Imports

In [1]:
```
library("BayesFactor")
library("MCMCpack")
```

```
Loading required package: coda

Loading required package: Matrix

************
Welcome to BayesFactor 0.9.12-4.2. If you have questions, please contact Richard
Morey (richarddmorey@gmail.com).

Type BFManual() to open the manual.
************

Loading required package: MASS

##
## Markov Chain Monte Carlo Package (MCMCpack)

## Copyright (C) 2003-2021 Andrew D. Martin, Kevin M. Quinn, and Jong Hee Park

##
## Support provided by the U.S. National Science Foundation

## (Grants SES-0350646 and SES-0350613)
##
```

Read Data

US Vaccination Records

- DTP1 = First dose of Diphtheria/Pertussis/Tetanus vaccine;
- HepB_BD = Hepatitis B, Birth Dose;
- Pol3 = Polio third dose;
- Hib3 – Influenza third dose;
- MCV1 = Measles first dose!

In [2]:
```
load("Data/usVaccines.RData")
str(usVaccines)
head(usVaccines)
```

```
Time-Series [1:38, 1:5] from 1980 to 2017: 83 84 83 84 84 85 88 88 89 81 ...
- attr(*, "dimnames")=List of 2
  ..$ : NULL
  ..$ : chr [1:5] "DTP1" "HepB_BD" "Pol3" "Hib3" ...
```

A matrix: 6 × 5 of type dbl

DTP1	HepB_BD	Pol3	Hib3	MCV1
83	16	95	85	86

DTP1	HepB_BD	Pol3	Hib3	MCV1
84	16	96	85	97
83	17	97	84	97
84	17	97	83	98
84	16	97	85	98
85	17	96	85	97

School Reports

In [3]:

```
load("Data/allSchoolsReportStatus.RData")
str(allSchoolsReportStatus)
head(allSchoolsReportStatus)
```

```
'data.frame':	7381 obs. of  3 variables:
 $ name    : chr  "AGUA DULCE ELEMENTARY" "MEADOWLARK ELEMENTARY" "CALIFORNIA SC
HOOL FOR THE DEAF-FREMONT" "HIDDEN VALLEY ELEMENTARY" ...
 $ pubpriv : chr  "PUBLIC" "PUBLIC" "PUBLIC" "PUBLIC" ...
 $ reported: chr  "Y" "Y" "Y" "Y" ...
```

A data.frame: 6 × 3

	name	pubpriv	reported
	<chr>	<chr>	<chr>
1	AGUA DULCE ELEMENTARY	PUBLIC	Y
2	MEADOWLARK ELEMENTARY	PUBLIC	Y
3	CALIFORNIA SCHOOL FOR THE DEAF-FREMONT	PUBLIC	Y
4	HIDDEN VALLEY ELEMENTARY	PUBLIC	Y
5	MANOR ELEMENTARY	PUBLIC	Y
6	BROOKSIDE ELEMENTARY	PUBLIC	Y

District

In [4]:

```
load("Data/districts21.RData")
str(districts)
head(districts)
```

```
'data.frame':	700 obs. of  13 variables:
 $ DistrictName     : chr  "Belleview Elementary" "Luther Burbank" "South Whittie
r Elementary" "Lawndale Elementary" ...
 $ WithoutDTP       : num  20 5 7 8 9 9 7 2 1 12 ...
 $ WithoutPolio     : num  20 4 7 8 8 9 6 2 1 12 ...
 $ WithoutMMR       : num  20 1 6 9 9 9 6 2 1 15 ...
 $ WithoutHepB      : num  20 2 2 3 4 4 3 2 1 8 ...
 $ PctUpToDate      : num  80 92 88 89 89 90 93 98 99 85 ...
 $ DistrictComplete: logi  TRUE TRUE TRUE TRUE TRUE TRUE ...
 $ PctBeliefExempt : num  20 0 0 1 2 0 2 0 1 0 ...
 $ PctChildPoverty : num  13 24 27 28 23 32 4 28 17 31 ...
 $ PctFreeMeal      : num  51 80 74 71 38 64 0 78 25 45 ...
 $ PctFamilyPoverty: num  9 12 12 12 30 20 2 15 2 12 ...
```

```
$ Enrolled        : num  20 96 357 674 1037 ...
$ TotalSchools    : num  1 1 5 6 15 11 3 1 1 1 ...
```

A data.fra

	DistrictName	WithoutDTP	WithoutPolio	WithoutMMR	WithoutHepB	PctUpToDate	District(
	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	
577	Belleview Elementary	20	20	20	20	80	
442	Luther Burbank	5	4	1	2	92	
112	South Whittier Elementary	7	7	6	2	88	
97	Lawndale Elementary	8	8	9	3	89	
351	Jefferson Elementary	9	8	9	4	89	
5	National Elementary	9	9	9	4	90	

Introductory / Descriptive Reports

Question 1

1. How have U.S. vaccination rates varied over time? Are vaccination rates increasing or decreasing? Which vaccination has the highest rate at the conclusion of the time series? Which vaccination has the lowest rate at the conclusion of the time series? Which vaccine has the greatest volatility?

- DTP1 = First dose of Diphtheria/Pertussis/Tetanus vaccine;
- HepB_BD = Hepatitis B, Birth Dose;
- Pol3 = Polio third dose;
- Hib3 – Influenza third dose;
- MCV1 = Measles first dose!

In [5]:

```
head(usVaccines, 1)
tail(usVaccines, 1)
```

A matrix: 1 × 5 of type dbl

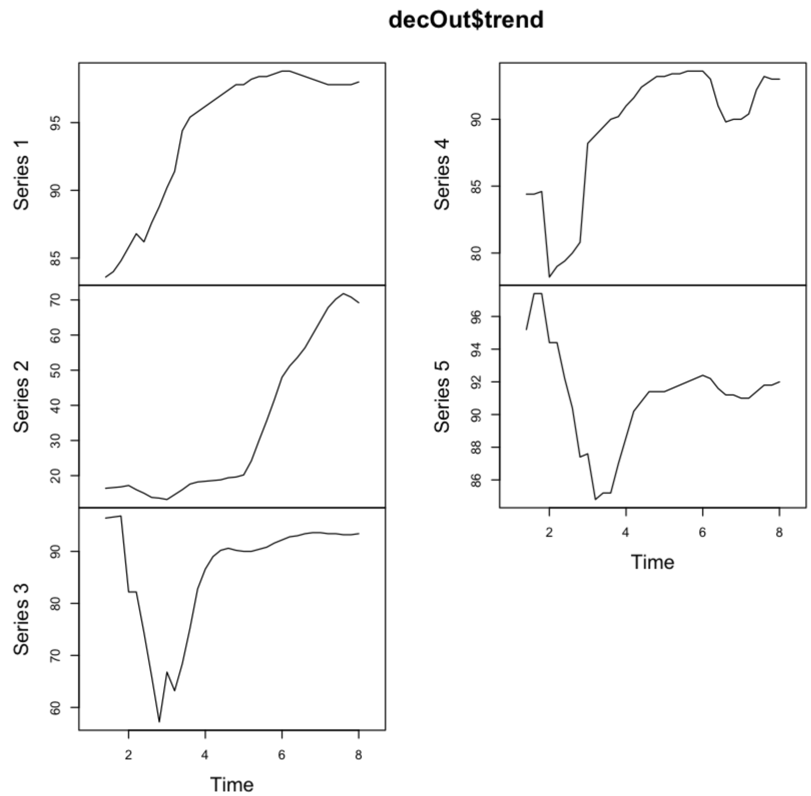
DTP1	HepB_BD	Pol3	Hib3	MCV1
83	16	95	85	86

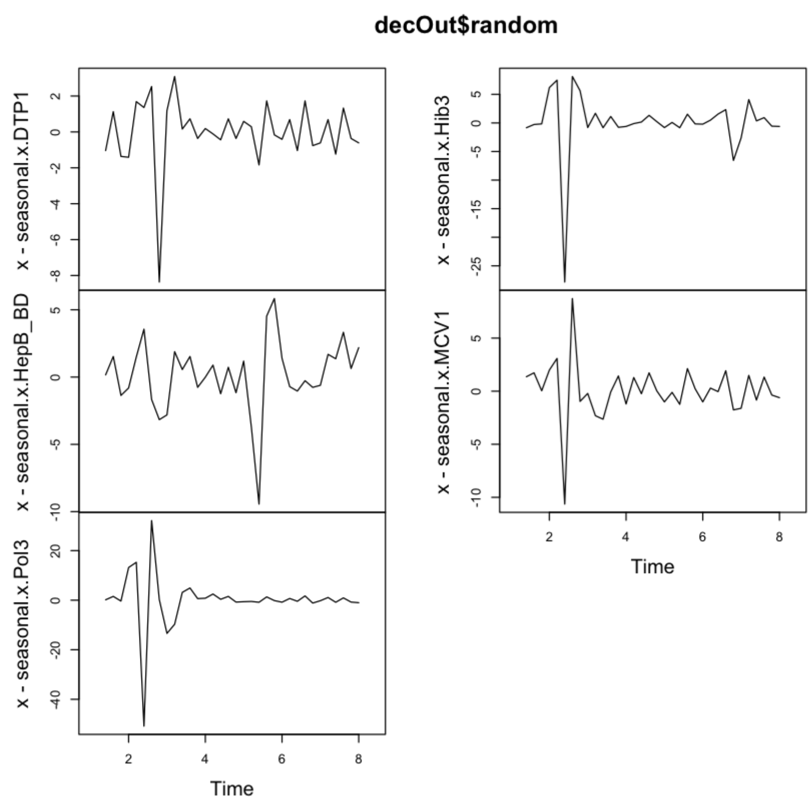
A matrix: 1 × 5 of type dbl

	DTP1	HepB_BD	Pol3	Hib3	MCV1
[38,]	98	64	94	93	92

In [179…

```
decOut = decompose(ts(usVaccines, frequency=5))
plot(decOut$trend)
plot(decOut$random)
```

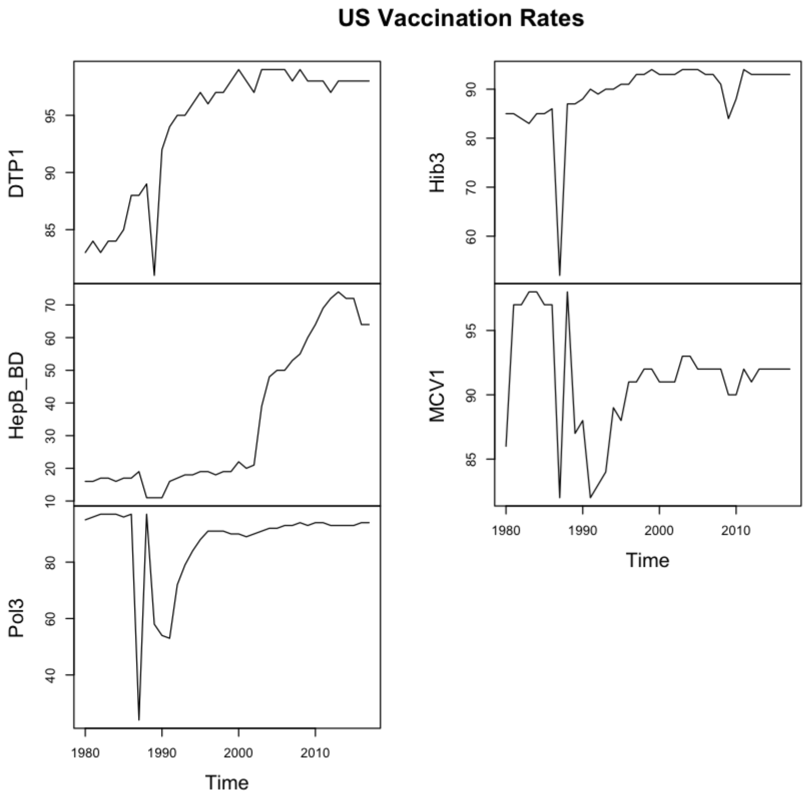




In [ ]:

