36-467 Homework 11

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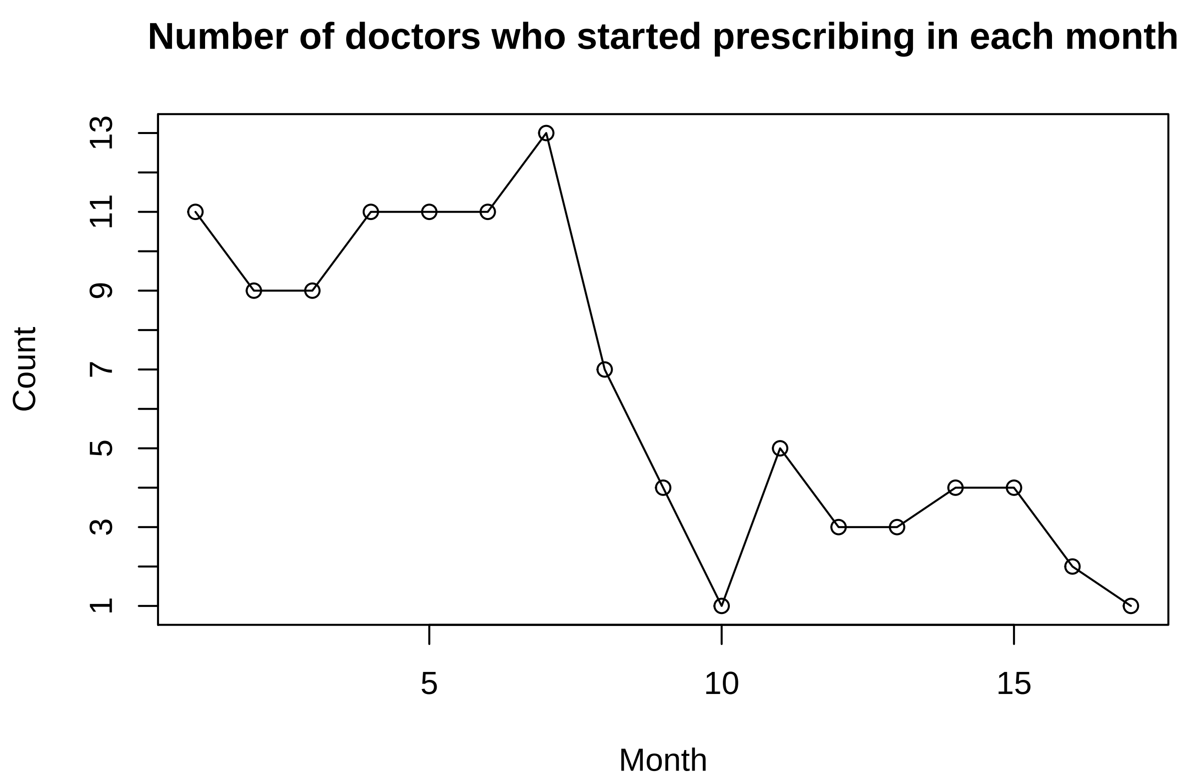
Q1

