1.   i) Together, (1) and (2) define a hierarchical model since they relate observed values D_{ij} drawn inde-
        pendently based on parameters β_i to a set of hyperparameters π_0 and σ_b in such a way that the D_{ij}
        can provide inference on each other through the hyperparameters. In other words, even though the
        observations are conditionally independent, they are still informative on each other through the hy-
        perparameters.Since the β_j are iid given the hyperparameters, they are necessarily exchangeable. Not
        conditioned on π_0, σ_b, the β_j should still be exchangeable assuming the same value of π_0 and σ_b are
        used to draw each β_j; there is just additional variability in the initial draw of the hyperparameters.
        $D_{ij} \mid \beta, \sigma$ will be exchangeable for all i since they are iid, but $D_{ij} \mid \beta_j$ won't be exchangeable across j
        since $P(D_{ij} \mid \beta_j = a, D_{ij'} \mid \beta_{j'} = b) = P(D_{ij'} \mid \beta_{j'} = a, D_{ij} \mid \beta_j = b)$ only if $\beta_{j'} = \beta_j$. Finally, the D_{ij}
        should be exchangable accross i and j if unconditioned, or conditioned on π, σ_b, since then they will be
   iid.

    ii) This command will calculate β, D, and also the p-values.

```
## ii − simulate simple hierarchical model
p.values <− function(x){
    return(t.test(x)$p.value)
}

simulateD <− function(pi0,sigb,n=10,m=1000,sigj=1){
    output <− list()
    output$beta        <− ifelse(rbinom(m,1,pi0),0,rnorm(m,0,sigb))
    output$D           <− replicate(n,rnorm(m,output$beta,sigj))
    output$p.values <− apply(output$D,1,p.values)
    return(output)
```

    iii) I calculated the usual two sided t-test p-value using the R command. They were distributed as such:

Histogram, $\pi_0 = 1$, $\sigma_b = 1$ Histogram, $\pi_0 = 0.5$, $\sigma_b = 3$
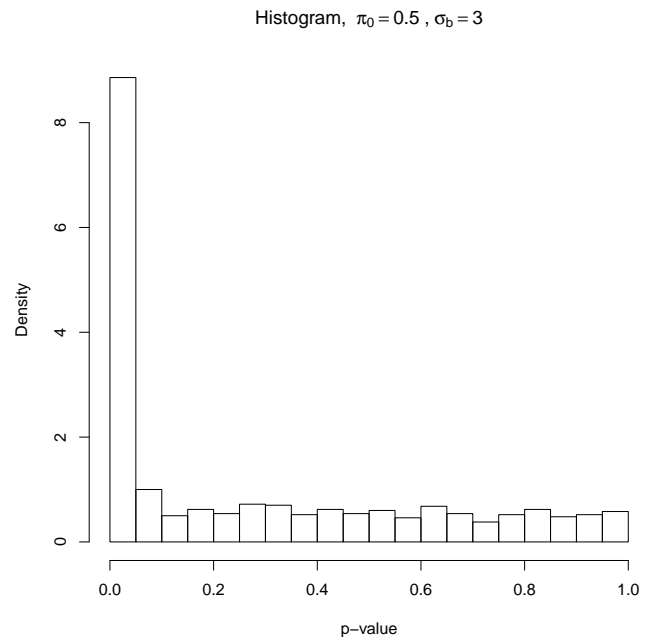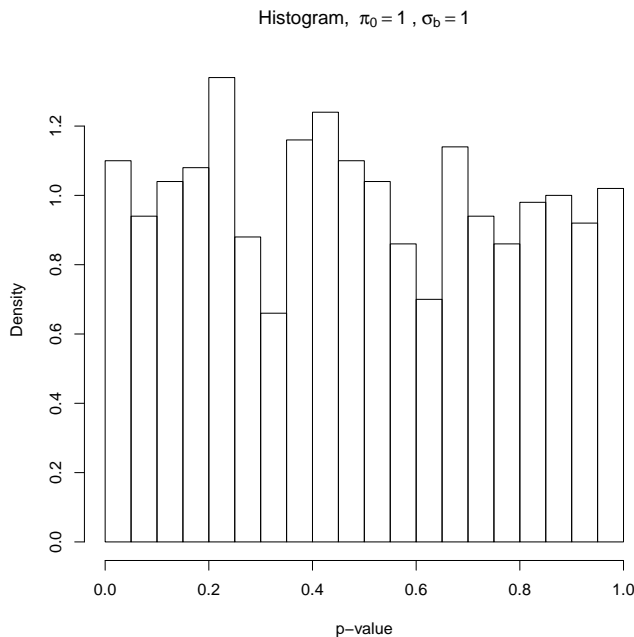
Histogram, $\pi_0 = 0$, $\sigma_b = 3$
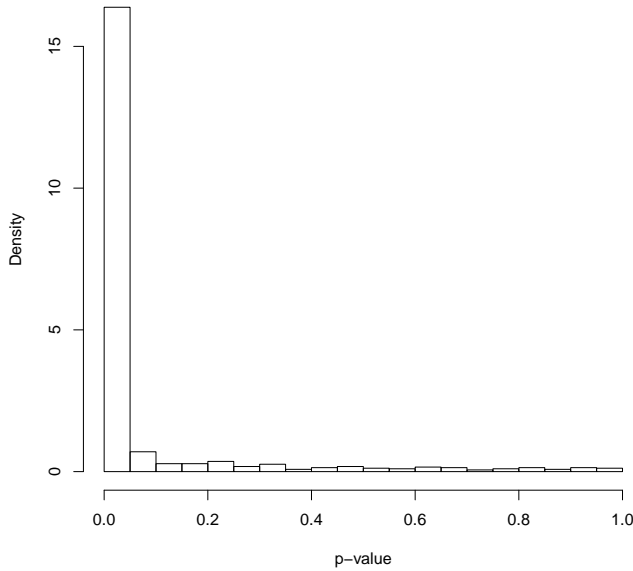
As one would expect, for the first one where the β are all 0, the p-values are uniformly distributed. In the second, with $\pi_0 = .5$, we see a big lump of low p-values near 0 corresponding to most of the β_j which are non-zero, and a approximately uniform distribution over the rest of the p-values corresponding to the β_j which are 0. Finally, in the last histogram, where none of the β_j are 0, we see overwhelmingly low p-values corresponding to the strong evidence against $\beta_j = 0$.

