STAT 457 Homework 05

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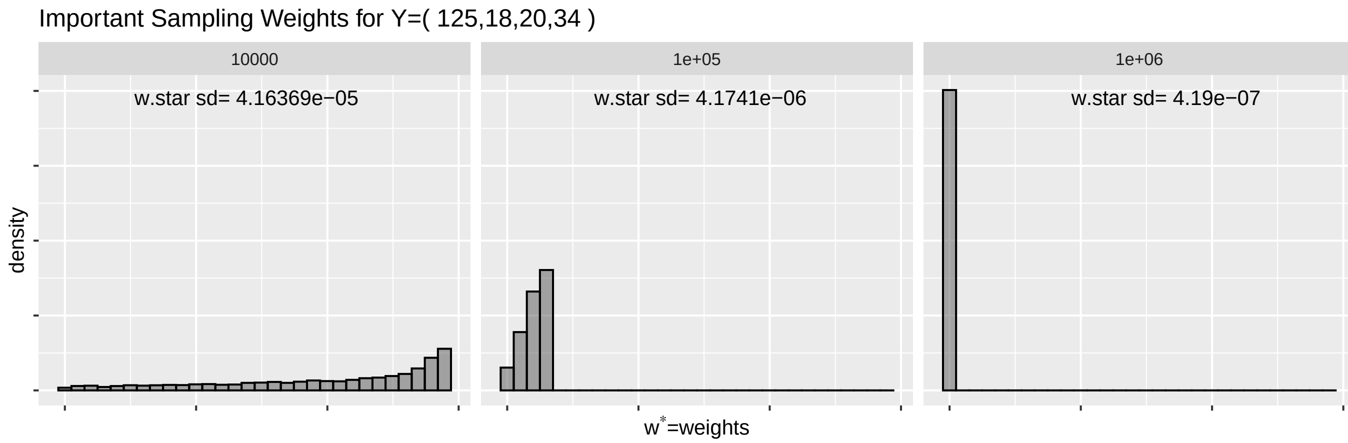
Problem 3a

For the genetic linkage model: use importance sampling to obtain the posterior mean for data $Y = (125, 18, 20, 34)$. Use the matching normal distribution as the importance function. Compare your importance sampling estimates of the posterior mean to those obtained via Laplace's method. Draw the histogram of the weights and compute their standard deviation. Normal Approxiamation for $Y = (125, 18, 20, 34) \sim \mathcal{N}(\mu = 0.62682,\ \sigma = 0.05382)$



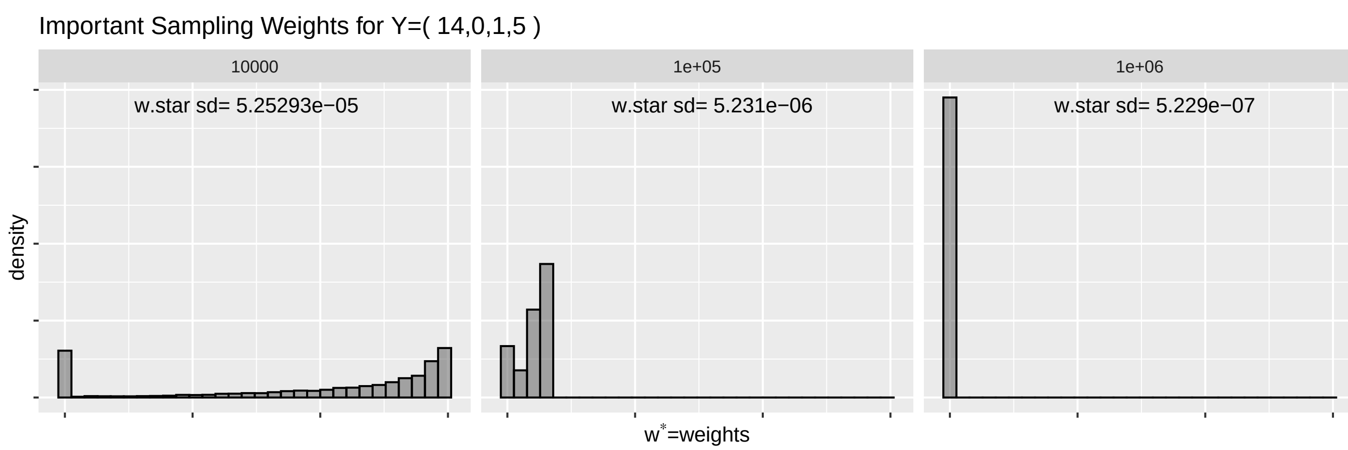
	IS	Norm.Apprx	Diff
mean	0.62365	0.62682	−0.00317
sd	0.03715	0.05382	−0.01667