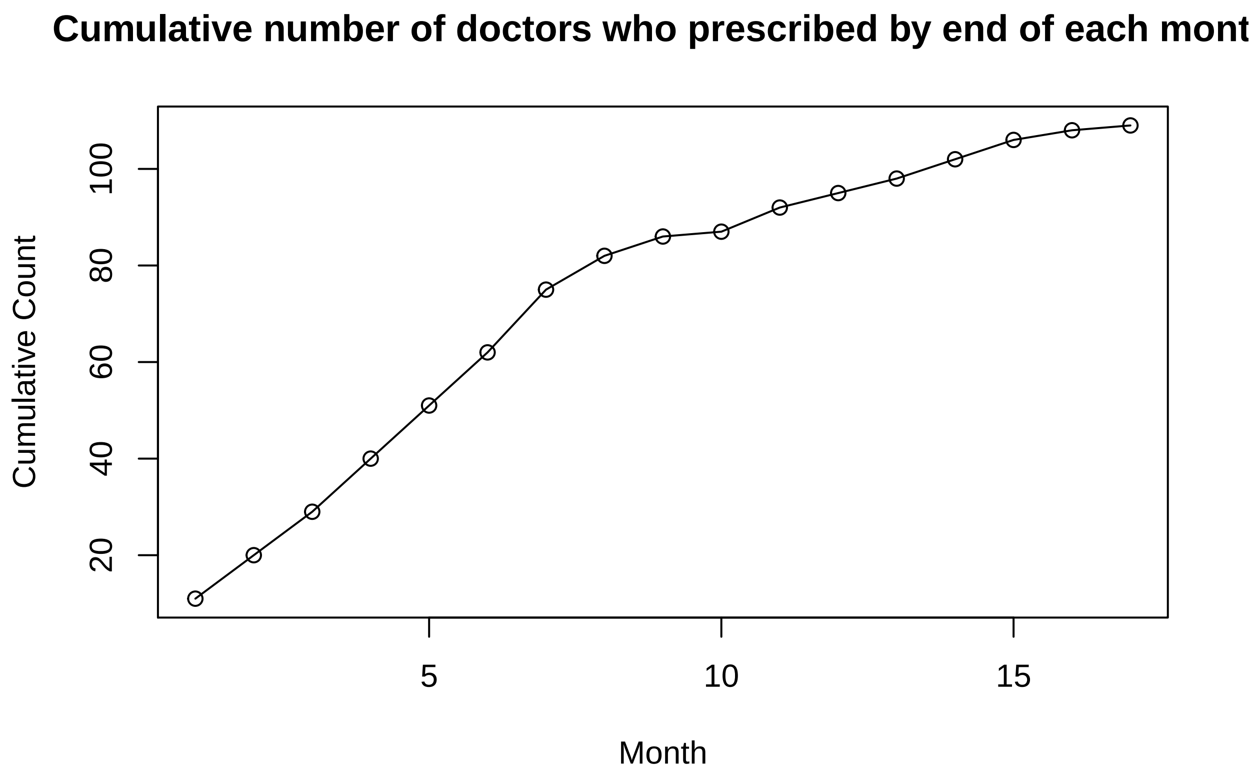
Table 1: Number of doctors without unknown adoption dates

