

First Simulation of Different Scientific Questions

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Small simulation

I want to do a quick simulation showing that with the same observations (same data) you get different evidence for different questions. This is somewhat obvious, but maybe it is not entirely intuitive how this plays out in the sample size limit, and what exactly the differences are depending on different questions.

For now, I consider a simple case of a correlational design. I will simulate from the following model

$$\begin{aligned}X_i &\sim \text{Normal}(10, 10^2), \\Y_i &\sim \text{Normal}(x_i\zeta + 2, \delta^2 10^2),\end{aligned}$$

Where ζ is either 0 or 1, indicating whether the correlation between \mathbf{x} and \mathbf{y} is truly zero or not, and δ is a scale on the standard deviation of Y indicating the size of the correlation (smaller correlation with larger δ). I simulate the data for some range of sample size N , and for true positive and true null correlations.

Scientific questions

- *Is there an effect?* This question indicates the comparison between a spike null hypothesis and an unconstrained model over the full range of possible correlation coefficients. The model comparison corresponding to this question is illustrated in Figure 1A.
- *Is there an effect in the expected direction, or is there no effect?* This question indicates the comparison between a spike null hypothesis and a positive-effects model that only considers correlation coefficients between 0 and 1. The model comparison corresponding to this question is illustrated in Figure 1B.
- *Is there an effect in the expected direction, or is an effect in the opposite direction?* This question indicates the comparison between a positive-effects model that only considers correlation coefficients between 0 and 1, and a negative-effects model that only considers correlation coefficients between -1 and 0. The model comparison corresponding to this question is illustrated in Figure 1C.
- *Is there an effect that is at least as large as x , where $[-x, x]$ corresponds to a range of values I consider equivalent to zero?* This question appears to be somewhat popular in psychology recently. The question indicates the comparison between an equivalence region around zero, and a model that excludes the equivalence region but includes all other coefficients between -1 and 1. The model comparison corresponding to this question will be illustrated in Figure 1D as soon as I find out how.

Thanks to Bayesian model comparison, all of these questions can be combined by calculating the Bayes factors between all of the models of interest. We therefore do not need to restrict ourselves to one question of interest. Yet, it is useful to consider how these questions differ. One way they differ is in the amount of evidence that can be acquired with increasing sample size. I therefore did a small simulation study with varying sample sizes to compare the evidence acquired for these four different questions. I repeated this simulation for a true positive, a true zero, and a true negative correlation, where the observed correlation varies for each simulation draw.

```
rsim <- function(n, z = 1, sdscale = 7){  
  x <- rnorm(n, 10, 10)  
  y <- rnorm(n, z * x + 2, sdscale * 10)  
  r1 <- correlationBF(y, x)  
  r2 <- correlationBF(y, x, nullInterval = c(-1, 0))  
  r3 <- correlationBF(y, x, nullInterval = c(-.05, .05))  
}
```

