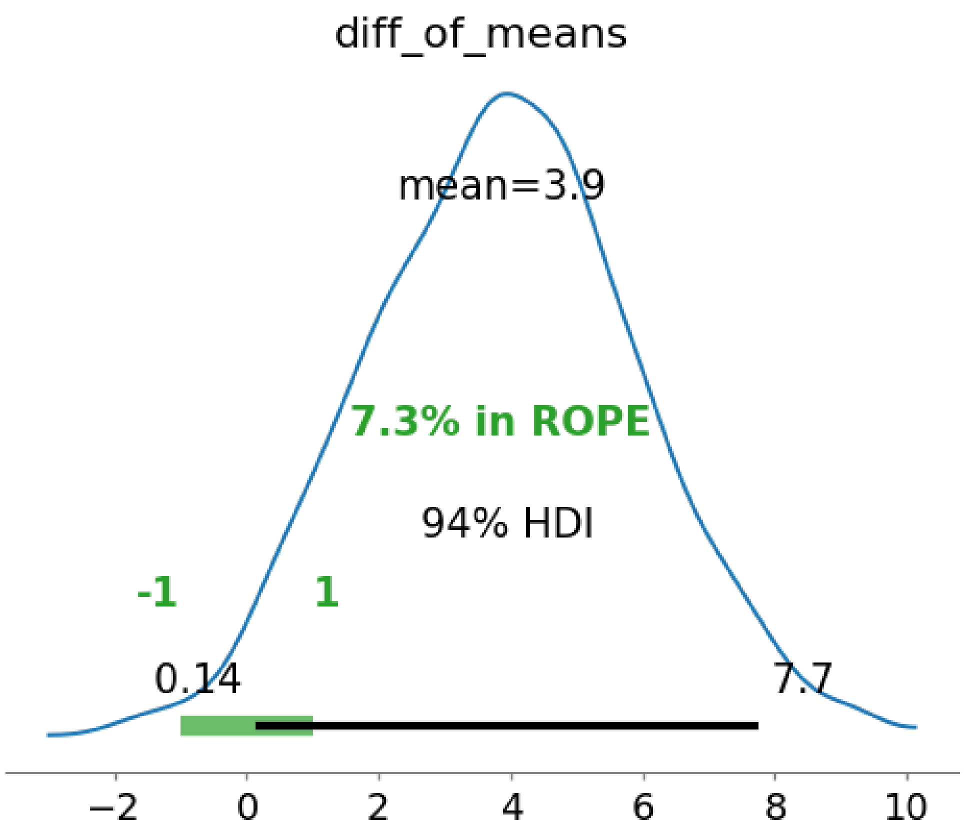
Now the question we got to ask ourselves is whether the 0 difference mean between the two states is plausible with our data or not. To do so, we need to check if 0 lies on the 95% High Density Interval, which it does in this case but its at the very limit, indicating that H0 could likely be rejected, proving the mean between New York and California being different

[19]:
```
az.plot_posterior(trace_ht_1_correct_prior,  var_names="diff_of_means",␣
↪ref_val=0, hdi_prob=0.95);
```



In the plot below we can see how the difference of means falls withing our ROPE indicator. This tells us the region (in this case, between -1 and 1) in which the difference between the two groups is insignificant. The more our difference mean falls within the ROPE, the more we can exclude any significant difference between the two groups. The mean difference between the two states is of 3.9 The HDI includes the zero by very little, almost insignificantly, and the percentage of the posterior distribution within the ROPE (Range of Practical Equivalence) is 7.3%, suggesting that the difference is practically significant and that we can fairly conclude that there is a solid difference between the graduation rate of the two states

[20]:
```
az.plot_posterior(trace_ht_1_correct_prior, var_names="diff_of_means",␣
↪rope=[-1,1]);
```



Another way to interpret the results of the difference of means analysis is to compute the probabilities, over the samples of the posterior, of the difference being either around 0 or significantly lower greater than the ROPE range. From the results we got here we c an estabilish that there is: - 91.7% probability of the difference being greater significantly greater than 1. This means that in 91.7% of the posterior samples, the graduation rate of New-York was better than the California one by at least 1% - 7.4% (as the percentage of the posterior being in the ROPE) probability of the difference being around 0 - 0.9% probability of the difference being less than 1, meaning the porbability that a California college would have a greater graduation rate than a New York one by at least 1%

[21]:
```
samples                  = az.extract(trace_ht_1_correct_prior)
diff_samples             = samples.diff_of_means.values
p_significant_positive   = (diff_samples > 1).sum() / len(diff_samples)
p_significant_negative   = (diff_samples < -1).sum() / len(diff_samples)
p_practically_eq         = 1 - p_significant_negative - p_significant_positive

print("p_significant_positive: ", "%.3f" % p_significant_positive)
print("p_practically_eq: ", "%.3f" % p_practically_eq)
print("p_significant_negative: ", "%.3f" % p_significant_negative)
```

```
p_significant_positive:  0.916
```

```
p_practically_eq:  0.074
p_significant_negative:  0.011
```

Based on the whole analysis performed, we can be reasonably confident in saying that the difference in graduation rate between New York and California is significantly different, having New York coming out on top with respect to California.

1.3 Hypothesis test: Difference in Graduation between Western and Eastern States

In history there were many rivalries between the two coasts of America: the Western laying on the Pacific Ocean, and the Eastern touching the Atlantic one. Among these rivalries, we thought of one in particular: aren't some of the best universities in the Eastern coast of USA? Among those are present such universities as Harvard, Stanford, Cambridge just to cite a few. With that in mind, we discussed about what we would expect the best coast to be in terms of graduation rate, and we arrived at the hypothesis of the Eastern coast graduating more frequently.

Formalizing the hypothesis, it would be:

$$H_0 : \mu_{\text{east}} \leq \mu_{\text{west}}$$
$$H_1 : \mu_{\text{east}} > \mu_{\text{west}}$$

At first we split the dataset in two, one for each coast

```
[22]: eastern_states = ['Maine', 'New Hampshire', 'Vermont', 'Massachusetts', 'Rhode␣
       ↪Island', 'Connecticut', 'New York', 'Pennsylvania', 'New Jersey',
      'Delaware', 'Maryland', 'Virginia', 'West Virginia', 'North Carolina', 'South␣
       ↪Carolina', 'Georgia', 'Florida',
      'Kentucky', 'Tennessee', 'Ohio', 'Indiana', 'Michigan', 'Wisconsin',␣
       ↪'Illinois', 'Alabama']

      eastern_df = grad_150_df[grad_150_df['state'].isin(eastern_states)]
      western_df = grad_150_df[~grad_150_df['state'].isin(eastern_states)]
```

1.3.1 Choice of prior and likelihood

Prior for μ_{east} and μ_{west} We decided for the prior concerning the mean of a certain coast to keep the same ones as previously stated, but we'll consider a smaller standard deviation since, having more data from different states, makes us except a smaller variation in the mean.

$$\mu_{\text{east}} \sim N(55, 5)$$
$$\mu_{\text{west}} \sim N(55, 5)$$

Prior for σ_{east} and σ_{west} As above, we decided to keep the same standard deviation for the two means. To simulate it through the HalfNormal distribution, we tune the half-normal prior in order to get a median close to 5. The value we got is 7.5

$$\sigma_{\text{east}} \sim HN(7.5)$$

$$\sigma_{\text{west}} \sim HN(7.5)$$

```
[23]: pd.DataFrame(halfnorm.rvs(scale=7.5, size=10000)).describe()
```

```
[23]:                    0
      count  10000.000000
      mean       6.051701
      std        4.571954
      min        0.000389
      25%        2.400086
      50%        5.130666
      75%        8.692258
      max       30.207031
```

Likelihood

- Like before, we assumed the distributions of the means for both the coasts to follow a Normal distribution, with the parameters of μ and σ being the priors we defined before

$$\vec{y}_{east} \sim N(\mu_{\text{east}}, \sigma_{\text{east}})$$

$$\vec{y}_{west} \sim N(\mu_{\text{west}}, \sigma_{\text{west}})$$

- With the whole prior and likelihood ready, we can build the new probabilistic model to represent easter and western data

$$\begin{aligned}
\mu_{\text{east}} &\sim N(55, 5)\\
\sigma_{\text{east}} &\sim HN(7.5)\\
\vec{y}_{\text{east}} &\sim N(\mu_{\text{east}}, \sigma_{\text{east}})\\
\\
\mu_{\text{west}} &\sim N(55, 5)\\
\sigma_{\text{west}} &\sim HN(7.5)\\
\vec{y}_{\text{west}} &\sim N(\mu_{\text{west}}, \sigma_{\text{west}})
\end{aligned}$$

Model

- As before, in order to compute the hypothes test later one, we need a *Deterministic* variable, representing the difference between the two means.

$$\mu_{\text{east}} - \mu_{\text{west}}$$

- The information regarding this deterministic difference will be stored in the computed trace

[24]:
```python
# Our defined priors
if os.path.exists('trace_ht_2_correct_prior.nc'):
    trace_ht_2_correct_prior = az.from_netcdf('trace_ht_2_correct_prior.nc')
else:
    with pm.Model() as model_initial_prior:
        mu_east          = pm.Normal     ('mu_east',  mu = 55,  sigma = 5)
        mu_west       = pm.Normal     ('mu_west', mu = 55,  sigma = 5)
        sigma_east       = pm.HalfNormal ('sigma_east',  sigma=7.5)
        sigma_west    = pm.HalfNormal ('sigma_west', sigma=7.5)

        y_east = pm.Normal  ('y_east',  mu=mu_east,      sigma=sigma_east,     ␣
 ↪ observed=eastern_df['grad_150_value'])
        y_west = pm.Normal  ('y_west',  mu=mu_west, sigma=sigma_west, observed=␣
 ↪western_df['grad_150_value'])

        diff_of_means = pm.Deterministic ('diff_of_means', mu_east - mu_west)

        trace_ht_2_correct_prior   = pm.sample(return_inferencedata=True)
        az.to_netcdf(trace_ht_2_correct_prior, 'trace_ht_2_correct_prior.nc')
```