	IS	Norm.Apprx	Diff
mean	0.62338	0.62682	−0.00344
sd	0.03706	0.05382	−0.01676

	IS	Norm.Apprx	Diff
mean	0.62347	0.62682	−0.00335
sd	0.03716	0.05382	−0.01666

Problem 3b

Repeat (a) for the data $Y = (14, 0, 1, 5)$. Normal Approximation for $Y = (125, 18, 20, 34) \sim \mathcal{N}(\mu = 0.90344,\ \sigma = 0.09348)$



	IS	Norm.Apprx	Diff
mean	0.87758	0.90344	−0.02586
sd	0.06194	0.09348	−0.03154

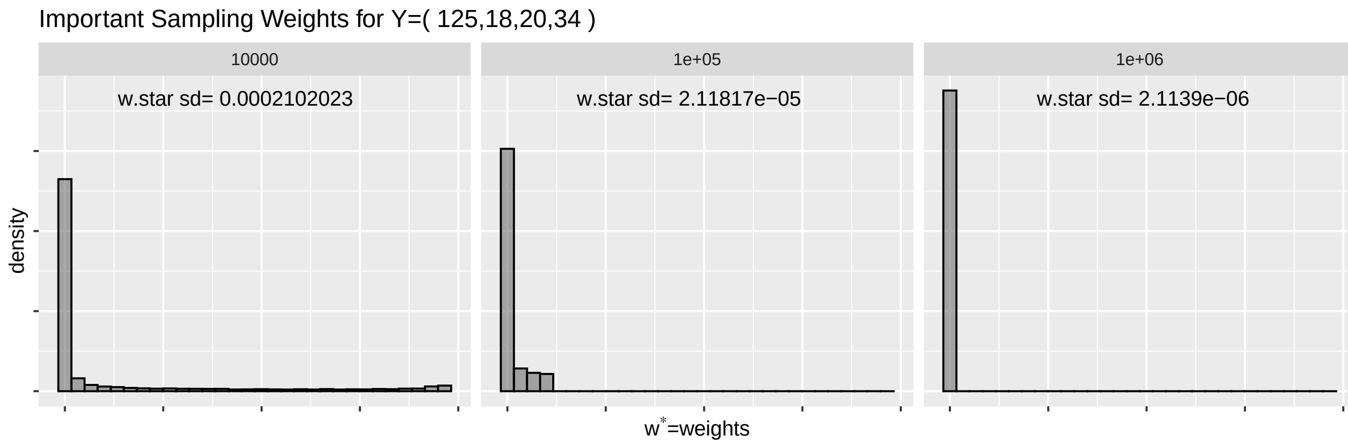
	IS	Norm.Apprx	Diff
mean	0.87714	0.90344	−0.0263
sd	0.06214	0.09348	−0.03134

	IS	Norm.Apprx	Diff
mean	0.87713	0.90344	−0.02631
sd	0.0622	0.09348	−0.03128

Using a normal important sampling function to estiamte the posterior mean is closer for $Y = (125, 18, 20, 34)$ normal approximation than $Y = (14, 0, 1, 5)$. This makes sense as in the last homework, we showed the likelihood for the first data follows the approximate normal distribution very closely whereas the second data likelihood did not follow the normal approximation well.