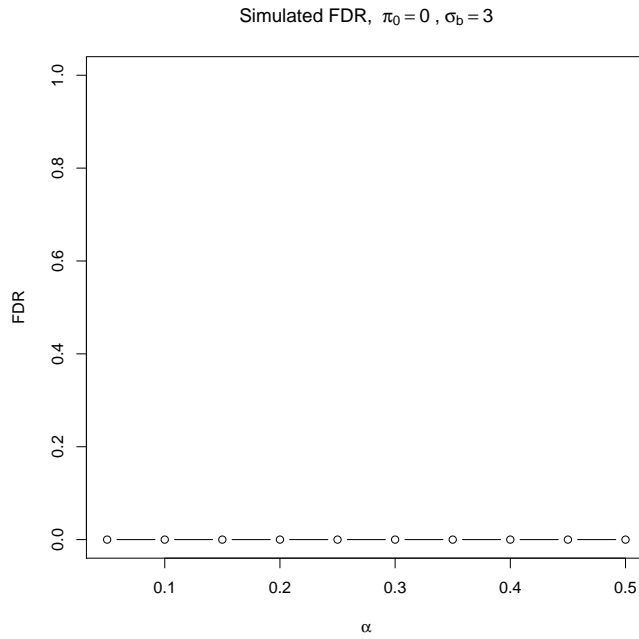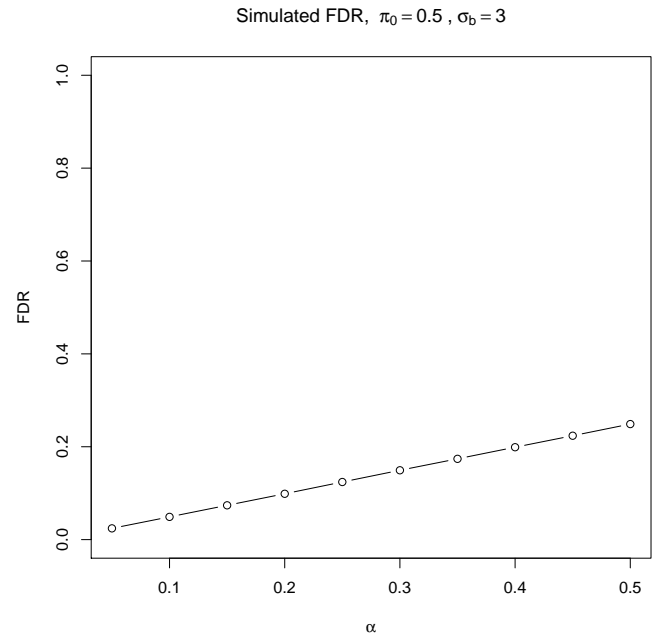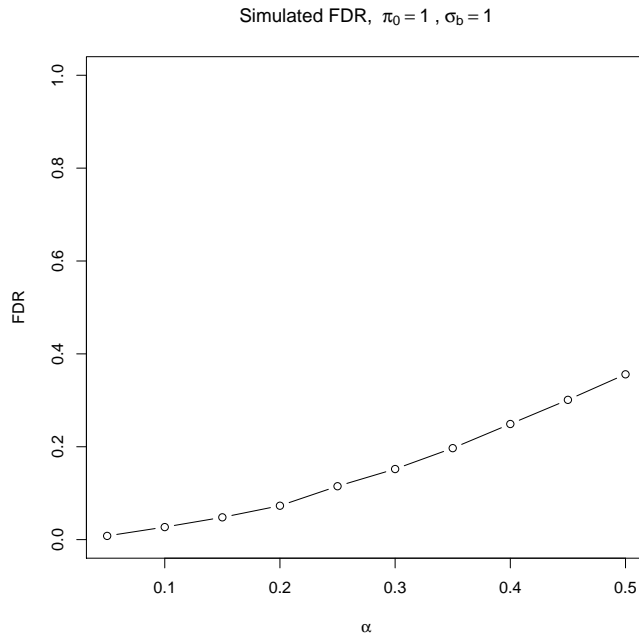iv) This is my function to apply Benjamini-Hochberg:

```
}

## iv - implement Benjamini-Hochberg
BH <- function(pvals, alpha){
    m    <- length(pvals)
    ord  <- order(pvals)
    test <- pvals[ord]< (1:m)*alpha/m
```