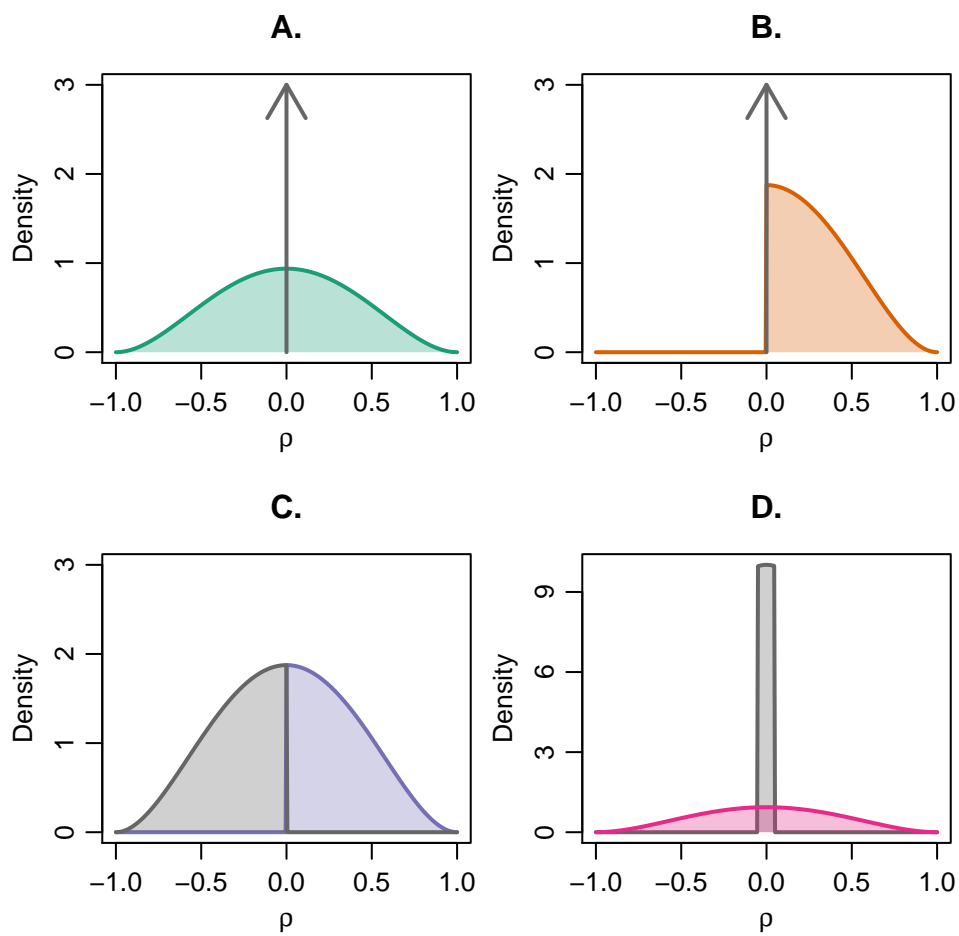


Figure 1: Four possible scientific questions illustrated.

```

return(c('n' = n
        , 'r' = cor(x, y)
        , 'BF10' = as.numeric(extractBF(r1)[1])
        , 'BFp0' = extractBF(r2)[2, 1]
        , 'BFpn' = extractBF(r2)[2, 1]/extractBF(r2)[1, 1]
        , 'BF1e' = extractBF(r3)[2, 1]/extractBF(r3)[1, 1]
        , 'BFe0' = extractBF(r3)[2, 1]))
}

# general settings
reps <- 25 #25 repetitions per sample size
N <- rep(((2:20)^3), reps) # vector of sample sizes between 8 and 8000

```

True positive correlation

```

set.seed(123)
res <- data.frame(t(sapply(N, rsim, simplify = T)))
avgs <- matrix(NA, nrow = 4, ncol = length(N)/reps)
for(i in 1:4){
  avgs[i, ] <- tapply(res[, i+2], res$n, median)
}

