

Exercise4

February 19, 2018

1 Exercise 4

1.1 Some Theory

For the data in this exercise the dose-response relation can be modelled as $\text{logit}(i)=+x_i$.

The liklihood for each group for such a model is:

$$p(y_i|\alpha, \beta, n_i, x_i) \propto [\text{logit}^{-1}(\alpha + \beta x_i)]^{y_i} [\text{logit}^{-1}(\alpha + \beta x_i)]^{n_i - y_i}$$

Given the prior distribution of the parameters $p(\alpha, \beta)$ it is also possible to compute their posterior distribution as:

$$p(\alpha, \beta|y, n, x) \propto p(\alpha, \beta) \prod_{i=1}^k p(y_i|\alpha, \beta, n_i, x_i)$$

1.2 4.a

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In [1]: %matplotlib inline
        from scipy.stats import multivariate_normal
        from scipy.special import expit # aka logistic
        import numpy as np
        import matplotlib.pyplot as plt
        import matplotlib
        from utilities_and_data import plot_tools

In [2]: # edit default plot settings
        plt.rc('font', size=12)
        # apply custom background plotting style
        plt.style.use(plot_tools.custom_styles['gray_background'])

In [3]: # Data from the Animal trials
        x = np.array([-0.86, -0.30, -0.05, 0.73])
        n = np.array([5, 5, 5, 5])
        y = np.array([0, 1, 3, 5])

In [4]: alpha_mean = 0
        alpha_var = 2**2
        beta_mean = 10
        beta_var = 10**2
        corr = 0.5
        cov = np.sqrt(alpha_var) * np.sqrt(beta_var) * corr
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N = 500
A = np.linspace(-10, 10, N)
B = np.linspace(-10, 40, N)
AB = np.dstack(np.meshgrid(A, B))
prior = multivariate_normal.pdf(AB, [alpha_mean, beta_mean], [[alpha_var, cov], [cov, beta_var]])

theta = 1 / (np.exp(-(A[:, None] + B[:, None, None] * x)) + 1)
loglike = np.sum(np.log(theta ** y * (1 - theta) ** (n - y)), axis=2)
logp = loglike + np.log(prior)
logp -= logp.max()
p = np.exp(logp)
p = p/np.sum(p)

# sample from the grid
nsamp = 1000
samp_indices = np.unravel_index(
    np.random.choice(p.size, size=nsamp, p=p.ravel()),
    p.shape
)
samp_A = A[samp_indices[1]]
samp_B = B[samp_indices[0]]
# add random jitter, see BDA3 p. 76
samp_A += (np.random.rand(nsamp) - 0.5) * (A[1] - A[0])
samp_B += (np.random.rand(nsamp) - 0.5) * (B[1] - B[0])

# samples of LD50 conditional beta > 0
bpi = samp_B > 0
samp_ld50 = -samp_A[bpi] / samp_B[bpi]

# ===== Plotting
plt.figure(figsize=(10, 24))

plt.subplot(5, 1, 1)
plt.imshow(prior, origin='lower', aspect='auto', extent=(A[0], A[-1], B[0], B[-1]), interpolation='nearest')
plt.xlim([A[0], A[-1]])
plt.ylim([B[0], B[-1]])
plt.xlabel(r'$\alpha$', fontsize=20)
plt.ylabel(r'$\beta$', fontsize=20)
plt.title('prior')

plt.subplot(5, 1, 2)
plt.imshow(np.exp(loglike), origin='lower', aspect='auto', extent=(A[0], A[-1], B[0], B[-1]), interpolation='nearest')
plt.xlim([A[0], A[-1]])
plt.ylim([B[0], B[-1]])
plt.xlabel(r'$\alpha$', fontsize=20)
plt.ylabel(r'$\beta$', fontsize=20)
plt.title('likelihood')

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plt.subplot(5, 1, 3)
plt.imshow(p, origin='lower', aspect='auto', extent=(A[0], A[-1], B[0], B[-1]), interpol
plt.xlim([A[0], A[-1]])
plt.ylim([B[0], B[-1]])
plt.xlabel(r'$\alpha$', fontsize=20)
plt.ylabel(r'$\beta$', fontsize=20)
plt.title('posterior')