x
125

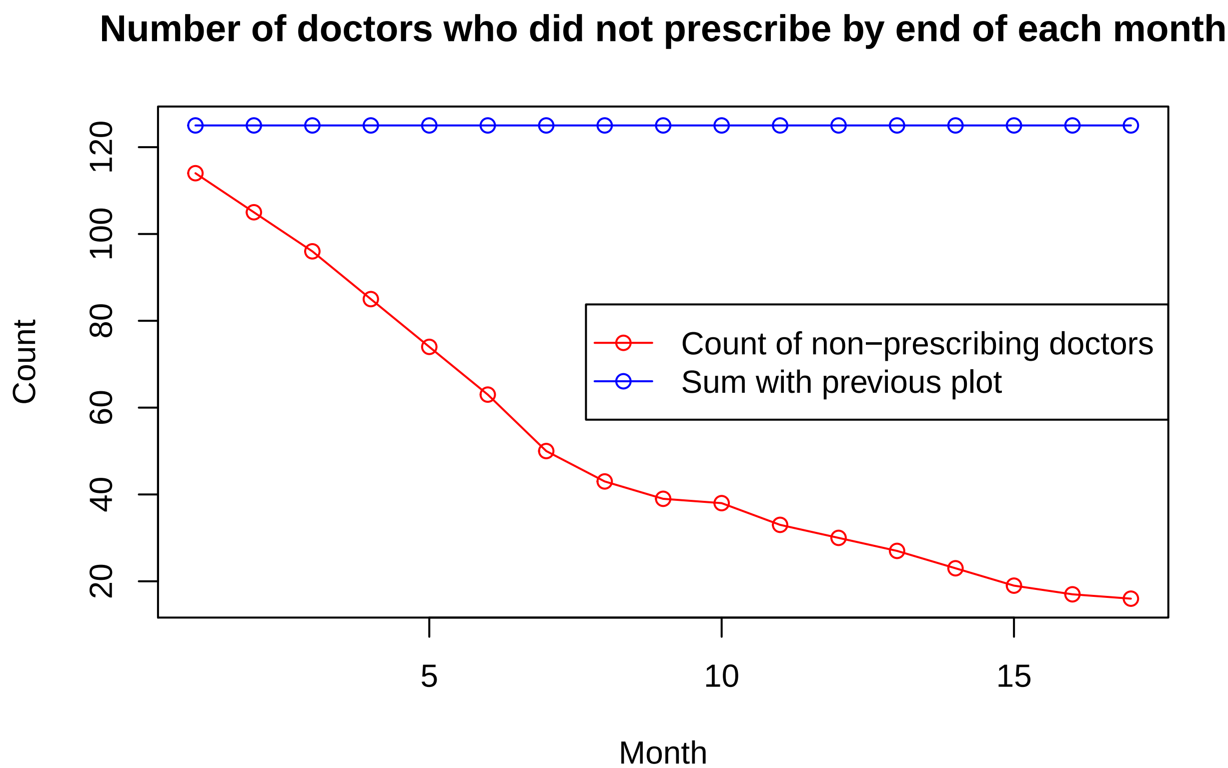
Q2



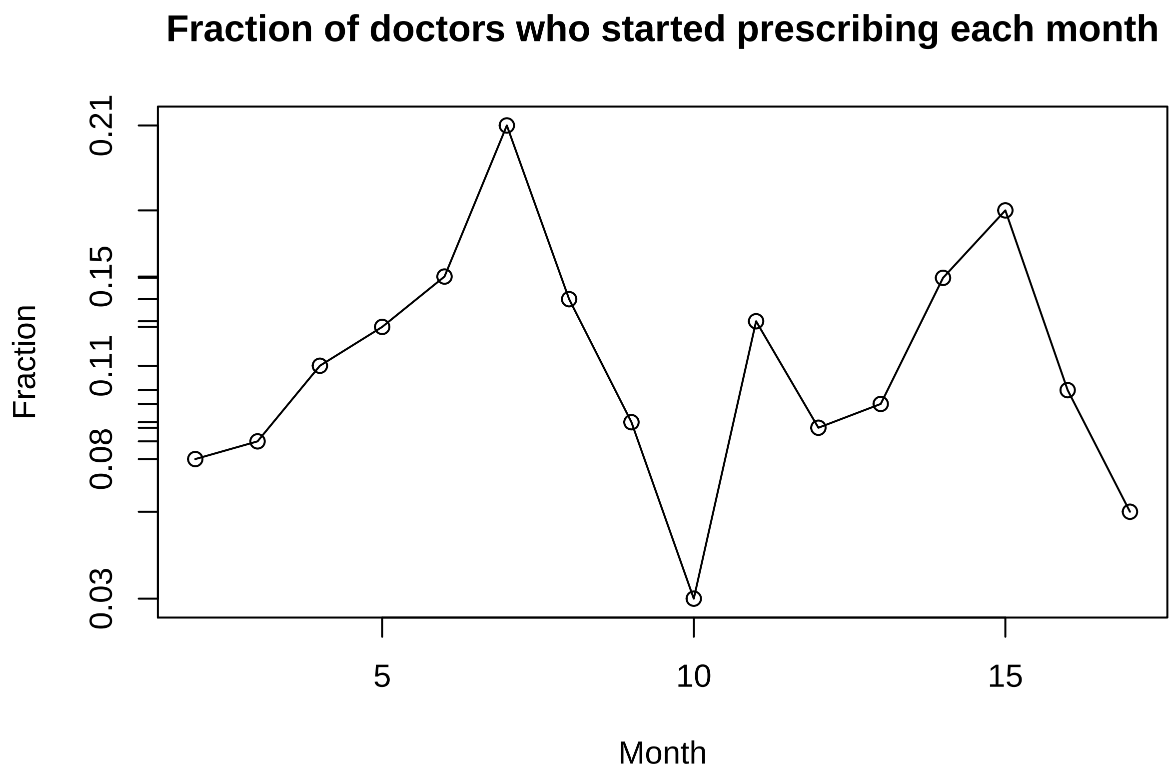
Q3


Cumulative number of doctors who prescribed by end of each mont
Cumulative Count
20
40
60
80
100
5
10
15
Month

