

1. 1) For both of them, $\text{Lambda} = 1/\text{mean}(X)$.
The value is 0.8995502
2) First we use analytic formula and get the value of 0.8996094
Then we use numeric optim and get the value of 0.8995117.
They are almost the same with a little difference.
2. 1) For a chi-square distribution. $M = \text{mean}(X) = 100.8$
2) For a one side 90% CI we just need to know the lower side of the value.
It is [98.58908, Inf]
3. A) ALL.mean -0.56760633 -0.03546518 with two side 95% CI
AML.mean 1.383931 1.795593 with two side 95% CI
B) ALL.var 0.3448388 0.6531934 with two side 95% CI
AML.var 0.04703777 0.20658102 with two side 95% CI
C) ALL.median -0.73507 0.31432 with two side 95% CI
AML.median 1.22814 1.82829 with two side 95% CI
D) for ALL and AML data, with two side 95% CI both the mean and median vary a little, it is very likely that the gene expression is quite different for them.
4. a) Included in the R code.
b) $\text{lambda} = 0.1$ 1) mean 0.864
2) var 0.544
 $\text{lambda} = 1$ 1) mean 0.907
2) var 0.84
 $\text{lambda} = 10$ 1) mean 0.909
2) var 0.874
c) I will choose the sample mean as my CI formulas because it is more stable. Especially when lambda is small, the sample variance would vary a lot, sometimes too big sometimes too small. It is not as stable as the sample mean.