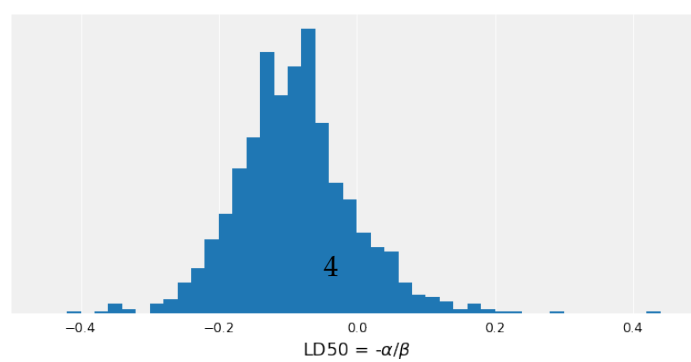
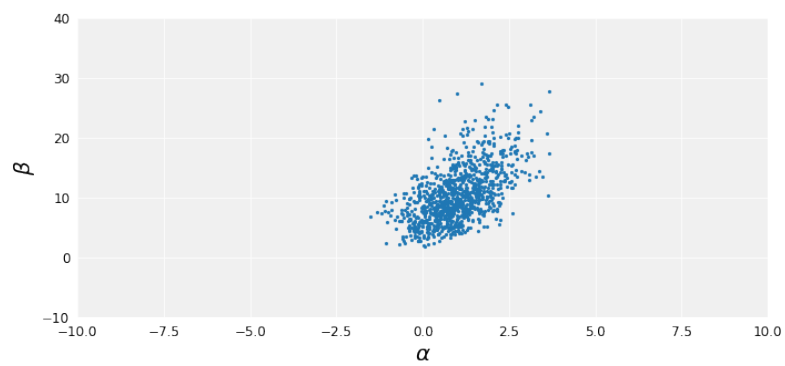
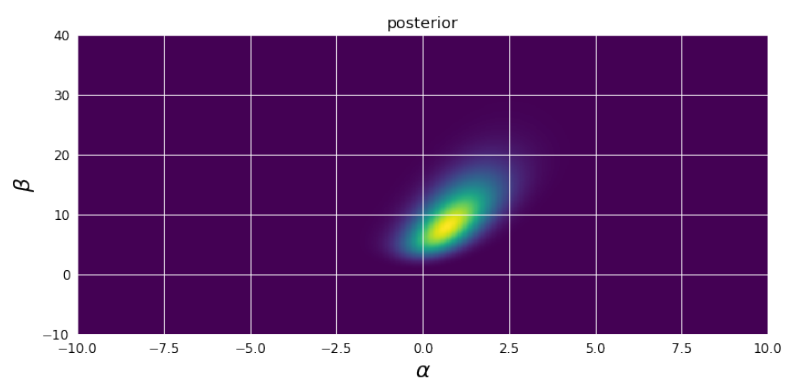
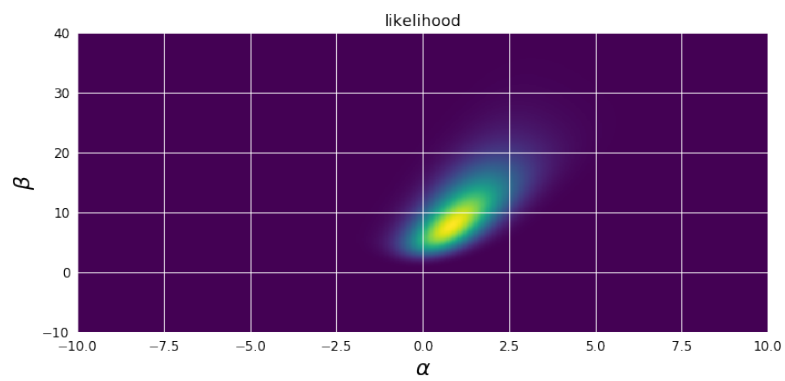
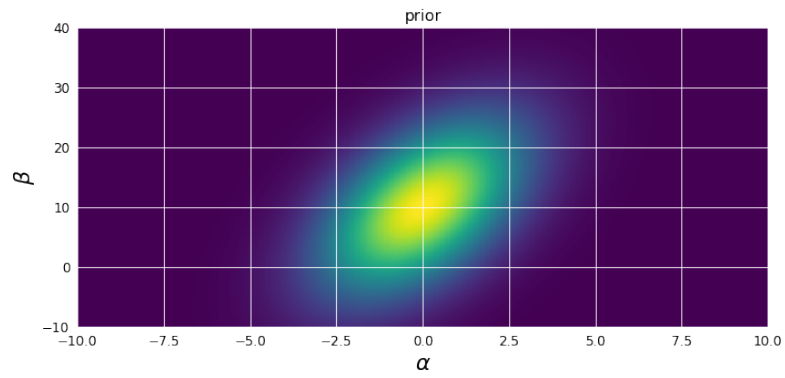
# plot the samples
plt.subplot(5, 1, 4)
plt.scatter(samp_A, samp_B, 10, linewidth=0)
plt.xlim([A[0], A[-1]])
plt.ylim([B[0], B[-1]])
plt.xlabel(r'$\alpha$', fontsize=20)
plt.ylabel(r'$\beta$', fontsize=20)

# plot the histogram of LD50
plt.subplot(5, 1, 5)
plt.hist(samp_ld50, np.arange(-0.5, 0.51, 0.02))
plt.xlim([-0.5, 0.5])
plt.xlabel(r'LD50 =  $-\alpha/\beta$ ', fontsize=16)
plt.yticks(())
plt.tight_layout()
plt.show()

print(np.mean(samp_ld50))
print(np.var(samp_ld50))

print("p(beta>0|x,y) > %d/%d" % ((np.sum(samp_B>0)-1), samp_B.size))

```



```
-0.0894483548711  
0.00756591955043  
p(beta>0|x,y) > 999/1000
```

1.3 4.b

Looking at the contour plots you can see that the posterior has been rounded in respect to the likelihood. this rounding is provided by the oval prior

1.4 4.c

From the 1000 draws of the posterior distribution, it is possible to estimate $p(>0 | x, n, y)$, that is the probability that the drug is harmful. Since of the 1000 draws all of them had positive values of , that probability is roughly estimated to exceed 0.999.