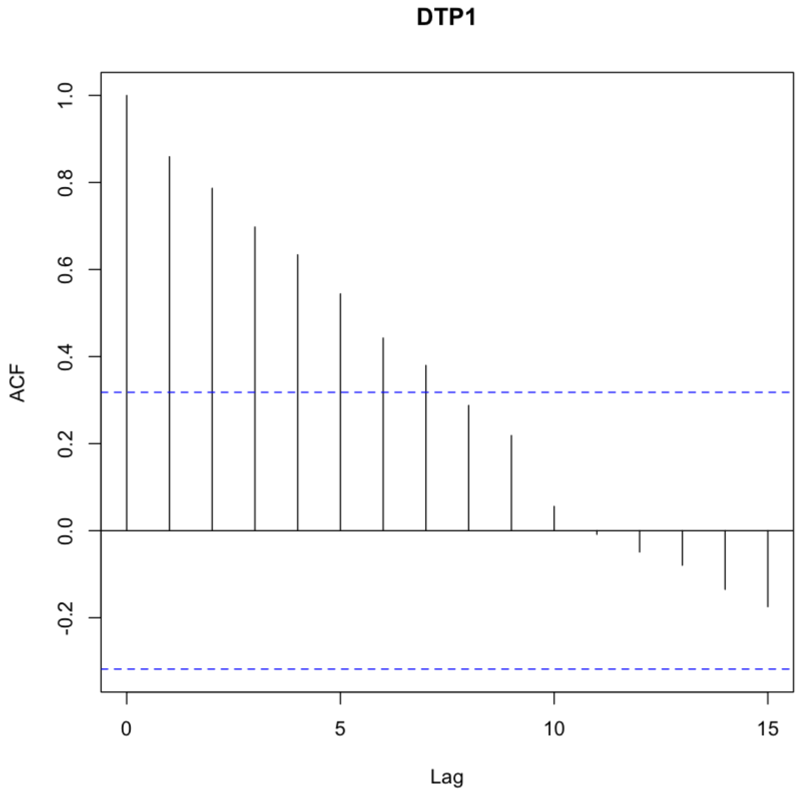
In [165…

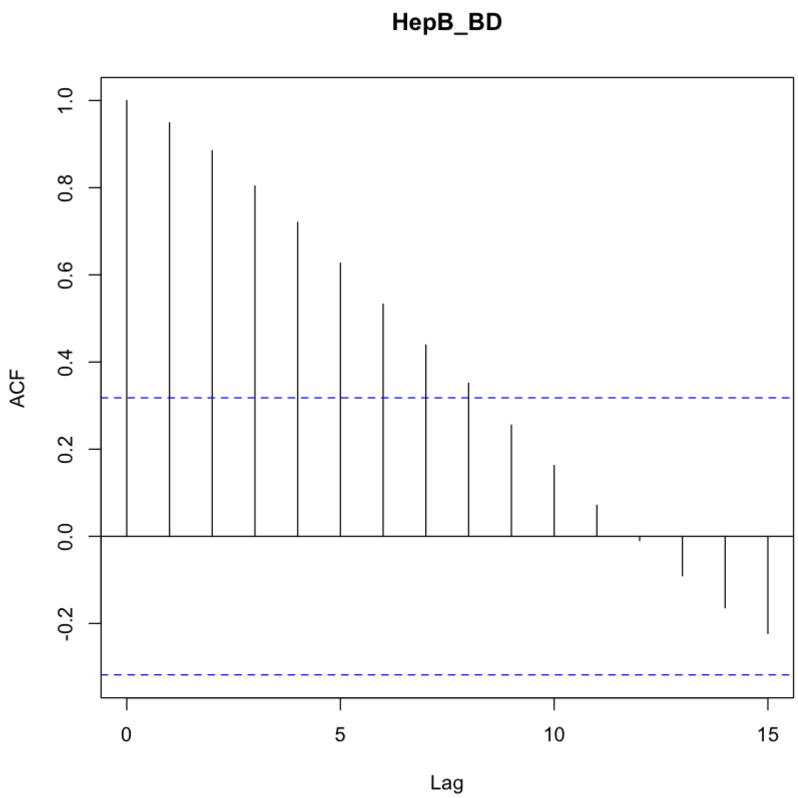
```
plot(usVaccines, main='US Vaccination Rates', ylim=c(0, 100))
```

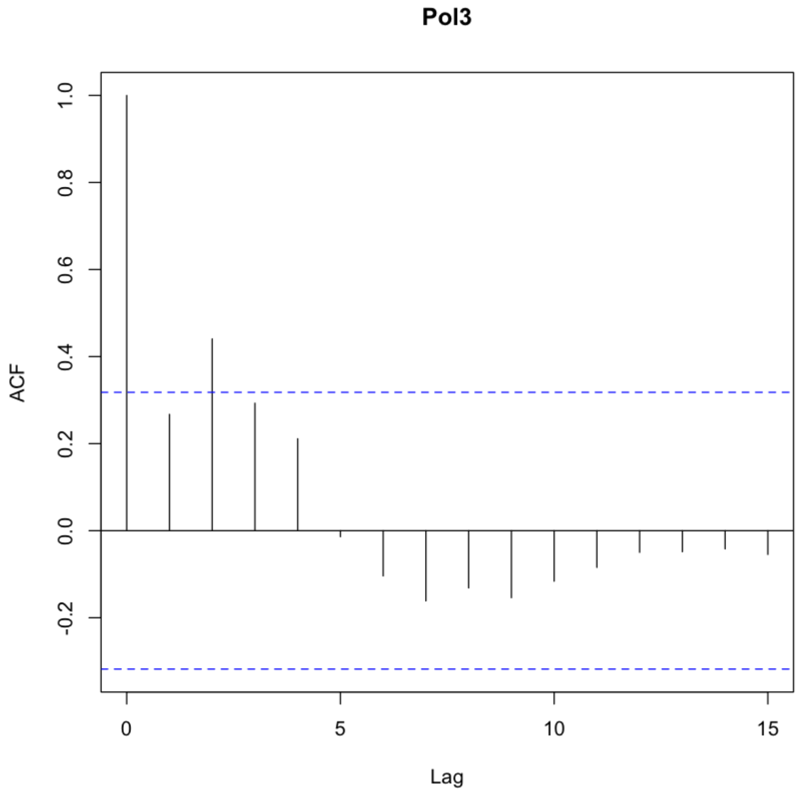


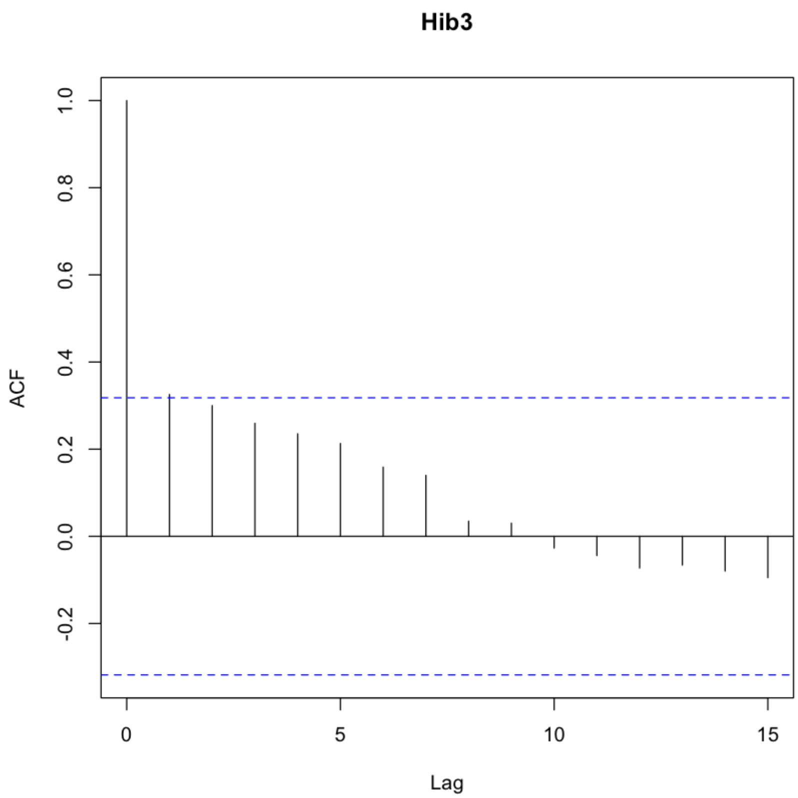
In [168…

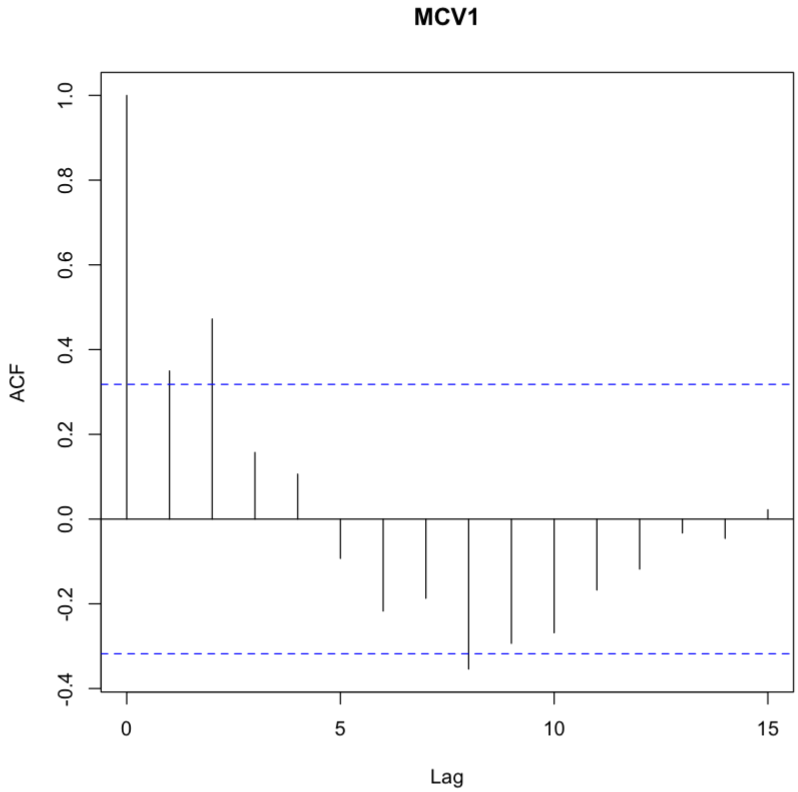
```
library(tseries)
for (col in colnames(usVaccines)) {
    acf(usVaccines[, col], main=col)
}
```


DTP1
ACF
1.0
0.8
0.6
0.4
0.2
0.0
-0.2
0
5
10
15
Lag

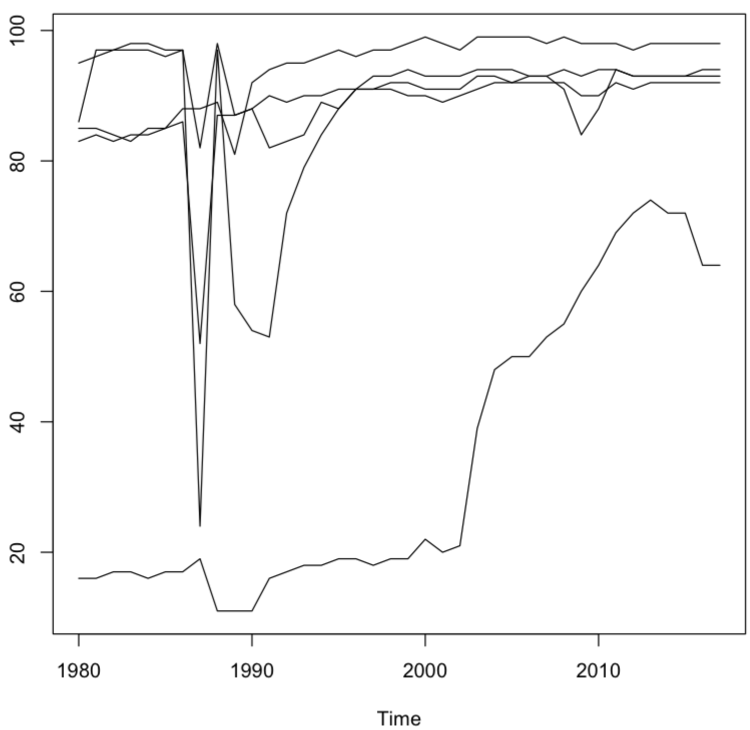

HepB_BD
ACF
1.0
0.8
0.6
0.4
0.2
0.0
-0.2
0
5
10
15
Lag


Pol3
ACF
1.0
0.8
0.6
0.4
0.2
0.0
-0.2
0
5
10
15
Lag


Hib3
ACF
1.0
0.8
0.6
0.4
0.2
0.0
-0.2
0
5
10
15
Lag



In [7]:
```
ts.plot(usVaccines)
```



In [8]:
```
summary(usVaccines)
```

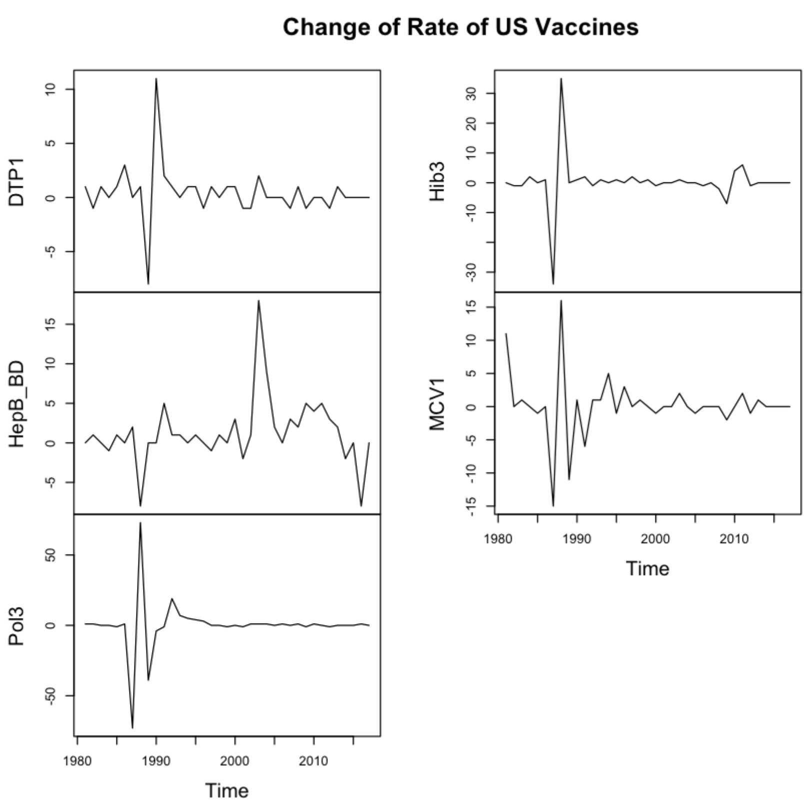
```
      DTP1          HepB_BD           Pol3           Hib3
```

```
 Min.   :81.00   Min.   :11.00   Min.   :24.00   Min.   :52.00  
 1st Qu.:89.75   1st Qu.:17.00   1st Qu.:90.00   1st Qu.:87.00  
 Median :97.00   Median :19.00   Median :93.00   Median :91.00  
 Mean   :94.05   Mean   :34.21   Mean   :87.16   Mean   :89.21  
 3rd Qu.:98.00   3rd Qu.:54.50   3rd Qu.:94.00   3rd Qu.:93.00  
 Max.   :99.00   Max.   :74.00   Max.   :97.00   Max.   :94.00  
      MCV1      
 Min.   :82.00  
 1st Qu.:90.00  
 Median :92.00  
 Mean   :91.24  
 3rd Qu.:92.00  
 Max.   :98.00  
```

In [181…

```
plot(diff(usVaccines), main='Change of Rate of US Vaccines')
summary(diff(usVaccines))
```

```
      DTP1              HepB_BD            Pol3                 Hib3         
 Min.   :-8.0000   Min.   :-8.000   Min.   :-73.00000   Min.   :-34.0000  
 1st Qu.: 0.0000   1st Qu.: 0.000   1st Qu.:  0.00000   1st Qu.:  0.0000  
 Median : 0.0000   Median : 1.000   Median :  0.00000   Median :  0.0000  
 Mean   : 0.4054   Mean   : 1.297   Mean   : -0.02703   Mean   :  0.2162  
 3rd Qu.: 1.0000   3rd Qu.: 2.000   3rd Qu.:  1.00000   3rd Qu.:  1.0000  
 Max.   :11.0000   Max.   :18.000   Max.   : 73.00000   Max.   : 35.0000  
      MCV1         
 Min.   :-15.0000  
 1st Qu.:  0.0000  
 Median :  0.0000  
 Mean   :  0.1622  
 3rd Qu.:  1.0000  
 Max.   : 16.0000  
```



Solution

- How have U.S. vaccination rates varied over time?