Q4

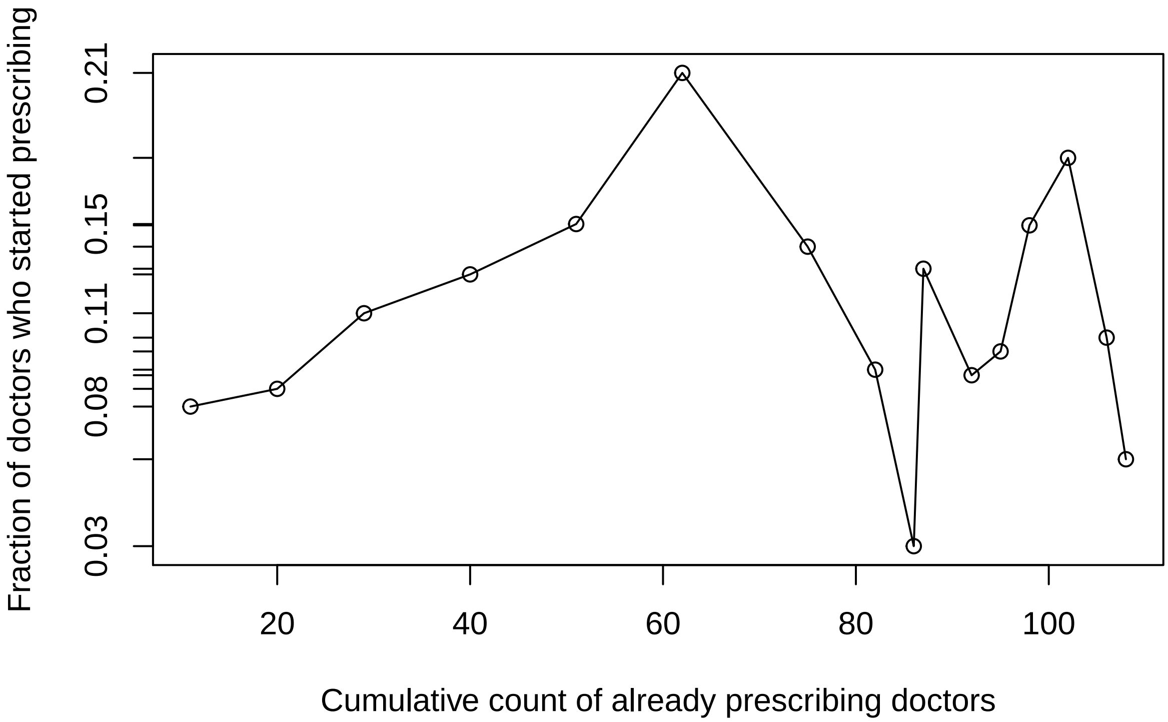

Number of doctors who did not prescribe by end of each month
Count
120
100
80
60
40
20
5
10
15
Month
Count of non−prescribing doctors
Sum with previous plot

