Lab 4_MCM

April 23, 2018

```
In [3]: import numpy as np
        import matplotlib.pyplot as plt
        from scipy.special import gamma as gamma
        import scipy.stats as stats

        %matplotlib inline
```

1 Lab 4: Heirarchial Models in Meta-Study Analysis

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```
In [46]: def posterior(fx):

             mu = fx[0]
             tau_sq = fx[1]
            # print (mu, tau_sq)

             odds_ratio = [1.06, -0.1, 0.62, 0.02, 1.07, -0.02, -0.12, -0.38, 0.51, 0.0, 0.38, 0
             sigma_i = [0.37, 0.11, 0.22, 0.11, 0.12, 0.12, 0.22, 0.23, 0.18, 0.32, 0.20, 0.25]

             prior = np.log(stats.norm.pdf(mu, 0, 1000.*tau_sq))+ np.log(stats.gamma.pdf(1/tau_s

             overall_likelihood = 0
             for i in range(len(odds_ratio)):
                 exp_part1 = (mu*sigma_i[i]**2 + odds_ratio[i]*tau_sq)**2/(sigma_i[i]**2 + tau_s
                 exp_part_all = (-mu**2*sigma_i[i]**2 - odds_ratio[i]**2*tau_sq + exp_part1)/(2*
                 olstep_i = np.log(1/np.sqrt(2*np.pi*(sigma_i[i]**2 + tau_sq))) + exp_part_all
                 overall_likelihood = overall_likelihood + olstep_i

             return overall_likelihood + prior

In [48]: # proposal
         def proposal(xc, delta):
             # change tau_sq and mu with delta
             tau_sq = -1
             mu = np.random.normal(xc[0], delta[0])
             while tau_sq < 0:
                tau_sq = np.random.normal(xc[1], delta[1])

            return [mu, tau_sq]
```

```
In [52]: # acceptance test
         def accept(x_old, x_new, posterior):
             accept_r = False

             # calculate posterior_new/posterior_old
             ratio = np.exp(posterior(x_new) - posterior(x_old))

             # if posterior_ratio is greater than some random value, accept proposal
             if ratio > 1.:
                 accept_r = True
             elif ratio > np.random.rand():
                 accept_r = True
             else:
                 accept_r = False

             # return acceptance (bool)
             return accept_r
```

```
In [50]: # metropolis driver
         def metropolis_MCMC(nmcs, delta, init):

             x = np.zeros((nmcs, 2))
             xc = init
             Acc = 0.0

             # for loop n steps (nmcs)
             for i in range(nmcs):

                 # log current state
                 x[i] = xc
                 # new state, proposed
                 xn = proposal(xc, delta)
                 # if accept,
                 if (accept(xc, xn, posterior)):
                     # current state = new state
                     xc = xn
                     # inc number of sucesses
                     Acc = Acc + 1
             # return all states, and ratio of success
             return x, Acc/nmcs
```