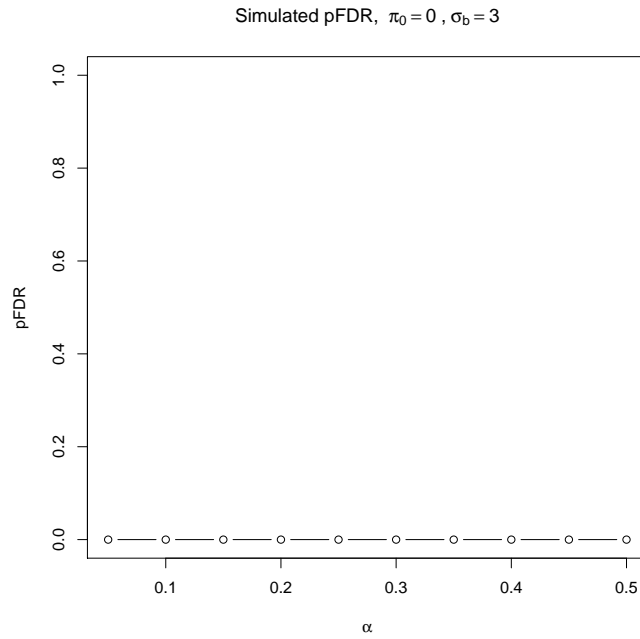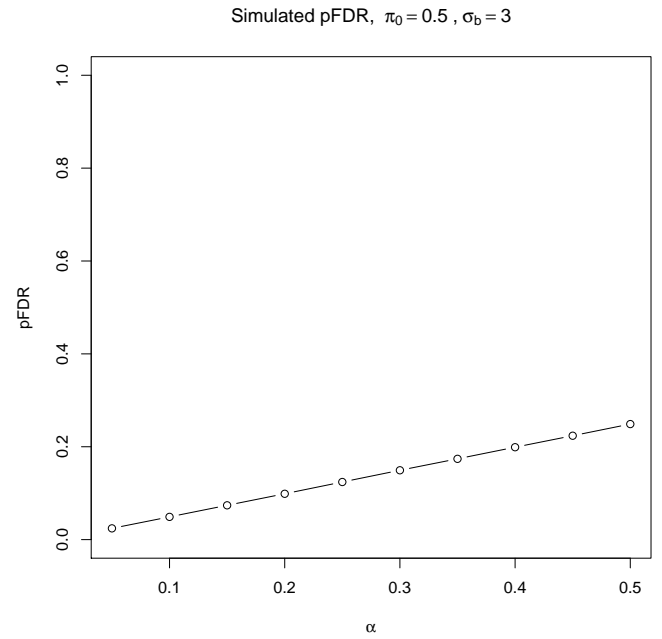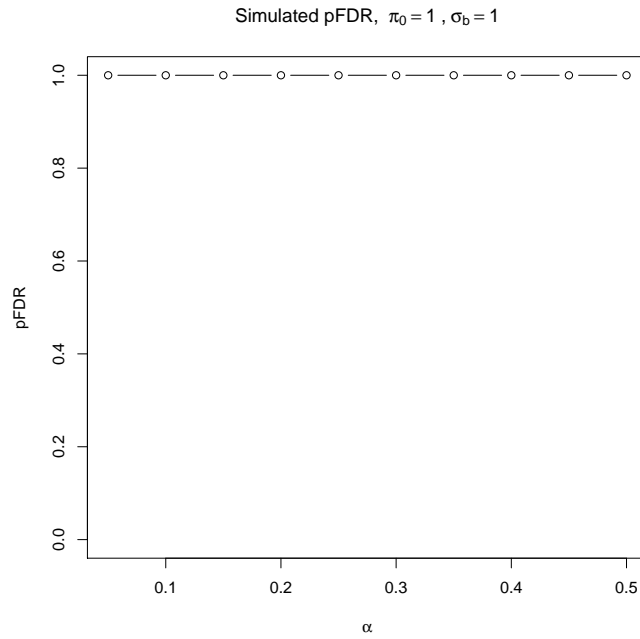v) This is my function to computer the empirical FDR (and pFDR):

```
}

## v - implement FDR
FDR <- function(beta, gamma, pFDR=FALSE){
    R <- sum(gamma)
    V <- sum(gamma & beta==0)
```

