Bayesian Data Analysis - Assignment 4

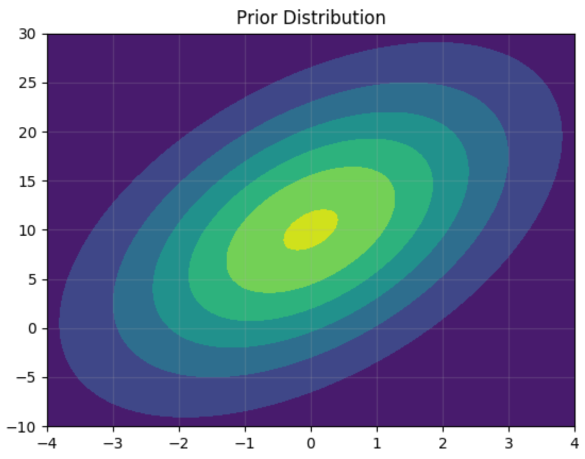
October 7, 2018

We can derive σ, μ and *convarience matrix* from the given normal distributions of $\alpha \sim N(0, 2^2)$ and $\beta \sim N(10, 10^2)$.

```python
sigma_a = 2
sigma_b = 10
mu_a = 0
mu_b = 10
cor = 0.5
cov_matrix = np.array([
    [sigma_a**2,                cor * sigma_a * sigma_b],
    [cor * sigma_a * sigma_b,   sigma_b**2]]
)
```

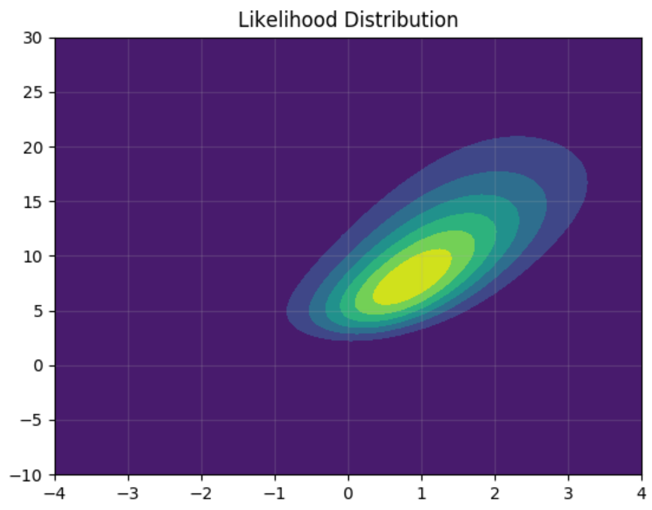
This initialization allows us to calculate and plot **prior distribution**:

```python
# create a grid and it's points using x and y ranges
alpha, beta = np.meshgrid(np.linspace(-4, 4, 100), np.linspace(-10, 30, 100))
points = np.dstack((alpha, beta))

# prior distribution
mean = np.array([mu_a, mu_b])
prior_multivar_nor = stats.multivariate_normal(mean, cov_matrix)
prior = prior_multivar_nor.pdf(points)
plt.contourf(alpha, beta, prior)
```



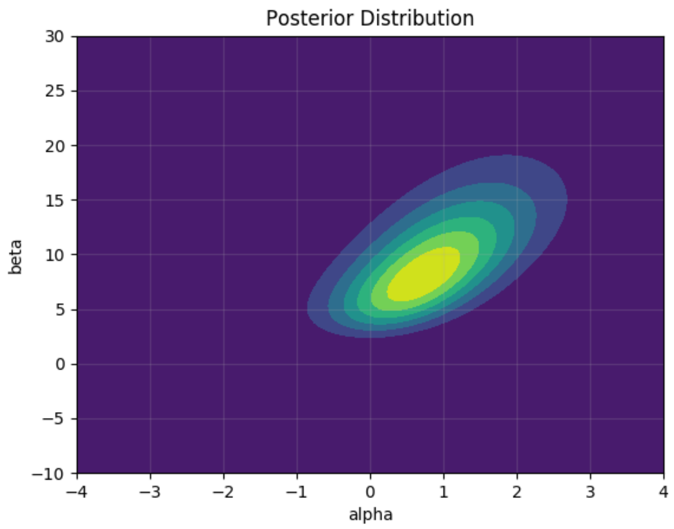
To calculate the **likelihood** though, we have to take into consideration the data from the book that indicates the values of *doses*, *deaths* and *number of animals*; and use the bioassaylp function:

```
doses = np.array([-0.86, -0.3, -0.05, 0.72])
deaths = np.array([0, 1, 3, 5])
number_of_animals = np.array([5, 5, 5, 5])

likelihood = bioassaylp(alpha, beta, doses, deaths, number_of_animals)
plt.contourf(alpha, beta, np.exp(likelihood))
```