- Are vaccination rates increasing or decreasing?
- Which vaccination has the highest rate at the conclusion of the time series?
- Which vaccination has the lowest rate at the conclusion of the time series?
- Which vaccine has the greatest volatility?

Question 2

1. What proportion of public schools reported vaccination data? What proportion of private schools reported vaccination data? Was there any credible difference in overall reporting proportions between public and private schools?

In [10]:

```
head(allSchoolsReportStatus, 2)
ct_sch_vax = table(allSchoolsReportStatus[, c("pubpriv", "reported")])
ct_sch_vax_mar = addmargins(ct_sch_vax)
ct_sch_vax_perc = 100*ct_sch_vax/ct_sch_vax_mar[c('PRIVATE', 'PUBLIC'), 'Sum']
ct_sch_vax
ct_sch_vax_mar
ct_sch_vax_perc
```

A data.frame: 2 × 3

	name	pubpriv	reported
	<chr>	<chr>	<chr>
1	AGUA DULCE ELEMENTARY	PUBLIC	Y
2	MEADOWLARK ELEMENTARY	PUBLIC	Y

```
         reported
pubpriv      N    Y
  PRIVATE  252 1397
  PUBLIC   148 5584
```

A table: 3 × 3 of type dbl

	N	Y	Sum
PRIVATE	252	1397	1649
PUBLIC	148	5584	5732
Sum	400	6981	7381

```
         reported
pubpriv           N         Y
  PRIVATE 15.281989 84.718011
  PUBLIC   2.581996 97.418004
```

In [11]:

```
# Chi-Squared Test for a Categorical Association
sch_vax_Xsq <- chisq.test(ct_sch_vax)
sch_vax_Xsq
sch_vax_exp <- addmargins(sch_vax_Xsq$expect)
print("Expected Value Table")
print(sch_vax_exp)
```

```
	Pearson's Chi-squared test with Yates' continuity correction

data:  ct_sch_vax
X-squared = 400.49, df = 1, p-value < 2.2e-16
[1] "Expected Value Table"
```

```
         reported
pubpriv           N        Y  Sum
  PRIVATE  89.36458 1559.635 1649
  PUBLIC  310.63542 5421.365 5732
  Sum     400.00000 6981.000 7381
```

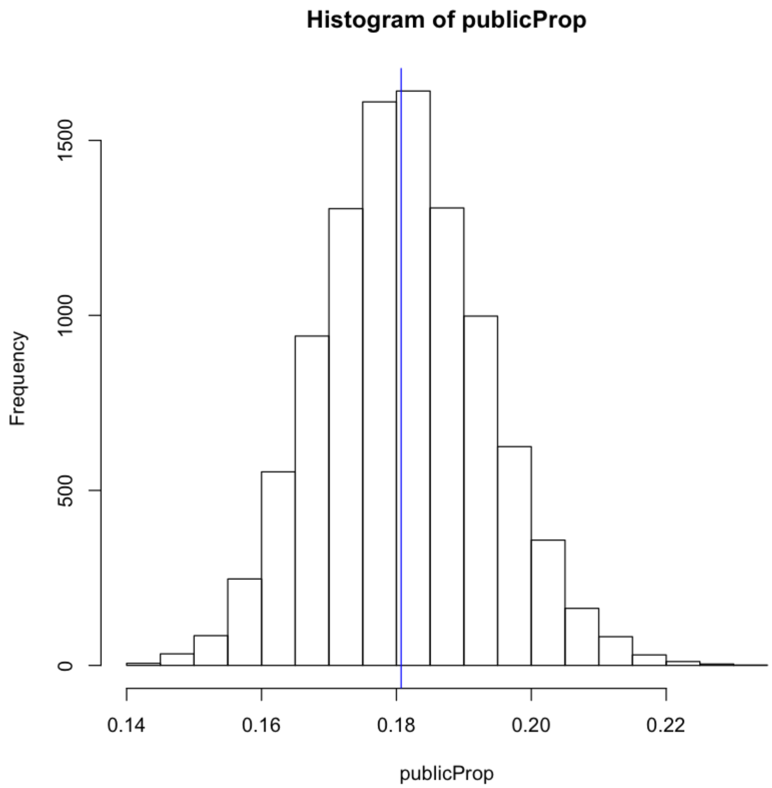
In [12]:

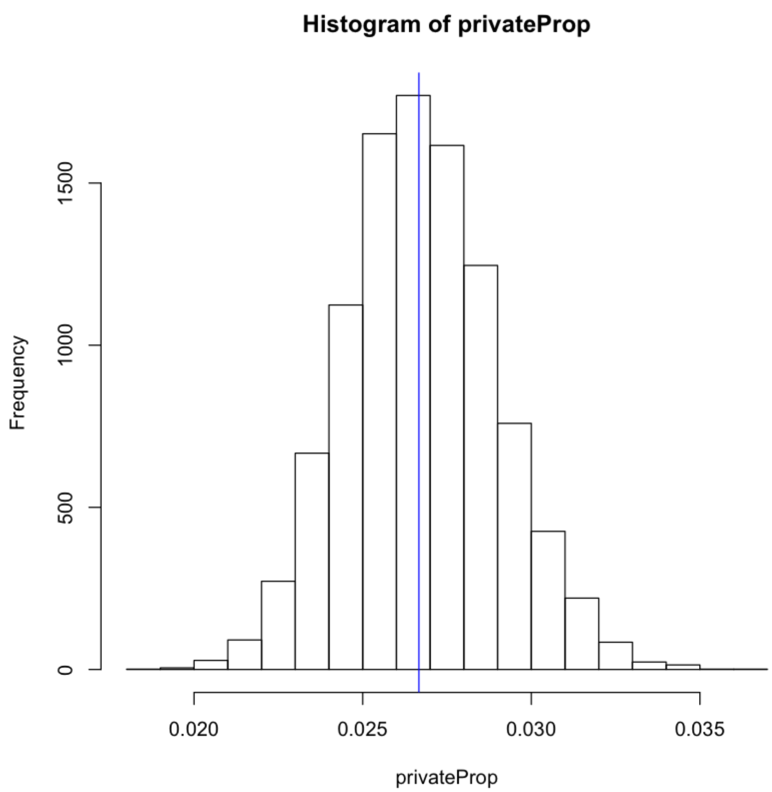
```
# Anova Contingency Table BF
ctBFout <- contingencyTableBF(ct_sch_vax,sampleType="poisson", posterior=FALSE)
print(ctBFout)
sch_vax_ctMCMCout <- contingencyTableBF(ct_sch_vax,sampleType="poisson", posteri
print(summary(sch_vax_ctMCMCout))
```

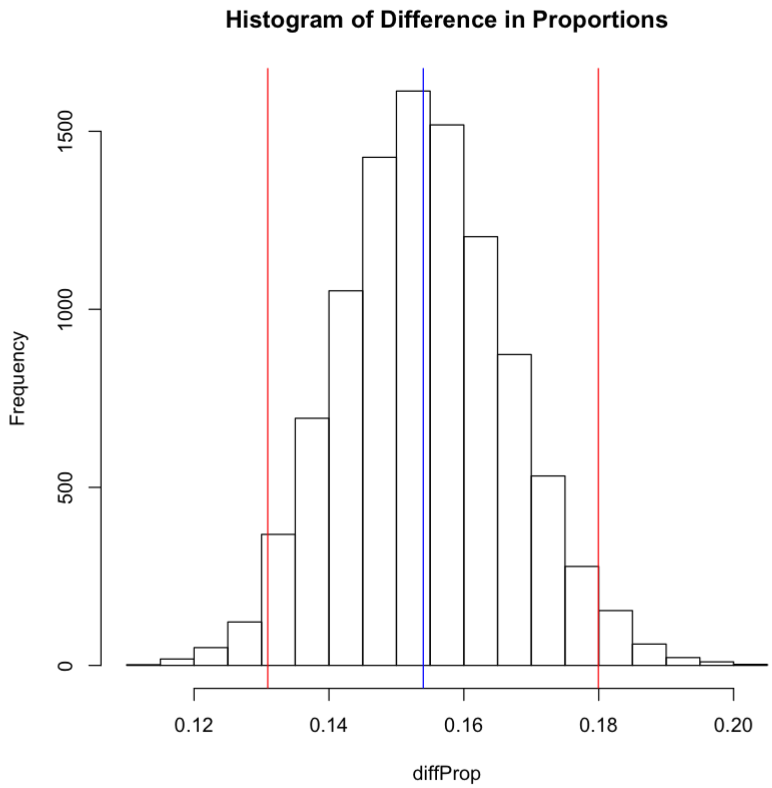
```
Bayes factor analysis
--------------
[1] Non-indep. (a=1) : 1.150548e+69 ±0%

Against denominator:
  Null, independence, a = 1
---
Bayes factor type: BFcontingencyTable, poisson


Iterations = 1:10000
Thinning interval = 1
Number of chains = 1
Sample size per chain = 10000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

              Mean    SD Naive SE Time-series SE
lambda[1,1]  252.7 15.67   0.1567         0.1567
lambda[2,1]  149.2 12.27   0.1227         0.1227
lambda[1,2] 1396.9 37.24   0.3724         0.3652
lambda[2,2] 5582.5 75.69   0.7569         0.7569

2. Quantiles for each variable:

              2.5%    25%    50%    75%  97.5%
lambda[1,1]  222.7  242.0  252.2  263.0  284.4
lambda[2,1]  126.0  140.8  148.8  157.3  174.6
lambda[1,2] 1325.4 1371.6 1396.1 1421.8 1471.4
lambda[2,2] 5435.5 5532.0 5582.2 5632.7 5733.1
```

In [183…

```
# BF Contingency Table Posterior Results
publicProp <- sch_vax_ctMCMCout[,"lambda[1,1]"]/sch_vax_ctMCMCout[,"lambda[1,2]"
hist(publicProp)
abline(v=unname(quantile(publicProp, .5)), col='blue')

privateProp <- sch_vax_ctMCMCout[,"lambda[2,1]"]/sch_vax_ctMCMCout[,"lambda[2,2]
hist(privateProp)
abline(v=unname(quantile(privateProp, .5)), col='blue')

diffProp <- publicProp-privateProp
hist(diffProp, main='Histogram of Difference in Proportions')
abline(v=unname(quantile(diffProp, .5)), col='blue')
abline(v=unname(quantile(diffProp, .025)), col='red')
abline(v=unname(quantile(diffProp, .975)), col='red')
```


Histogram of publicProp
Frequency
0
500
1000
1500
0.14
0.16
0.18
0.20
0.22
publicProp


Histogram of privateProp
Frequency
0
500
1000
1500
0.020
0.025
0.030
0.035
privateProp



Solution

- What proportion of public schools reported vaccination data?

> 5584/5732 ~ 97.4%

- What proportion of private schools reported vaccination data?

> 1397/1649 ~ 84.7%

- Was there any credible difference in overall reporting proportions between public and private schools?

> To check for a difference in Public and Private school vaccination reporting rate, we ran a Chi-Squared Test for a Categorical Association, and its Bayesian equivalent using a Bayes Factor package. In both tests, we found significant evidence to say the proportions of reporting rates are different with the Public Schools reporting rate being higher than Private Schools. The Bayesian Posterior analysis showed the difference in proportions to always be positive in the resulting HDI which means Public Schools are more likely to report vaccination records. Similarly, the Baysian Factor resulted in a value too big to write down which means there is a difference between the two school types. Finally, the frequestist test of chi-squared resulted in a p-value less than 0.05 which means we reject the null of the school types having the same proportions.

Question 3

1. What are 2013 vaccination rates for individual vaccines (i.e., DOT, Polio, MMR, and HepB) in California public schools? How do these rates for individual vaccines in California districts compare with overall US vaccination rates (make an informal comparison to the final observations in the time series)?