```

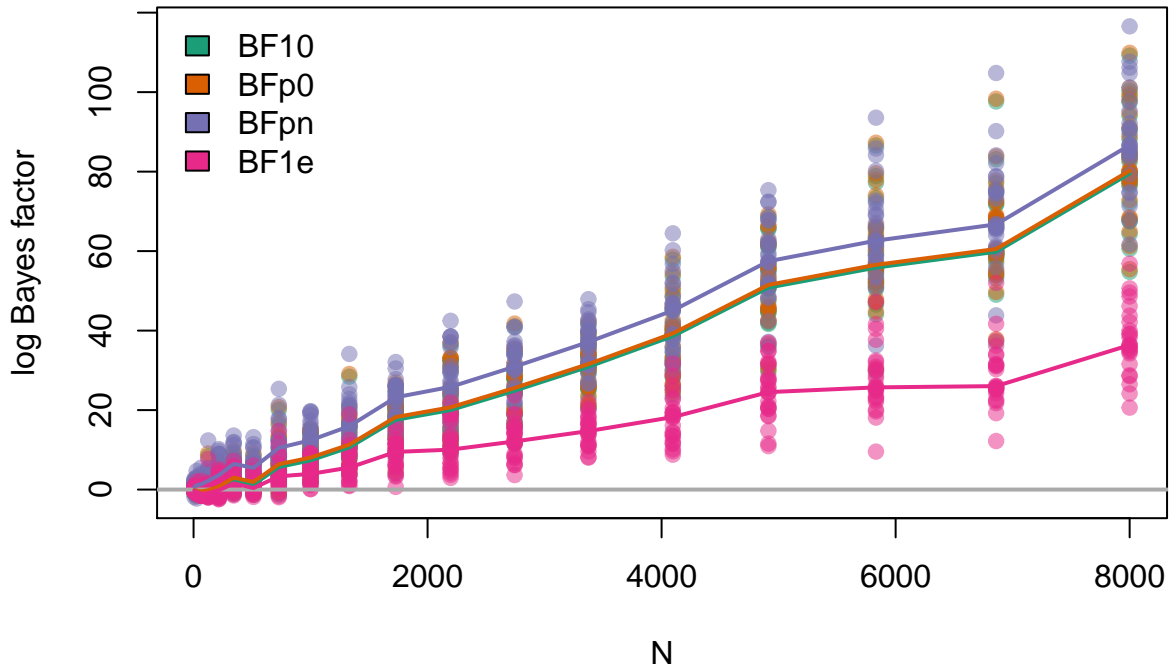
True correlation is $r = 0.14$.

```

matplot(N, log(res[,3:6])
        , type = "p", lty = 1, pch = 19
        , col = adjustcolor(cols, .5)
        , ylab = "log Bayes factor"
        , main = paste("Correlation r =", round(mean(res$r), 2)))
legend("topleft", colnames(res[,3:6]), fill = cols, bty = "n")
abline(h = 0, col = "darkgrey", lwd = 2)
matplot(unique(N), log(t(avgs)), type = "l", lwd = 2, col = cols, lty = 1, add = T)