Calculating **posterior** is straight forward, we have to just multiply the likelihood with prior:

```
posterior = prior * np.exp(likelihood)
plt.contourf(alpha, beta, posterior)
```



Using the prior distribution we can **draw a sample with a size = 10000**:

```
samples_from_prior = prior_multivar_nor.rvs(10000)
```

We can then compute **the importance ratios for each draw** like:

```
logit = 1 / (
    1 + np.exp(
        -(samples_from_prior[:, 0, None] + samples_from_prior[:, 1, None] * doses)
    )
)

weights_of_likelihood = np.prod(
    logit**deaths * (1 - logit)**(number_of_animals - deaths),
    axis=1
)
print('Shape of the weights of the likelihood: ', weights_of_likelihood.shape)
```

Consequently, **the effective sample size** S_{eff} would be calculated as:

```
weights_norm = (weights_of_likelihood) / np.sum(weights_of_likelihood)
S_eff = 1 / np.sum(weights_norm**2)
print('The effective sample size: ', round(S_eff, 4))
```

Which outputs:

```
$ The effective sample size:  2725.6818
```

We can then easily compute the **posterior mean** using importance sampling:

```
mean_posterior = sum(
  weights_of_likelihood[ : , None] * samples_from_prior
) / sum(weights_of_likelihood)
print('The posterior mean of alpha : ', round(mean_posterior[0], 4))
print('The posterior mean of beta  : ', round(mean_posterior[1], 4))
```

Which are:

```
$ The posterior mean of alpha :  0.9786
$ The posterior mean of beta  :  10.4321
```

Using importance resampling we can obtain a **posterior sample of size 1000** of alpha and beta:

```
gen_nums = np.random.RandomState(0).choice(
  a=10000, size=1000, replace=False, p=weights_norm
)
resamples = samples_from_prior[gen_nums]
print('The posterior mean of alpha: ', round(np.mean(resamples[:, 0]), 4))
print('The posterior mean of beta: ', round(np.mean(resamples[:, 1]), 4))
```

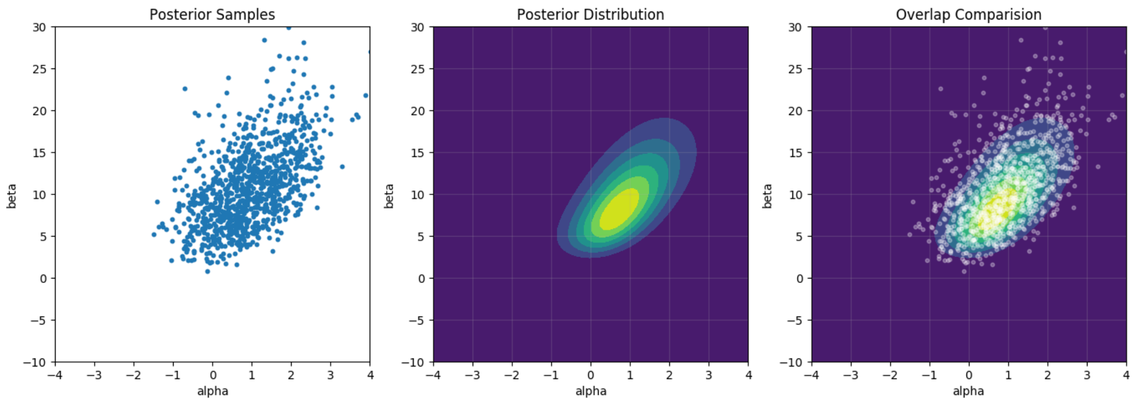
Which are:

```
$ The posterior mean of alpha:  0.9359
$ The posterior mean of beta:  10.3614
```

If we combine these two we will have $\alpha = [\mathbf{0.9359,\ 0.9786}]$ and $beta = [\mathbf{10.4321,\ 10.3614}]$.

