```
[1] "# of discriminatory genes = 99"

[1] "fold change for discriminatory genes: 0.5"

[1] "fold change for nondiscriminatory genes: 0.1"

choose_k
  2
100
```

The optimal number of clusters K is set as the most frequently found K from the 100 simulations tabulated above. It is found by using the BIC criterion after running the unpenalized EM algorithm on K spanning from 2 to 8.

Using the last set of simulated counts, I ran a grid search across varying tuning parameters. As done in Pan et al, I fixed $\lambda_1 = 1$, and searched over $\lambda_2 = (0.1, 0.2, ..., .2)$ and $\tau = (0.1, 0.2, ..., 2)$:

```
[1] "lambda1, lambda2, tau, BIC:"

     [,1] [,2] [,3]     [,4]
[1,]    1  0.2  0.1 19634.1
[2,]    1  0.2  0.2 19634.1
```

The results of the final run based on optimal tuning parameters are below:
Below are the summary of results:

```
[1] "Mean pi: 0.514782608695652" "Mean pi: 0.485217391304348"

[1] "First 3 genes:"

        [,1]     [,2]
[1,] 3.598888 4.134588
[2,] 4.825616 5.368282
[3,] 4.339378 4.872001

[1] "Last 3 genes:"

          [,1]     [,2]
 [98,] 6.130155 6.668114
 [99,] 5.681757 6.219005
[100,] 6.333579 6.427589

[1] "Mean % of nondiscriminatory genes: 0.0094"

[1] "Mean ARI: 1"

[1] "Mean sensitivity: 1"

[1] "Mean false positive rate: 0.06"
```