

# Supplement of “Bayesian Reanalysis of Null Results Reported in the New England Journal of Medicine: Strong yet Variable Evidence for the Absence of Treatment Effects”

- This is a supplement of “Bayesian Reanalysis of Null Results Reported in the New England Journal of Medicine: Strong yet Variable Evidence for the Absence of Treatment Effects” by Hoekstra R, Monden R, van Ravenzwaaij D and Wagenmaker EJ. This document was written by Rei Monden (November, 2016).
- These plots were generated based on the 43 test statistics reported in the New England Journal of Medicine 2015.

Data

(nomisdata)

##	P.value	BF01	Total.N
## 1	0.420	6.190	3856
## 2	0.870	13.150	981
## 3	0.190	12.300	981
## 4	0.240	11.950	2033
## 5	0.470	68.540	6109
## 6	0.930	107.300	7945
## 7	0.620	89.650	5985
## 8	0.930	84.450	7768
## 9	0.700	18.860	86
## 10	0.360	11.470	10003
## 11	0.530	8.610	524
## 12	0.230	45.100	18446
## 13	0.480	85.340	10003
## 14	1.000	27.840	1044
## 15	0.900	77.690	10063
## 16	0.750	3.790	106
## 17	0.760	16.360	1053
## 18	0.190	9.940	549
## 19	0.160	2.530	260
## 20	0.970	10.870	517
## 21	0.370	17.090	2070
## 22	0.170	6.840	310
## 23	0.630	19.230	1832
## 24	0.890	2.660	33
## 25	0.450	40.210	7213
## 26	0.110	14.560	7213
## 27	0.800	11.040	791
## 28	0.260	7.320	1325
## 29	0.190	2.420	259
## 30	0.380	15.440	404
## 31	0.600	15.280	1612
## 32	0.720	7.440	404
## 33	0.660	9.140	369
## 34	1.000	18.310	2059
## 35	0.400	10.460	1523

```
## 36  0.220  3.130    252
## 37  0.190 12.440   1990
## 38  0.870 21.710   2287
## 39  0.500  9.050    826
## 40  0.930  5.610    162
## 41  0.820 44.240   6068
## 42  0.985  4.023    101
## 43  0.860 560.900  2447
```

**Figure 2**

```
par(cex.main = 1.1, mar = c(4.5, 6, 2, 9) + 0.1, mgp = c(3, 1, 0), cex.lab = 1.1,
    font.lab = 2, cex.axis = 1.1, las = 1)
plot(nomisdata$P.value, log(nomisdata$BF01), xlim = c(0, 1), ylim = c(log(1), log(1000)),
     xlab = "", ylab = "", cex.lab = 2, cex.axis = 2, las = 1, yaxt = "n", xaxt="n",cex=2,
     bty = "n", type = "p", pch = 21, bg = "grey")

labelsUpper = log(c(1000,300,100, 30, 10, 3, 1))

criticalP = c( 0, labelsUpper)
for (idx in 1:length(criticalP)) {
  abline(h = criticalP[idx], col = "darkgrey", lwd = 1, lty = 2)
}
abline(h = 0)
axis(side = 4, at = criticalP, tick = c(TRUE,FALSE,rep(TRUE,5)), las = 2,
     cex.axis = 1, labels = FALSE)
axis(side = 4, at = labelsUpper + 0.602, tick = FALSE, cex.axis = 1.2,
     labels = c("", "", "Extreme", "Very strong", "Strong", "Moderate", "Anecdotal"))

axis(side = 2, at = c(criticalP), tick = TRUE, las = 2, cex.axis = 1.1,
     labels = c("1", "1,000", "300", "100", "30", "10", "3", ""))

mtext("Bayes factor in favor of the null hypothesis", side = 2.5, line = 3.2, las = 0, cex = 1.2)
grid::grid.text("Evidence", 0.97, 0.5, rot = 270, gp = grid::gpar(cex = 1.2))
mtext("P-values", side = 1, line = 2.5, las = 1, cex = 1.1)

axis(at=seq(0,1,by=0.1),side=1)
```

