303-HW2-Rpart

Set the seed and initialize vectors

```
set.seed(303)
x1 <- rgamma(1000, shape = 1.5, scale = .5)
x2 <- rgamma(5000, shape = 1.5, scale = .5)
```

Define negative loglikelihood function for gamma

```
gamma_loglik <- function(parm,X){
    alpha <- parm[1]
    beta <- parm[2]
    loglik <- sum(dgamma(X, shape=alpha, scale=beta, log=TRUE))
    return(-loglik)
}
```

Optimize for x1

```
nlm(gamma_loglik, p = c(1,1), X = x1)
```

```
## $minimum
## [1] 709.5882
##
## $estimate
## [1] 1.5654530 0.5040026
##
## $gradient
## [1] 3.631116e-07 1.136868e-06
##
## $code
## [1] 1
##
## $iterations
## [1] 10
```

Optimize for x2

```
nlm(gamma_loglik, p = c(1,1), X = x2)
```

```
## $minimum
## [1] 3324.725
##
## $estimate
## [1] 1.4828518 0.5031744
##
## $gradient
```

```
## [1] -2.760037e-05 -8.899406e-04
##
## $code
## [1] 1
##
## $iterations
## [1] 10
```

We see that more observations yield better estimations as these are done via approximations. We know that the parameters are 1.5 & 0.5, and both results are satisfactory. Rounding both to 1st digit yields the same results. But x2 has more precision becuase size is bigger.