575_HW2

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```r
#Mice from group A are approximately Poisson-distributed with a mean of 12. We dont know what mice from
y_A <- c(12,9,12,14,13,13,15,8,15,6)
sy_A <- sum(y_A); n_A <- length(y_A)

y_B <- c(11,11,10,9,9,8,7,10,6,8,8,9,7)
sy_B <- sum(y_B); n_B <- length(y_B)

#Prior A
a_A <- 120
b_A <- 10

#Prior B
a_B <- 12
b_B <- 1


posterior_stats_gamma_poisson <- function(y, a, b, cred_level = 0.95) {
  sy <- sum(y)
  n  <- length(y)

  post_a <- a + sy
  post_b <- b + n

  alpha_low  <- (1 - cred_level)/2
  alpha_high <- 1 - alpha_low
  ci <- pgamma(c(alpha_low, alpha_high), shape = post_a, rate = post_b)

  post_mean <- post_a / post_b
  post_var  <- post_a / (post_b^2)

  cat("Posterior shape:", post_a, "\n")
  cat("Posterior rate: ", post_b, "\n")
  cat(paste0(100*cred_level, "% Credible Interval: [",
             ci[1], ", ", ci[2], "]\n"))
  cat("Posterior Mean:    ", round(post_mean, 3), "\n")
  cat("Posterior Variance:", round(post_var, 3), "\n\n")

  return(invisible(list(shape = post_a,
                        rate  = post_b,
                        ci    = ci,
```

```
                        mean  = post_mean,
                        var   = post_var)))
}

cat("Results for Population A:\n")
```

Results for Population A:

```
res_A <- posterior_stats_gamma_poisson(y_A, a_A, b_A)
```

```
## Posterior shape: 237
## Posterior rate:  20
## 95% Credible Interval: [0, 6.79812201970516e-165]
## Posterior Mean:     11.85
## Posterior Variance: 0.593
```

```
cat("Results for Population B:\n")
```

Results for Population B:

```
res_B <- posterior_stats_gamma_poisson(y_B, a_B, b_B)
```

```
## Posterior shape: 125
## Posterior rate:  14
## 95% Credible Interval: [3.82767136296272e-267, 5.47561723379974e-74]
## Posterior Mean:      8.929
## Posterior Variance: 0.638
```
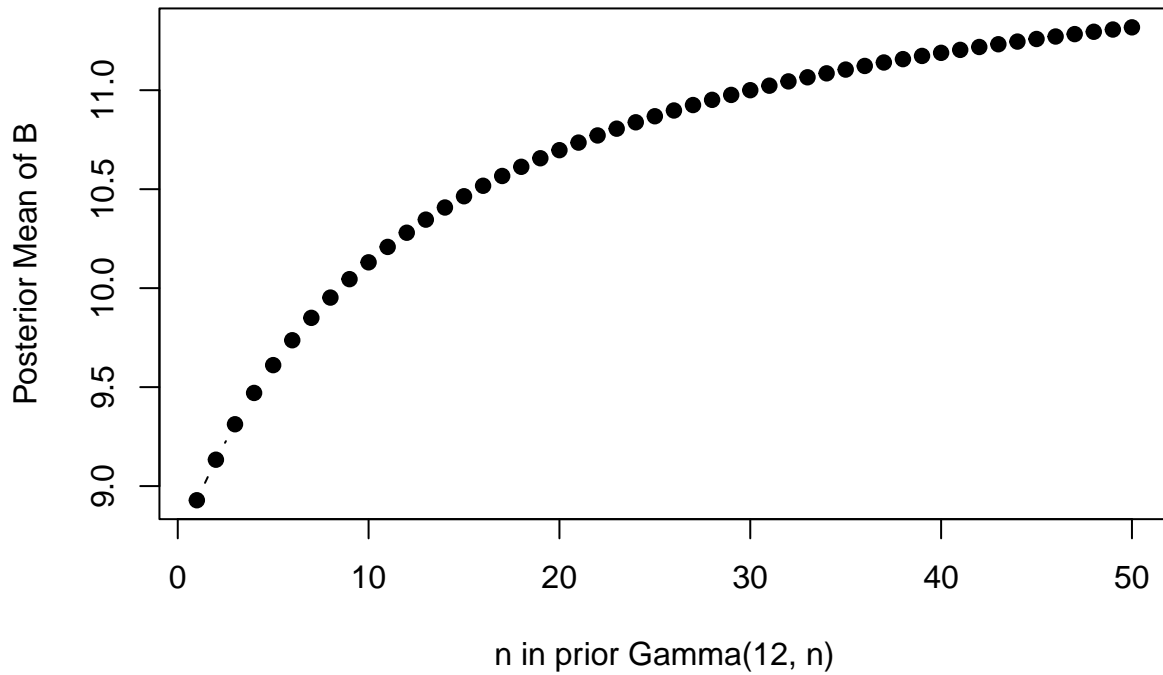
```
n_seq <- 1:50
posterior_means_B <- sapply(n_seq, function(n_cur) {
  post_a_B <- a_B*n_cur + sy_B
  post_b_B <- n_cur + n_B
  post_a_B / post_b_B
})

plot(n_seq, posterior_means_B, type="b", pch=19,
     xlab="n in prior Gamma(12, n)", ylab="Posterior Mean of B",
     main="Posterior Mean vs. Prior Rate 'n' (for Gamma(12, n))")
abline(h=res_A$mean, col="red", lty=2)
```

Posterior Mean vs. Prior Rate 'n' (for Gamma(12, n))

b) you would need to amost entirely sure about your priror belife for this to be the case.

c) This Statement assumes independence, but this does not make sense as the types of mice are related. Even each sample bieng mice would indicate that they have similarities and we can learn about one from the other. It is far less of a stretch to learn about type B mice from type A mice than to learn about humans from type a mice, but this is a common practice.