Overall Calculations

In [14]:

```
districts$WithDTP <- districts$Enrolled - districts$WithoutDTP*(districts$Enroll
districts$WithPolio <- districts$Enrolled - districts$WithoutPolio*(districts$En
districts$WithMMR <- districts$Enrolled - districts$WithoutMMR*(districts$Enroll
districts$WithHepB <- districts$Enrolled - districts$WithoutHepB*(districts$Enro
```

In [15]:

```
sum_dist <- colSums(districts[, c('WithDTP', 'WithPolio','WithMMR', 'WithHepB',
sum_dist
sum_dist <- 100*sum_dist[c('WithDTP', 'WithPolio','WithMMR', 'WithHepB')]/sum_di
sum_dist
```

WithDTP: 406939.7 **WithPolio:** 409143.86 **WithMMR:** 408080.38 **WithHepB:** 417981.16 **Enrolled:** 439276

WithDTP: 92.6387282710642 **WithPolio:** 93.1404993671405 **WithMMR:** 92.8984010052905 **WithHepB:** 95.152286944882

Distribution Calculations

In [16]:

```
districts$WithDTPPerc <- 100*districts$WithDTP/districts$Enrolled
districts$WithPolioPerc <- 100*districts$WithPolio/districts$Enrolled
districts$WithMMRPerc <- 100*districts$WithMMR/districts$Enrolled
districts$WithHepBPerc <- 100*districts$WithHepB/districts$Enrolled
```

In [17]:

```
summary(districts[, c('WithDTPPerc', 'WithPolioPerc','WithMMRPerc', 'WithHepBPer
```

```
  WithDTPPerc      WithPolioPerc     WithMMRPerc      WithHepBPerc
 Min.   : 23.00   Min.   : 23.00   Min.   : 23.0   Min.   : 23.0
 1st Qu.: 86.00   1st Qu.: 87.00   1st Qu.: 86.0   1st Qu.: 90.0
 Median : 93.00   Median : 94.00   Median : 94.0   Median : 96.0
 Mean   : 89.75   Mean   : 90.16   Mean   : 89.8   Mean   : 92.2
 3rd Qu.: 97.00   3rd Qu.: 97.00   3rd Qu.: 97.0   3rd Qu.: 98.0
 Max.   :100.00   Max.   :100.00   Max.   :100.0   Max.   :100.0
```

In [209…

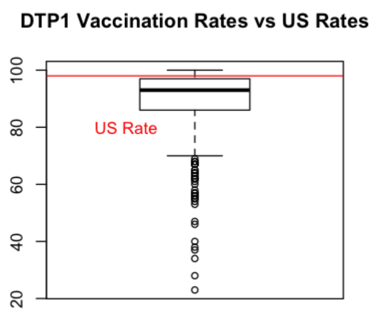
```
last_vax_rec = c(tail(usVaccines, 1)[, c('DTP1', 'Pol3', 'MCV1', 'HepB_BD')])
last_vax_rec
```

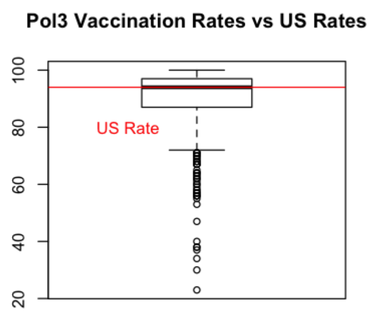
DTP1: 98 **Pol3:** 94 **MCV1:** 92 **HepB_BD:** 64

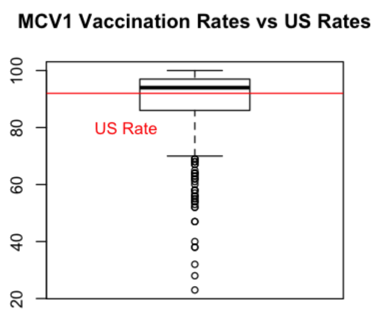
In [208…

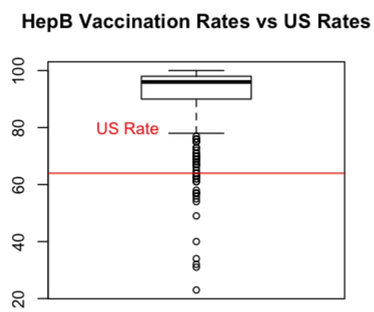
```
par(mfrow = c(2,2))
boxplot(districts[, 'WithDTPPerc'], main='DTP1 Vaccination Rates vs US Rates')
abline(h=last_vax_rec['DTP1'], col="red")
text(.75,80, "US Rate", col="red")
```

```
boxplot(districts[, 'WithPolioPerc'], main='Pol3 Vaccination Rates vs US Rates')
abline(h=last_vax_rec['Pol3'], col="red")
text(.75,80, "US Rate", col="red")

boxplot(districts[, 'WithMMRPerc'], main='MCV1 Vaccination Rates vs US Rates')
abline(h=last_vax_rec['MCV1'], col="red")
text(.75,80, "US Rate", col="red")

boxplot(districts[, 'WithHepBPerc'], main='HepB Vaccination Rates vs US Rates')
abline(h=last_vax_rec['HepB_BD'], col="red")
text(.75,80, "US Rate", col="red")
```









In [214…

```
ttest_res$estimate
ttest_res$p.value
ttest_res$conf[1]
ttest_res$conf[2]
```

mean of x: 89.75

DTP1: 7.19262267293189e-69

88.926378001478

90.573621998522

In [218…

```
seq(1, length(last_vax_rec))
```

1 · 2 · 3 · 4

In [238…

```
last_vax_rec = c(tail(usVaccines, 1)[, c('DTP1', 'Pol3', 'MCV1', 'HepB_BD')])
distric_vax_cols = c('WithDTPPerc','WithPolioPerc','WithMMRPerc','WithHepBPerc')
```

```
vax_L = c('DTP1', 'Pol3', 'MCV1', 'HepB_BD')
ttest_resL = list()

for (i in seq(1, length(last_vax_rec))) {
    ttest_res = t.test(districts[, distric_vax_cols[i]], mu=last_vax_rec[i])

    ttest_res <- data.frame(vax = vax_L[i],
                            mean = ttest_res$estimate,
                            p_val = ttest_res$p.value,
                            conf_int_lower = ttest_res$conf[1],
                            conf_int_upper = ttest_res$conf[2],
                            national_rate = last_vax_rec[i]
                           )
    ttest_resL[[i]] <- ttest_res # add it to your list
}

ttest_res <- do.call(rbind, ttest_resL)
ttest_res
```

A data.frame: 4 × 6

	vax	mean	p_val	conf_int_lower	conf_int_upper	national_rate
	<fct>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
mean of x	DTP1	89.75000	7.192623e-69	88.92638	90.57362	98
mean of x1	Pol3	90.16429	5.245779e-19	89.34296	90.98561	94
mean of x2	MCV1	89.79714	4.113745e-07	88.95114	90.64315	92
mean of x3	HepB_BD	92.20143	0.000000e+00	91.46007	92.94279	64

In [244…

```
library("BEST")

last_vax_rec = c(tail(usVaccines, 1)[, c('DTP1', 'Pol3', 'MCV1', 'HepB_BD')])
distric_vax_cols = c('WithDTPPerc','WithPolioPerc','WithMMRPerc','WithHepBPerc')
vax_L = c('DTP1', 'Pol3', 'MCV1', 'HepB_BD')

ttest_bf_resL = list()

for (i in seq(1, length(last_vax_rec))) {

    ttest_bf_res = summary(BESTmcmc(districts[, distric_vax_cols[i]], last_vax_r

    ttest_bf_res <- data.frame(vax = vax_L[i],
                            conf_int_lower = ttest_bf_res['HDIlo'],
                            median = ttest_bf_res['median'],
                            conf_int_upper = ttest_bf_res['HDIup'],
                            mean = ttest_bf_res['mean'],
                            national_rate = last_vax_rec[i]
                           )
    ttest_bf_resL[[i]] <- ttest_bf_res # add it to your list
}

ttest_bf_res <- do.call(rbind, ttest_bf_resL)
ttest_bf_res
```

```
Waiting for parallel processing to complete...
done.
```

```
Waiting for parallel processing to complete...
done.

Waiting for parallel processing to complete...
done.

Waiting for parallel processing to complete...
done.
```

A data.frame: 4 × 6

	vax	conf_int_lower	median	conf_int_upper	mean	national_rate
	<fct>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
HDIlo	DTP1	92.99018	93.62116	94.19976	93.61627	98
HDIlo1	Pol3	93.55201	94.13346	94.70487	94.13019	94
HDIlo2	MCV1	93.44835	94.04691	94.63047	94.03974	92
HDIlo3	HepB_BD	95.58904	96.00747	96.41360	96.00305	64

Question 4

1. Among districts, how are the vaccination rates for individual vaccines related? In other words, if students are missing one vaccine are they missing all of the others?

- Correlation between numbers missing
- Check how many schools have equal vax missing in all vaxes

In [247…

```
# Check if Percentage is the same for All
districts$PctNotUpToDate <- 100 - districts$PctUpToDate

districts$WithoutAll <- ifelse(((districts$WithoutDTP==districts$WithoutPolio)
                               & (districts$WithoutDTP==districts$WithoutMMR)
                               & (districts$WithoutDTP==districts$WithoutHepB)
                               & (districts$WithoutDTP==districts$PctNotUpToDat

districts$AllVax <- ifelse((districts$PctUpToDate==100),"Yes","No")
table(districts[, c('WithoutAll', 'AllVax')])

# If not all individuals are vaccinated, then 161/(496+161) ~ 24.5% of schools h
```

```
          AllVax
WithoutAll  No Yes
       No  535   0
       Yes 122  43
```

Correlation Analysis Frequentist

In [132…

```
# Correlation Analysis Frequentist
sc_inperf = districts[districts$PctUpToDate!=100, ] # Get inperfect schools (dro

sc_inperf$Without <- 100-sc_inperf$PctUpToDate
round(cor(sc_inperf[, c('WithoutDTP', 'WithoutPolio','WithoutMMR', 'WithoutHepB'

# Perform Corr Test for each Combination
without_cols <- c('WithoutDTP', 'WithoutPolio','WithoutMMR', 'WithoutHepB', 'Wit
```

```
cor_resL = list()
count <- 1
for (x in seq(1,length(without_cols)-1)) {

    for (y in seq(x+1,length(without_cols))){


        cor_res <- cor.test(sc_inperf[, without_cols[x]], sc_inperf[, without_co
        cor_res <- data.frame(x = without_cols[x],
                              y = without_cols[y],
                              cor = cor_res$estimate,
                              p_val = cor_res$p.value,
                              conf_int_lower = cor_res$conf[1],
                              conf_int_upper = cor_res$conf[2],
                              num_diff = nrow(sc_inperf[sc_inperf[,without_cols[
                              total = nrow(sc_inperf),
                              avg_diff = mean(abs(sc_inperf[,without_cols[x]] -
                             )
        cor_resL[[count]] <- cor_res # add it to your list

        count <- count + 1
    }
}

cor.test(sc_inperf[, 'WithoutDTP'], sc_inperf[, 'WithoutHepB'])

cor_res = do.call(rbind, cor_resL)
cor_res
```

A matrix: 5 × 5 of type dbl

	WithoutDTP	WithoutPolio	WithoutMMR	WithoutHepB	Without
WithoutDTP	1.00	0.98	0.98	0.89	0.96
WithoutPolio	0.98	1.00	0.97	0.90	0.94
WithoutMMR	0.98	0.97	1.00	0.89	0.97
WithoutHepB	0.89	0.90	0.89	1.00	0.84
Without	0.96	0.94	0.97	0.84	1.00

```
        Pearson's product-moment correlation

data:  sc_inperf[, "WithoutDTP"] and sc_inperf[, "WithoutHepB"]
t = 50.007, df = 655, p-value < 2.2e-16
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 0.8731533 0.9050544
sample estimates:
      cor
0.8901899
```

A data.frame: 10 × 9

	x	y	cor	p_val	conf_int_lower	conf_int_upper	num_
	<fct>	<fct>	<dbl>	<dbl>	<dbl>	<dbl>	<
cor	WithoutDTP	WithoutPolio	0.9814509	0.000000e+00	0.9784114	0.9840659	
cor1	WithoutDTP	WithoutMMR	0.9814299	0.000000e+00	0.9783870	0.9840479	
cor2	WithoutDTP	WithoutHepB	0.8901899	8.125305e-226	0.8731533	0.9050544	

	x	y	cor	p_val	conf_int_lower	conf_int_upper	num_
	<fct>	<fct>	<dbl>	<dbl>	<dbl>	<dbl>	<
cor3	WithoutDTP	Without	0.9600451	0.000000e+00	0.9535801	0.9656256	
cor4	WithoutPolio	WithoutMMR	0.9726613	0.000000e+00	0.9682046	0.9765008	
cor5	WithoutPolio	WithoutHepB	0.9043900	1.870970e-244	0.8894275	0.9174162	
cor6	WithoutPolio	Without	0.9423949	1.001752e-313	0.9331713	0.9503782	
cor7	WithoutMMR	WithoutHepB	0.8938302	2.436573e-230	0.8773216	0.9082258	
cor8	WithoutMMR	Without	0.9656428	0.000000e+00	0.9600651	0.9704532	
cor9	WithoutHepB	Without	0.8423243	5.536536e-178	0.8185743	0.8631992	

