HW8

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```r
suppressPackageStartupMessages({
  library(MASS)
  library(tidyverse)
})
```

5.3

a)

I found it easier to find the complement of event $1 - A_n = A_n^c$ first,

With $\mu = 0$, we see that the probability is 1. Then $1 - A_n^c = 1 - 1 = 0$

```r
n=10000
mu=0
sd=1
a = (sqrt(n) / sd) * ((1/n^.25) - mu)
b = (sqrt(n) / sd) * (-(1/n^.25) - mu)

1 - pnorm(a,0,1) - pnorm(b,0,1)
```

```
[1] -7.619853e-24
```

and with $\mu \neq 0$, the probability is 0, so the compliment,$1 - A_n^c = 1 - 0 = 1$

```r
n=10000
mu=10
sd=1
```

```
a = (sqrt(n) / sd) * ((1/n^.25) - mu)
b = (sqrt(n) / sd) * (-(1/n^.25) - mu)

1 - pnorm(a,0,1) - pnorm(b,0,1)
```

```
[1] 1
```

e)

ii)

Again using the complement, I evaluate A_n^c using n $=$ 10,000, h $=$ 5, and sd=1. We see that this equals 0 $\forall \mu_n$.

```
n=10000
h = 5
mu_n = 5/sqrt(n)
sd=1
a = (sqrt(n) / sd) * ((1/n^.25) - mu_n)
b = (sqrt(n) / sd) * (-(1/n^.25) - mu_n)

1 - pnorm(a,0,1) - pnorm(b,0,1)
```

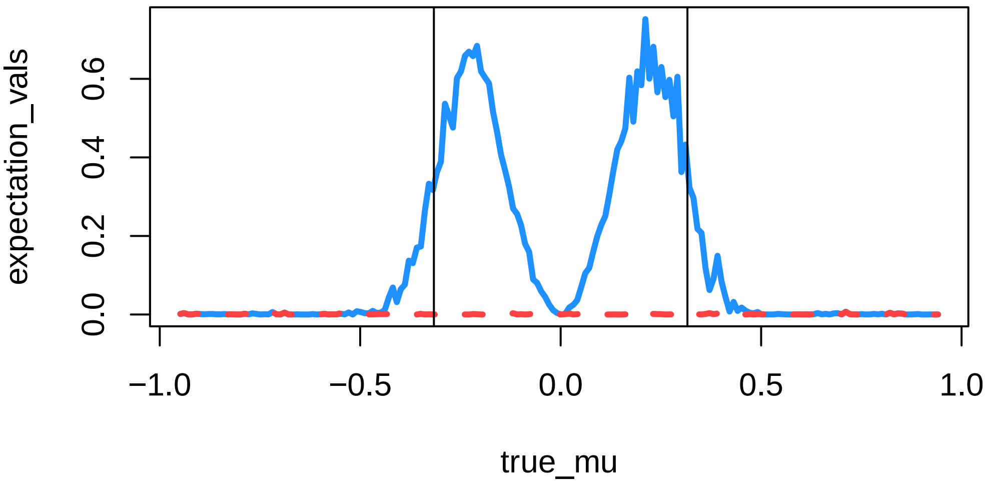
```
[1] 2.866516e-07
```

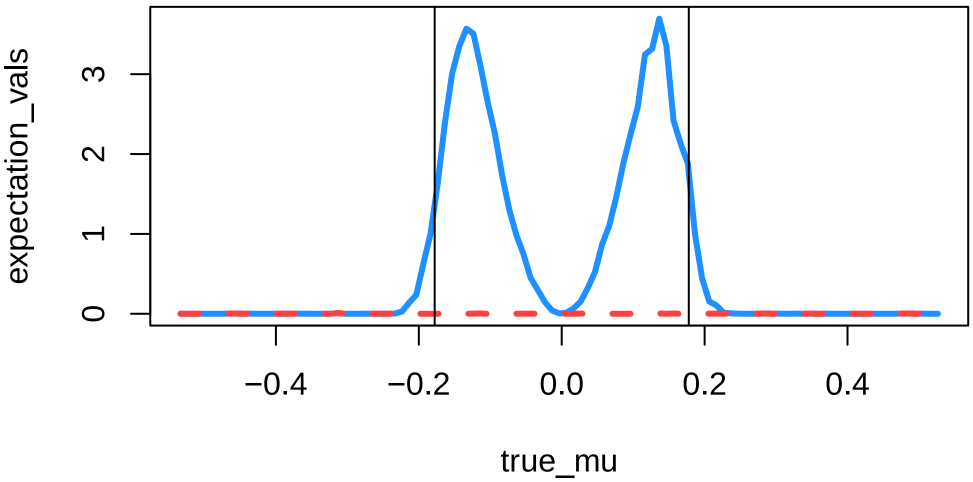
g)

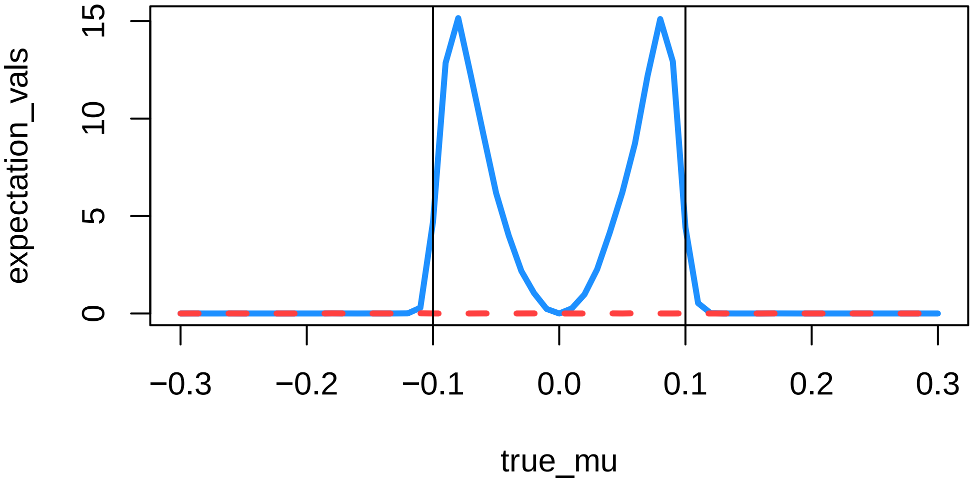
Irregularity is problematic because, and confirming with the plots below, $\tilde{\mu}$ does a very poor job of estimating the true parameter from about -0.1 to 0.1. This violates what we want from the N-P Paradigm, so we could not have good error controls over the entire model space using this estimator. So because $\hat{\mu}$ is not irregular we see that it has a constistent value for the expectation over the whole range of true mu values while $\tilde{\mu}$ spikes over certain ranges of values. However, it does well at a true $\mu = 0$, though we wouldn't want to use it unless we were almost certain the true μ was in fact 0.