vi) To simulate $E(V/R)$, I generated the dataset D 1000 times for each scenario, and averaged the emperical FDR for each *alpha* over the data sets. The results are ploted below:

2

Simulated FDR, $\pi_0 = 1$, $\sigma_b = 1$

Simulated FDR, $\pi_0 = 0.5$, $\sigma_b = 3$
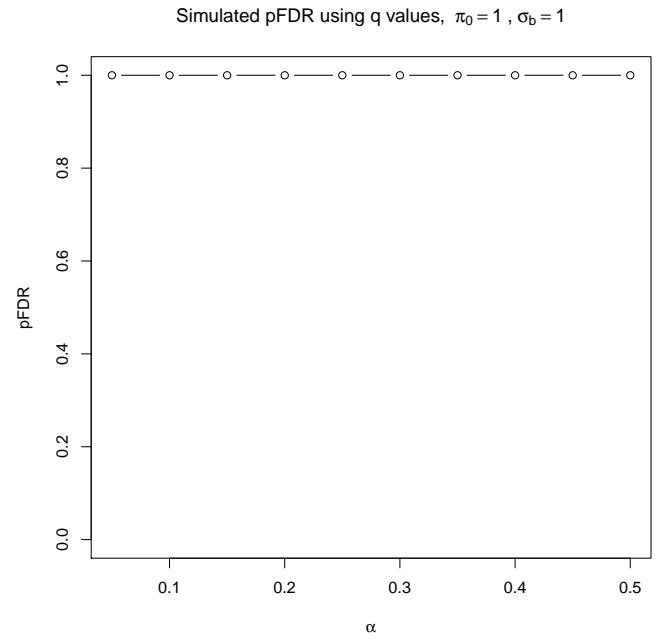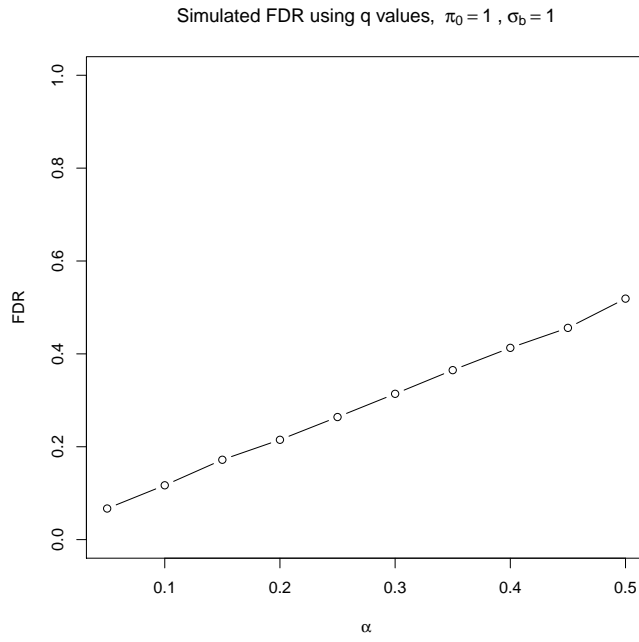
Simulated FDR, $\pi_0 = 0$, $\sigma_b = 3$

In the first scenario, despite the fact that all the discoveries are false, our FDR statistic is less than 1, which is due to the definiton. In