Correlation Analysis Bayes Factor

In [160…

```
cor_post_res[]$quantiles['97.5%']
```

97.5%: 0.882353164460003

In [163…

```
# Correlation Analysis Bayes Factor
bfCorTest <- function (x,y) # Get r from BayesFactor
{
    zx <- scale(x) # Standardize X
    zy <- scale(y) # Standardize Y
    zData <- data.frame(x=zx,rhoNot0=zy) # Put in a data frame
    bfOut <- generalTestBF(x ~ rhoNot0, data=zData) # linear coefficient
    mcmcOut <- posterior(bfOut,iterations=10000) # posterior samples
#     print(summary(mcmcOut[,"rhoNot0"])) # Get the HDI for rho
#     plot(mcmcOut)
    return(bfOut) # Return Bayes factor object
}
postCorTest <- function (x,y) # Get r from BayesFactor
{
    zx <- scale(x) # Standardize X
    zy <- scale(y) # Standardize Y
    zData <- data.frame(x=zx,rhoNot0=zy) # Put in a data frame
    bfOut <- generalTestBF(x ~ rhoNot0, data=zData) # linear coefficient
    mcmcOut <- posterior(bfOut,iterations=10000) # posterior samples
#     print(summary(mcmcOut[,"rhoNot0"])) # Get the HDI for rho
#     plot(mcmcOut)
    return(mcmcOut) # Return Bayes factor object
}


cor_bf_resL = list()
count <- 1
for (x in seq(1,length(without_cols)-1)) {
    for (y in seq(x+1,length(without_cols))) {
        cor_bf_res <- bfCorTest(sc_inperf[, without_cols[x]], sc_inperf[, withou
        cor_post_res <- summary(postCorTest(sc_inperf[, without_cols[x]], sc_inp

        cor_bf_res <- data.frame(x = without_cols[x],
```

```
                                y = without_cols[y],
                                bf = extractBF(cor_bf_res)$bf,
                                conf_int_lower = cor_post_res$quantiles['2.5%'],
                                median = cor_post_res$quantiles['50%'],
                                conf_int_upper = cor_post_res$quantiles['97.5%'],
                                mean = cor_post_res$statistics['Mean'],
                                sd = cor_post_res$statistics['SD']
                               )
        cor_bf_resL[[count]] <- cor_bf_res # add it to your list

        count <- count + 1
    }
}

cor_bf_res = do.call(rbind, cor_bf_resL)
cor_bf_res
```

A data.frame: 10 × 8

	x	y	bf	conf_int_lower	median	conf_int_upper	
	<fct>	<fct>	<dbl>	<dbl>	<dbl>	<dbl>	
2.5%	WithoutDTP	WithoutPolio	Inf	0.9661810	0.9812760	0.9961160	0.!
2.5%1	WithoutDTP	WithoutMMR	Inf	0.9667598	0.9812939	0.9957762	0.!
2.5%2	WithoutDTP	WithoutHepB	2.653119e+221	0.8544770	0.8897247	0.9243606	0.8
2.5%3	WithoutDTP	Without	Inf	0.9385259	0.9599735	0.9817711	0.9
2.5%4	WithoutPolio	WithoutMMR	Inf	0.9547910	0.9726297	0.9904393	0.!
2.5%5	WithoutPolio	WithoutHepB	1.033976e+240	0.8716391	0.9038877	0.9367270	0.9
2.5%6	WithoutPolio	Without	Inf	0.9158948	0.9418794	0.9680240	0.!
2.5%7	WithoutMMR	WithoutHepB	8.612511e+225	0.8590916	0.8934828	0.9281075	0.
2.5%8	WithoutMMR	Without	Inf	0.9449771	0.9651849	0.9849702	0.
2.5%9	WithoutHepB	Without	5.342760e+173	0.7996716	0.8413853	0.8826529	0.8

Solution

Extremly high correlation with DTP, Polio and MMR when at least one individual does not have all vaccines. On the other hand, not having HepB is less correlated to the rest of the vaccines.

Predictive Analysis

(For all of these analyses, use PctChildPoverty, PctFreeMeal, PctFamilyPoverty, Enrolled, and TotalSchools as predictors. Transform variables as necessary to improve prediction and/or interpretability. In general, if there is a Bayesian version of an analysis available, you are expected to run that analysis in addition to the frequentist version of the analysis.)

In [24]:

```
logistic <- function(logistX)
{
```

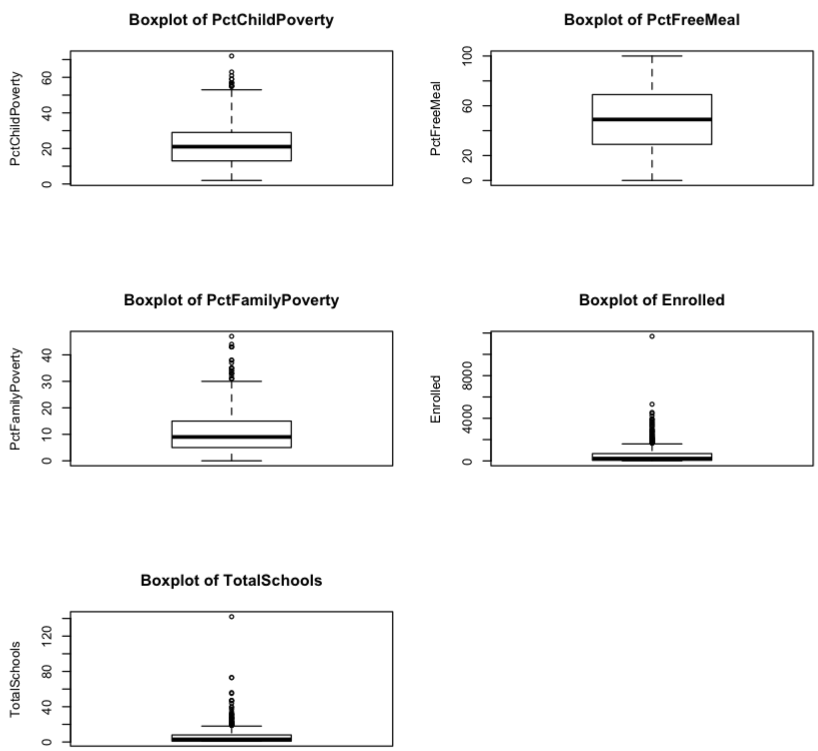
```
  exp(logistX)/(exp(logistX)+1)
}
```

In [25]:

```
pred_cols <- c('PctChildPoverty', 'PctFreeMeal', 'PctFamilyPoverty', 'Enrolled',
```

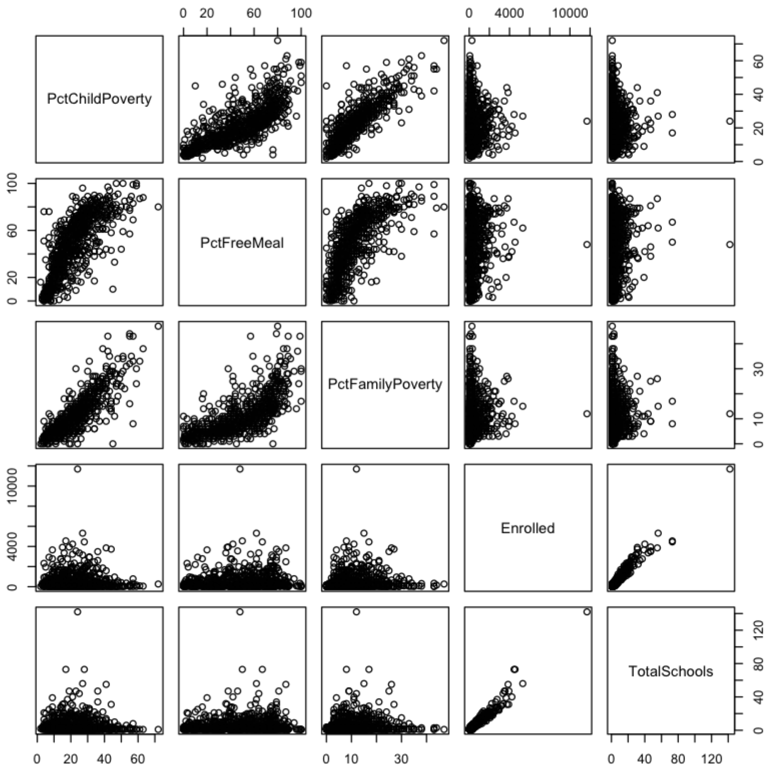
In [288…

```
par(mfrow = c(3,2))
for (i in seq(1, length(pred_cols))) {
    boxplot(districts[, pred_cols[i]], main=paste('Boxplot of', pred_cols[i]), y
}
```



In [285…

```
pairs(districts[, pred_cols])
```



In [284…

```
districts <- districts[districts[, 'TotalSchools']<200, ]
```

Question 5

1. What variables predict whether or not a district's reporting was complete?

In [ ]:

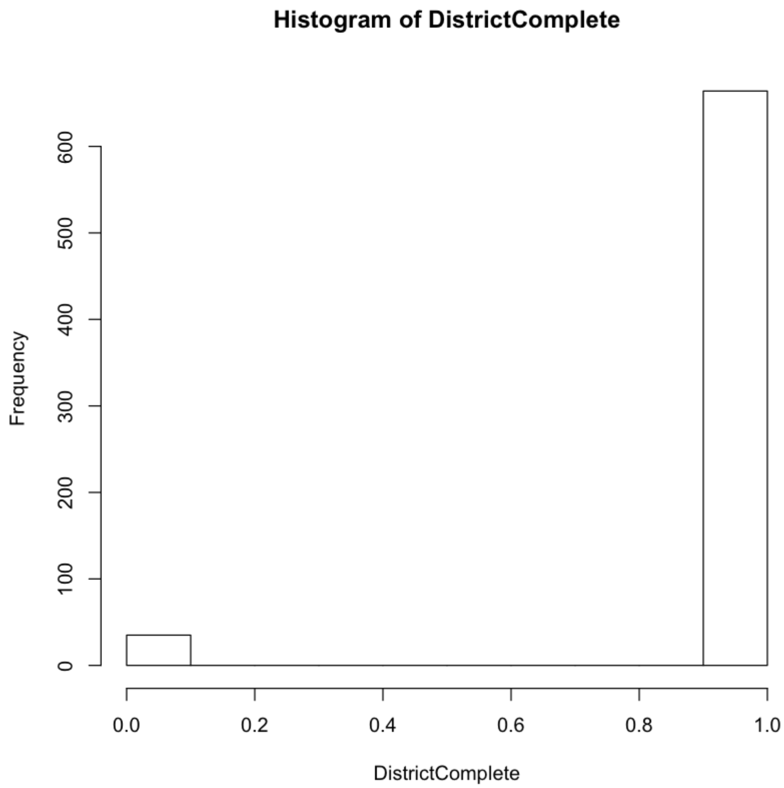
```

```

In [385…

```
pred_col <- 'DistrictComplete'
pred_col_factor <- paste(pred_col,'Factor', sep="")
pred_col_num <- paste(pred_col,'Num', sep="")

districts[, pred_col_factor] <- factor(districts$DistrictComplete, labels=c(0, 1
districts[, pred_col_num] <- as.numeric(districts$DistrictCompleteFactor) - 1
```

In [389…

```
hist(districts[, pred_col_num], main=paste('Histogram of', pred_col), xlab=pred_
```

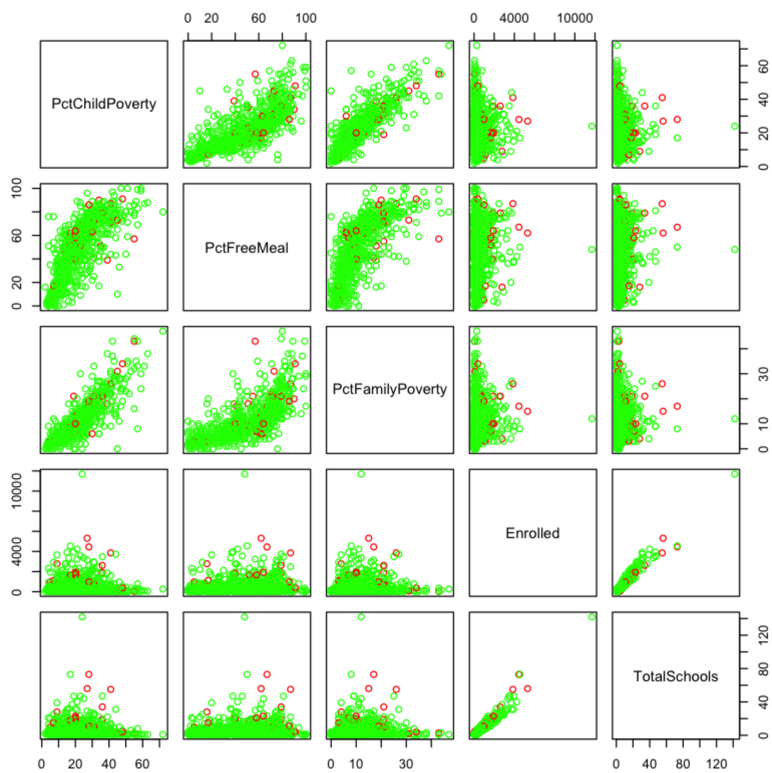


In [289…

```
cols <- character(nrow(districts))
cols[] <- "black"
cols[districts[, pred_col] == TRUE] <- "green"
cols[districts[, pred_col] == FALSE] <- "red"

pairs(districts[, pred_cols], col=cols)
cor(districts[, pred_cols])
```

A matrix: 5 × 5 of type dbl

	PctChildPoverty	PctFreeMeal	PctFamilyPoverty	Enrolled	TotalSchools
PctChildPoverty	1.00000000	0.75187546	0.85101699	-0.01439864	-0.02409280
PctFreeMeal	0.75187546	1.00000000	0.71644320	0.08390907	0.06661373
PctFamilyPoverty	0.85101699	0.71644320	1.00000000	0.04084347	0.02580181
Enrolled	-0.01439864	0.08390907	0.04084347	1.00000000	0.97015737
TotalSchools	-0.02409280	0.06661373	0.02580181	0.97015737	1.00000000