```
A_n = function(X){
  # function to calculate indicator
  n = length(X)
  ind = abs(mean(X)) > (1/n)^0.25
  return(ind)
  }

n_list = c(100, 1000, 10000)
for (n in n_list){
  true_mu = seq(-3 * n^(-0.25), 3 * n^(-0.25), 0.01)
  expectation_vals = c()
  x_bar_means = c()
  for (mu in true_mu) {

    # initialize
    mc_vals = c()
    x_bar_vals = c()

    for (i in 1:1000){

      # monte carlo
      X = rnorm(n, mu, 1)
      X_bar = mean(X)
      Y_n = (1+A_n(X))/2
      mu_tilde = X_bar * Y_n

      # store values
      mc_vals = c(mc_vals, mu_tilde)
      x_bar_vals = c(x_bar_vals, X_bar)
    }
    # calculation
    mc_mean = mean(mc_vals)
    xbar_mean = mean(x_bar_vals)
    expectation = n * mean((mc_mean - mu)^2)
    x_bar_expect = n * mean((xbar_mean - mu)^2)

    # storing means
    expectation_vals = c(expectation_vals, expectation)
    x_bar_means = c(x_bar_means, x_bar_expect)
  }

  plot(true_mu, expectation_vals, type='l', lwd=3, lty=1, col='dodgerblue')
  lines(true_mu, x_bar_means, type='l', lwd=3, lty=2, col='brown1')
  abline(v = n^(-1/4))
  abline(v = -n^(-1/4))
```