Finally, we can **plot a scatterplot of the obtained posterior sample** from importance resampling and compare it to the heatmap:

```
fig, axes = plt.subplots(1, 3, figsize=(16, 5))
axes[0].scatter(resamples[:, 0], resamples[:, 1], 10)
axes[1].grid(linewidth=0.9, alpha=0.2)
axes[2].contourf(alpha, beta, posterior)
axes[2].scatter(resamples[:, 0], resamples[:, 1], 10, alpha=0.3, color='w')
```



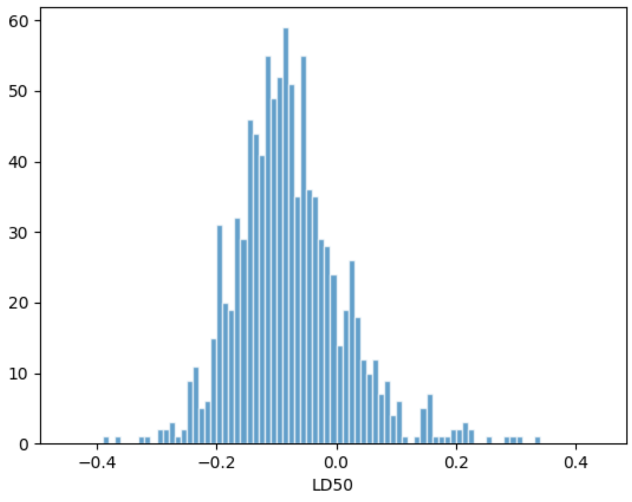
The **estimate** $p(beta > 0|x, n, y)$ **probability** can be calculated as:

```
beta_resample = resamples[:, 1]
alpha_resample = resamples[:,0]
pos = beta_resample > 0
probab_drug_harmful = (beta_resample[pos].size/(beta_resample.size))
print('Probability of the drug being harmful: ', round(probab_drug_harmful, 3))
```

```
$ Probability of the drug being harmful is very close to:  1
```

And the **histogram** can be plotted like:

```
sample_ld50 = -alpha_resample[pos]/beta_resample[pos]
y_range = np.arange(-0.45, 0.45, 0.01)
plt.hist(sample_ld50, y_range, ec='white', alpha=0.7)
```