Problem 3c

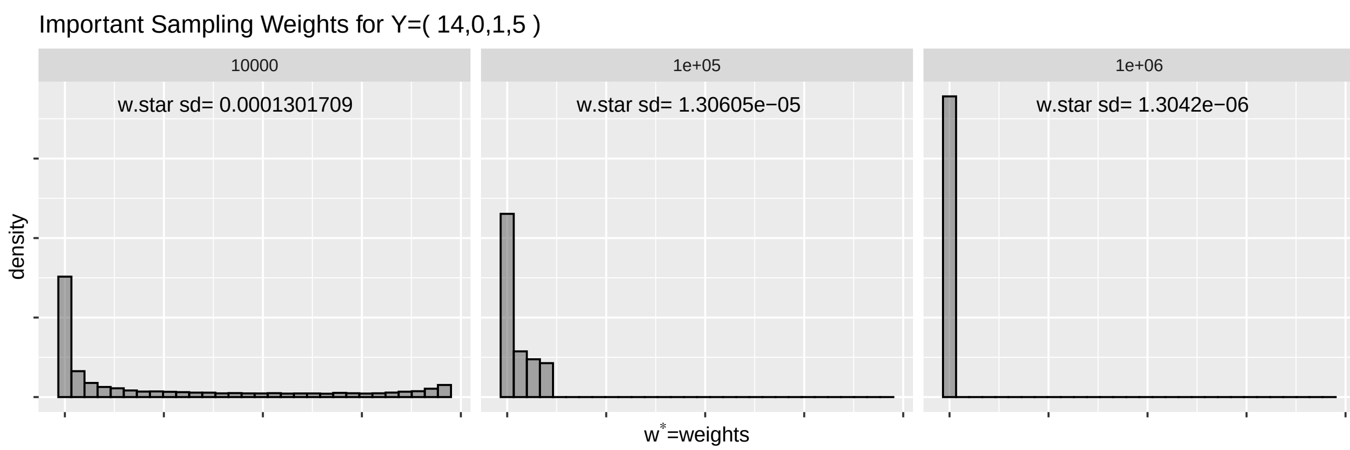
Repeat (a) and (b) with a Uniform[0, 1] importance function.