In [291…

```
by(districts[,append(pred_cols, c(pred_col))], districts[, pred_col], function(x
```

```
districts[, pred_col]: FALSE
                 PctChildPoverty PctFreeMeal PctFamilyPoverty    Enrolled
PctChildPoverty       1.00000000   0.6759884       0.91604384 -0.02693970
PctFreeMeal           0.67598839   1.0000000       0.61812122  0.11740847
PctFamilyPoverty      0.91604384   0.6181212       1.00000000 -0.01836814
Enrolled             -0.02693970   0.1174085      -0.01836814  1.00000000
TotalSchools          0.02228511   0.1599768       0.02235951  0.96742752
                 TotalSchools
PctChildPoverty    0.02228511
PctFreeMeal        0.15997678
PctFamilyPoverty   0.02235951
Enrolled           0.96742752
TotalSchools       1.00000000
------------------------------------------------------------
districts[, pred_col]: TRUE
                 PctChildPoverty PctFreeMeal PctFamilyPoverty    Enrolled
PctChildPoverty       1.00000000  0.75424911      0.846855557 -0.02448142
PctFreeMeal           0.75424911  1.00000000      0.720910428  0.07096035
PctFamilyPoverty      0.84685556  0.72091043      1.000000000  0.03189031
Enrolled             -0.02448142  0.07096035      0.031890314  1.00000000
TotalSchools         -0.04380199  0.04487945      0.006335537  0.97177529
                 TotalSchools
PctChildPoverty  -0.043801988
PctFreeMeal       0.044879454
PctFamilyPoverty  0.006335537
Enrolled          0.971775293
TotalSchools      1.000000000
```

GSL with Logistic Regression

Linear Regression for Collinearity Frequentist

In [327…

```
formula_str = paste(pred_col_factor, ' ~ PctChildPoverty + PctFreeMeal + PctFami
glmOut <- glm(formula_str, data=districts, family=binomial())
summary(glmOut)
exp(confint(glmOut))
anova(glmOut, test="Chisq") # Compare null model to one predictor
round(coef(glmOut), 2)# Convert log odds to odds (Intercept) logistX
round(exp(coef(glmOut)), 2)# Convert log odds to odds (Intercept) logistX
```

```
Call:
glm(formula = formula_str, family = binomial(), data = districts)

Deviance Residuals: 
    Min       1Q   Median       3Q      Max  
-2.7711   0.2298   0.2707   0.3250   1.8375  

Coefficients:
                   Estimate Std. Error z value Pr(>|z|)    
(Intercept)       3.9566197  0.5016414   7.887 3.09e-15 ***
PctChildPoverty   0.0248614  0.0316583   0.785  0.43228    
PctFreeMeal      -0.0111337  0.0118946  -0.936  0.34926    
PctFamilyPoverty -0.0596358  0.0396739  -1.503  0.13280    
Enrolled          0.0018163  0.0008216   2.211  0.02706 *  
TotalSchools     -0.1794111  0.0655295  -2.738  0.00618 ** 
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 277.82  on 698  degrees of freedom
Residual deviance: 252.18  on 693  degrees of freedom
AIC: 264.18

Number of Fisher Scoring iterations: 6
Waiting for profiling to be done...
```

A matrix: 6 × 2 of type dbl

	2.5 %	97.5 %
(Intercept)	20.9430950	151.3195305
PctChildPoverty	0.9659396	1.0930889
PctFreeMeal	0.9656662	1.0119119
PctFamilyPoverty	0.8720020	1.0191471
Enrolled	1.0003902	1.0036610
TotalSchools	0.7209873	0.9361211

A anova: 6 × 5

	Df	Deviance	Resid. Df	Resid. Dev	Pr(>Chi)
	<int>	<dbl>	<int>	<dbl>	<dbl>
NULL	NA	NA	698	277.8187	NA
PctChildPoverty	1	3.241521	697	274.5772	0.071793976
PctFreeMeal	1	1.995714	696	272.5814	0.157744748
PctFamilyPoverty	1	2.288687	695	270.2928	0.130320157
Enrolled	1	7.406391	694	262.8864	0.006499257

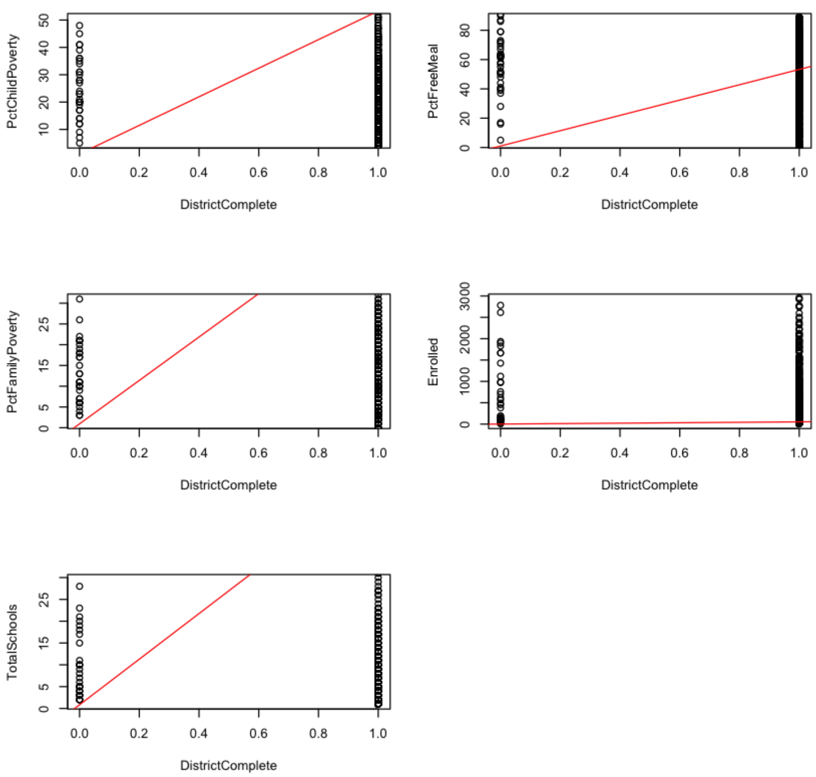
	Df	Deviance	Resid. Df	Resid. Dev	Pr(>Chi)
	<int>	<dbl>	<int>	<dbl>	<dbl>
TotalSchools	1	10.701974	693	252.1844	0.001070213

(Intercept): 3.96 **PctChildPoverty:** 0.02 **PctFreeMeal:** -0.01 **PctFamilyPoverty:** -0.06 **Enrolled:** 0 **TotalSchools:** -0.18

(Intercept): 52.28 **PctChildPoverty:** 1.03 **PctFreeMeal:** 0.99 **PctFamilyPoverty:** 0.94 **Enrolled:** 1 **TotalSchools:** 0.84

In [328…

```
par(mfrow = c(3,2))
for (x in pred_cols){
    plot(districts[, pred_col], districts[, x],
         ylab=x, xlab=pred_col,
         ylim=c(quantile(districts[, x], .025), quantile(districts[, x], .975)))
    abline(a=exp(coef(glmOut))[x], b=exp(coef(glmOut))['(Intercept)'], col = "re
}
```



In [329…

```
districts[, 'Enrolled100'] <- districts[, 'Enrolled']/100

formula_str = paste(pred_col_factor, ' ~ PctChildPoverty + PctFreeMeal + PctFami
glmOut <- glm(formula_str, data=districts, family=binomial())
summary(glmOut)
exp(confint(glmOut))
anova(glmOut, test="Chisq") # Compare null model to one predictor
round(exp(coef(glmOut)), 3)# Convert log odds to odds (Intercept) logistX
```

```
Call:
glm(formula = formula_str, family = binomial(), data = districts)
```

```
Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.7711   0.2298   0.2707   0.3250   1.8375

Coefficients:
                 Estimate Std. Error z value Pr(>|z|)
(Intercept)       3.95662    0.50164   7.887 3.09e-15 ***
PctChildPoverty   0.02486    0.03166   0.785  0.43228
PctFreeMeal      -0.01113    0.01189  -0.936  0.34926
PctFamilyPoverty -0.05964    0.03967  -1.503  0.13280
Enrolled100       0.18163    0.08216   2.211  0.02706 *
TotalSchools     -0.17941    0.06553  -2.738  0.00618 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

    Null deviance: 277.82  on 698  degrees of freedom
Residual deviance: 252.18  on 693  degrees of freedom
AIC: 264.18

Number of Fisher Scoring iterations: 6
Waiting for profiling to be done...
```

A matrix: 6 × 2 of type dbl

	2.5 %	97.5 %
(Intercept)	20.9430950	151.3195305
PctChildPoverty	0.9659396	1.0930889
PctFreeMeal	0.9656662	1.0119119
PctFamilyPoverty	0.8720020	1.0191471
Enrolled100	1.0397830	1.4411302
TotalSchools	0.7209873	0.9361211

A anova: 6 × 5

	Df	Deviance	Resid. Df	Resid. Dev	Pr(>Chi)
	<int>	<dbl>	<int>	<dbl>	<dbl>
NULL	NA	NA	698	277.8187	NA
PctChildPoverty	1	3.241521	697	274.5772	0.071793976
PctFreeMeal	1	1.995714	696	272.5814	0.157744748
PctFamilyPoverty	1	2.288687	695	270.2928	0.130320157
Enrolled100	1	7.406391	694	262.8864	0.006499257
TotalSchools	1	10.701974	693	252.1844	0.001070213

(Intercept): 52.28 **PctChildPoverty:** 1.025 **PctFreeMeal:** 0.989 **PctFamilyPoverty:** 0.942 **Enrolled100:** 1.199 **TotalSchools:** 0.836

Linear Regression for Collinearity Bayesian

In [313…

```
formula_str = paste(pred_col_num, '~ PctChildPoverty + PctFreeMeal + PctFamilyPo
regOutMCMC <- lmBF(as.formula(formula_str), data=districts, posterior=TRUE, iter
```

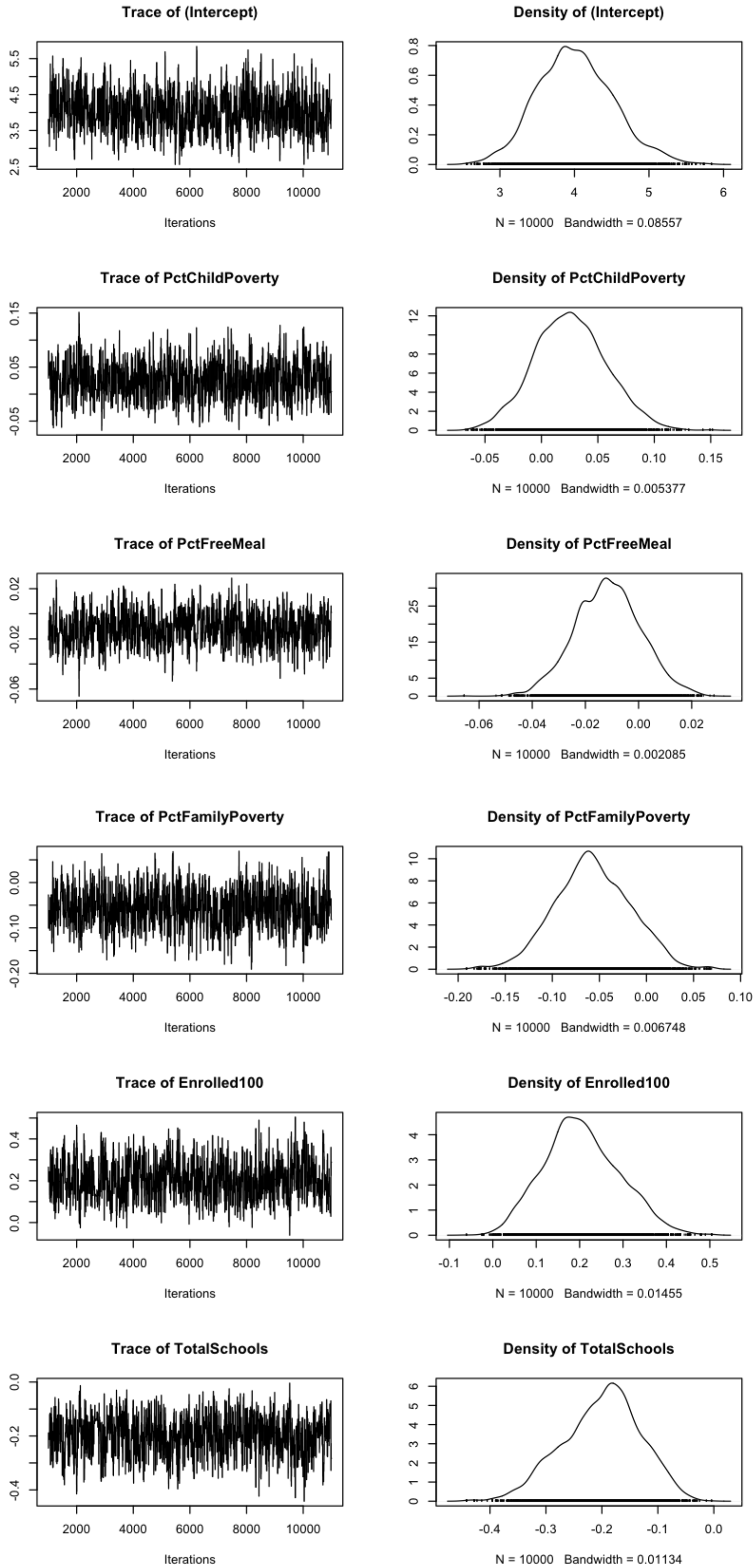
```r
summary(regOutMCMC)
```

```
Iterations = 1:10000
Thinning interval = 1
Number of chains = 1
Sample size per chain = 10000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

                       Mean        SD  Naive SE Time-series SE
mu                0.9498972 0.0079713 7.971e-05      8.063e-05
PctChildPoverty   0.0009167 0.0013703 1.370e-05      1.371e-05
PctFreeMeal      -0.0003171 0.0005049 5.049e-06      5.049e-06
PctFamilyPoverty -0.0032667 0.0019064 1.906e-05      1.906e-05
Enrolled100       0.0161594 0.0037414 3.741e-05      3.741e-05
TotalSchools     -0.0174399 0.0032804 3.280e-05      3.280e-05
sig2              0.0445568 0.0023745 2.374e-05      2.374e-05
g                 0.0501555 0.0483902 4.839e-04      4.839e-04

2. Quantiles for each variable:

                      2.5%        25%        50%        75%      97.5%
mu                0.934239  9.446e-01  0.9497859  9.553e-01  0.9652256
PctChildPoverty  -0.001743 -2.089e-05  0.0009259  1.836e-03  0.0036103
PctFreeMeal      -0.001310 -6.543e-04 -0.0003175  2.268e-05  0.0006639
PctFamilyPoverty -0.006976 -4.567e-03 -0.0032578 -1.988e-03  0.0005146
Enrolled100       0.008940  1.365e-02  0.0161640  1.872e-02  0.0234694
TotalSchools     -0.023884 -1.966e-02 -0.0174484 -1.524e-02 -0.0110384
sig2              0.040159  4.291e-02  0.0444757  4.611e-02  0.0494119
g                 0.013538  2.547e-02  0.0373653  5.794e-02  0.1616180
```