```

Correlation $r = 0.14$

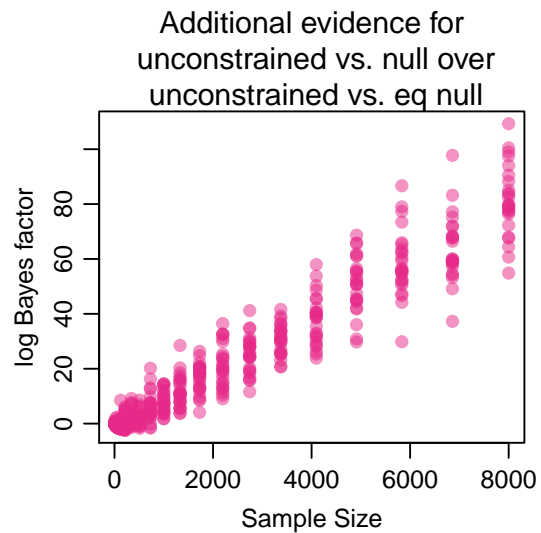
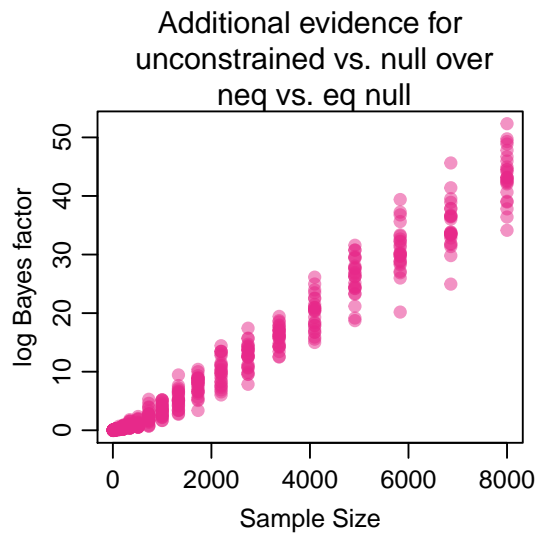
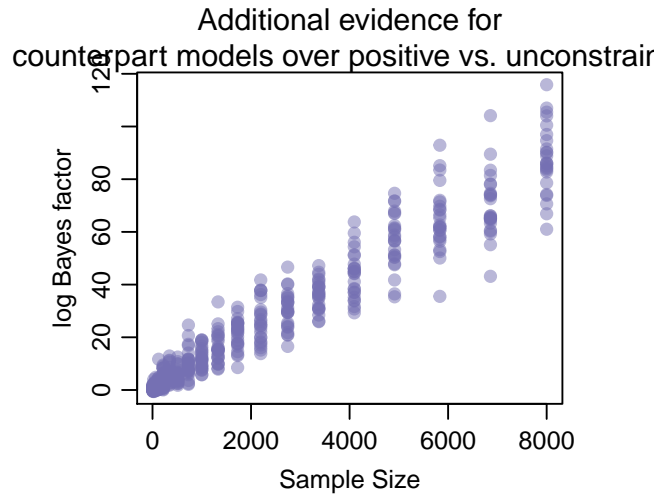
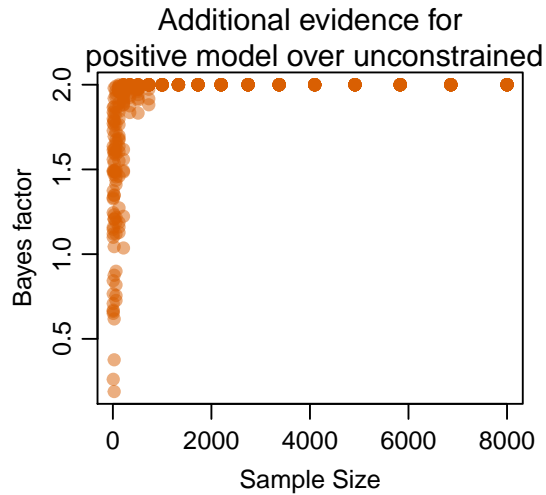


```
par(mgp = c(2, .7, 0), mar = c(4,4,4,3))
res$BFp1 <- res$BFp0/res$BF10
res$BFoppenc <- res$BFpn/res$BFp1
res$BF0estar <- res$BF10/res$BF1e
res$BF0e2 <- res$BF0e
layout(matrix(1:4, ncol = 2, byrow = T))
plot(res$n, res$BFp1
     , col = adjustcolor(cols[2], .5), pch = 19
     , xlab = "Sample Size"
     , ylab = "Bayes factor"
     )
mtext("Additional evidence for\n positive model over unconstrained", 3)

plot(res$n, log(res$BFoppenc)
     , col = adjustcolor(cols[3], .5), pch = 19
     , xlab = "Sample Size"
     , ylab = "log Bayes factor")
mtext("Additional evidence for\n counterpart models over positive vs. unconstrained", 3)

plot(res$n, log(res$BF0estar)
     , col = adjustcolor(cols[4], .5), pch = 19
     , xlab = "Sample Size"
     , ylab = "log Bayes factor")
mtext("Additional evidence for\n unconstrained vs. null over\n neq vs. eq null", 3)

plot(res$n, log(res$BF0e2)
     , col = adjustcolor(cols[4], .5), pch = 19
     , xlab = "Sample Size"
     , ylab = "log Bayes factor")
mtext("Additional evidence for\n unconstrained vs. null over\n unconstrained vs. eq null", 3)
```