	IS	Norm.Apprx	Diff
mean	0.61867	0.90344	−0.28477
sd	0.05209	0.09348	−0.04139

	IS	Norm.Apprx	Diff
mean	0.61838	0.90344	−0.28506
sd	0.05169	0.09348	−0.04179

	IS	Norm.Apprx	Diff
mean	0.61855	0.90344	−0.28489
sd	0.05143	0.09348	−0.04205



	IS	Norm.Apprx	Diff
mean	0.81241	0.90344	−0.09103
sd	0.11825	0.09348	0.02477

	IS	Norm.Apprx	Diff
mean	0.81389	0.90344	−0.08955
sd	0.11782	0.09348	0.02434

	IS	Norm.Apprx	Diff
mean	0.81412	0.90344	−0.08932
sd	0.11791	0.09348	0.02443

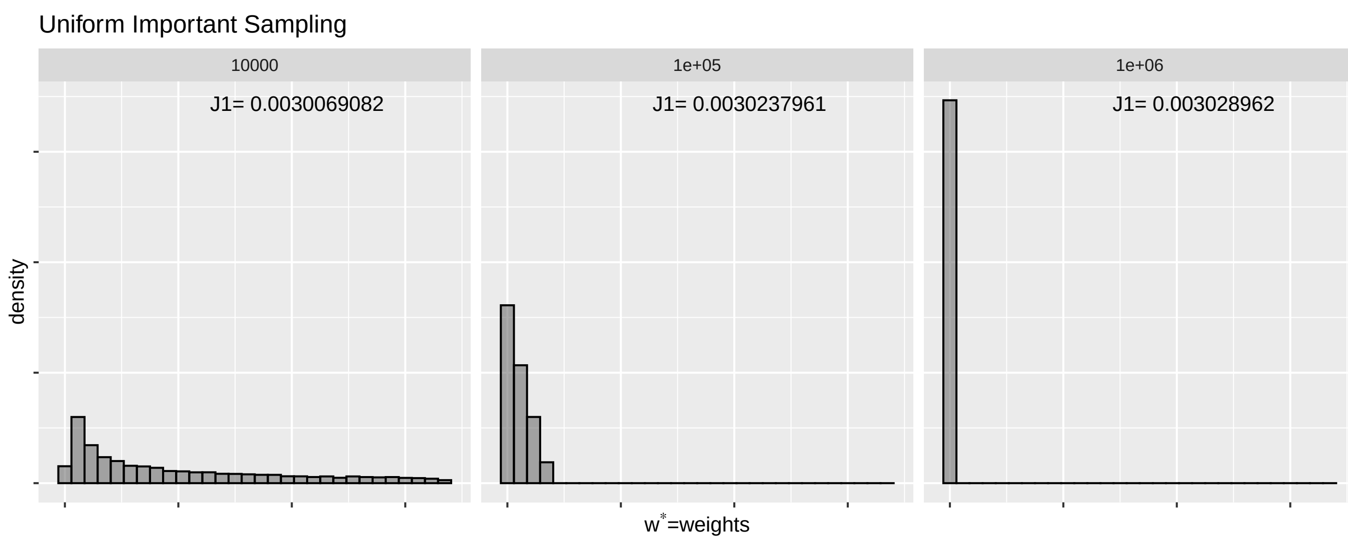
Note that the histograms of the weights, w^*, are very similar for both sets of data. This is because the importance function is not dependent on the data (like it was for when using the normal approximation data for a norma importance function).