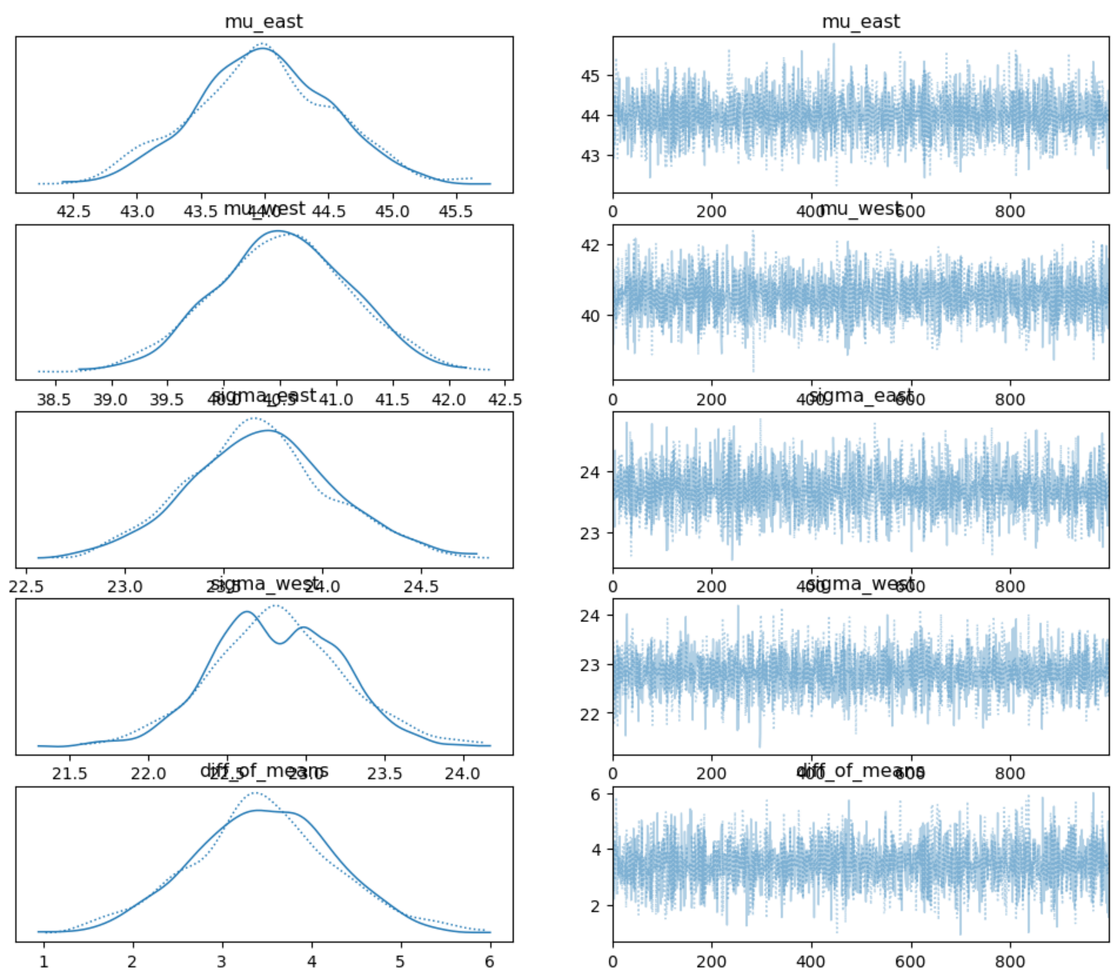
```
<IPython.core.display.HTML object>

<IPython.core.display.HTML object>

<IPython.core.display.HTML object>

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

1.3.2 Convergence diagnostics

To check for convergence, we did as before, meaning analyzing the following aspects: - Density plots: the sampling chains are converging as before, forming a Gaussian-like distribution - Trace plots: the sampling frequencies are distributed evenly and correctly around the mean - r_hat: as before, all values of r_hat are equal to 1, indicating convergence - ess_bulk / ess_tail: showing a high amount for both, these two parameters confirm ulteriorly convergence

As before, we overestimated

[25]:
```python
az.plot_trace(trace_ht_2_correct_prior);
```



[26]:
```
az.summary(trace_ht_2_correct_prior, hdi_prob=0.95)
```

[26]:
```
                 mean     sd  hdi_2.5%  hdi_97.5%  mcse_mean  mcse_sd  \
mu_east        43.987  0.548    42.926     45.046      0.008    0.006
mu_west        40.521  0.603    39.312     41.664      0.009    0.006
sigma_east     23.689  0.373    22.997     24.486      0.006    0.005
sigma_west     22.816  0.419    21.968     23.622      0.008    0.005
diff_of_means   3.467  0.815     1.717      4.945      0.012    0.009

               ess_bulk  ess_tail  r_hat
mu_east          4128.0    1725.0    1.0
mu_west          4599.0    1680.0    1.0
sigma_east       3415.0    1786.0    1.0
sigma_west       3081.0    1454.0    1.0
diff_of_means    4396.0    1549.0    1.0
```

1.3.3 Prior sensitivity

In the previous HT we noticed that choosing different, but still reasonable priors, didn't affect the posterior sampling and distributions. We except the same behaviour also for this hypothesis test, but we still want to check if that is indeed the case.

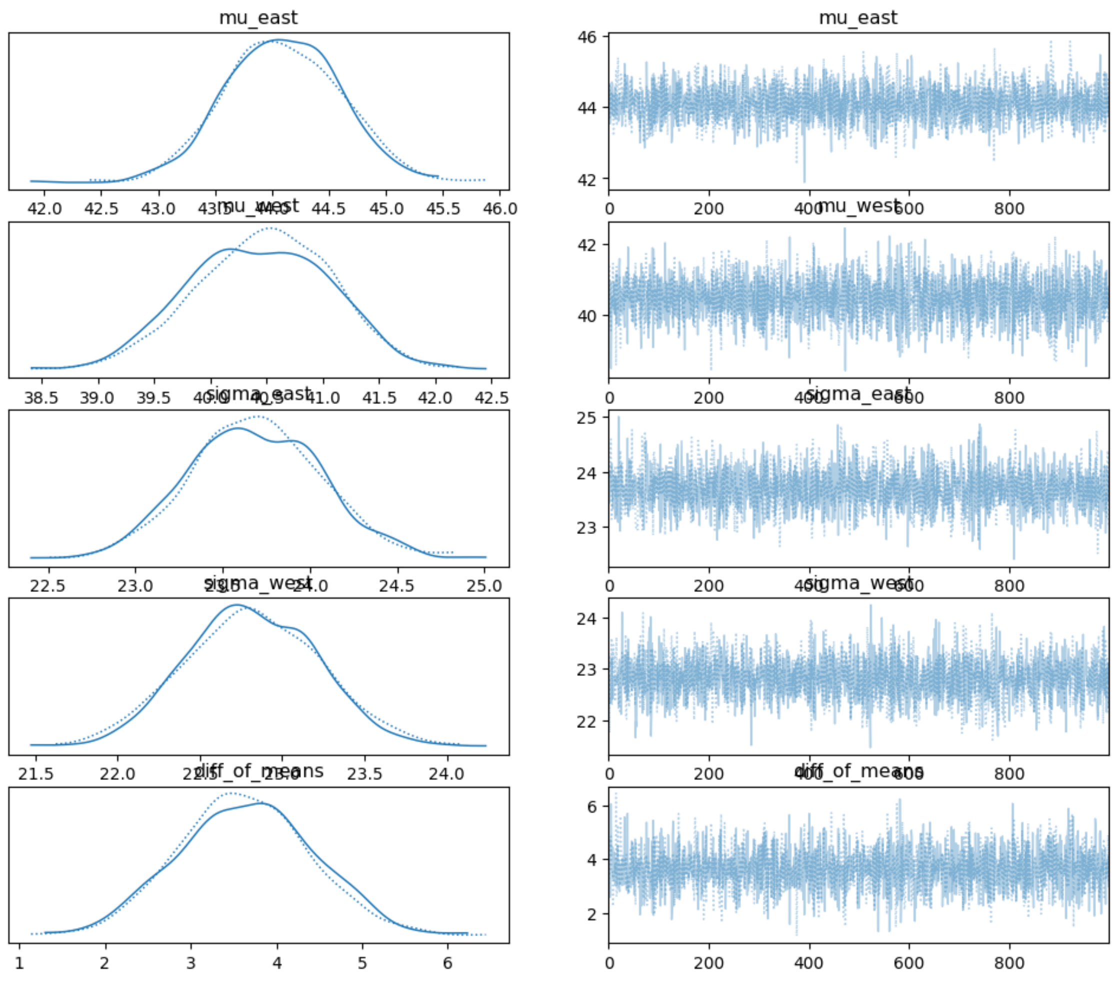
We chose priors that were agian reasonable for this problem. We decided to apply changes only to the mean parameter of the two μ parameters, raising the one of the eastern distribution and lowering the western one, both by 5.

Even with these priors, the two groups are able to converge in the same bell-shaped distributions, the "fuzzy caterpillar" appeared the same again, and the summary variables such as r_hat and ess_bulk / ess_tail are all showing good results of model convergence

[27]:
```
# Our defined priors
if os.path.exists('trace_ht_2_different_prior.nc'):
    trace_ht_2_different_prior = az.from_netcdf('trace_ht_2_different_prior.nc')
else:
    with pm.Model() as model_initial_prior:
        mu_east         = pm.Normal     ('mu_east',  mu = 65,  sigma = 5)
        mu_west      = pm.Normal     ('mu_west', mu = 50,  sigma = 5)
        sigma_east      = pm.HalfNormal ('sigma_east',  sigma=7.5)
        sigma_west   = pm.HalfNormal ('sigma_west', sigma=7.5)

        y_east = pm.Normal  ('y_east',  mu=mu_east,      sigma=sigma_east,     ␣
 ↪ observed=eastern_df['grad_150_value'])
        y_west = pm.Normal  ('y_west',  mu=mu_west, sigma=sigma_west, observed=␣
 ↪western_df['grad_150_value'])

        diff_of_means = pm.Deterministic ('diff_of_means', mu_east - mu_west)

        trace_ht_2_different_prior   = pm.sample(return_inferencedata=True)
        az.to_netcdf(trace_ht_2_different_prior, 'trace_ht_2_different_prior.
 ↪nc')
```

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

<IPython.core.display.HTML object>

<IPython.core.display.HTML object>

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

[28]:
```
az.plot_trace(trace_ht_2_different_prior);
```