any event, The FDR rate is properly controlled, coming in under α. For the second scenario, the FDR rate seems to come in at almost exactly half of α for all levels, providing conservative control. For the final scenario, since all $\beta \neq 0$, the FDR is necessarily 0, so FDR is inherently controlled.

vii) I repeated the same procedure as above, but this time caclulated the pFDR. The results are below:
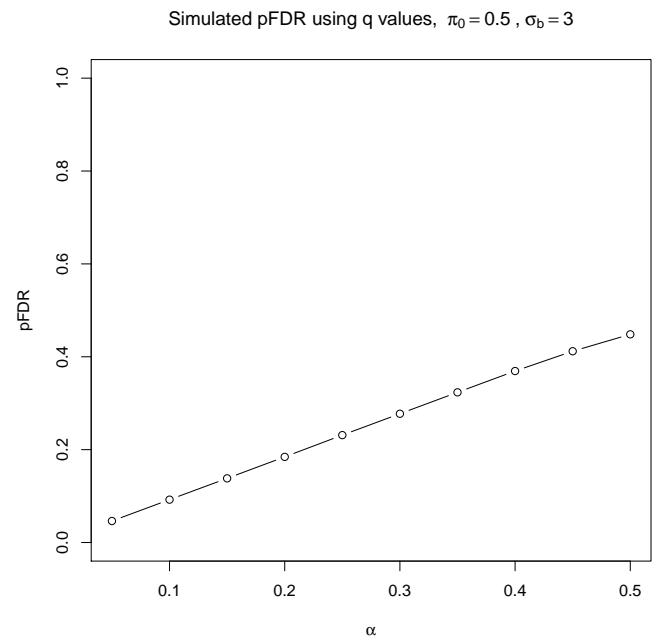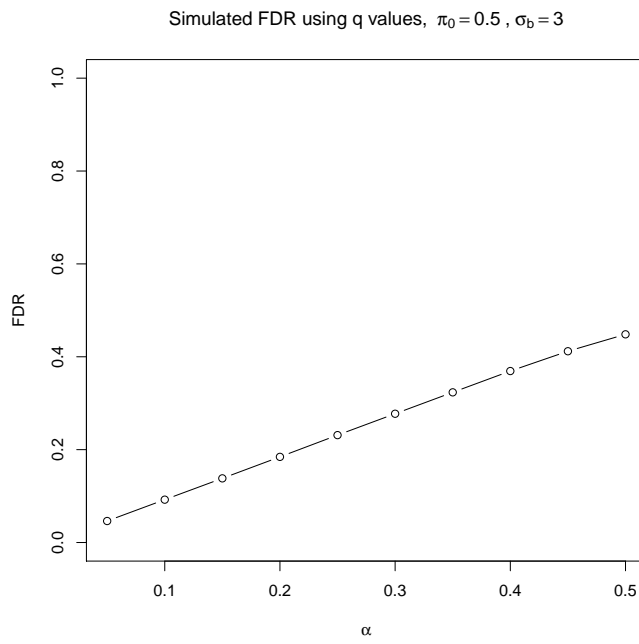
Simulated pFDR, $\pi_0 = 1$, $\sigma_b = 1$