In [314…

```r
formula_str = paste(pred_col_num, '~ PctChildPoverty + PctFreeMeal + PctFamilyPo
bayesLogitOut <- MCMClogit(formula =as.formula(formula_str), data=districts)
summary(bayesLogitOut) # Summarize the results
plot(bayesLogitOut)
```

```
Iterations = 1001:11000
Thinning interval = 1
Number of chains = 1
Sample size per chain = 10000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

                     Mean      SD  Naive SE Time-series SE
(Intercept)       4.01328 0.50934 0.0050934      0.0226669
PctChildPoverty   0.02573 0.03201 0.0003201      0.0013932
PctFreeMeal      -0.01153 0.01241 0.0001241      0.0005645
PctFamilyPoverty -0.05701 0.04017 0.0004017      0.0017857
Enrolled100       0.20523 0.08740 0.0008740      0.0040273
TotalSchools     -0.20065 0.06936 0.0006936      0.0031933

2. Quantiles for each variable:

                     2.5%       25%      50%       75%    97.5%
(Intercept)       3.06040  3.650729  3.99612  4.348260  5.09580
PctChildPoverty  -0.03583  0.003625  0.02475  0.046571  0.09117
PctFreeMeal      -0.03606 -0.020213 -0.01163 -0.003511  0.01329
PctFamilyPoverty -0.13379 -0.084138 -0.05861 -0.030024  0.01937
Enrolled100       0.04793  0.146983  0.19892  0.263033  0.38353
TotalSchools     -0.34319 -0.244555 -0.19325 -0.154071 -0.07748
```



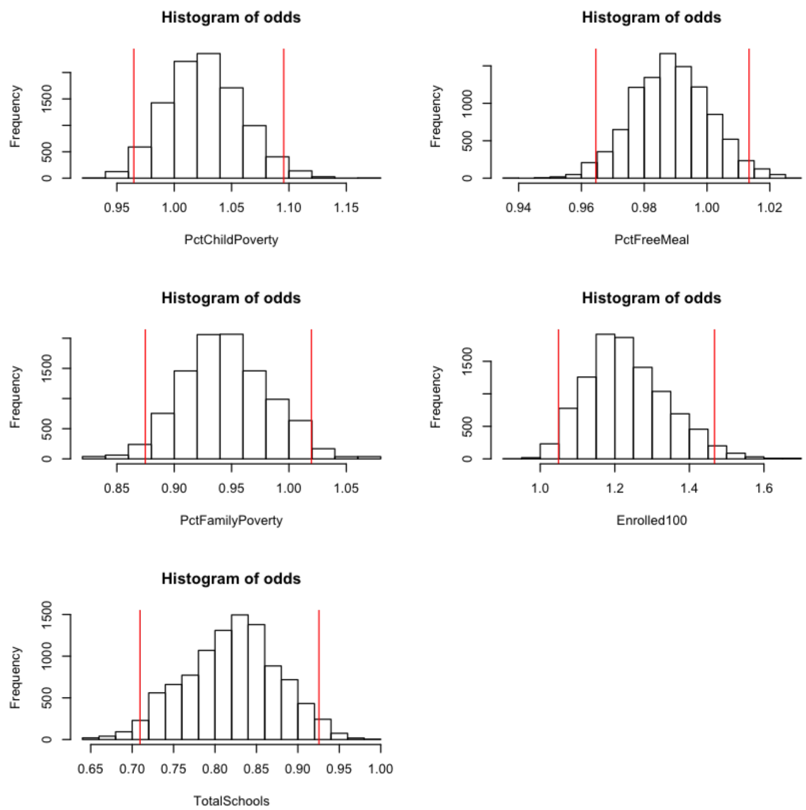
In [321…

```
exp(summary(bayesLogitOut)$statistics[, 'Mean'])
```

(Intercept): 55.3281251130829 **PctChildPoverty:** 1.0260667911197 **PctFreeMeal:** 0.988532807130316 **PctFamilyPoverty:** 0.944580955153545 **Enrolled100:** 1.22780863879524 **TotalSchools:** 0.818196921129187

In [317…

```
par(mfrow = c(3,2))
for (x in c('PctChildPoverty','PctFreeMeal','PctFamilyPoverty','Enrolled100','To
    odds <- as.matrix(bayesLogitOut[,x]) # Create a matrix for apply()
    odds <- apply(odds,1,exp) # apply() runs exp() for each one
    hist(odds, xlab=x) # Show a histogram
    abline(v=quantile(odds,c(0.025)),col="red") # Left edge of 95% HDI
    abline(v=quantile(odds,c(0.975)),col="red") # Right edge of 95% HDI
}
```



Question 6

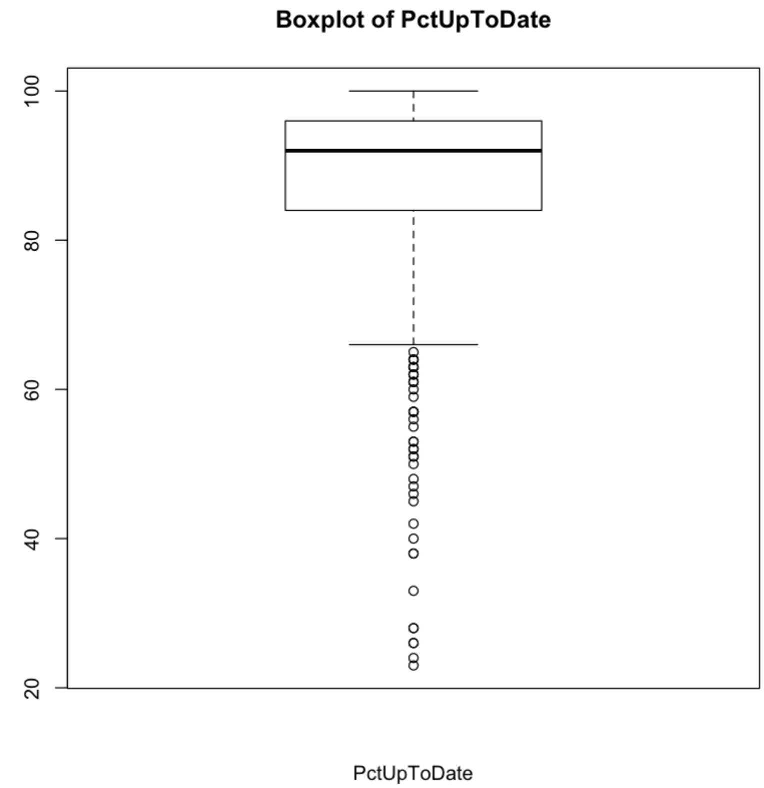
1. What variables predict the percentage of all enrolled students with completely up-to-date vaccines?

In [382…

```
pred_col <- 'PctUpToDate'
```

In [384…

```
boxplot(districts[, pred_col], main=paste('Boxplot of', pred_col), xlab=pred_col
```

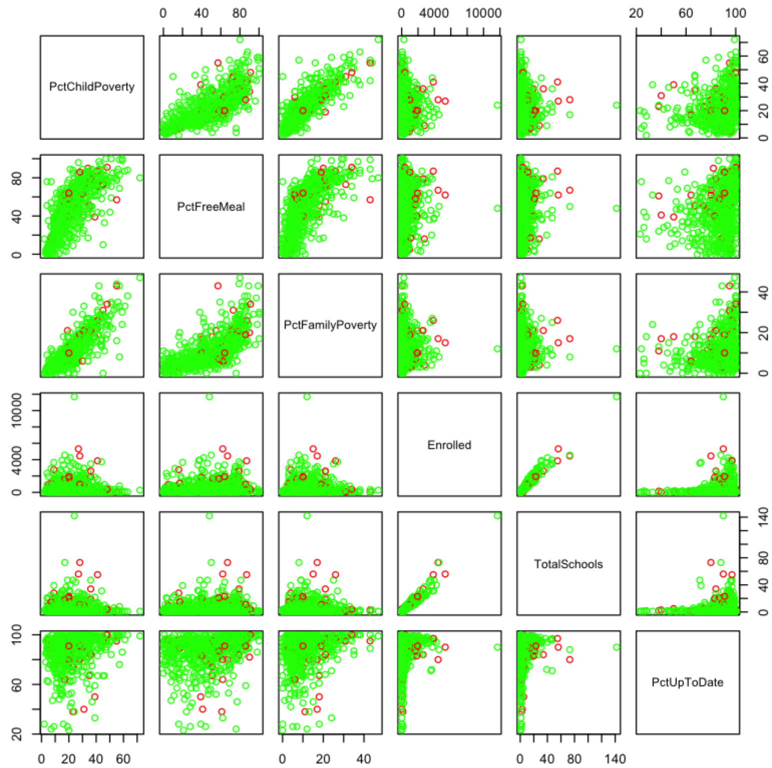


In [337…

```
pairs(districts[, append(pred_cols, c(pred_col))], col=cols)
cor(districts[,append(pred_cols, c(pred_col))])
```

A matrix: 6 × 6 of type dbl

	PctChildPoverty	PctFreeMeal	PctFamilyPoverty	Enrolled	TotalSchools	Pct
PctChildPoverty	1.00000000	0.75187546	0.85101699	-0.01439864	-0.02409280	
PctFreeMeal	0.75187546	1.00000000	0.71644320	0.08390907	0.06661373	(
PctFamilyPoverty	0.85101699	0.71644320	1.00000000	0.04084347	0.02580181	
Enrolled	-0.01439864	0.08390907	0.04084347	1.00000000	0.97015737	
TotalSchools	-0.02409280	0.06661373	0.02580181	0.97015737	1.00000000	
PctUpToDate	0.19140352	0.25056018	0.23922143	0.18047920	0.13774562	



GSM with Logistic Regression

Linear Regression for Collinearity Frequentist

In [346…

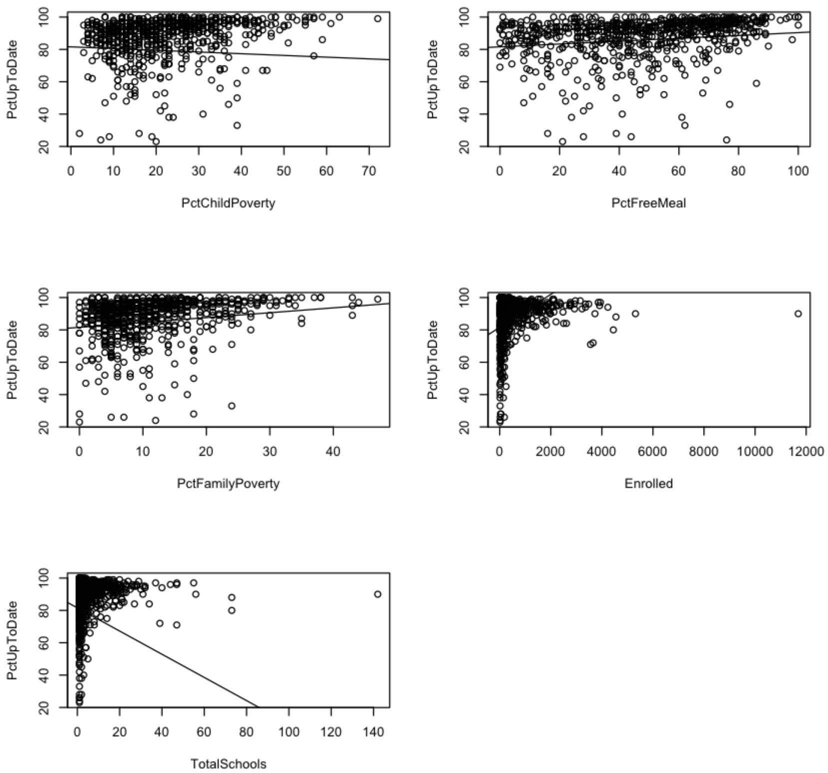
```
formula_str = paste(pred_col, ' ~ PctChildPoverty + PctFreeMeal + PctFamilyPover
lmOut <- lm(formula_str, data=districts)
summary(lmOut)
round(coef(lmOut), 3)
```

```
Call:
lm(formula = formula_str, data = districts)

Residuals:
    Min      1Q  Median      3Q     Max 
-66.603  -3.301   2.862   7.322  19.368 

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)    
(Intercept)      81.584071   1.095964  74.440  < 2e-16 ***
PctChildPoverty  -0.106260   0.079393  -1.338 0.181202    
PctFreeMeal       0.087962   0.029228   3.010 0.002712 ** 
PctFamilyPoverty  0.301841   0.111558   2.706 0.006984 ** 
Enrolled          0.010185   0.002134   4.773 2.21e-06 ***
TotalSchools     -0.717208   0.187052  -3.834 0.000137 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 11.97 on 693 degrees of freedom
Multiple R-squared:  0.1179,	Adjusted R-squared:  0.1115 
F-statistic: 18.52 on 5 and 693 DF,  p-value: < 2.2e-16
```