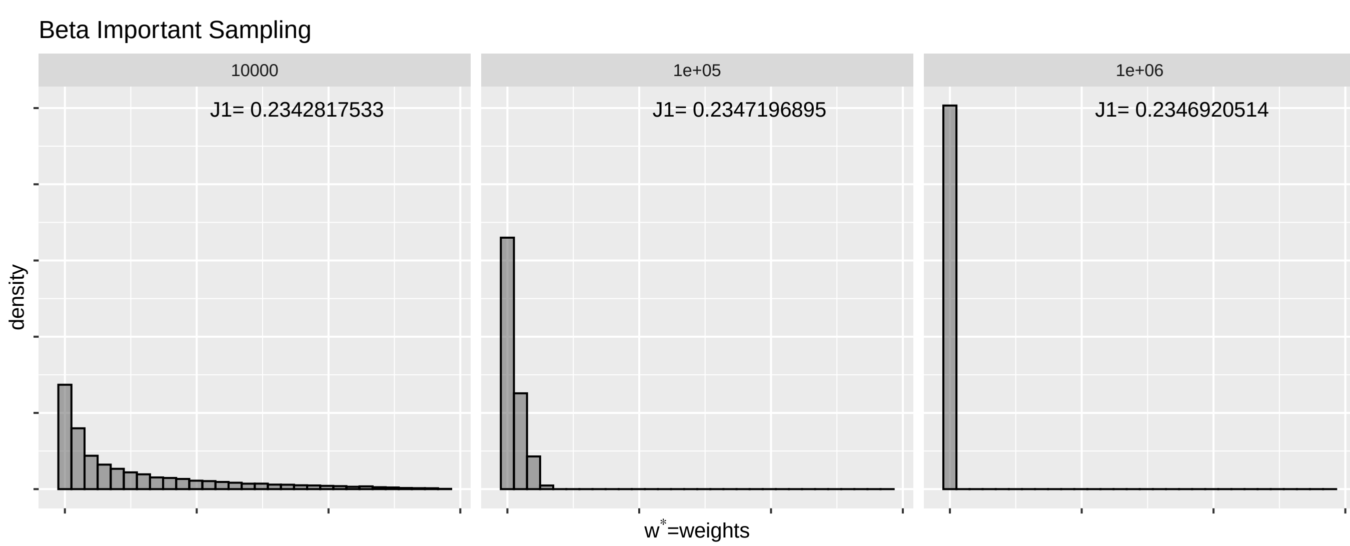
Problem 4

Problem 4a

Solve the following problem posted by the Reverend Thomas Bayes in his essay "Essay Towards Solving a Problem in the Doctrine of Chances," which was published in the *Philosophical Transactions of the Royal Society* (London) in 1763: *Given* the number of times in which an unknown event has happened and failed: *Required* the chance that the probability of its happening in a single trial lies somewhere between any tow degrees of probability that can be named.
In other words, if the number of the successful happenings of the event is p and the failures q, and if the named "degrees" of the probability are b and f, respectively, compute: $\int_b^f x^p(1-x)^q dx / \int_0^1 x^p(1-x)^q dx$ via important sampling. Take $p = 1,\ q = 4,\ b = 0.7,\ f = 0.9$.

Let $J_1 = \int_b^f x^p(1-x)^q dx$





4A:OUTSTANDING

Problem 4b

Repeat the calculation using numerical integration. Compare the results of (a) and (b).

```
## Warning in rbind(iteration, round(J1.vec, 6), round(diff.J1, 6)): number of
## columns of result is not a multiple of vector length (arg 1)
```

```
##                 [,1]      [,2]      [,3]      [,4]      [,5]
## Iteration       "N/A"     "10000"   "1e+05"   "1e+06"   "N/A"
```

```
## J1              "0.000363" "0.003007" "0.003024" "0.003029" "0.234282"
## J1-Integration "0"        "0.002644" "0.002661" "0.002666" "0.233919"
##                [,6]       [,7]
## Iteration      "10000"    "1e+05"
## J1             "0.23472"  "0.234692"
## J1-Integration "0.234357" "0.234329"
```

	Integration	IS - Uniform			IS - Beta		
Iteration	N/A	10000	1e+05	1e+06	N/A	10000	1e+05
J1	0.000363	0.003007	0.003024	0.003029	0.234282	0.23472	0.234692
J1-Integration	0	0.002644	0.002661	0.002666	0.233919	0.234357	0.234329

The standard error is pretty high and the estimates differ by about 0.003.

```
## [1] 0.003006188
```

```
## [1] 35.74961
```

```
## 0.0003626667 with absolute error < 4e-18
```

4B:OUTSTANDING

Problem 6a

Under the likelihood $\theta^k(1-\theta)^{n-x}$ and the Beta(a,b) prior (a and b known) compute the exact posterior mean. Repeat the calculation using the second-order Laplace approximation. evaluate the relative error for the data $n=5,\ x=3$ and the prior values $a=b={}^1\!/_2$. What is the relative error when $n=25,\ x=15$ (same prior)?

6A:OUTSTANDING

Problem 1

Recall the genetic linkage model of Section 4.1.

Problem 1a

For the data $Y=(125,18,202,34)$ implement the *EM* algorithm. Use a flat prior on θ. Try starting your algorithm at $\theta=.1,.2,.3,.4,.6$ and .8. Did the algorithm converge for all of these starting values? How do you access convergence? How many iterations were required for convergence? 1A:OUTSTANDING

Problem 1c

Plot the normal approximation along with the normalized likelihood. Is the normal approximation appropriate in this case?
1C:OUTSTANDING

Problem 1d

Repeat (a) and (c) for the data $Y=(14,0,1,5)$. did the algorithm coverage for all of the above starting values?
1D:OUTSTANDING

Problem 2

Repeat Problem 1 (a) and (d) using the Monte Carlo *EM*. How did you assess convergence.
2A:OUTSTANDING
2D:OUTSTANDING