```
In [75]: x, acc_percent = metropolis_MCMC(10000, [0.1, 0.1], [1.0, 1.0])
         acc_percent
```

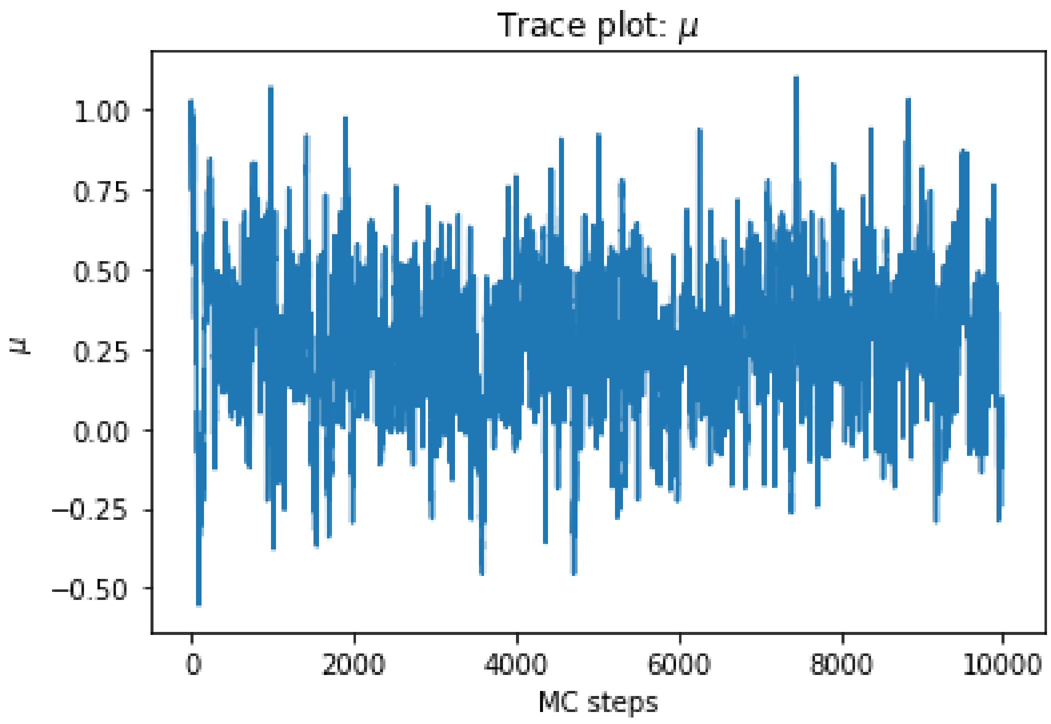
```
/home/celine/anaconda2/lib/python2.7/site-packages/ipykernel_launcher.py:10: RuntimeWarning: div
```

```
  # Remove the CWD from sys.path while we load stuff.
```

```
Out[75]: 0.7659
```

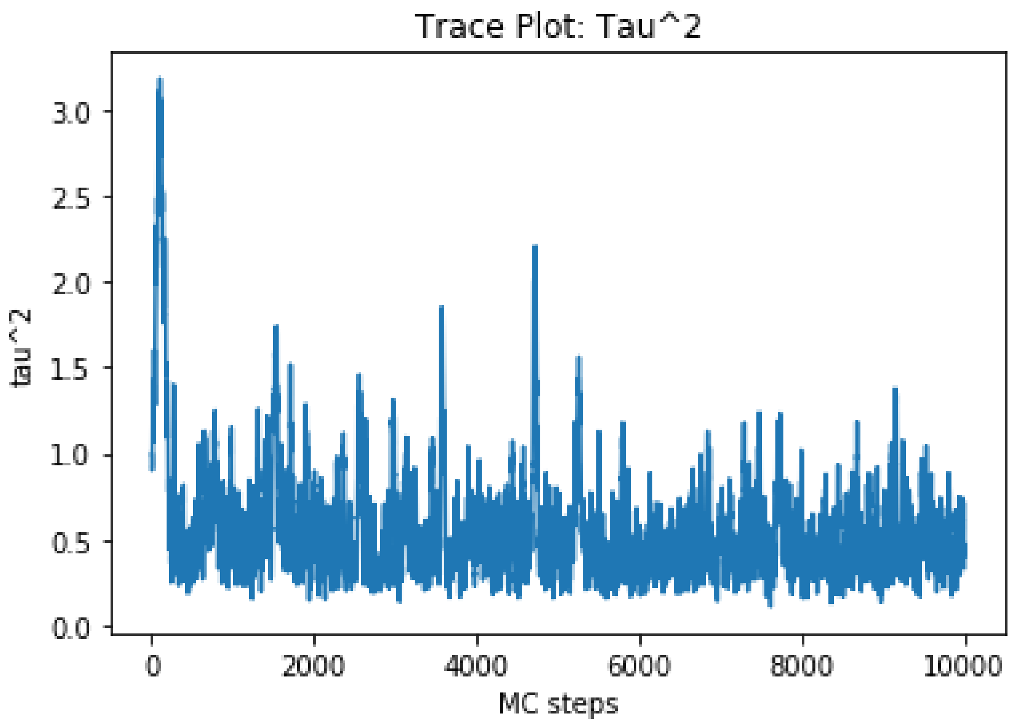
```
In [79]: t = np.linspace(0, 10000, len(x[:, 0]))

         plt.plot(t, x[:, 0])
         plt.ylabel("$\mu$")
         plt.xlabel("MC steps")
         plt.title("Trace plot: $\mu$")
```