```
}
```


expectation_vals
0.0
0.2
0.4
0.6
−1.0
−0.5
0.0
0.5
1.0
true_mu


expectation_vals
0
1
2
3
−0.4
−0.2
0.0
0.2
0.4
true_mu



5.5

a)

iii) and v)

My methodology was to loop through the countries, rows, and columns, and calculate the statistics of interest. Then, as a comparison, find the difference between $2log\Lambda(X_k, H_I)$ and T_k. It seems the values are close in countries like Italy, Yugoslavia, and Finland, and far away in countries like Spain, the Phillipines and Spain.

vi)

vi) is also calculated below, and is performed by taking the sum of the test statistic across all countries

```r
global_sum = c()
country_name = names(data)
for (i in 1:length(data)){

  t = data[[i]]
  country = country_name[i]

  vals = c() # likelihood ratio vals
  T_k_values = c() # chi square values
  n_k = sum(t)
  r_sum = rowSums(t)
  c_sum = colSums(t)

  for (i in 1:3){
    for (j in 1:3){
      # select xij value
      xij = t[i,j]

      # calculate statistics
      E_ij = (r_sum[i] * c_sum[j])/n_k
      f = 2 * ((xij * log(xij) - xij) - ((xij * log(E_ij)) - E_ij))
      vals = c(vals,f)

      #chi squared stat
      T_ijk = (xij - E_ij)^2 / E_ij
      T_k_values = c(T_k_values, T_ijk)
    }
  }

  T_k = sum(T_k_values)
  V_sum = sum(vals)
  global_sum = c(global_sum, V_sum)
  compare = V_sum - T_k
  p_value = pchisq(V_sum, 4, lower.tail = F)
  cat(country, 'Difference : ', compare, "; P Value : ", p_value, "\n")
}
```

```
Australia Difference :  -71.09597 ; P Value :  1.547168e-96
Belgium Difference :  -105.8371 ; P Value :  1.237476e-134
Frane Difference :  -75.91532 ; P Value :  0
Hungary Difference :  -31.00982 ; P Value :  0
Italy Difference :  -1.409348 ; P Value :  1.119295e-142
Japan Difference :  12.61146 ; P Value :  1.13328e-121
Phillipines Difference :  -280.0931 ; P Value :  5.53404e-273
Spain Difference :  425.7491 ; P Value :  0
USA Difference :  -85.97342 ; P Value :  0
WestGermany Difference :  -121.3209 ; P Value :  0
WestMalaysia Difference :  -59.93569 ; P Value :  4.297791e-273
Yugoslavia Difference :  -1.285559 ; P Value :  4.602893e-37
Denmark Difference :  -4.908024 ; P Value :  2.59003e-43
Finland Difference :  -0.06585406 ; P Value :  1.629016e-25
```

```
Norway Difference :  -5.496425 ; P Value :  6.292721e-19
Sweden Difference :  -15.61604 ; P Value :  2.465429e-25
```

```
total = sum(global_sum)
global_p = pchisq(total, 64, lower.tail=F)
cat("Global P-Value : ", global_p)
```

```
Global P-Value :  0
```

b)

iii) / iv) / vi)

Code to optimize and find the maximum log likelihood is below, along with individual country p-values and a global p-value for part vi). In part iv), the test statistic value is 0.855 verified below, and we see that δ_1 and δ_3 are positive, indicating positive inheritance, while δ_2 indicates negative inheritance. So sons actively avoided blue-collar work if their father's had blue collar jobs but were more likely to choose white-collar or farm work if those were their father's professions.

It looks like this is almost completely true for the other countries, which is a bit surprising that farm work does not have negative inheritance. Maybe if the father owns a farm, the son is very likely to take over. It also makes sense that sons with white-collar fathers would most likely not take up a blue-collar job.