```
[29]: az.summary(trace_ht_2_different_prior, hdi_prob=0.95)
```

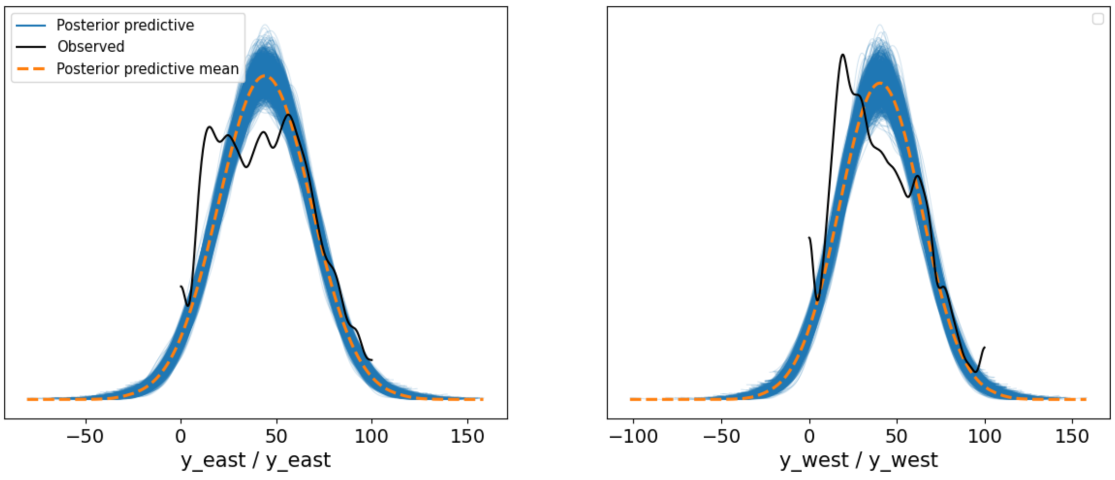
```
[29]:                  mean     sd  hdi_2.5%  hdi_97.5%  mcse_mean  mcse_sd  \
      mu_east        44.095  0.497    43.121     45.036      0.009    0.007
      mu_west        40.458  0.618    39.250     41.578      0.010    0.007
      sigma_east     23.688  0.376    22.935     24.401      0.007    0.005
      sigma_west     22.815  0.410    21.981     23.575      0.008    0.006
      diff_of_means   3.637  0.783     2.109      5.070      0.013    0.010

                     ess_bulk  ess_tail  r_hat
      mu_east          2922.0    1710.0    1.0
      mu_west          4180.0    1852.0    1.0
      sigma_east       2767.0    1394.0    1.0
      sigma_west       2614.0    1416.0    1.0
      diff_of_means    3543.0    1968.0    1.0
```

1.3.4 Posterior predictive check

After sampling, the posterior needs to be checked, same as before, to be two modal in the center, New York a bit less and California a bit more. This doesn't impact though on the final results, being those distributions approximated pretty well - There is no need to take the Robust Likelihood approach, the one less sensitive to the outliers, since our outliers outside of the +-2σ range are still captured

```
[30]: if not os.path.exists("trace_ht_2_correct_prior"):
        with model_initial_prior:
            ppc = pm.sample_posterior_predictive(trace_ht_2_correct_prior)
        az.plot_ppc(ppc);
```

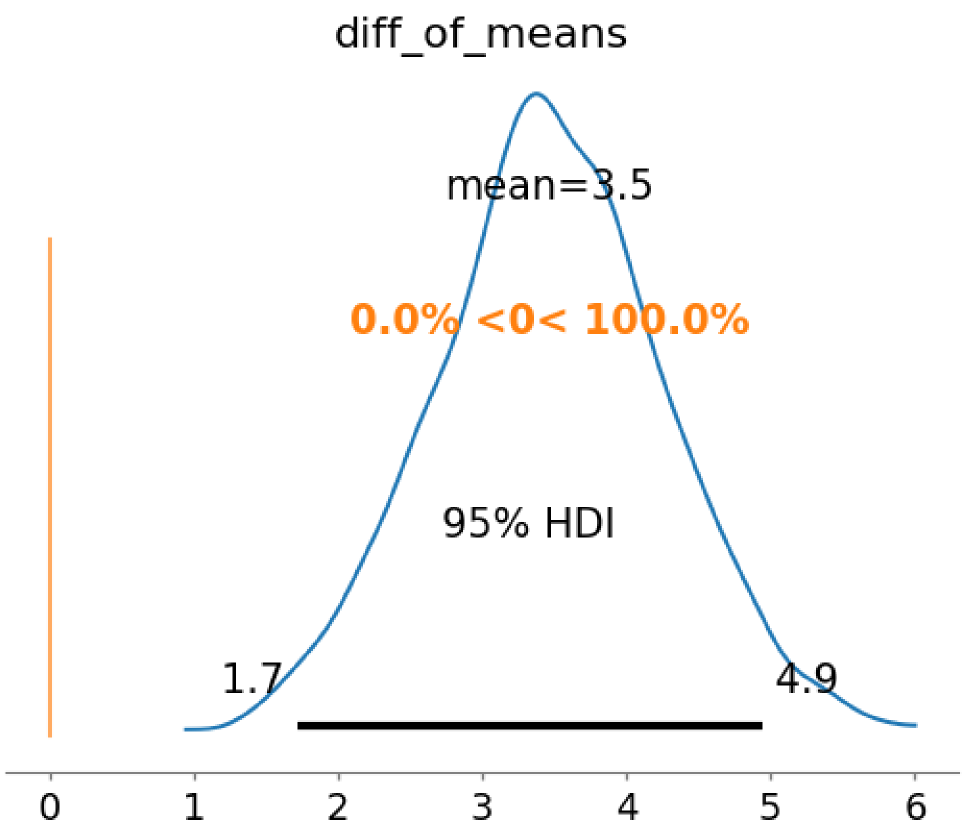
```
<IPython.core.display.HTML object>

<IPython.core.display.HTML object>

/usr/local/lib/python3.10/dist-packages/IPython/core/pylabtools.py:151:
UserWarning: Creating legend with loc="best" can be slow with large amounts of
data.
  fig.canvas.print_figure(bytes_io, **kw)
```



1.3.5 Conclusions based on posterior, including a meaningful definition of ROPE

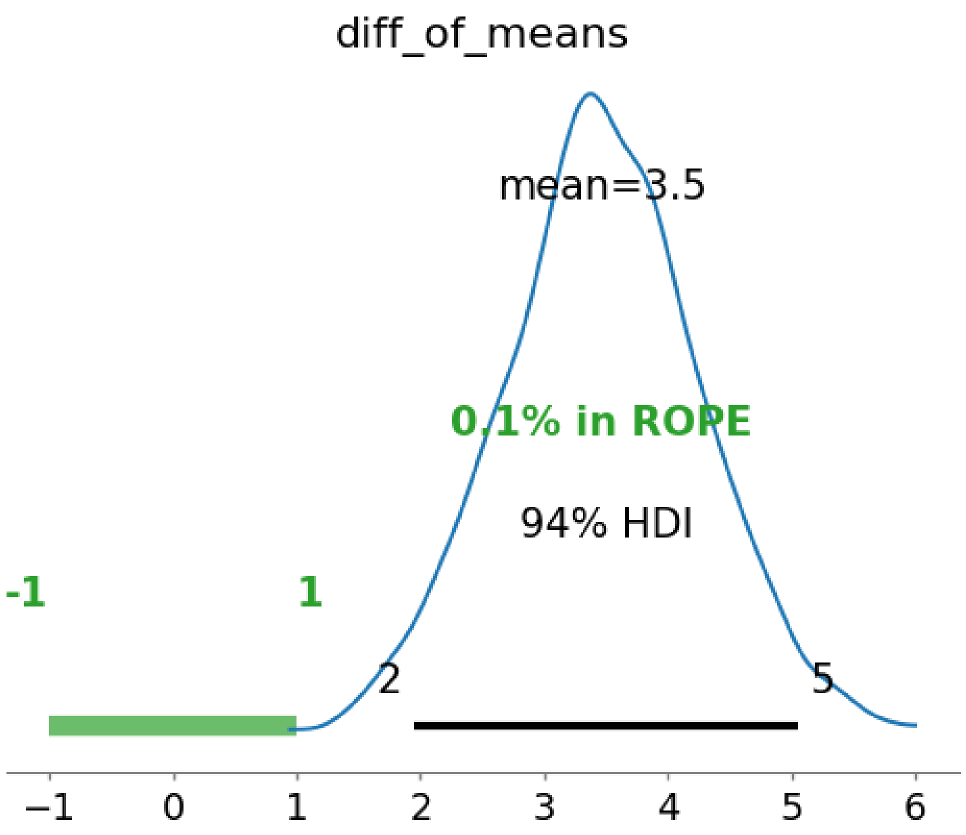
To check the hypothesis possible result, a possible indication is to see if the reference value of 0 is in the HDI, which is not, in fact its way out far from the distribution itself, which does not include it as value

```
[31]: az.plot_posterior(trace_ht_2_correct_prior,  var_names="diff_of_means",␣
        ↪ref_val=0, hdi_prob=0.95);
```



We may observe how the mean difference falls within our ROPE indicator in the plot below. This indicates the range (in this case, -1 to 1) in which there is little variation between the two groups. We can rule out any meaningful difference between the two groups the more our difference mean lies inside the ROPE. The mean difference between the two states is of 3.4 The ROPE range overlaps with the HDI by just 0.1%, makin us understand very clearly that the two means are far away one from another

[32]:
```
az.plot_posterior(trace_ht_2_correct_prior, var_names="diff_of_means",␣
 ↪rope=[-1,1]);
```



Calculating the probability over the posterior samples of the difference being either around 0 or much smaller than the ROPE range is another method to evaluate the results of the difference of means study. From the results we got here we can estabilish that there is not a chance that the mean of the Western states is bigger than the one of the Eastern states, therefore we can succesfully reject H0 and accept H1.

[33]:
```
samples                   = az.extract(trace_ht_2_correct_prior)
diff_samples              = samples.diff_of_means.values
p_significant_positive    = (diff_samples > 1).sum() / len(diff_samples)
p_significant_negative    = (diff_samples < -1).sum() / len(diff_samples)
p_practically_eq          = 1 - p_significant_negative - p_significant_positive

print("p_significant_positive: ", "%.3f" % p_significant_positive)
print("p_practically_eq: ", "%.3f" % p_practically_eq)
print("p_significant_negative: ", "%.3f" % p_significant_negative)
```