Appendix A Source code

```python
import matplotlib
matplotlib.use('TkAgg')
import matplotlib.pyplot as plt
from mpl_toolkits.mplot3d import Axes3D
from scipy import stats
import numpy as np

def bioassaylp(a, b, x, y, n):
    # last axis for the data points
    a = np.expand_dims(a, axis=-1)
    b = np.expand_dims(b, axis=-1)
    # these help using chain rule in derivation
    t = a + b*x
    et = np.exp(t)
    z = et/(1.+et)
    # negative log posterior (error function to be minimized)
    lp = np.sum(y*np.log(z)+ (n-y)*np.log(1.0-z), axis=-1)
    return lp

# Init all the params based on the description
sigma_a = 2
sigma_b = 10
mu_a = 0
mu_b = 10
cor = 0.5
cov_matrix = np.array([
  [sigma_a**2,                cor * sigma_a * sigma_b],
  [cor * sigma_a * sigma_b,   sigma_b**2]]
)

# create a grid and it's points using x and y ranges
alpha, beta = np.meshgrid(np.linspace(-4, 4, 100), np.linspace(-10, 30, 100))
```

```python
points = np.dstack((alpha, beta))

# prior distribution
mean = np.array([mu_a, mu_b])
prior_multivar_nor = stats.multivariate_normal(mean, cov_matrix)
prior = prior_multivar_nor.pdf(points)

plt.contourf(alpha, beta, prior)
plt.title('Prior Distribution')
plt.grid(linewidth=0.9, alpha=0.2)
plt.savefig('./ex4/report/1_prior_distribution.png')
plt.figure()

# likelihood
doses = np.array([-0.86, -0.3, -0.05, 0.72])
deaths = np.array([0, 1, 3, 5])
number_of_animals = np.array([5, 5, 5, 5])

likelihood = bioassaylp(alpha, beta, doses, deaths, number_of_animals)
plt.contourf(alpha, beta, np.exp(likelihood))
plt.title('Likelihood Distribution')
plt.grid(linewidth=0.9, alpha=0.2)
plt.savefig('./ex4/report/2_likelihood_distribution.png')
plt.figure()

'''
1. Calculate the posterior density in a grid of points around the prior
(alpha: 0 +- 4, beta: 10 +- 20) and plot a heatmap of the density.
'''
posterior = prior * np.exp(likelihood)
plt.contourf(alpha, beta, posterior)
plt.xlabel('alpha')
plt.ylabel('beta')
plt.title('Posterior Distribution')
plt.grid(linewidth=0.9, alpha=0.2)
plt.savefig('./ex4/report/3_posterior_distribution.png')
plt.figure()

'''
2. Sample draws of alpha and beta from the prior distribution.
'''
samples_from_prior = prior_multivar_nor.rvs(10000)
print('Shape of the samples from prior: ', samples_from_prior.shape)

'''
3. Compute the importance ratios for each draw (target distribution is the posterior).
'''
logit = 1 / (
    1 + np.exp(
        -(samples_from_prior[:, 0, None] + samples_from_prior[:, 1, None] * doses)
    )
)

weights_of_likelihood = np.prod(
    logit**deaths * (1 - logit)**(number_of_animals - deaths),
    axis=1
)
print('Shape of the weights of the likelihood: ', weights_of_likelihood.shape)

'''
4. Using the importance ratios, compute the effective sample size Seff and report it.
If Seff is less than 1000, repeat the importance sampling with more draws.
'''
weights_norm = (weights_of_likelihood) / np.sum(weights_of_likelihood)
S_eff = 1 / np.sum(weights_norm**2)
print('The effective sample size: ', round(S_eff, 4))

'''
5. Compute the posterior mean using importance sampling and report it.
'''
mean_posterior = sum(
  weights_of_likelihood[ : , None] * samples_from_prior
  ) / sum(weights_of_likelihood)
print('The posterior mean of alpha : ', round(mean_posterior[0], 4))
print('The posterior mean of beta  : ', round(mean_posterior[1], 4))

'''
6. Use importance resampling to obtain a posterior sample of size 1000
  of alpha and beta.
'''
gen_nums = np.random.RandomState(0).choice(
  a=10000, size=1000, replace=False, p=weights_norm
)
resamples = samples_from_prior[gen_nums]
print('Mean alpha: ', round(np.mean(resamples[:, 0]), 4))
print('Mean beta: ', round(np.mean(resamples[:, 1]), 4))

'''
7. Using the posterior sample obtained via importance resampling:
    7.1 Plot a scatterplot of the obtained posterior sample and compare that to
        the heatmap plotted earlier.
'''
fig, axes = plt.subplots(1, 3, figsize=(16, 5))
axes[0].set_xlim([-4, 4])
axes[0].set_ylim([-10, 30])
axes[0].set_xlabel('alpha')
axes[0].set_ylabel('beta')
axes[0].set_title('Posterior Samples')
axes[0].scatter(resamples[:, 0], resamples[:, 1], 10)

axes[1].set_xlim([-4, 4])
axes[1].set_ylim([-10, 30])
axes[1].set_xlabel('alpha')
axes[1].set_ylabel('beta')
axes[1].set_title('Posterior Distribution')
axes[1].contourf(alpha, beta, posterior)
axes[1].grid(linewidth=0.9, alpha=0.2)

axes[2].set_xlim([-4, 4])
axes[2].set_ylim([-10, 30])
```

```python
axes[2].set_xlabel('alpha')
axes[2].set_ylabel('beta')
axes[2].set_title('Overlap Comparision')
axes[2].contourf(alpha, beta, posterior)
axes[2].scatter(resamples[:, 0], resamples[:, 1], 10, alpha=0.3, color='w')
axes[2].grid(linewidth=0.9, alpha=0.2)

plt.subplots_adjust(left=0.1, right=0.9, top=0.9, bottom=0.1)
plt.savefig('./ex4/report/4_posterior_comparision.png')
plt.figure()

'''
    7.2 Report an estimate for p(beta > 0|x, n, y), that is, the
    probability that the drug is harmful.
'''
beta_resample = resamples[:, 1]
alpha_resample = resamples[:,0]
pos = beta_resample > 0
probab_drug_harmful = (beta_resample[pos].size/(beta_resample.size))
print('Probability of the drug being harmful: ', round(probab_drug_harmful, 3))

'''
    7.3 Draw a histogram of the draws from the posterior distribution of the LD50
        conditional on beta > 0 (see Figure 3.4).
'''
sample_ld50 = -alpha_resample[pos]/beta_resample[pos]
y_range = np.arange(-0.45, 0.45, 0.01)
plt.hist(sample_ld50, y_range, ec='white', alpha=0.7)

plt.xlabel('LD50')
plt.savefig('./ex4/report/5_histogram.png')
plt.figure()
```