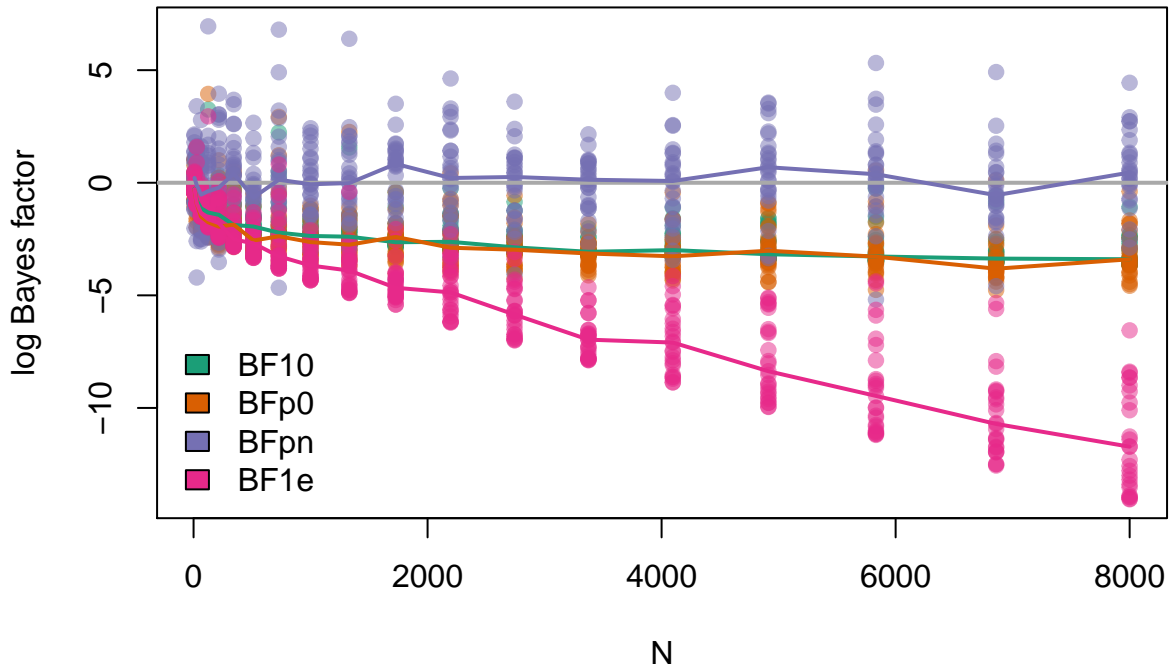
True null correlation

```
set.seed(123)
res <- data.frame(t(sapply(N, rsim, z = 0, simplify = T)))
avgs <- matrix(NA, nrow = 4, ncol = length(N)/reps)
for(i in 1:4){
  avgs[i, ] <- tapply(res[, i+2], res$n, median)
}
```

True correlation is $r = 0$.

```
matplot(N, log(res[,3:6])
  , type = "p", lty = 1, pch = 19
  , col = adjustcolor(cols, .5)
  , ylab = "log Bayes factor"
  , main = paste("Correlation r =", round(mean(res$r), 2)))
legend("bottomleft", colnames(res[,3:6]), fill = cols, bty = "n")
abline(h = 0, col = "darkgrey", lwd = 2)
matplot(unique(N), log(t(avgs)), type = "l", lwd = 2, col = cols, lty = 1, add = T)
```