```
p_significant_positive:  1.000
p_practically_eq:  0.000
p_significant_negative:  0.000
```

1.4 Hierarchical model

1.4.1 Choice of prior and likelihood

Having the nature of the model to be hierarchical, the setting of prior comes from defining a prior for each smallest group (in this case, for each state), where that prior is believed to come from a broader distribution that captures overall trends across states.

- The j subscript refers to the j-th state (we have 50 states).
- n_j: number of colleges present in the state j.
- y_{ij}: number of students who graduated within 150% of the normal time from the i-th college of a state j
  - $j \in \{1, 2, ..., 50\}$, $i \in \{1, 2, ..., n_j\}$.
- State j has its own mean graduation rate of colleges, μ_j

The full probabilistic model is composed of several parts which include: * Prior beliefs about the graduation rate of the states in the population * Distributions representing: - Graduation rate of a particular state j - Graduation rate of a particular college y_{ij}

$$\begin{aligned}
\mu_{\text{pop}} &\sim N(\mu_{\text{prior}}, \sigma_{\text{prior}}) \quad \text{prior beliefs about graduation rate of a state in the population} \\
\sigma_{\text{pop}} &\sim HN(\xi_{prior}) \quad \text{prior beliefs about std of a state's graduation rate in the population} \\
\\
\mu_j &\sim N(\mu_{\text{pop}}, \sigma_{\text{pop}}) \quad \mu_j \text{ is a sample from the population of states} \\
\sigma_{\text{grad}} &\sim HN(\xi) \quad \text{prior common to all the states} \\
\\
y_{ij} &\sim N(\mu_j, \sigma_{\text{grad}}) \text{ distrib of graduation rate of the colleges of a state } j
\end{aligned} \tag{1}$$

Starting from the very top level of the hierarchy, we need to set the prior believes regarding the graduation rate of a college in the population. We can use the same priors that were used for the previous part of the two Hypothesis Tests, meaning

$$\mu_{\text{pop}} \sim N(55, 7.5)$$
$$\sigma_{\text{pop}} \sim HN(15)$$

Having these parameters, μ_j can follow a Normal with that prior as parameters. Now σ_{grad} needs to be tuned in order to fit correctly the distribution of our data. The values of the column grad_150_value range between 0 and 100, and since it can be interpreted as +-2 stds, a value of 25 can be taken as std. The HalfNormal now needs to have as ξ a value that would approximately get to 25 as median value. After tuning, we got to 37 as such value, therefore

$$\sigma_{\text{grad}} \sim \text{Half Normal}(37)$$

```
[34]: pd.DataFrame(halfnorm.rvs(scale=37, size=10000)).describe()
```

```
[34]:                    0
       count  10000.000000
```

```
mean      29.827704
std       22.501199
min        0.004423
25%       11.886676
50%       25.377878
75%       42.908386
max      148.361184
```

1.4.2 Model

For further analysis, below a specific code is assigned to each state present in our dataset. This way, when we need to compute predictive distributions for a certain group of data, such as a state like New York, the state_code can be used

[35]:
```
grad_150_df["state"] = grad_150_df["state"].astype("category")
states = list(grad_150_df["state"].cat.categories)
grad_150_df['state_code']  = grad_150_df['state'].astype('category').cat.codes
grad_150_df.sample(n = 5, random_state = 24)
```

[35]:
```
                                   chronname       state  grad_150_value  \
154                 Barstow Community College  California            17.2
277                      MTI College (Calif.)  California            70.5
284                             Menlo College  California            40.8
3259  ITT Technical Institute at Little Rock    Arkansas            18.2
743                John Wood Community College    Illinois            30.8

      med_sat_value  state_code
154             NaN           4
277             NaN           4
284          1001.0           4
3259            NaN           3
743             NaN          12
```

With PyMC we defined the prior and the likelihood functions, which we use later to compute the posterior and predictive distributions later on

[36]:
```
n_states = 50 # states in df
if os.path.exists('trace_hier.nc'):
    trace_hier = az.from_netcdf('trace_hier.nc')
else:
    with pm.Model() as hier_model:

        # Priors
        mu_pop      = pm.Normal ('mu_pop', 45, 10)
        sigma_pop   = pm.HalfNormal ('sigma_pop', 15)
        mu_state    =  pm.Normal ('mu_state', mu=mu_pop, sigma=sigma_pop, shape=␣
↪n_states)
        sigma_colleges   =  pm.HalfNormal ('sigma_colleges', sigma = 37)
        # Likelihood
        grad_150_value   =  pm.Normal ('grad_150_value', mu =␣
↪mu_state[grad_150_df['state_code']],  sigma = sigma_colleges, observed =␣
↪grad_150_df["grad_150_value"])

        trace_hier   = pm.sample(return_inferencedata=True)
        az.to_netcdf(trace_hier, 'trace_hier.nc')
```

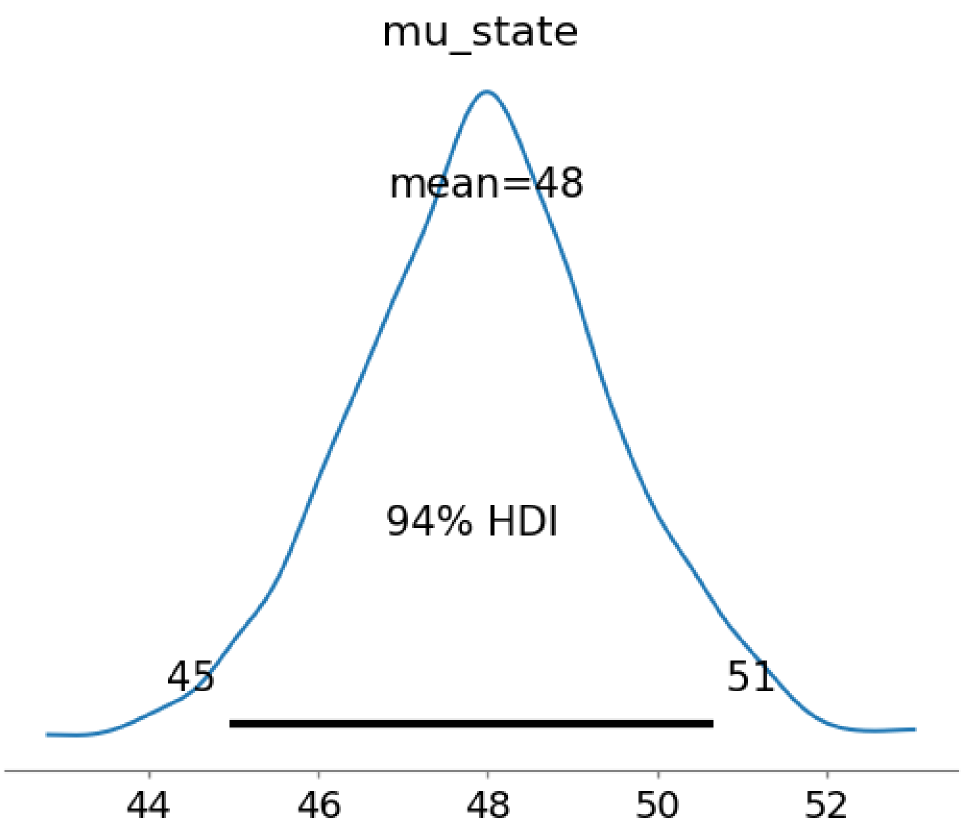
```
<IPython.core.display.HTML object>

<IPython.core.display.HTML object>

<IPython.core.display.HTML object>

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

1.4.3 Posterior distribution of the mean: New York

Once the trace was computed, we were able to plot the posterior distibution for the New York state. In order to do so, we needed to retrieve the state's code, the one we defined above. From the plot, once again, we can observe the prior being higher than the one is really found, wih less spread of data. The prior didn't influence much the final result since many rows were available for New York

[37]:
```
# Unique code of the New York state
new_york_code = grad_150_df[grad_150_df['state'] == 'New York'].iloc[0, -1]
print("New York unique code: ", new_york_code)

#  posterior distribution of the mean for the New York state
coords = {"mu_state_dim_0": new_york_code}
with pm.Model() as h_model:
    az.plot_posterior(trace_hier, var_names=["mu_state"],␣
 ↪point_estimate='mean', coords=coords)
```

```
New York unique code:  31
```



1.4.4 Predictive distribution: New York

In order to compute the predictive distribution, for each sample of the New York posterior we need to get the mean and the standard deviation of it, and use those as sampling parameters for the predictive distribution

- For each posterior samples $< \mu_{\text{new-york},s}, \sigma_s >$:
  - sample $y^{\text{new}}_{\text{new-york},s}$ from a normal distribution.

$$\begin{bmatrix} \mu_{\text{new-york},1} & \sigma_{\text{colleges},1} \\ \mu_{\text{new-york},2} & \sigma_{\text{colleges},2} \\ \vdots & \vdots \\ \mu_{\text{new-york},4000} & \sigma_{\text{colleges},4000} \end{bmatrix} \longrightarrow \begin{bmatrix} y^{\text{new}}_{\text{new-york},1} \\ y^{\text{new}}_{\text{new-york},2} \\ \vdots \\ y^{\text{new}}_{\text{new-york},4000} \end{bmatrix}$$

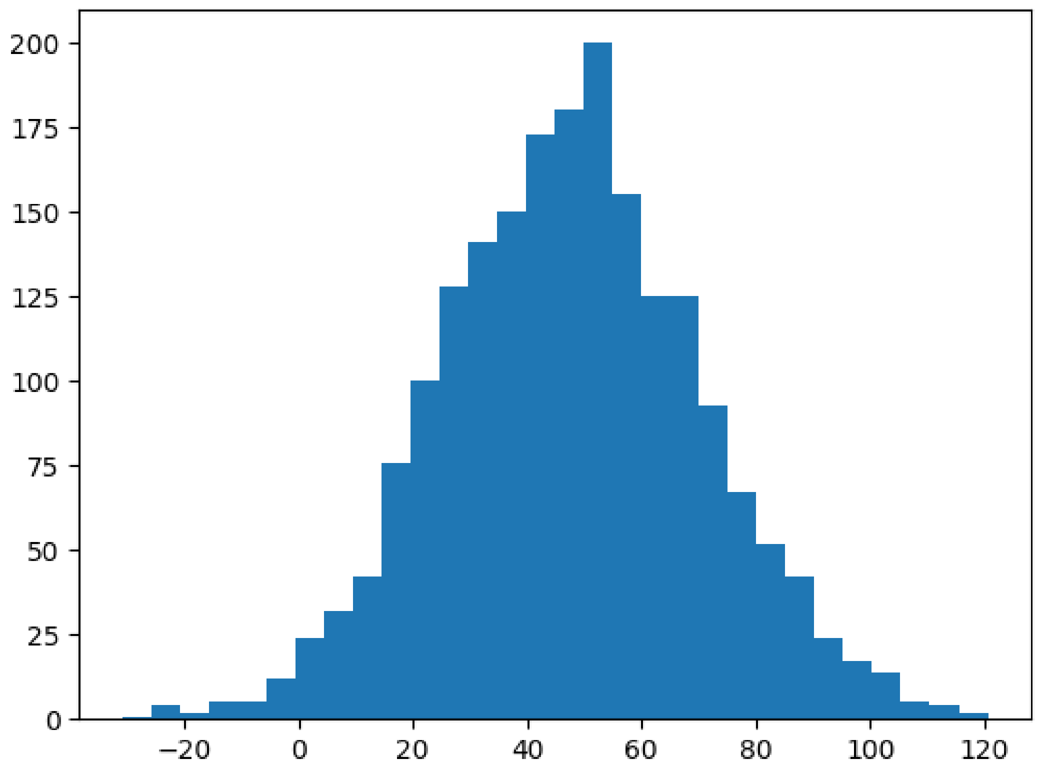
From the summary dataframe of the predictive distribution, we can see that the minimum and maximum values of the two tails are out of the true data bounds, since the graduation rate goes from 0 to 100, but looking at the 2.5% and 97.5% percentiles, it's clearly observable that the majority of the density lies within the correct bounds, representing very well the true distribution of data, having some at the tails but the main concentration around the mean