```
Out[79]: Text(0.5,1,u'Trace plot: $\\mu$')
```

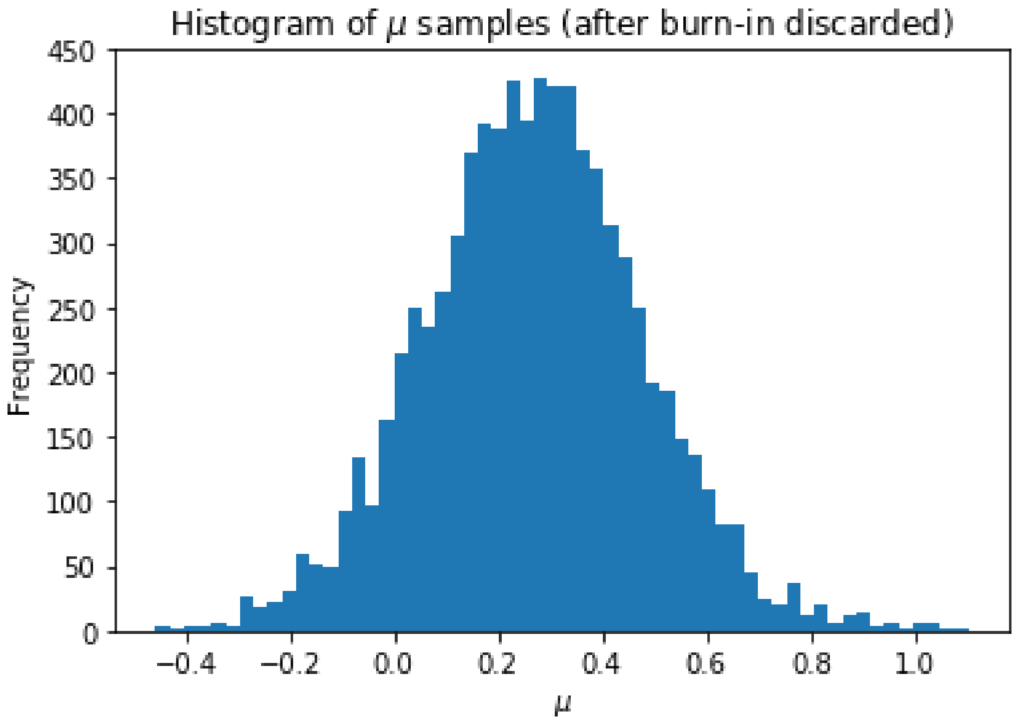


```
In [80]: t = np.linspace(0, 10000, len(x[:, 0]))

         plt.plot(t, x[:, 1])
         plt.ylabel("tau^2")
         plt.xlabel("MC steps")
         plt.title("Trace Plot: Tau^2")
```

```
Out[80]: Text(0.5,1,u'Trace Plot: Tau^2')
```



```
In [86]: # discarded burn-in

         plt.hist(x[2000:, 0], bins='auto')
         plt.ylabel("Frequency")
         plt.xlabel("$\mu$")
         plt.title("Histogram of $\mu$ samples (after burn-in discarded)")
         plt.show()
```



```
In [76]: # the expected value of mu
         np.mean(x[2000:, 0])
```

```
Out[76]: 0.26882826910603042
```

The expected value of μ is 0.2688. The "true" log odds ratio for the population is μ, and the logarithm of the odds ratio ranges between $-\infty$ through 0, to ∞. Since the estimation of μ turns out to be closest to 0, this follows that the trait produces no enhancement in disease (no effect). Although the expected value is not exactly 0, you still have to factor in Measurement error and Sampling Error