Correlation $r = 0$

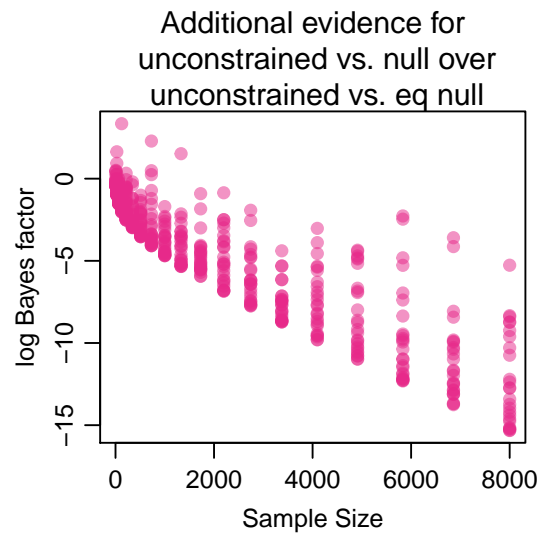
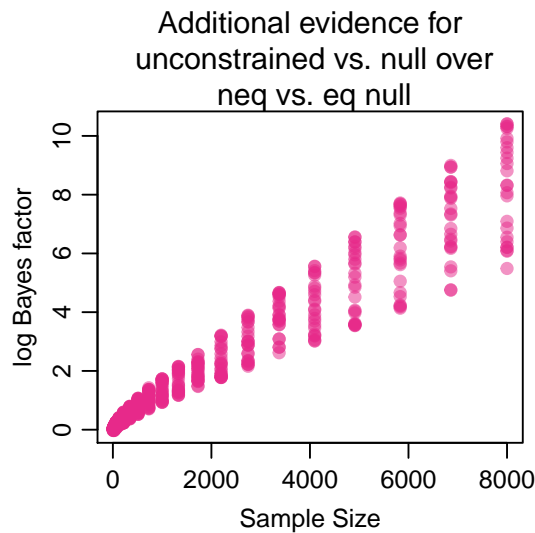
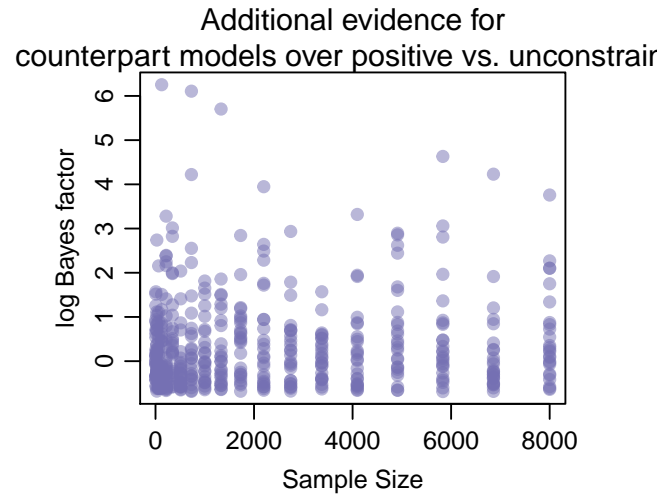
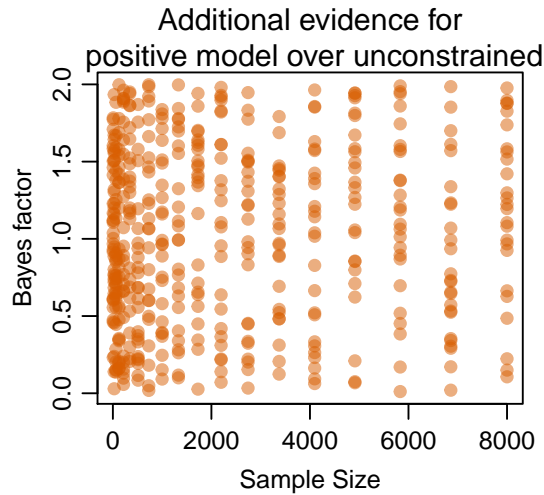


```
par(mgp = c(2, .7, 0), mar = c(4,4,4,3))
res$BFp1 <- res$BFp0/res$BF10
res$BFoppenc <- res$BFpn/res$BFp1
res$BF0estar <- res$BF10/res$BF1e
res$BF0e2 <- res$BF0e
layout(matrix(1:4, ncol = 2, byrow = T))
plot(res$n, res$BFp1
     , col = adjustcolor(cols[2], .5), pch = 19
     , xlab = "Sample Size"
     , ylab = "Bayes factor"
     )
mtext("Additional evidence for\n positive model over unconstrained", 3)

plot(res$n, log(res$BFoppenc)
     , col = adjustcolor(cols[3], .5), pch = 19
     , xlab = "Sample Size"
     , ylab = "log Bayes factor")
mtext("Additional evidence for\n counterpart models over positive vs. unconstrained", 3)

plot(res$n, log(res$BF0estar)
     , col = adjustcolor(cols[4], .5), pch = 19
     , xlab = "Sample Size"
     , ylab = "log Bayes factor")
mtext("Additional evidence for\n unconstrained vs. null over\n neq vs. eq null", 3)

plot(res$n, log(res$BF0e)
     , col = adjustcolor(cols[4], .5), pch = 19
     , xlab = "Sample Size"
     , ylab = "log Bayes factor")
mtext("Additional evidence for\n unconstrained vs. null over\n unconstrained vs. eq null", 3)
```