[38]:
```
post_hier = az.extract_dataset(trace_hier.posterior)

mu_new_york_hier    = post_hier.mu_state[new_york_code].values
sigma_colleges_hier  = post_hier.sigma_colleges.values

y_new_york_hier     = np.zeros(len(mu_new_york_hier))

for i, current_mu in enumerate(mu_new_york_hier):
        y_new_york_hier[i]      = np.random.normal (loc = mu_new_york_hier[i],␣
 ↪scale = sigma_colleges_hier[i])

pd.DataFrame(y_new_york_hier).describe(percentiles=[0.025, 0.975])
```

```
<ipython-input-38-7f845c86cd98>:1: FutureWarning: extract_dataset has been
deprecated, please use extract
  post_hier = az.extract_dataset(trace_hier.posterior)
```

[38]:
```
                 0
count  2000.000000
mean     47.778277
std      22.693957
min     -30.875277
2.5%      3.791271
50%      47.936017
97.5%    93.825485
max     120.585550
```

[39]:
```
plt.hist(y_new_york_hier, bins=30);
```



1.4.5 Posterior distribution of a novel group

To compute the posterior's distribution for a new group that wasn't present in our dataset, the following steps were performed: 1. Obtain the values of μ_{pop} and σ_{pop} from the posterior trace 2. Initialize an array that will contain the new values μ_{new} 3. Iterating through the values of μ_{pop} and σ_{pop} previously stored, sample from a Normal with the current values of μ_{pop} and σ_{pop} 4. Extracts the posterior samples for the standard deviation of colleges σ_{grad} from the hierarchical model's trace. 5. Initialize an array grad_new_college_new_state to store new college graduation rates for a new state, with the same length as the σ_{grad} array. 6. Iterate over the μ_{new} array and for each element, sample from a normal distribution using the generated state mean μ_{new} and corresponding σ_{grad} to generate a new college graduation rate for the new state.

While the posterior distribution for an existing state was staying within the bounds of the graduation, in this case it's more prevalent the error, showing also on the histogram below that there is not an insignificant amount of data in the out-of-bounds regions. The mean and standard deviation though are computed well with respect to the general population

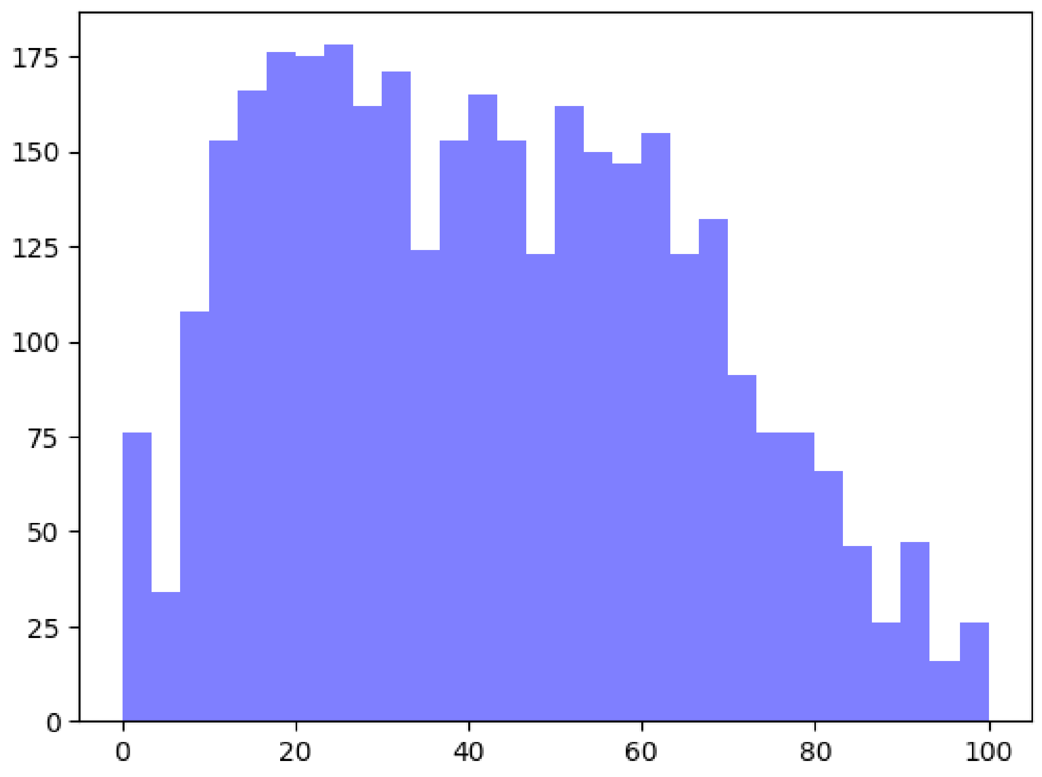
[40]:
```
post_hier   = az.extract(trace_hier.posterior)

mu_population    = post_hier.mu_pop.values
sigma_population = post_hier.sigma_pop.values

mu_new_state  = np.zeros(len(mu_population))
```

```
for i, current_mu in enumerate(mu_population):
        mu_new_state[i] = np.random.normal (loc = mu_population[i], scale =␣
 ↪sigma_population[i])

sigma_colleges = post_hier.sigma_colleges.values
grad_new_college_new_state  = np.zeros(len(sigma_colleges))

for i, current_mu in enumerate(mu_population):
        grad_new_college_new_state[i] = np.random.normal (loc =␣
 ↪mu_new_state[i], scale = sigma_colleges[i])

pd.DataFrame(grad_new_college_new_state).describe(percentiles=[0.025, 0.975])
```

[40]:
```
                 0
count  2000.000000
mean     40.029253
std      23.014189
min     -41.876117
2.5%     -5.460753
50%      40.690362
97.5%    84.955820
max     118.393985
```

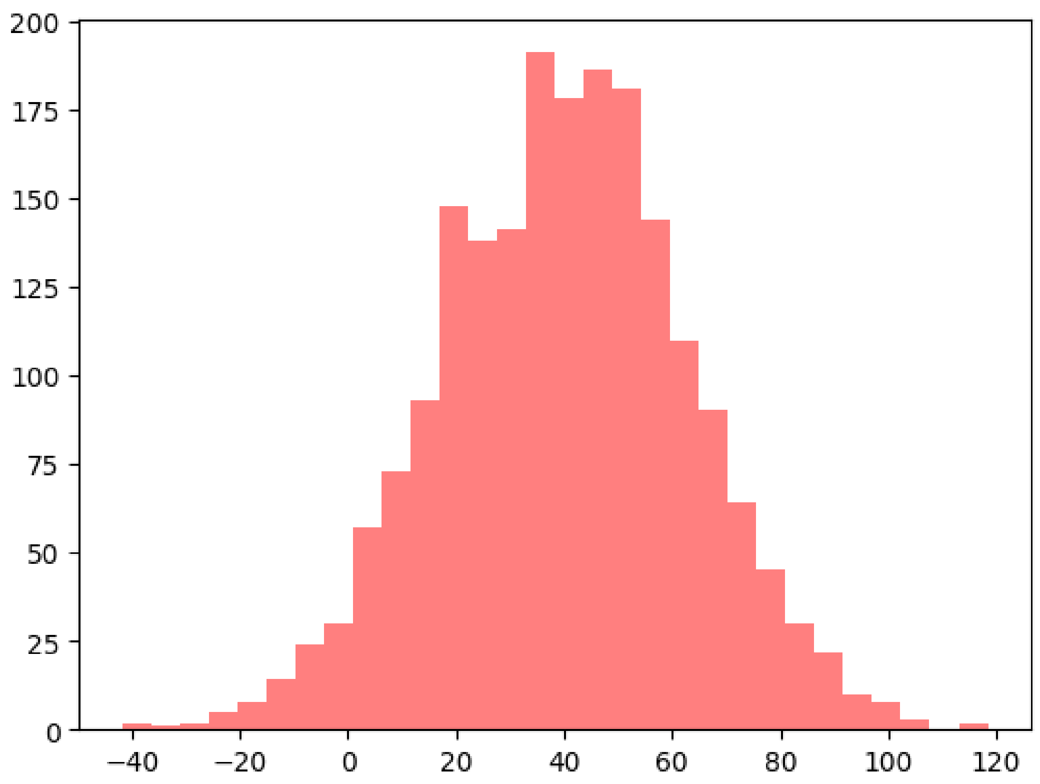
[41]:
```
plt.hist(grad_150_df['grad_150_value'], bins=30, color="blue", alpha=0.5)
```

[41]:
```
(array([ 76.,  34., 108., 153., 166., 176., 175., 178., 162., 171., 124.,
        153., 165., 153., 123., 162., 150., 147., 155., 123., 132.,  91.,
         76.,  76.,  66.,  46.,  26.,  47.,  16.,  26.]),
 array([  0.        ,   3.33333333,   6.66666667,  10.        ,
         13.33333333,  16.66666667,  20.        ,  23.33333333,
         26.66666667,  30.        ,  33.33333333,  36.66666667,
         40.        ,  43.33333333,  46.66666667,  50.        ,
         53.33333333,  56.66666667,  60.        ,  63.33333333,
         66.66666667,  70.        ,  73.33333333,  76.66666667,
         80.        ,  83.33333333,  86.66666667,  90.        ,
         93.33333333,  96.66666667, 100.        ]),
 <BarContainer object of 30 artists>)
```



```
[42]: plt.hist(grad_new_college_new_state, bins=30, color="red", alpha=0.5)
```

```
[42]: (array([  2.,   1.,   2.,   5.,   8.,  14.,  24.,  30.,  57.,  73.,  93.,
              148., 138., 141., 191., 178., 186., 181., 144., 110.,  90.,  64.,
               45.,  30.,  22.,  10.,   8.,   3.,   0.,   2.]),
       array([-41.87611683, -36.5337801 , -31.19144337, -25.84910664,
              -20.50676991, -15.16443318,  -9.82209645,  -4.47975972,
                0.86257701,   6.20491374,  11.54725047,  16.8895872 ,
               22.23192394,  27.57426067,  32.9165974 ,  38.25893413,
               43.60127086,  48.94360759,  54.28594432,  59.62828105,
               64.97061778,  70.31295451,  75.65529124,  80.99762797,
               86.3399647 ,  91.68230143,  97.02463816, 102.36697489,
              107.70931162, 113.05164835, 118.39398509]),
       <BarContainer object of 30 artists>)
```



1.5 Probabilistic Regression model: Median SAT value to predict Graduation rate

1.5.1 Variables involved

- We want to predict the value of Y given the observation of X.
- X and Y are random variables:
  - Y is the *response* variable: grad_150_value
  - X is the *explanatory variable* variable: med_sat_value
- The way Y is predicted is through usage of a Normal distribution that looks the following way

[43]:
```
X = np.array(median_sat_values_df['med_sat_value'].values)
Y = np.array(median_sat_values_df['grad_150_value'].values)
```

$$Y \sim N(\mu = \alpha + X\beta, \sigma)$$

- We must specify a prior distribution for each of parameter: α, β, σ.