pFDR

α

Simulated pFDR, $\pi_0 = 0.5$, $\sigma_b = 3$

pFDR

α

Simulated pFDR, $\pi_0 = 0$, $\sigma_b = 3$

pFDR

α

In the first case, with all discoveries false, the pFDR is naturally at 1 for all α and not controlled. The second case is nearly identical as with FDR, controlled at about half of α. Again, for the final case, since no discoveries are false, the pFDR is controlled perfectly at 0.
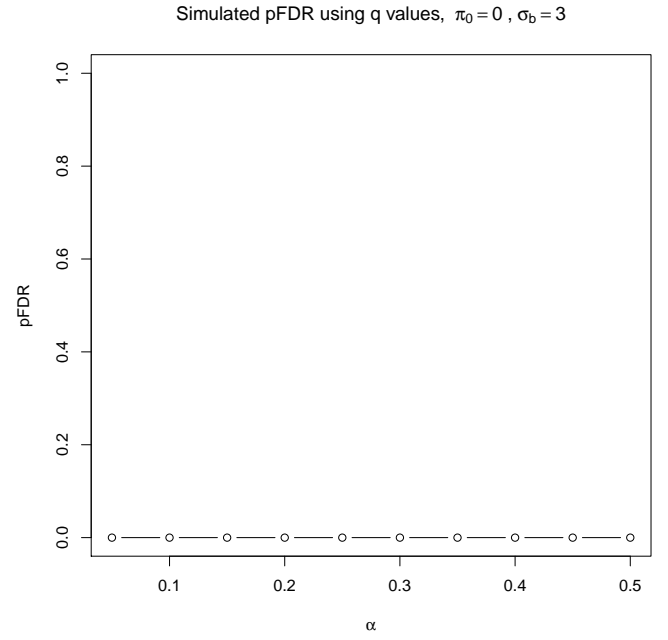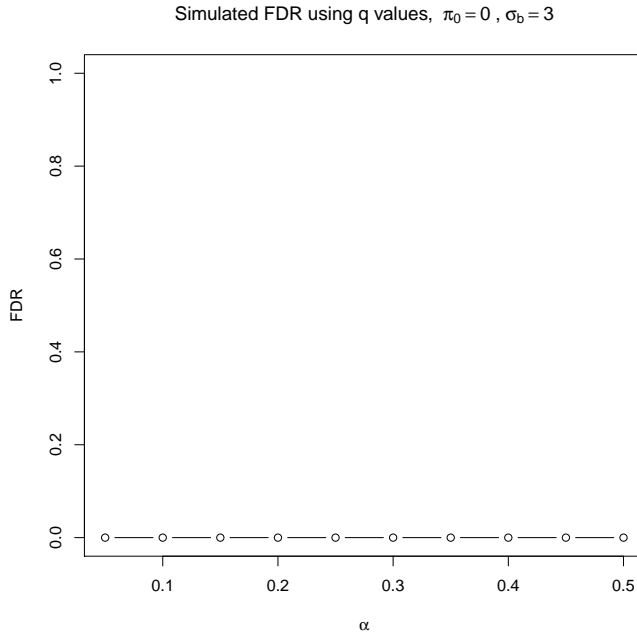
2.   i) Repeating the same procedure as above, except with reject decisions based on q values, I get these results:

Simulated FDR using q values, $\pi_0 = 1$, $\sigma_b = 1$ — Simulated pFDR using q values, $\pi_0 = 1$, $\sigma_b = 1$

In this first scenario, the FDR seems to be controlled at pretty much exactly the desired rate, while the pFDR is still necessarily 1.