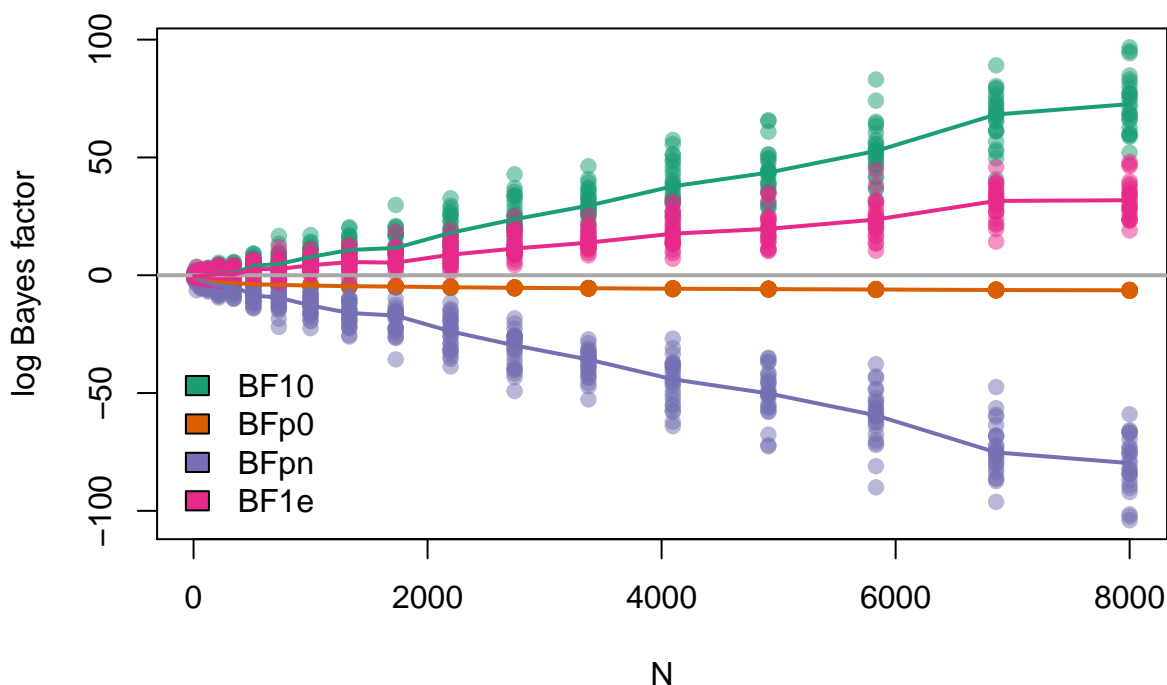
True negative correlation

```
set.seed(123)
res <- data.frame(t(sapply(N, rsim, z = -1, simplify = T)))
avgs <- matrix(NA, nrow = 4, ncol = length(N)/reps)
for(i in 1:4){
  avgs[i, ] <- tapply(res[, i+2], res$n, median)
}
```

True correlation is $r = -0.14$.

```
matplot(N, log(res[,3:6])
  , type = "p", lty = 1, pch = 19
  , col = adjustcolor(cols, .5)
  , ylab = "log Bayes factor"
  , main = paste("Correlation r =", round(mean(res$r), 2)))
legend("bottomleft", colnames(res[,3:6]), fill = cols, bty = "n")
abline(h = 0, col = "darkgrey", lwd = 2)
matplot(unique(N), log(t(avgs)), type = "l", lwd = 2, col = cols, lty = 1, add = T)
```

Correlation $r = -0.14$



```
par(mgp = c(2, .7, 0), mar = c(4,4,4,3))
res$BFp1 <- res$BFp0/res$BF10
res$BFoppenc <- res$BFpn/res$BFp1
res$BF0estar <- res$BF10/res$BF1e
res$BF0e2 <- res$BF0e
layout(matrix(1:4, ncol = 2, byrow = T))
plot(res$n, res$BFp1
      , col = adjustcolor(cols[2], .5), pch = 19
      , xlab = "Sample Size"
      , ylab = "Bayes factor"
      )
mtext("Additional evidence for\n positive model over unconstrained", 3)

plot(res$n, log(res$BFoppenc)
      , col = adjustcolor(cols[3], .5), pch = 19
      , xlab = "Sample Size"
      , ylab = "log Bayes factor")
mtext("Additional evidence for\n counterpart models over positive vs. unconstrained", 3)

plot(res$n, log(res$BF0estar)
      , col = adjustcolor(cols[4], .5), pch = 19
      , xlab = "Sample Size"
      , ylab = "log Bayes factor")
mtext("Additional evidence for\n unconstrained vs. null over\n neq vs. eq null", 3)

plot(res$n, log(res$BF0e2)
      , col = adjustcolor(cols[4], .5), pch = 19
      , xlab = "Sample Size"
      , ylab = "log Bayes factor")
mtext("Additional evidence for\n unconstrained vs. null over\n unconstrained vs. eq null", 3)
```