  - α (*intercept*): predicted value of Y for $X = 0$; can be seen as a constant which calibrates the shift along the y-axis.
  - β (*slope*): predicted change in Y for a unit change in X.
  - σ (*noise*): noise that accounts for the variation around the regression line

1.5.2 The effect of σ

- Large σ (left): large variability of the observations around the linear model, weak relationship.
- Small σ (right): the observations deviates little from the model; strong relationship.

1.5.3 Regression with centered data + Choice of Priors

The regression function in case of centered data, like ours, is needed, since we know that the median SAT score is centered around a certain mean

- *Centered* median SAT value X, where $\bar{x}$ is the average med_sat_value:

$$X_c = X - \bar{x}$$

$$\begin{aligned}
Y &= \alpha + \beta X \\
Y &= \alpha + \beta \underbrace{(X - \bar{x})}_{X_c} + \beta\bar{x} \\
Y &= \alpha + \beta X_c + \beta\bar{x} \\
Y &= \underbrace{\alpha + \beta\bar{x}}_{\alpha_c} + \beta X_c \\
Y &= \alpha_c + \beta X_c
\end{aligned}$$

- The intercept with centered data α_c is the expected value of Y when $X_c = 0$ i.e., when $X = \bar{x}$.
- α_c is the average value of Y when X is at its mean.
- The meaning of β does not change.

1.5.4 Priors and Likelihood choice

Since there is no particular prior knowledge regarding this model, we're forced to go for the weakly informative data-driven approach.

- $\alpha_c \sim N(\bar{y}, 2s_y)$:
  - we expect α_c to be close to $\bar{y}$, yet we allow large variability around it (while remaining in the same scale of the data)
  - $\bar{y}$ are the mean and the standard deviation of Y in the sample.
- $\beta \sim N(0, 2.5\frac{s_y}{s_x})$

    – a priori the relation has equal probability of being increasing or decreasing; this justifies the prior mean being 0;
    – the prior is broad since in simple linear regression $\hat{\beta} = R\frac{s_y}{s_x}$, where R is the correlation between X and Y.

- $\sigma \sim HN(1.5s_y)$. The prior for σ is large compared to the standard deviation of the data, though remaining on the same scale.
- s_x and s_y are respectively the standard deviation of the samples from the X an Y values

1.5.5 Convergence diagnostics

We setup now our PyMC model with the prior functions defined before, and run it, computing likelihood and posterior trace.

[44]:
```
#implementation with data-dependent priors
x_c = (X - X.mean())
s_x = x_c.std()
s_y = Y.std()
y_bar = Y.mean()

if os.path.exists('gaussian_trace.pkl'):
    gaussian_trace = az.from_netcdf('gaussian_trace.nc')
else:
    with pm.Model() as gaussian_model:
        # Data driven priors
        alpha   = pm.Normal ('alpha', mu=y_bar, sigma=2 * s_y)
        beta    = pm.Normal ('beta',  mu=0,  sigma= 2.5 * s_y / s_x)
        sigma   = pm.HalfNormal ('sigma', sigma= 1.5 * s_y)

        # likelihood
        y_pred   = pm.Normal ('y_pred', mu= alpha + beta * x_c,  sigma=sigma,␣
↪observed=Y)

        gaussian_trace   = pm.sample(idata_kwargs={"log_likelihood": True})
        az.to_netcdf(gaussian_trace, 'gaussian_trace.nc')
```

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

<IPython.core.display.HTML object>

<IPython.core.display.HTML object>

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

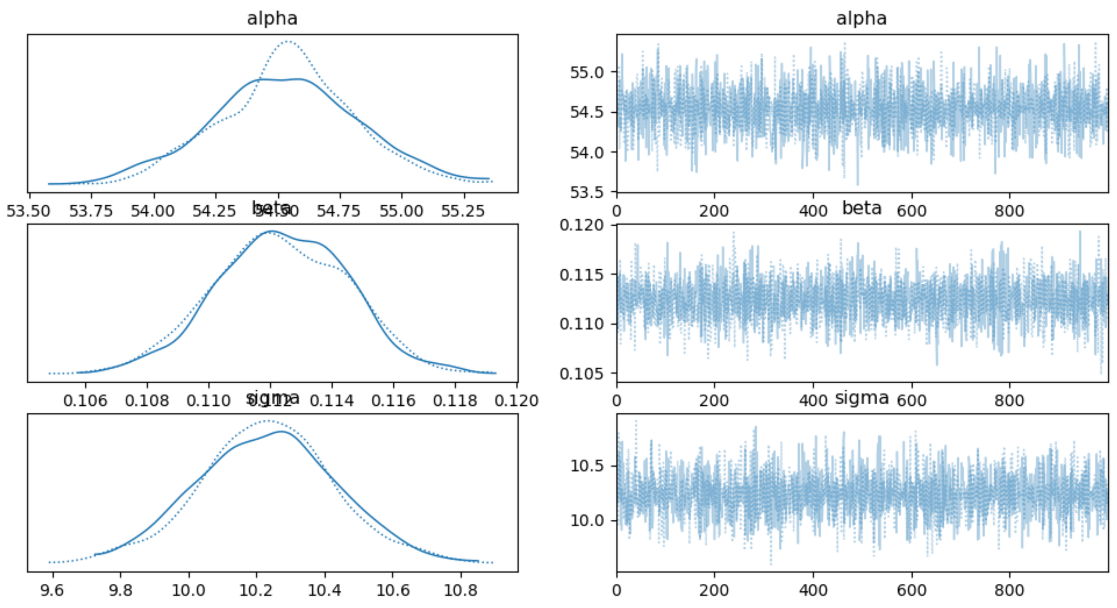
The model can be seen converging towards stable posterior distributions, both from the chains and from the samples, r_hat and the ess_bulk / ess_tail

[45]:
```
x_bar = X.mean()
print(x_bar)
az.summary(gaussian_trace)
```

```
1061.489006823351
```

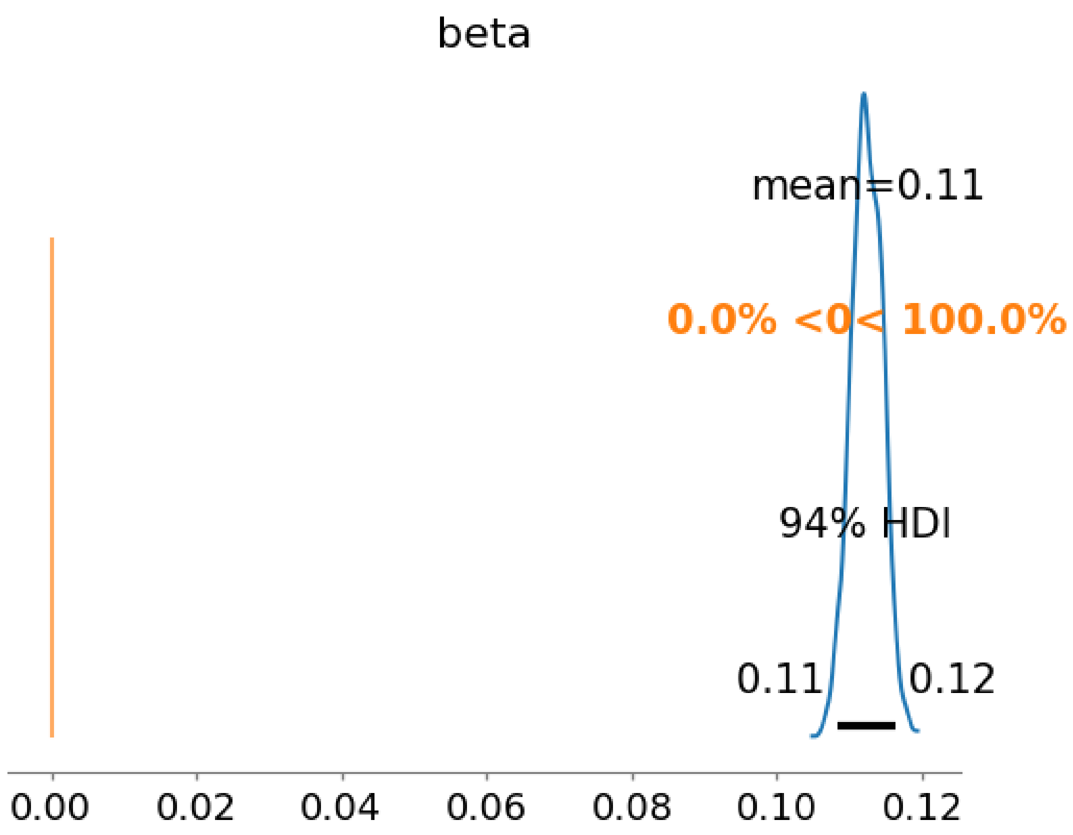
[45]:
```
          mean     sd  hdi_3%  hdi_97%  mcse_mean  mcse_sd  ess_bulk  ess_tail  \
alpha   54.534  0.283  53.997   55.078      0.005    0.004    3090.0    1756.0
beta     0.112  0.002   0.108    0.116      0.000    0.000    3010.0    1412.0
sigma   10.233  0.201   9.814   10.588      0.004    0.003    2989.0    1670.0

       r_hat
alpha   1.01
beta    1.00
sigma   1.00
```

[46]:
```python
az.plot_trace(gaussian_trace);
```



Having the β parameter as prior mean 0, and being the σ a division of the sampling stds. of two variables X and Y, which are assumed to follow a normal distribution, we can expect there to be a very low value of standard deviation, because of which the plot shows the distribution of beta pretty far away from the 0 mean

[47]:
```python
az.plot_posterior(gaussian_trace, var_names = "beta", ref_val=0);
```



