APMTH 207: Advanced Scientific Computing:

Stochastic Methods for Data Analysis, Inference and Optimization

Homework 11

Harvard University Spring 2017

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Due Date: Monday, April 23rd, 2018 at 11:59pm

Instructions:

- Upload your final answers as an iPython notebook containing all work to Canvas.
- Structure your notebook and your work to maximize readability.

```
In [1]: import numpy as np
   import pandas as pd
   import pymc3 as pm
   import theano.tensor as T

   import matplotlib
   import matplotlib.pyplot as plt

   import seaborn as sns
   sns.set_style("whitegrid", {'axes.grid' : False})
   sns.set_context('talk')
   %matplotlib inline
```

The AM207 Cambridge Nursery

A plant nursery in Cambridge is exprimentally cross-breeding two types of hibiscus flowers: blue and pink. The goal is to create an exotic flower whose petals are pink with a ring of blue on each.

There are four types of child plant that can result from this cross-breeding:

- Type 1: blue petals
- Type 2: pink petals
- Type 3: purple petals
- Type 4: pink petals with a blue ring on each (the desired effect).

Out of 197 initial cross-breedings, the nursery obtained the following distribution over the four types of child plants:

$$Y = (y_1, y_2, y_3, y_4) = (125, 18, 20, 34)$$

where y_i represents the number of child plants that are of type i.

The nursery then consulted a famed Harvard plant geneticist, who informed them that the probability of obtaining each type of child plant in any single breeding experiment is as follows:

$$\frac{\theta+2}{4}, \frac{1-\theta}{4}, \frac{1-\theta}{4}, \frac{\theta}{4}.$$

Unfortunately, the geneticist did not specify the quantity θ .

Clearly, the nursery is interested in understanding how many cross-breeding they must perform, on average, in order to obtain a certain number of child plants with the exotic blue rings. To do this they must be able to compute θ .

The owners of the nursery, being top students in AM207, decided to model the experiment in hopes of discovering θ using the results from their 197 initial experiments.

They chose to model the observed data using a multinomial model and thus calculated the likelihood to be:

$$p(y| heta) \propto (2+ heta)^{y_1}(1- heta)^{y_2+y_3}\, heta^{y_4}$$

Being good Bayesians, they also imposed a prior on θ , Beta(a, b).

Thus, the posterior is:

$$p(\theta|Y) = (2+ heta)^{y_1}(1- heta)^{y_2+y_3}\, heta^{y_4}\, heta^{a-1}\,(1- heta)^{b-1}.$$

If the nursery owners are able to sample from the posterior, they would be able to understand the distribution of θ and make appropriate estimates.

Problem 1. Sampling using data augmentation

Realizing that it would be difficult to sample from the posterior directly and after being repeatedly frustrated by attempts of Metropolis-Hastings and Gibbs sampling for this model, the nursery owners decided to augment their model and hopefully obtain a friendlier looking distribution that allows for easy sampling.

They augment the data with a new variable z such that:

$$z+(y_1-z)=y_1.$$

That is, using z, we are breaking y_1 , the number of type I child plants, into two subtypes. Let the probability of obtaining the two subtype be 1/2 and $\theta/4$, respectively. Now, we can interpret y_1 to be the total number of trials in a binomial trial. Thus, the new likelihood can be written as

$$p(y,z| heta) \propto inom{y_1}{z}igg(rac{1}{2}igg)^{y_1-z}igg(rac{ heta}{4}igg)^z(1- heta)^{y_2+y_3} heta^{y_4}$$

Derive the joint posterior $p(\theta, z|y)$ and sample from it using Gibbs sampling.

Visualize the distribution of theta and, from this distribution, estimate the probability of obtaining a type 4 child plant (with the blue rings) in any cross-breeding experiment.

Answer to Problem 1

We know $heta\sim ext{Beta}(a,b)$, and $p(y,z| heta)\propto inom{y_1}{z}ig(rac{1}{2}ig)^{y_1-z}\Big(rac{ heta}{4}\Big)^z(1- heta)^{y_2+y_3}\, heta^{y_4}$. Thus

$$p(heta,z|y) \propto p(y,z| heta) \, p(heta) = inom{y_1}{z} igg(rac{1}{2}igg)^{y_1-z} igg(rac{ heta}{4}igg)^z (1- heta)^{y_2+y_3} \, heta^{y_4} \, heta^{a-1} (1- heta)^{b-1}$$

To obtain conditionals, we keep the relevant variables.