Q5



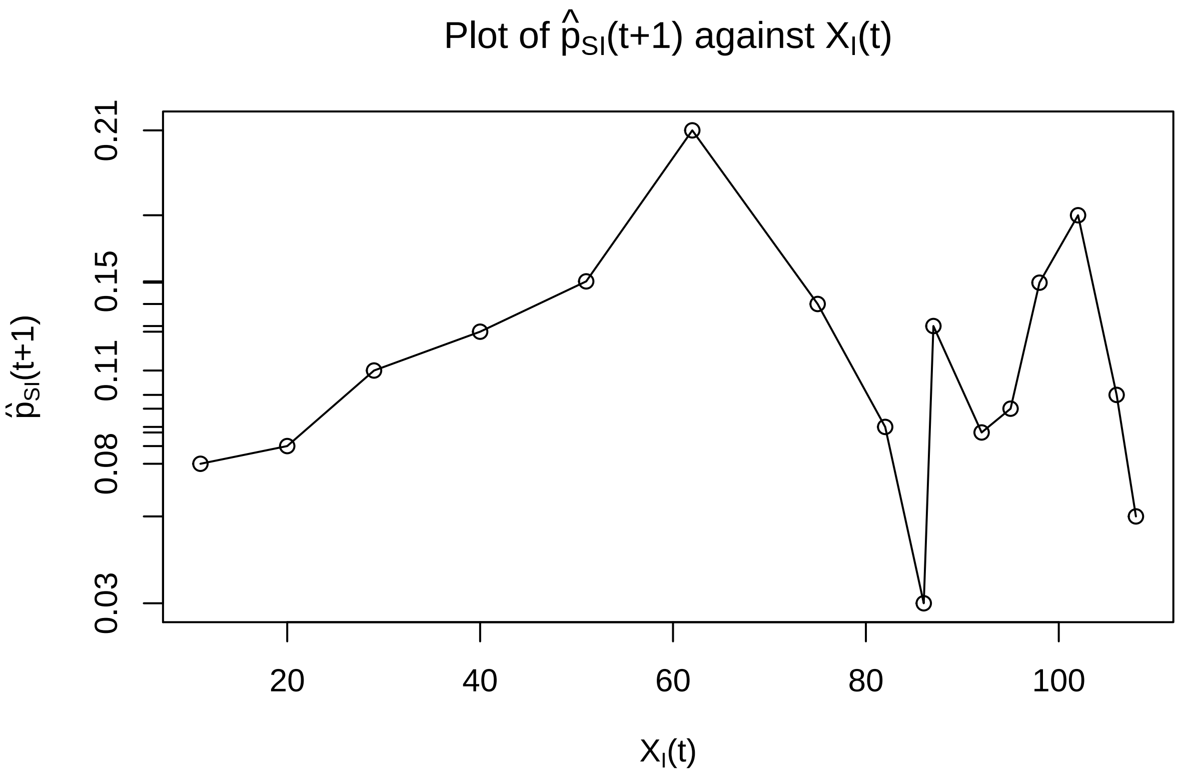
Fraction of doctors who started prescribing each month
Fraction
0.21
0.15
0.11
0.08
0.03
5
10
15
Month

Q6



The shape is shows an increasing fraction of doctors who start prescribing as more doctors already prescribe. However, this is only up to a certain point, where it sharply decreases, then starts roughly increasing again, followed finally by another sharp decrease. This resembles some form of a damped oscillation.

Q7



$\hat{p}_{SI}(t+1)$ is represented by `adoption.fraction`, as it counts the proportion of those who had not been prescribing before, but transitioned into prescribing for each month. $X_I(t)$ is represented by `adoption.start.cum` in the code, as it counts the total number of doctors prescribing by the end of each month.