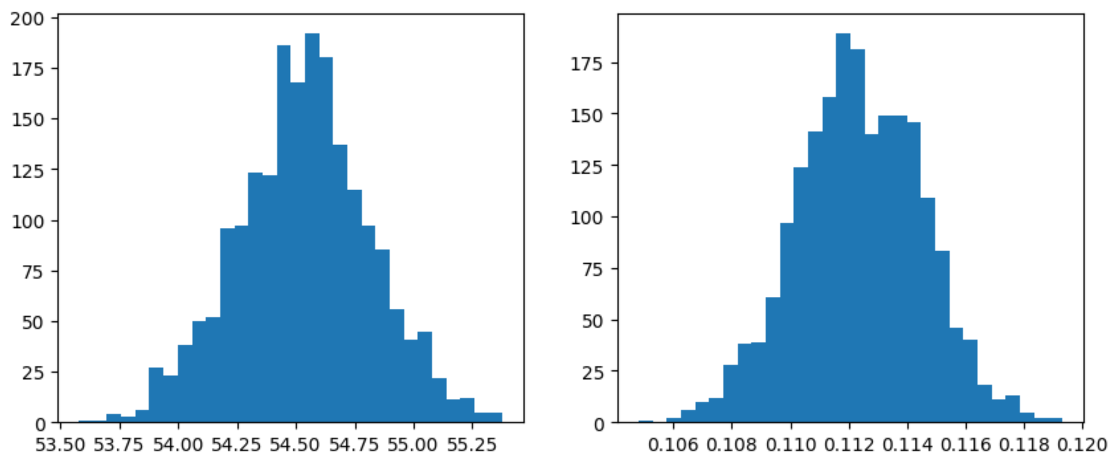
Below the values of the posterior mean of alpha and beta are stored

```
[48]: #posterior mean of the parameters, gaussian model
post_gauss  = az.extract_dataset(gaussian_trace)
alpha_values = post_gauss.alpha.values
beta_values = post_gauss.beta.values
a           = alpha_values.mean()
b           = beta_values.mean()
```

```
<ipython-input-48-b83812d7b98e>:2: FutureWarning: extract_dataset has been
deprecated, please use extract
  post_gauss  = az.extract_dataset(gaussian_trace)
```

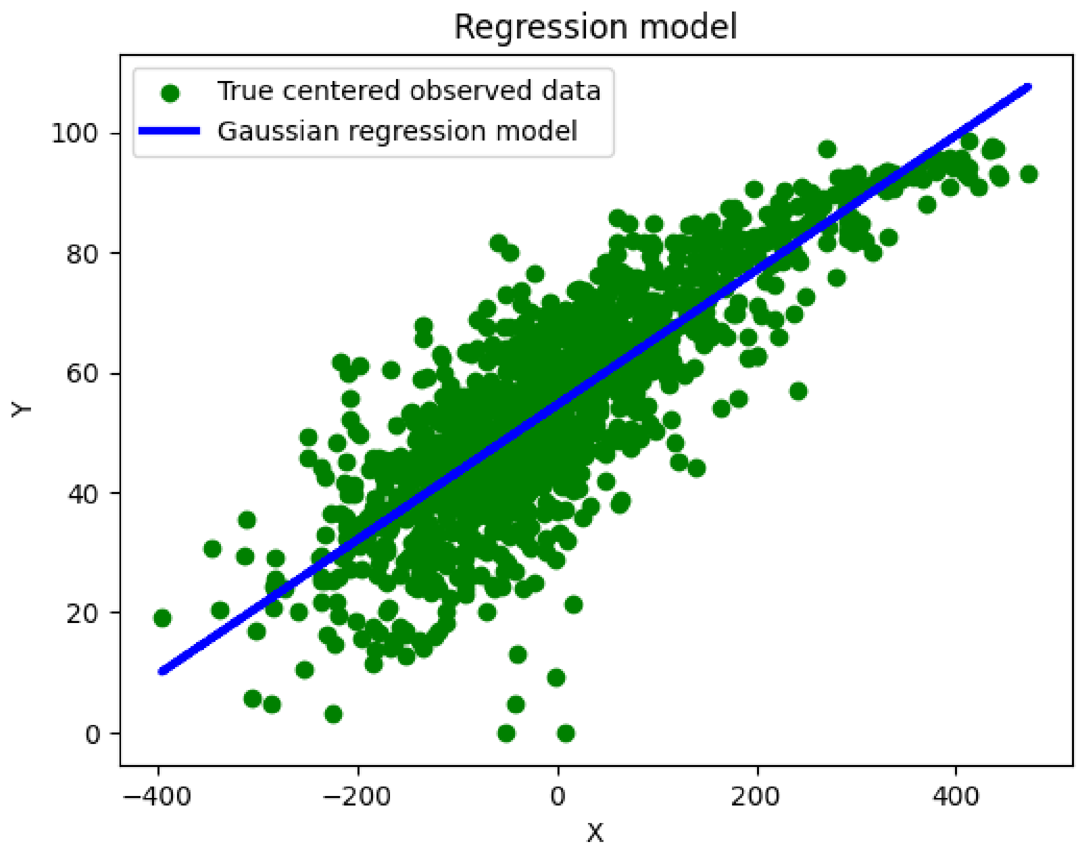
```
[49]: fig, ax = plt.subplots(ncols=2, figsize=(10, 4))
ax[0].hist(alpha_values, bins=30);
ax[1].hist(beta_values, bins=30);
```

```
[49]: (array([  1.,   0.,   2.,   6.,  10.,  12.,  28.,  38.,  39.,  61.,  97.,
        124., 141., 158., 189., 181., 140., 149., 149., 146., 109.,  83.,
         46.,  40.,  18.,  11.,  13.,   5.,   2.,   2.]),
 array([0.10479787, 0.10528211, 0.10576635, 0.1062506 , 0.10673484,
        0.10721908, 0.10770332, 0.10818756, 0.1086718 , 0.10915604,
        0.10964028, 0.11012452, 0.11060876, 0.111093  , 0.11157725,
        0.11206149, 0.11254573, 0.11302997, 0.11351421, 0.11399845,
        0.11448269, 0.11496693, 0.11545117, 0.11593541, 0.11641965,
        0.11690389, 0.11738814, 0.11787238, 0.11835662, 0.11884086,
        0.1193251 ]),
 <BarContainer object of 30 artists>)
```



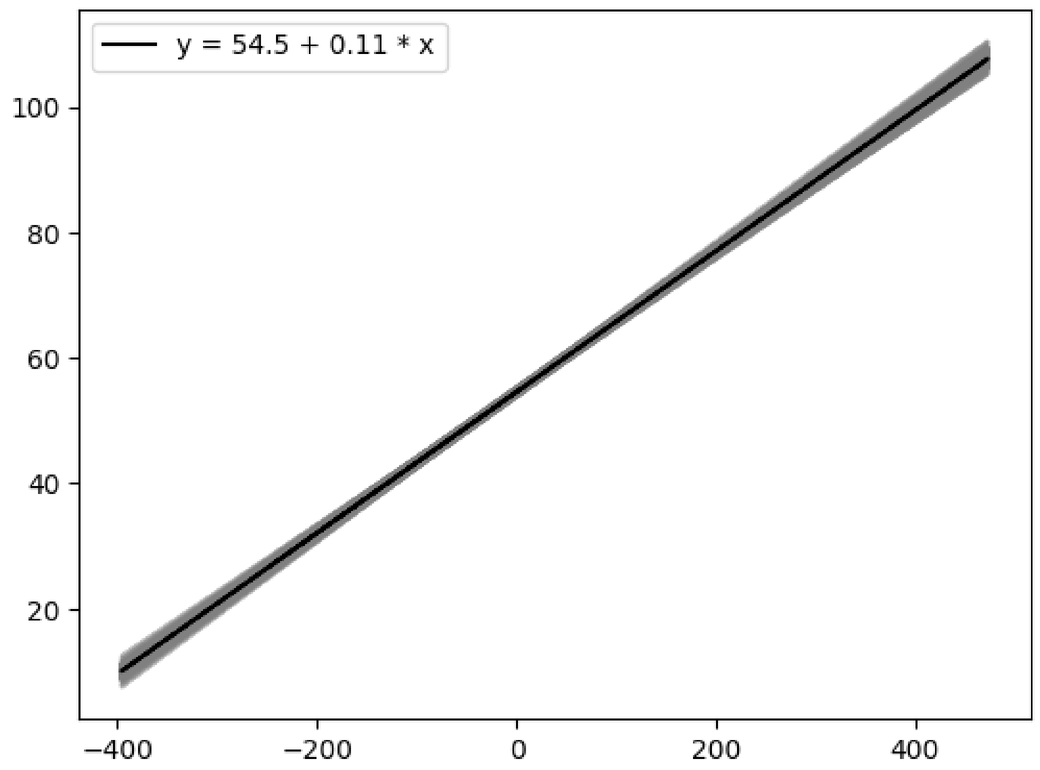
On the plot below, it can be seen that the regression line imputed using the centered X values and the obtained alpha and beta means is very good, indeed the regression model is able to capture the two variables correlation. This plot is also very similar compared to the data exploratory part one, meaning that the model seems ulteriorly converging into a good model

```
[50]: plt.scatter(x_c, Y, color='green', label='True centered observed data')
      plt.plot(x_c,  a+ b * x_c,  color='blue', lw=3, label='Gaussian regression␣
       ↪model')
      plt.title("Regression model")
      plt.xlabel('X')
      plt.ylabel('Y')
      plt.legend();
```



One of the main advantages of using the bayesian regression models is to being able to account for uncertainty of the data. From this plot though, it can be seen that there is a very little presence of it, showcasing once again the strong correlation between the two variables

[51]:
```
chosen_samples = range(0, len(alpha_values),10)

for i in range(len(chosen_samples)):
    plt.plot(x_c, post_gauss.alpha.values[i] + post_gauss.beta.values[i] * x_c,␣
 ↪c='gray', alpha=0.5)

plt.plot(x_c, a + b * x_c, c='k',label='y = {:.1f} + {:.2f} * x'.format(a, b))
plt.legend();
```



1.5.6 Predictive distribution for a an observation of the test set.

To understand how well our model performs when tested on data, we took a random sample from the dataset and used it to evaluate the model. The sample we got it the Adelphi University, New York. It has a median SAT value of 1098 and the corresponding rate within 150% of time of 62.5.