$$p(heta|y,z) \propto heta^{z+y_4+a-1}(1- heta)^{y_2+y_3+b-1}$$

i.e.,

$$heta|y,z\sim ext{Beta}(z+y_4+a,y_2+y_3+b).$$

And

$$p(z|y, heta) \propto inom{y_1}{z}igg(rac{2}{ heta+2}igg)^{y_1-z}igg(rac{ heta}{ heta+2}igg)^z$$

i.e.,

$$z|y, heta \sim ext{Binomial}(y_1,rac{ heta}{ heta+2}).$$

We can implement Gibbs sampling using the above conditionals. And we simply choose a uniform prior for θ (i.e., a=b=1).

```
In [2]: def corrplot(trace, maxlags=50):
    plt.acorr(trace-np.mean(trace), normed=True, maxlags=maxlags);
    plt.xlim([0, maxlags])

def effective_sample_size(data, step=1):
```

```
# References:
    # https://code.google.com/p/biopy/source/browse/trunk/biopy/bayesianStats.
py?r=67
    # https://am207.github.io/2018spring/wiki/tetchygibbs.html
    n = len(data)
    assert n > 1
    maxlags = min(n//3, 1000)
    gamma stat = [0, ] * maxlags
    var_stat = 0.0
    if type(data) != np.ndarray:
        data = np.array(data)
    data normed = data - data.mean()
    for lag in range(maxlags):
        v1 = data normed[:n-lag]
        v2 = data normed[lag:]
        v = v1 * v2
        gamma_stat[lag] = sum(v) / len(v)
        if lag == 0:
            var_stat = gamma_stat[0]
        elif lag % 2 == 0:
            s = gamma_stat[lag-1] + gamma_stat[lag]
            if s > 0:
                var_stat += 2 * s
            else:
                break
    act = step * var_stat / gamma_stat[0]
    ess = step * n / act
    return ess
def print ess(data):
    ess1 = effective_sample_size(data[:, 0])
    ess2 = effective_sample_size(data[:, 1])
    print('Effective size for theta:', ess1, ' of', len(data), 'samples; effec
tive rate:', ess1/len(data))
    print('Effective size for z:', ess2, ' of', len(data), 'samples; effective
 rate:', ess2/len(data))
class Gibbs:
    def init (self, a=1, b=1, y=np.array([125, 18, 20, 34])):
        self.a = a
        self.b = b
        self.y = y
    def run(self, n=20000, x_init=np.array([0.5, 0]), seed=0):
        a = self.a
        b = self.b
        y = self.y
```

```
a0 = y[3] + a
    b1 = y[1] + y[2] + b
    samples = np.empty((n+1, 2))
    samples[0] = x_init
    if seed is not None:
        np.random.seed(seed)
    for i in range(1, n+1):
        a1 = samples[i-1, 1] + a0
        samples[i, 0] = np.random.beta(a1, b1)
        p = samples[i, 0] / (samples[i, 0] + 2)
        samples[i, 1] = np.random.binomial(y[0], p)
    self.n = n
    self.samples = samples[1:]
    return self
def process(self, burnin=0, thin=1):
    self.burnin = burnin
    self.thin = thin
    self.samples2 = self.samples[burnin::thin]
    return self
```

```
In [3]: g0 = Gibbs().run().process(thin=2)
```

```
In [4]: plt.figure(figsize=(10, 3))

plt.subplot(1, 2, 1)
    corrplot(g0.samples[:, 0])
    plt.ylabel(r'autocorrelation($\theta$)')

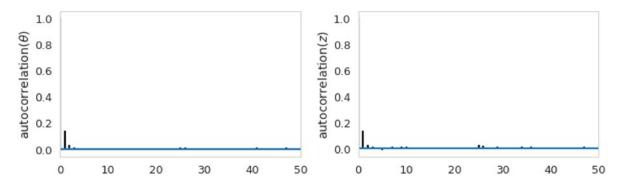
plt.subplot(1, 2, 2)
    corrplot(g0.samples[:, 1])
    plt.ylabel('autocorrelation($z$)')
    plt.tight_layout()

print('No burnin and thining:')
    print_ess(g0.samples)
```

No burnin and thining:

Effective size for theta: 14612.3871292 of 20000 samples; effective rate: 0. 73061935646