```
log_lkh = function(l_theta, x){
  theta = exp(l_theta)
  d1 = theta[1]
  d2 = theta[2]
  d3 = theta[3]
  alpha2 = theta[4]
  alpha3 = theta[5]
  beta2 = theta[6]
  beta3 = theta[7]
  lambda = theta[8]
  theta_mat = lambda * matrix(c(d1, beta2, beta3,
                              alpha2, d2 * alpha2 * beta2, alpha2 * beta3,
                              alpha3, alpha3 * beta2, d3 * alpha3 * beta3),3,3,
                              byrow=T)
  log_mat = log(theta_mat)
  f = -sum(x * log_mat - theta_mat)
  f
}

global_sum = c()
for (i in 1:length(data)){

  t = data[[i]]
  opt = optim(par = c(1,1,1,1,1,1,1,1), log_lkh, x = t, method="BFGS")
  delta = opt$par[1:3]
  mle = -opt$value
  country = country_name[i]

  vals = c() # likelihood ratio vals

  for (i in 1:3){
    for (j in 1:3){

      # select xij value
      xij = t[i,j]

      # calculate statistic
      f = xij * log(xij) - xij
      vals = c(vals,f)

    }
  }
  lrt = 2 * (sum(vals) - mle)
  global_sum = c(global_sum, lrt)
  p_value = pchisq(lrt, 4, lower.tail = F)
  cat(country, 'Value : ', lrt, "; P-Value : ", p_value, "\n")
  cat(country, 'delta values : ', delta, "\n", "\n")

}
```

```
Australia Value :  11.73796 ; P-Value :  0.01941003
Australia delta values :  1.030619 0.2265895 2.401344

Belgium Value :  10.6225 ; P-Value :  0.03115082
Belgium delta values :  1.404585 0.527517 3.259004

Frane Value :  22.97042 ; P-Value :  0.0001283611
Frane delta values :  1.354031 0.2661022 3.347636
```

```
Hungary Value :  0.8554593 ; P-Value :  0.9308621
Hungary delta values :  2.698505 -0.8539063 3.053352

Italy Value :  1.773136 ; P-Value :  0.7773934
Italy delta values :  2.134687 0.01783844 2.825704

Japan Value :  1.266833 ; P-Value :  0.8669771
Japan delta values :  1.363813 0.4536371 2.039854

Phillipines Value :  0.07651477 ; P-Value :  0.9992866
Phillipines delta values :  1.302148 0.636987 2.110648

Spain Value :  68.35058 ; P-Value :  5.059381e-14
Spain delta values :  1.767542 0.4450499 2.718206

USA Value :  20.95466 ; P-Value :  0.000323291
USA delta values :  1.745549 -0.3076404 2.798695

WestGermany Value :  6.342103 ; P-Value :  0.175015
WestGermany delta values :  1.588162 0.3669252 1.672962

WestMalaysia Value :  0.2243697 ; P-Value :  0.9941587
WestMalaysia delta values :  1.127708 0.1638802 1.912759

Yugoslavia Value :  0.6905396 ; P-Value :  0.9524904
Yugoslavia delta values :  1.498647 0.3263042 1.944188

Denmark Value :  0.09040986 ; P-Value :  0.9990085
Denmark delta values :  1.528356 0.09070624 3.207579

Finland Value :  2.797152 ; P-Value :  0.5923244
Finland delta values :  0.9738435 0.8804998 1.969367

Norway Value :  0.1690122 ; P-Value :  0.9966243
Norway delta values :  1.217378 0.1140759 1.933176

Sweden Value :  0.1430917 ; P-Value :  0.9975595
Sweden delta values :  1.636189 0.00663069 3.259265
```

```r
total = sum(global_sum)
global_p = pchisq(total, 64, lower.tail=F)
cat("Global P-Value : ", global_p)
```

```
Global P-Value :  9.674784e-09
```

v)

First, we note that we now have a chi-squared distribution with 1 degree of freedom, since the full parameter space has dimension 9 and our restricted space, Θ_Q has dimension 8 since we now have 8 parameters, $\lambda_k, \{\alpha_{ik}\}_2^3, \{\beta\}_2^3, and\ \delta_1, \delta_2, \delta_3$.

Now, I would grid search across ranges of the parameters, and for each distinct combination of parameters, create 10,000 synthetic data sets by drawing each X_{ijk} from a POIS($\theta_{ij}^{(k)}$), compute the statistic $2log\Lambda(X_k; H_Q)$, average across the data sets to create an MC average, plot a histogram of the average statistic, and visually compare to a χ_1^2 and see if they match. It should look similar regardless of the combination of parameters if it is truly from the distribution.