[52]:
```
prediction_sample = median_sat_values_df.sample(1, random_state=42).iloc[0]
print(prediction_sample['chronname'], "\n\t State: ",␣
 ↪prediction_sample['state'], "\n\t Median SAT score: ",␣
 ↪prediction_sample['med_sat_value'], "\n\t Graduation rate within 150% of␣
 ↪time: ", prediction_sample['grad_150_value'])
```

```
Adelphi University
         State:  New York
         Median SAT score:  1098.0
         Graduation rate within 150% of time:  62.5
```

- Predict the graduation rate within 150% of normal time of the Adelphi University of New York?
- The median SAT value of this college is 1098
- First, the model we have requires we center the value before being predicted: $x^* = 1098 - \bar{x} = 1098 - 1068 = 30$

- A simple way to make predictions is to use the posterior mean of the parameters:

$$y_{\text{pred}} = \bar{\alpha} + \bar{\beta} \cdot 30 = 54.4 + 0.11 \cdot 30 = 57.7$$

This ignores two sources of variability:

- the effect of the noise ϵ
- the uncertainty about the value of the parameters

To account for parameter uncertainty, we draw a prediction for each parameter sample $< \alpha_s, \beta_s, \sigma_s >$:

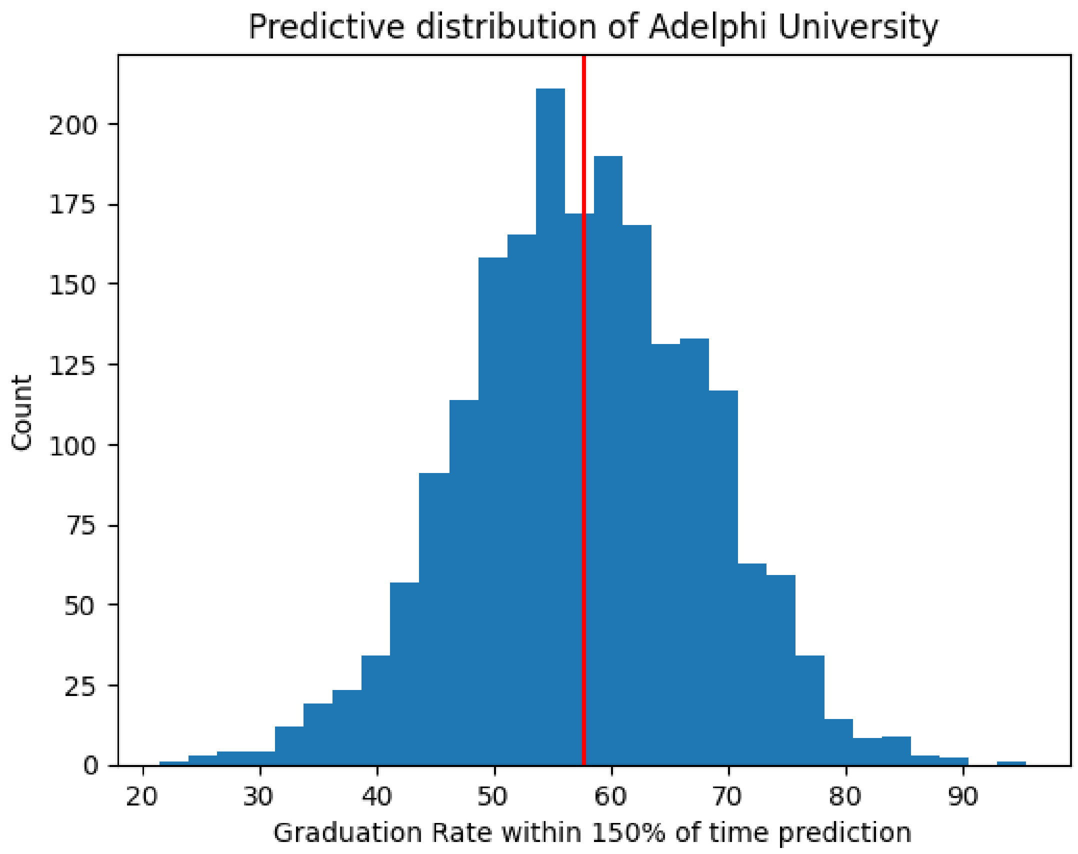
$$y_{\text{pred},s} \sim N(\alpha_s + \beta_s \cdot 30, \sigma_s)$$

$$\begin{bmatrix} \alpha_{c,1} & \beta_1 & \sigma_1 \\ \alpha_{c,2} & \beta_2 & \sigma_2 \\ \vdots & \vdots & \vdots \\ \alpha_{c,4000} & \beta_{4000} & \sigma_{4000} \end{bmatrix} \longrightarrow \begin{bmatrix} y_{\text{pred},1} \\ y_{\text{pred},2} \\ \vdots \\ y_{\text{pred},4000} \end{bmatrix}$$

[53]:
```
x_test = 30

post = az.extract_dataset(gaussian_trace)

sigma_s = post.sigma.values
alpha_s = post.alpha.values
beta_s  = post.beta.values

y_test = np.zeros(shape=len(sigma_s))

preds_sample  = np.random.normal (loc = alpha_s + beta_s * x_test, scale =␣
  ↪sigma_s)
```

```
<ipython-input-53-f7a239009069>:3: FutureWarning: extract_dataset has been
deprecated, please use extract
  post = az.extract_dataset(gaussian_trace)
```

[54]:
```
plt.hist(preds_sample, bins=30)
plt.axvline(preds_sample.mean(), color="red")
plt.title("Predictive distribution of Adelphi University")
plt.xlabel("Graduation Rate within 150% of time prediction")
plt.ylabel("Count");
```



The result of the prediction was pretty accurate with less than 5% of difference w.r.t reality. However, we decided to compute N = 50 samples in order to see what the RMSE would be. This metric would help to confirm any suspicions in quality of the model.

[55]:
```
true_sample_value = round(prediction_sample['grad_150_value'], 2)
print("True value: ", true_sample_value)
results = pd.DataFrame(preds_sample).describe (percentiles=[.025, .05, .5, .95,␣
 ↪.975])
print("Predicted value (mean of predictive distribution): ",␣
 ↪round(results[0]['mean'], 2))
```

```
True value:  62.5
Predicted value (mean of predictive distribution):  57.7
```

[56]:
```
n_samples = 50
rmse = 0
sampling_data_list = list()
for i in range(n_samples):
    sample = median_sat_values_df.sample(1).iloc[0]
    sampling_data = dict()
    x = sample['med_sat_value']
    y= sample['grad_150_value']

    x_test = x - x_bar

    preds  = np.random.normal (loc = alpha_s + beta_s * x_test, scale = sigma_s)
    results = pd.DataFrame(preds).describe()
    y_pred = round(float(results[0]['mean']), 2)
    residual = y_pred - y

    sampling_data['chronname'] = sample['chronname']
    sampling_data['state'] = sample['state']
    sampling_data['med_sat_value'] = sample['med_sat_value']
    sampling_data['med_sat_value_centered'] = x_test
    sampling_data['grad_150_value'] = sample['grad_150_value']
    sampling_data['grad_150_pred'] = y_pred
    sampling_data['residual'] = residual
    sampling_data_list.append(sampling_data)
    rmse += (residual)**2
rmse /= n_samples
rmse = np.sqrt(rmse)

print("RMSE for 10 samples: ", round(rmse, 4))
sampling_data_df = pd.DataFrame(data=sampling_data_list)
sampling_data_df.head()
```

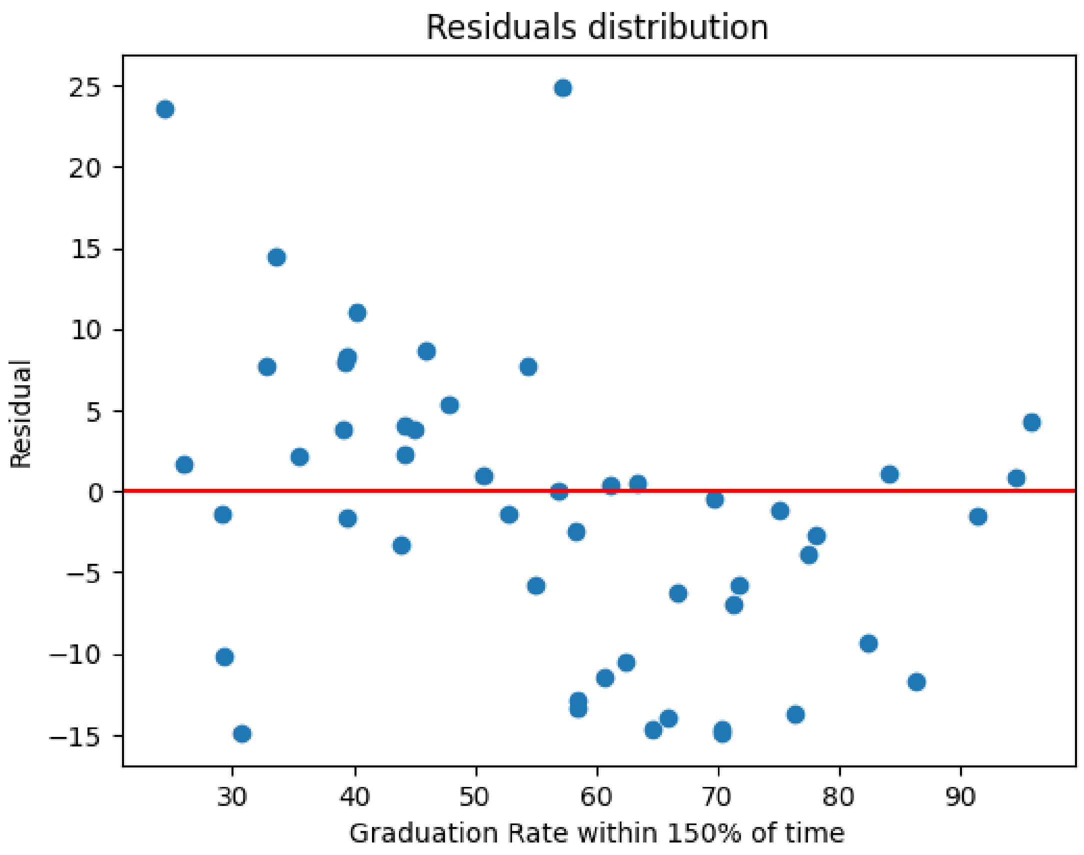
```
RMSE for 10 samples:  9.2873
```

[56]:

```
                                chronname        state  med_sat_value  \
0      Mississippi Valley State University  Mississippi          825.0
1  Millersville University of Pennsylvania  Pennsylvania        1014.0
2                   Gustavus Adolphus College    Minnesota       1224.0
3                                Lane College    Tennessee        716.0
4                  University of Evansville      Indiana        1147.0

   med_sat_value_centered  grad_150_value  grad_150_pred  residual
0             -236.489007            26.0          27.69      1.69
1              -47.489007            60.7          49.19    -11.51
2              162.510993            82.3          72.93     -9.37
3             -345.489007            30.8          15.94    -14.86
4               85.510993            63.3          63.82      0.52
```

This regression model is able to predict with good accuracy the graduation rate of a college having as data its median SAT score. The two are significantly correlated and the residuals are not that big. They are smaller if the average graduation rate is approximately close to the true data mean of the graduation rate, and a little bit sparse towards the tails of the true distribution, but overall we are satisfied with the results

[57]:
```
plt.scatter(sampling_data_df['grad_150_value'], sampling_data_df['residual'])
plt.axhline(0, color='red')
plt.title("Residuals distribution")
plt.xlabel("Graduation Rate within 150% of time")
plt.ylabel("Residual");
```


Residuals distribution
Residual
Graduation Rate within 150% of time