Effective size for z: 14841.4240569 of 20000 samples; effective rate: 0.7420 71202847



```
In [5]: plt.figure(figsize=(10, 3))

plt.subplot(1, 2, 1)
    corrplot(g0.samples2[:, 0])
    plt.ylabel(r'autocorrelation($\theta$)')

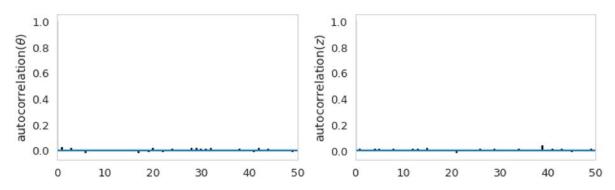
plt.subplot(1, 2, 2)
    corrplot(g0.samples2[:, 1])
    plt.ylabel('autocorrelation($z$)')
    plt.tight_layout()

print('burnin = {}, thining = {}:'.format(g0.burnin, g0.thin))
    print_ess(g0.samples2)
```

burnin = 0, thining = 2:

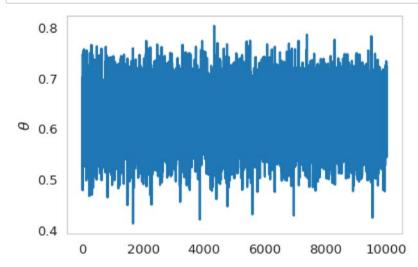
Effective size for theta: 9592.65625146 of 10000 samples; effective rate: 0. 959265625146

Effective size for z: 9406.20749842 of 10000 samples; effective rate: 0.9406 20749842



As we can see, autocorrelations are negligible after thining at 2.

```
In [6]: thetas = g0.samples2[:, 0]
    plt.plot(thetas);
    plt.ylabel(r'$\theta$');
```

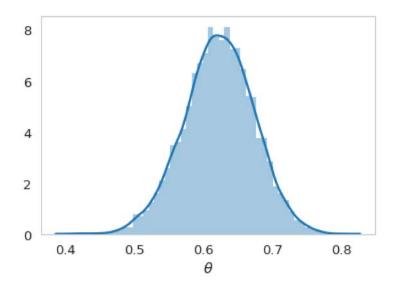


We can visualize the distribution of θ as follows.

```
In [7]: sns.distplot(thetas);
plt.xlabel(r'$\theta$');

print('mean(theta) = {}'.format(np.mean(thetas)))
print('std(theta) = {}'.format(np.std(thetas)))
```

mean(theta) = 0.6229266753714496 std(theta) = 0.05064704358302179



The estimate of the probability of obtaining a type 4 child plant is 0.1557. The 2-sigma envelope is [0.1304, 0.1811].

Problem 2. Finding the MLE using Expectation Maximization

Treat the augmented model as a latent variable model.

Part A.

Write down an expression (up to unimportant constants - you must decide what unimportant means) for each of the following:

- (1) the observed data log likelihood
- (2) the complete(full) data log likelihood

Hint: You should already have the observed data likelihood and the complete data likelihood from Problem 1, you just need to take their logs for this problem.

(3) the Auxilary function, $Q(\theta, \theta^{(t-1)})$, or the expected complete(full) data log likelihood, defined by $Q(\theta, \theta^{(t-1)}) = \mathbb{E}_{Z|Y=y,\Theta=\theta^{t-1}}[\text{the complete data log likelihood}]$

In other words $Z|Y=y,\Theta=\theta^{t-1}$ is $q(z,\theta_{old})$ from lecture at the end of the E-step and Q is the z-posterior expectation (at θ_{old}) of the full data log likelihood, which is the ELBO minus the entropy of q (which being evaluated at θ_{old} is not dependent on θ and thus irrelevant for maximization).

Part B:

We will maximize the likelihood through Expectation Maximization (EM). In order to preform EM, we must iterate through the following steps

- (Expectation) Compute the Auxilary function, $Q(heta, heta^{t-1})$ (the expectation of the full data likelihood)
- (Maximization) Compute $\theta^t = \mathrm{argmax}_{\theta} Q(\theta, \theta^{(t-1)})$

Thus, you must compute exact formulae for the following:

- 1. the Auxiliary function, $Q(\theta, \theta^{(t-1)})$, for a given $\theta^{(t-1)}$. That is, compute the expectation of the complete data log likelihood.
- 2. θ^t , by maximizing the Auxiliary function $Q(\theta, \theta^{(t-1)})$.

Hint: You don't actually need to do any difficult optimization for the M-step. After taking the expectation of the complete data log likelihood in the E-step, match your $Q(\theta, \theta^{(t-1)})$ to the log pdf of a familiar distribution, then use the known formula for the mode of this distribution to optimize $Q(\theta, \theta^{(t-1)})$.

Use these to **estimate the MLE** of θ using EM (choose your own reasonable criterion for convergence).

Answer to Problem 2 Part A

Let n be the total number of initial cross-breedings (n=197 in this case); let C_i represent unimportant constants.

