```
[1] "# of discriminatory genes = 2"

[1] "fold change for discriminatory genes: 0.3"

[1] "fold change for nondiscriminatory genes: 0"

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] "tau= 0.1" "tau= 0.2"

[1] "lambda1= 1"

[1] "lambda2= 0.2" "lambda2= 0.3"
```

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

```
[1] "Mean pi: 0.60260869449336" "Mean pi: 0.39739130550664"

[1] "First 3 genes:"

          [,1]      [,2]
[1,] 3.562036 4.156239
[2,] 4.794866 5.391399
[3,] 4.604305 4.604740

[1] "Last 3 genes:"

            [,1]      [,2]
 [98,] 6.398943 6.399278
 [99,] 5.951367 5.950685
[100,] 6.376974 6.378484

[1] "Mean % of nondiscriminatory genes: 0.9783"

[1] "Mean ARI: 1"

[1] "Mean sensitivity: 1"

[1] "Mean false positive rate: 0.00173469387755102"
```