```
[1] "# of discriminatory genes = 75"

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

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

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]     1.00     0.20     0.10 19162.72
```

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

```
[1] "Mean pi: 0.607826086956522" "Mean pi: 0.392173913043478"

[1] "First 3 genes:"

          [,1]     [,2]
[1,] 2.899429 4.846465
[2,] 4.112760 6.089739
[3,] 3.614634 5.601090

[1] "Last 3 genes:"

           [,1]     [,2]
 [98,] 5.899722 6.898534
 [99,] 5.455442 6.450401
[100,] 5.880523 6.877613

[1] "Mean % of nondiscriminatory genes: 0"

[1] "Mean ARI: 1"

[1] "Mean sensitivity: 1"

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