(1) the observed data log likelihood

$$y| heta \sim ext{Multinomial}\left(y; n, rac{ heta+2}{4}, rac{1- heta}{4}, rac{1- heta}{4}, rac{ heta}{4}
ight)$$

$$\log p(y|\theta) = y_1 \log(2+\theta) + (y_2 + y_3) \log(1-\theta) + y_4 \log \theta + C_0$$

(2) the complete (full) data log likelihood

$$\log p(y,z| heta) = \loginom{y_1}{z} + (y_1-z)\lograc{1}{2} + z\lograc{ heta}{4} + (y_2+y_3)\log(1- heta) + y_4\log heta + C_1$$

(3) the Auxilary function

We know from problem 1 that

$$z|y, heta \sim \mathrm{Binomial}(y_1,rac{ heta}{ heta+2})$$

. Thus,

$$\mathbb{E}_{z|y, heta^{t-1}}(z)=rac{y_1 heta^{t-1}}{ heta^{t-1}+2}.$$

Let $F(z, \theta^{t-1})$ represent terms not involving θ (including unimportant constants), then

$$egin{aligned} Q(heta, heta^{t-1}) &= \mathbb{E}_{z|y, heta^{t-1}}[\log p(y,z| heta)] = \ \mathbb{E}_{z|y, heta^{t-1}}\left[\loginom{y_1}{z} + (y_1-z)\lograc{1}{2} + z\lograc{ heta}{4} + (y_2+y_3)\log(1-t)
ight] \ &= F(z, heta^{t-1}) + \mathbb{E}_{z|y, heta^{t-1}}[z\log heta + y_4\log heta + (y_2+y_3)\log(1- heta)] \ &= F(z, heta^{t-1}) + (\mathbb{E}_{z|y, heta^{t-1}}(z) + y_4)\log heta + (y_2+y_3)\log(1- heta), \end{aligned}$$

where

$$\mathbb{E}_{z|y, heta^{t-1}}(z) = rac{y_1 heta^{t-1}}{ heta^{t-1}+2}.$$

Answer to Problem 2 Part B

At E-step, we need to evaluate

$$\mathbb{E}_{z|y, heta^{t-1}}(z) = rac{y_1 heta^{t-1}}{ heta^{t-1}+2}.$$

At M-step, we know

$$Q(heta, heta^{t-1}) = \ F(z, heta^{t-1}) + (\mathbb{E}_{z|y, heta^{t-1}}(z) + y_4) \log heta + (y_2 + y_3) \log (1 - heta).$$

Let
$$\frac{\partial Q(\theta, \theta^{t-1})}{\partial heta} = 0$$
, we get

$$heta^t = rac{y_4 + \mathbb{E}_{z|y, heta^{t-1}}(z)}{y_2 + y_3 + y_4 + \mathbb{E}_{z|y, heta^{t-1}}(z)}.$$

We can iterate the process until θ converges.

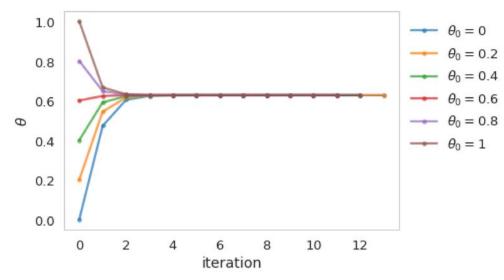
```
In [2]:
    def __init__(self, y=np.array([125, 18, 20, 34])):
        self.y = y

    def run(self, theta_init=0, max_iter=1000, thres=1e-10):
        y = self.y
        zs = []
        thetas = [theta_init]
        for _ in range(max_iter):
             zs.append(y[0]*thetas[-1]/(thetas[-1]+2))
             thetas.append((y[3]+zs[-1])/(y[1]+y[2]+y[3]+zs[-1]))
        if abs(thetas[-1]-thetas[-2]) < thres:
             break
        self.zs = zs
        self.thetas = thetas
        return self</pre>
```

We can run the algorithm from several different initial θ s to see whether they converge to the same point.

```
In [3]: ems = [EM().run(theta_init=t) for t in [0, 0.2, 0.4, 0.6, 0.8, 1]]

for em in ems:
    plt.plot(range(len(em.thetas)), em.thetas, '.-', alpha=0.7, label=r'$\theta = _0={}$'.format(em.thetas[0]));
    plt.legend(bbox_to_anchor=(1, 1));
    plt.xlabel('iteration');
    plt.ylabel(r'$\theta$');
```



As we can see, they all converge to the same point.

```
In [4]: print('The estimate of the MLE of theta using EM is {:.4f}.'.format(ems[0].the
    tas[-1]))
```

The estimate of the MLE of theta using EM is 0.6268.