Q8

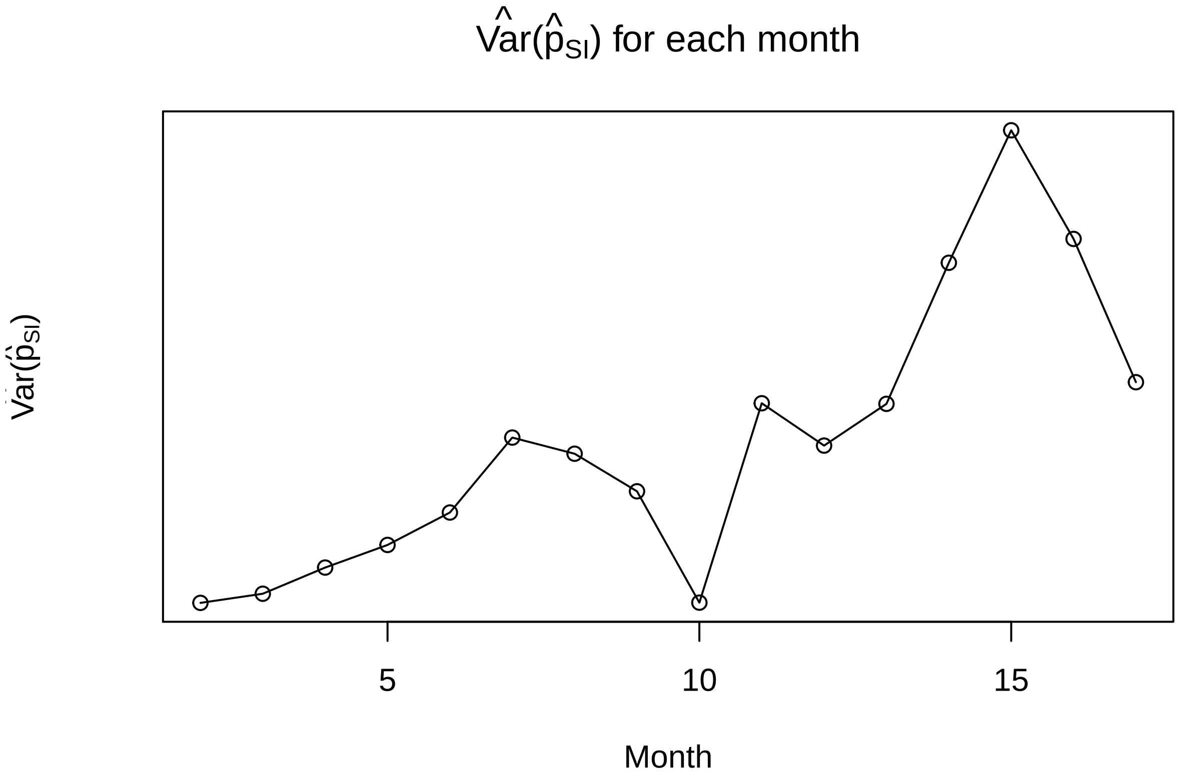


Table 2: Ratio of largest to smallest estimated variance

x
9.792934

Q9

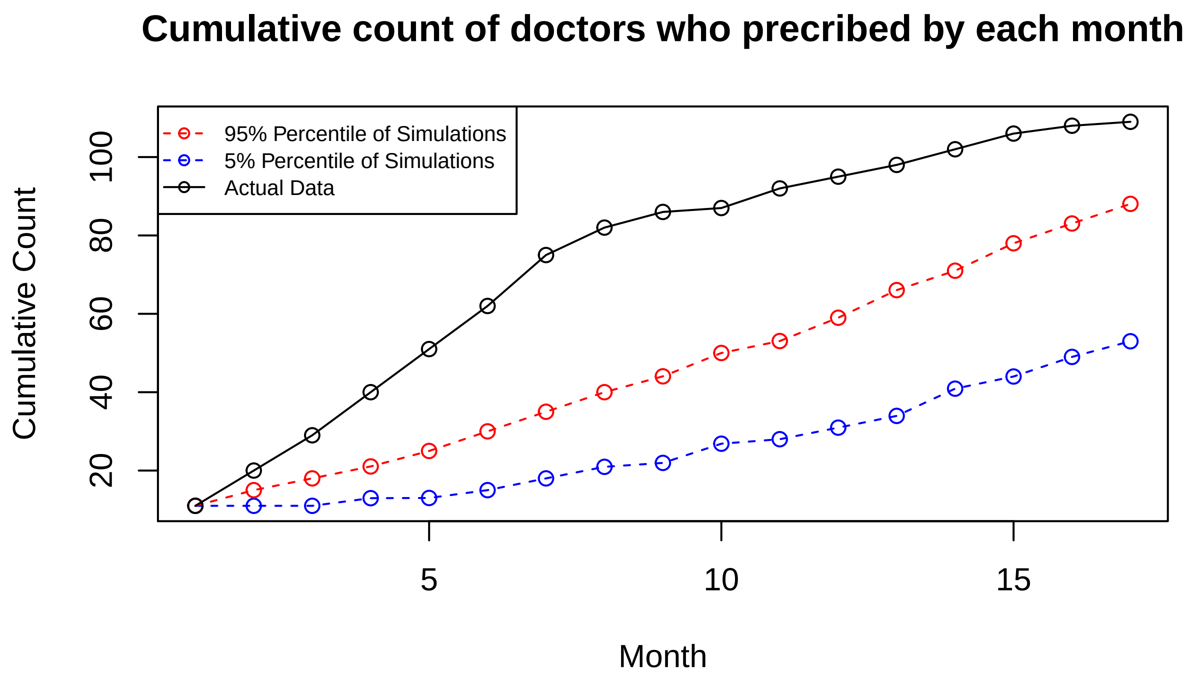
Table 3: Estimate of α

x
0.0013475

Q10

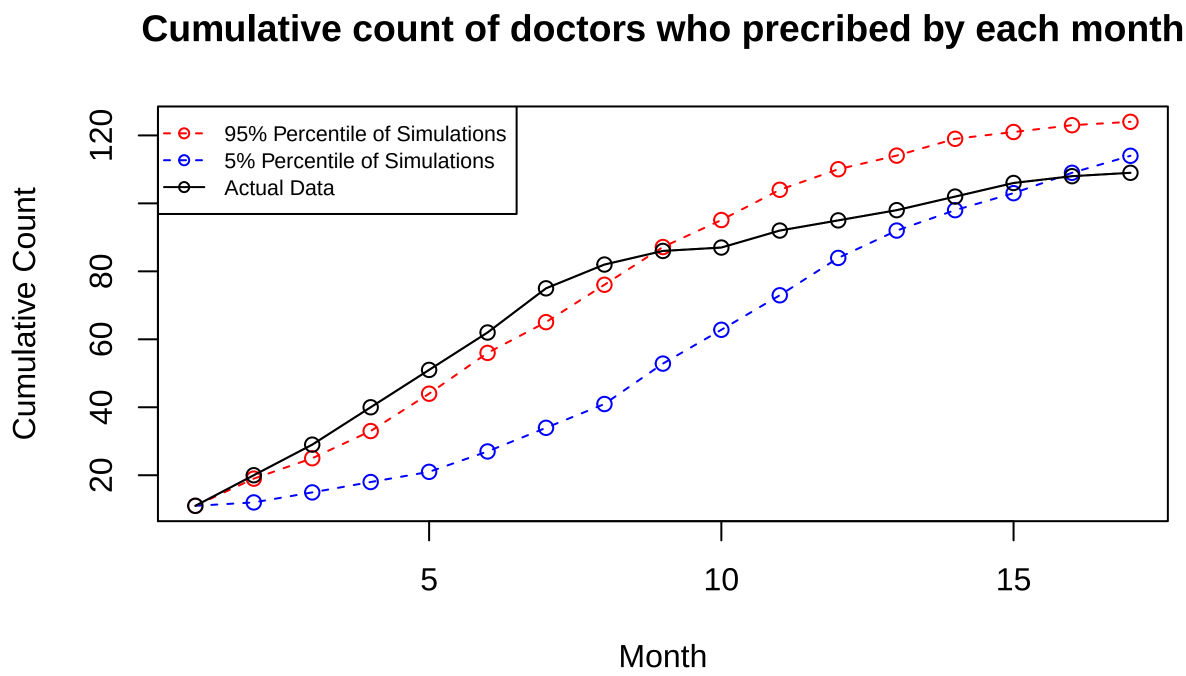
```r
sim.adoption <- function(alpha, n, X.I.init, months) {
    # alpha: weight such that p_SI(t) = alpha * X_I(t-1)
    # n: total number in population
    # X.I.init: Initial number of "infected"
    # months: number of months to simulate, where each time step is a month
    # Returns: Vector of counts of total infected by the month as indexed

    X.I <- vector(length = months)

    # Initial counts of "Infected"
    X.I[1] <- X.I.init

    # Edge case
    if (months < 2) {
        return(X.I)
    }

    # Simulate rest of the values
    for (t in 2:months) {
        # Count of "Susceptible" at t-1
        X.S <- n - X.I[t - 1]

        # Count of those transitioning from S to I follows binomial dist.
        # with m = X.S(t-1) and p.SI(t) = alpha * X.I(t-1)
        changed <- rbinom(1, X.S, alpha * X.I[t - 1])

        # Update those who changed from S to I
        X.I[t] <- X.I[t - 1] + changed
    }

    return(X.I)
}
```

Q11



The plot shows that the model, using the estimated value of $\alpha = 0.00135$, does not work well as the actual data is consistently above the 5^{th} and 95^{th} percentile of the simulations, hence is consistently underestimating.

Q12



Since our model with $\alpha = 0.00135$ consistently underestimates compared to the actual data, increasing α would cause the model to estimate more transitions from non-prescription to prescriptions with a higher probability, counteracting the effect of the underestimation. Hence, this model using $2 * \alpha$ seems to perform better, where more of the actual data seems to lie close to or within the bounds of the simulations.