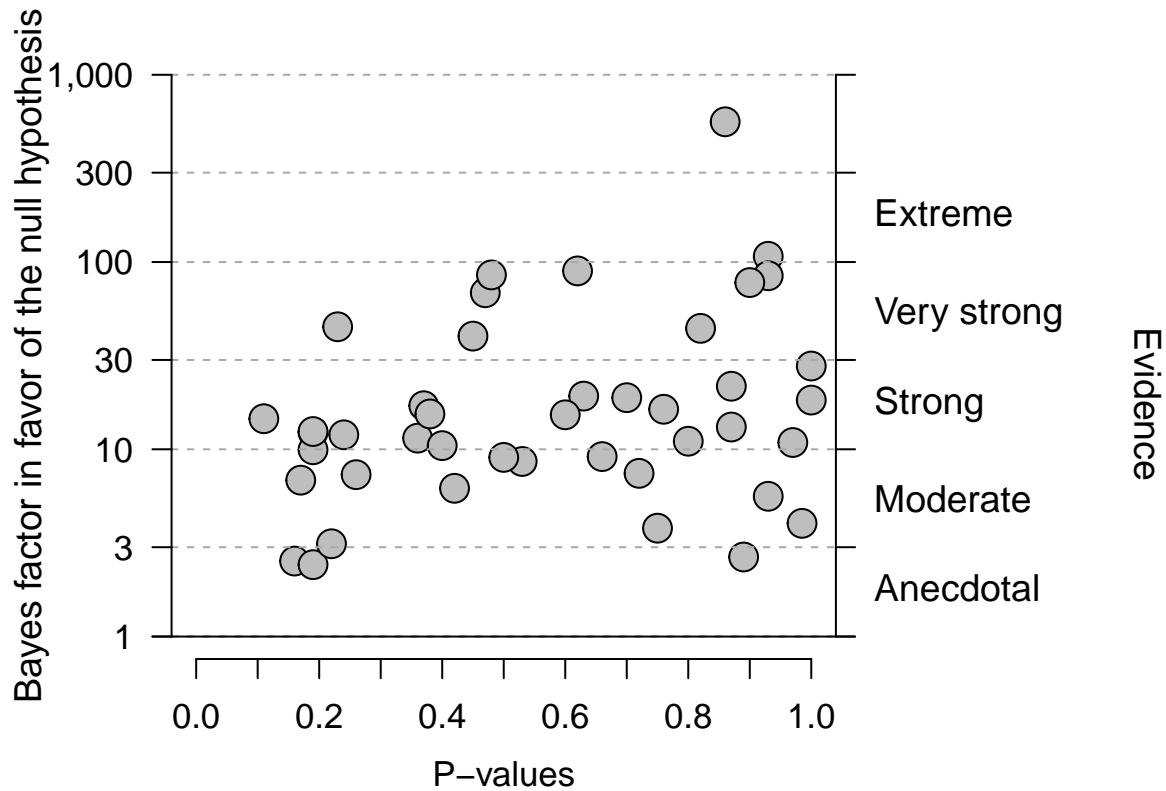


Figure 3

```

par(cex.main = 1.1, mar = c(4.5, 6, 2, 9) + 0.1, mgp = c(3, 1, 0), cex.lab = 1.1,
    font.lab = 2, cex.axis = 1.1, las = 1)
plot(log(nomisdata$Total.N), log(nomisdata$BF01), xlim = c(3, 11), ylim = c(log(1), log(1000)),
     xlab = "", ylab = "", cex.lab = 2, cex.axis = 2, las = 1, yaxt = "n", xaxt="n",cex=2,
     bty = "n", type = "p", pch = 21, bg = "grey")

labelsUpper = log(c(1000,300,100, 30, 10, 3, 1))

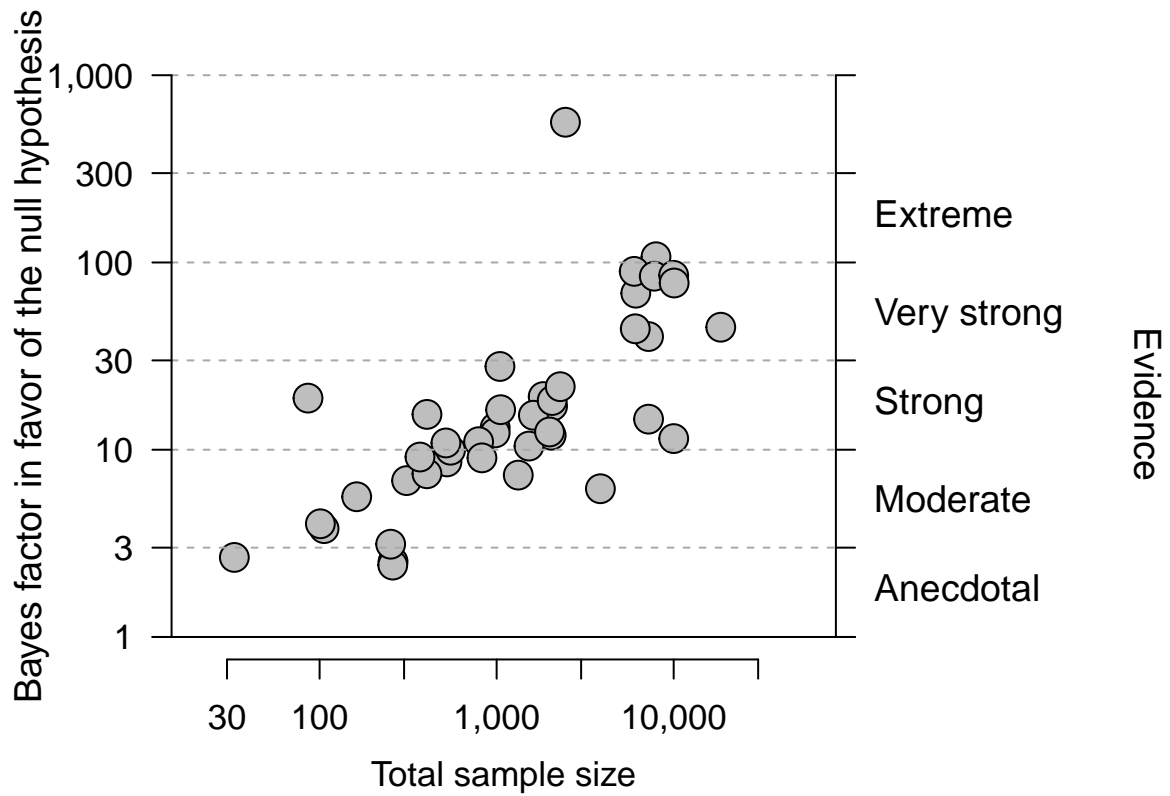
criticalP = c( 0, labelsUpper)
for (idx in 1:length(criticalP)) {
  abline(h = criticalP[idx], col = "darkgrey", lwd = 1, lty = 2)
}
abline(h = 0)
axis(side = 4, at = criticalP, tick = TRUE, las = 2, cex.axis = 1, labels = FALSE)
axis(side = 4, at = labelsUpper + 0.602, tick = FALSE, cex.axis = 1.2,
     labels = c("", "", "Extreme", "Very strong", "Strong", "Moderate", "Anecdotal"))

axis(side = 2, at = c(criticalP), tick = TRUE, las = 2, cex.axis = 1.1,
     labels = c("1", "1,000", "300", "100", "30", "10", "3", ""))

mtext("Bayes factor in favor of the null hypothesis", side = 2.5, line = 3.2, las = 0, cex = 1.2)
grid::grid.text("Evidence", 0.97, 0.5, rot = 270, gp = grid::gpar(cex = 1.2))
mtext("Total sample size", side = 1, line = 2.5, las = 1, cex = 1.1)

```

```
axis(at=c(log(30),log(100),log(300),log(1000),log(3000),log(10000),log(30000)),
     side=1,labels = c(30,100,300,"1,000","3,000","10,000","30,000"))
```



The correlation between Bayes factors and P-values:

```
cor(log(nomisdata$BF01),nomisdata$P.value)
```

```
## [1] 0.2896321
```

The correlation between Bayes factors and total sample sizes:

```
cor(log(nomisdata$BF01),log(nomisdata$Total.N))
```

```
## [1] 0.7198048
```