Simulated FDR using q values, $\pi_0 = 0.5$, $\sigma_b = 3$ — Simulated pFDR using q values, $\pi_0 = 0.5$, $\sigma_b = 3$

In this second scenario, we have control of both FDR and pFDR at the desired rate.

Simulated FDR using q values, $\pi_0 = 0$, $\sigma_b = 3$

Simulated pFDR using q values, $\pi_0 = 0$, $\sigma_b = 3$

With no false discoveries, FDR and pFDR are still 0.

2) I have plotted the estimated π_0 vs actual π_0 over a range of values for $\sigma_b = .5, 1, 2, 4$. Each estimate is the average over 100 simulations.

True vs. Estimated π_0, $\sigma_b = 0.5$

True vs. Estimated π_0, $\sigma_b = 1$
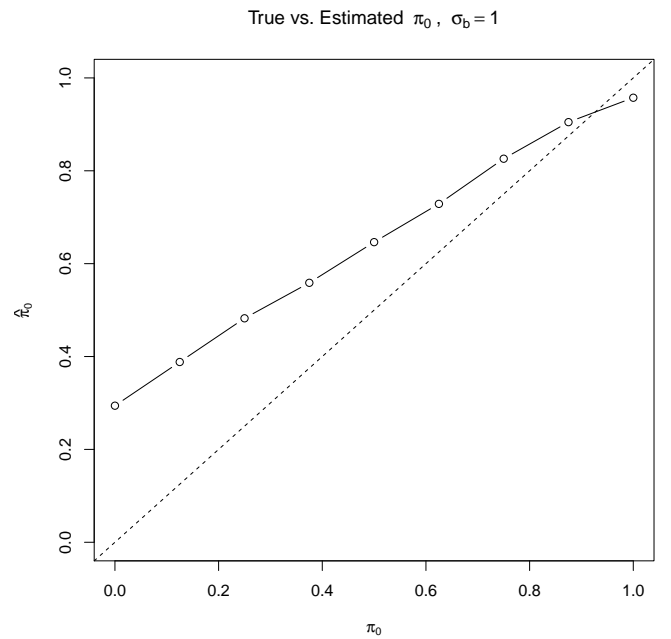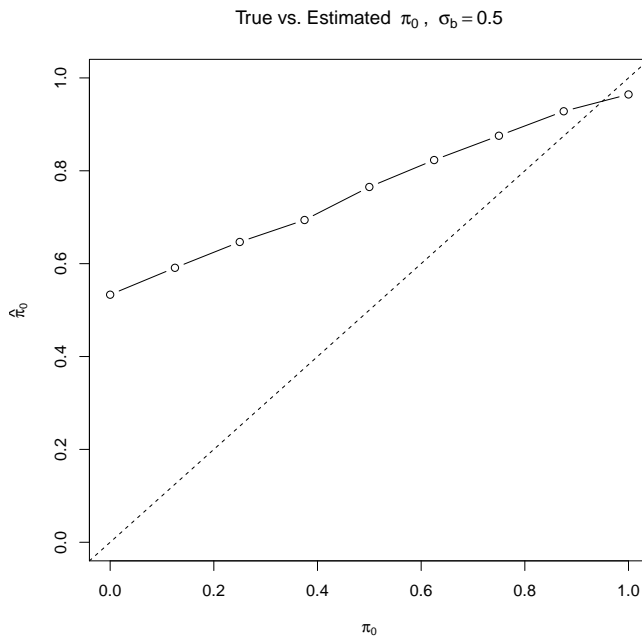
As we can see above and below, the estimates get increasingly good as the variance goes up and the β tend to fall farther from 0. The predictions are uniformly higher than the actual π_0, except for values near 1, and the worst predictions are for low values of π_0. In general, this method seem to provide a pretty solid estimate.

True vs. Estimated π_0, $\sigma_b = 2$

True vs. Estimated π_0, $\sigma_b = 4$