(Intercept): 81.584 **PctChildPoverty:** -0.106 **PctFreeMeal:** 0.088 **PctFamilyPoverty:** 0.302 **Enrolled:** 0.01 **TotalSchools:** -0.717

In [347…

```
par(mfrow = c(3,2))
for (x in pred_cols){
    plot(districts[, x], districts[, pred_col], xlab=x, ylab=pred_col)
    abline(lmOut$coefficients[c('(Intercept)', x)], col = "black")
}
```



Linear Regression for Collinearity Bayesian

In [360…

```
summary(regOutMCMC)$statistics[, 'Mean']
```

mu: 87.8569137030153 **PctChildPoverty:** -0.103101170607796 **PctFreeMeal:** 0.0849209607353594 **PctFamilyPoverty:** 0.292652871821446 **Enrolled:** 0.00987407295539862 **TotalSchools:** -0.695586465830675 **sig2:** 143.299736356767 **g:** 0.0636501083526082

In [375…

```
formula_str = paste(pred_col, '~ PctChildPoverty + PctFreeMeal + PctFamilyPovert
regOutMCMC <- lmBF(as.formula(formula_str), data=districts, posterior=TRUE, iter
regOutBF <- lmBF(as.formula(formula_str), data=districts)
summary(regOutMCMC)
summary(regOutMCMC)$statistics[, 'Mean']
regOutBF
```

```
Iterations = 1:10000
Thinning interval = 1
Number of chains = 1
Sample size per chain = 10000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

                         Mean        SD  Naive SE Time-series SE
```

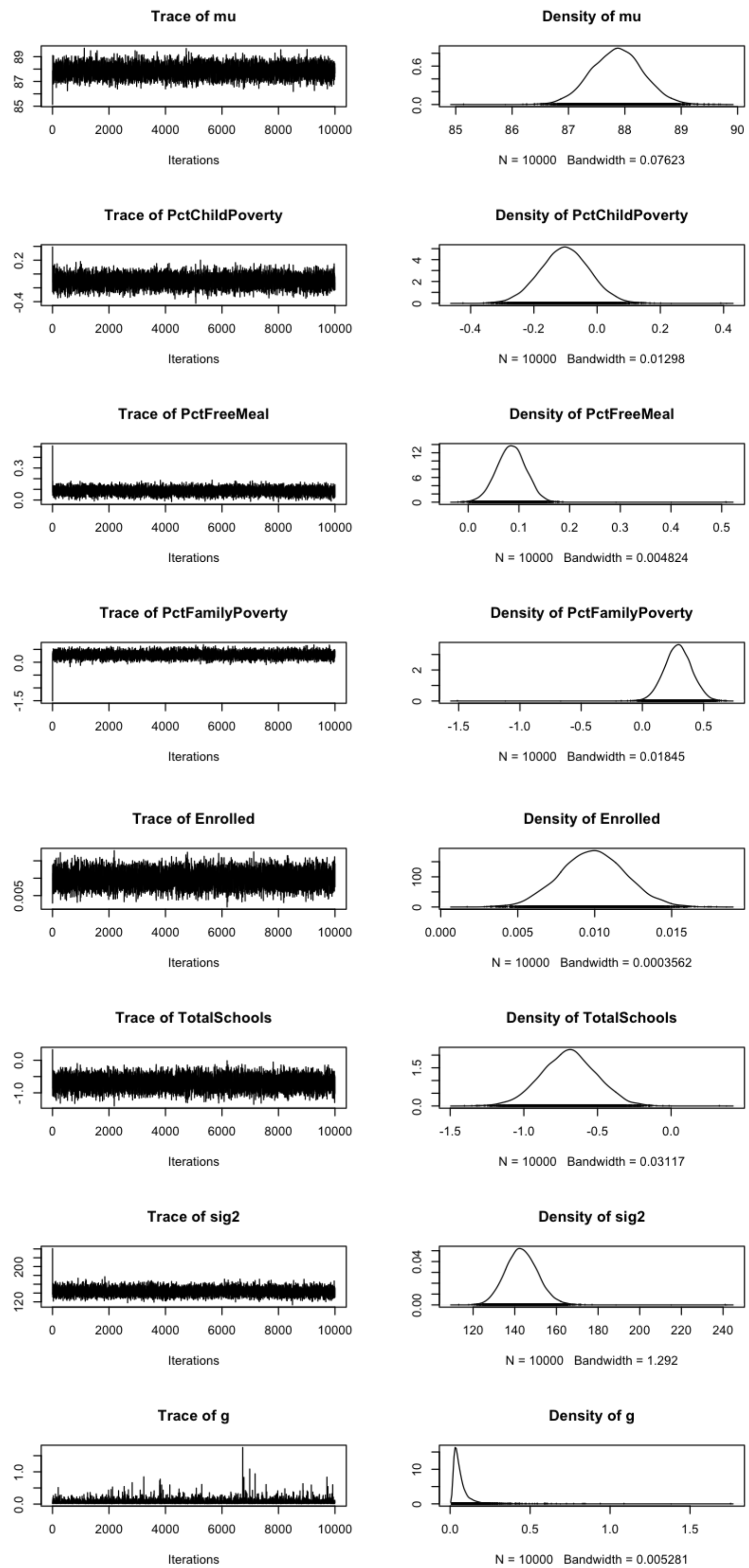
```
mu                 87.854643 0.451659 4.517e-03      4.517e-03
PctChildPoverty    -0.103859 0.078196 7.820e-04      7.820e-04
PctFreeMeal         0.085855 0.028926 2.893e-04      2.893e-04
PctFamilyPoverty    0.290449 0.110111 1.101e-03      1.101e-03
Enrolled            0.009812 0.002106 2.106e-05      2.106e-05
TotalSchools       -0.690303 0.183772 1.838e-03      1.838e-03
sig2              143.299136 7.724907 7.725e-02      7.725e-02
g                   0.063617 0.057932 5.793e-04      5.963e-04

2. Quantiles for each variable:

                        2.5%        25%        50%       75%     97.5%
mu                 86.983577  87.555129  87.849093  88.15394  88.74826
PctChildPoverty    -0.259276  -0.156214  -0.103801  -0.05270   0.04959
PctFreeMeal         0.030236   0.066097   0.085559   0.10536   0.14268
PctFamilyPoverty    0.074202   0.216253   0.289650   0.36375   0.50478
Enrolled            0.005731   0.008375   0.009789   0.01123   0.01400
TotalSchools       -1.051495  -0.814549  -0.688930  -0.56546  -0.33228
sig2              128.982570 137.908663 143.001483 148.28692 159.38479
g                   0.017176   0.032302   0.048240   0.07462   0.20812
```

mu: 87.8546428760571 **PctChildPoverty:** -0.103858809479828 **PctFreeMeal:** 0.0858551826118403 **PctFamilyPoverty:** 0.290449467896548 **Enrolled:** 0.00981175725109815 **TotalSchools:** -0.690303362349861 **sig2:** 143.299135557245 **g:** 0.0636174274180152

```
Bayes factor analysis
--------------
[1] PctChildPoverty + PctFreeMeal + PctFamilyPoverty + Enrolled + TotalSchools :
1.018477e+14 ±0.01%

Against denominator:
  Intercept only
---
Bayes factor type: BFlinearModel, JZS
```

In [349…

```
plot(regOutMCMC)
```

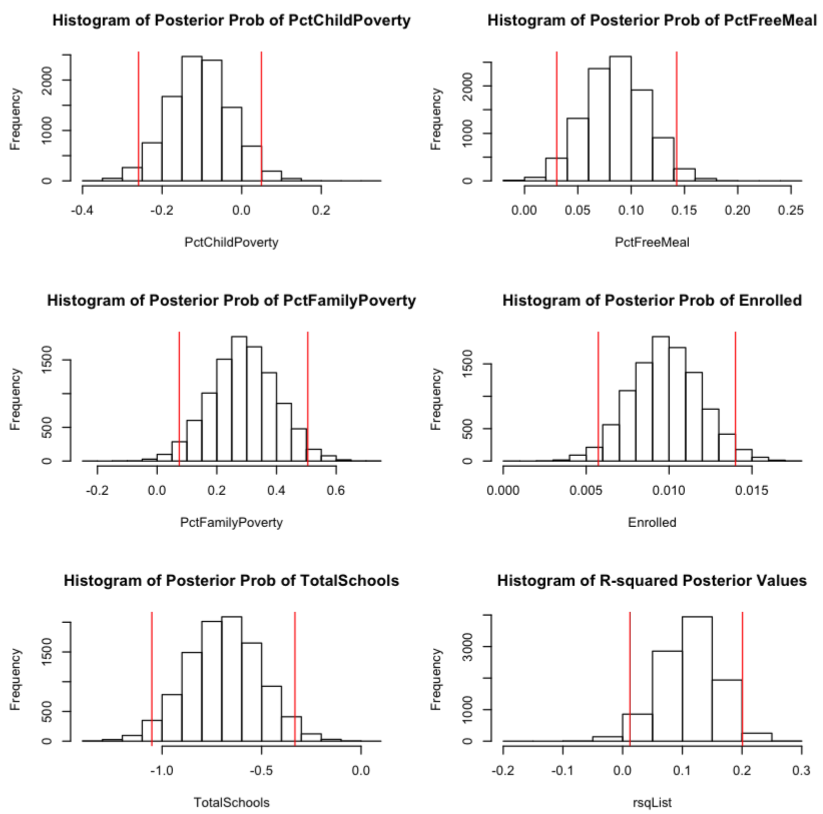


In [377…

```
rsqList <- 1 - (regOutMCMC[,"sig2"] / var(districts[, pred_col])) # sig2 from lm

par(mfrow = c(3,2))

for (x in pred_cols){
    hist(regOutMCMC[,x], xlab=x, main=paste('Histogram of Posterior Prob of', x)
```

```
    abline(v=quantile(regOutMCMC[,x],c(0.025)), col="red")
    abline(v=quantile(regOutMCMC[,x],c(0.975)), col="red")
}

mean(rsqList) # Overall mean R-squared is 0.75
hist(rsqList, main='Histogram of R-squared Posterior Values') # Show a histogram
# Lower bound of the 95% HDI
abline(v=quantile(rsqList,c(0.025)), col="red")
# Upper bound of the 95% HDI
abline(v=quantile(rsqList,c(0.975)), col="red")
```

0.111989704315883



Question 7

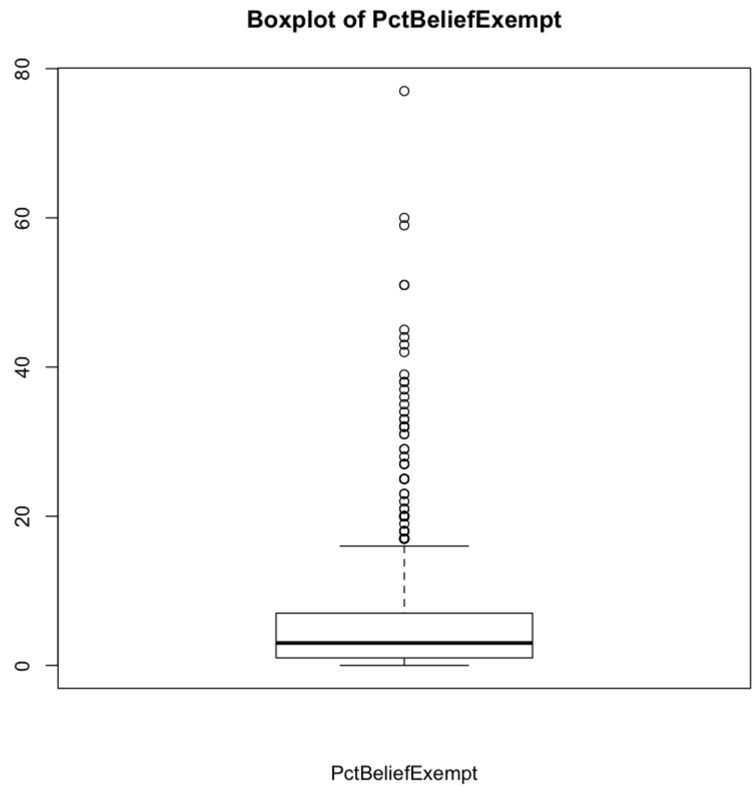
1. What variables predict the percentage of all enrolled students with belief exceptions?

In [393…

```
pred_col <- 'PctBeliefExempt'
```

In [394…

```
boxplot(districts[, pred_col], main=paste('Boxplot of', pred_col), xlab=pred_col
```

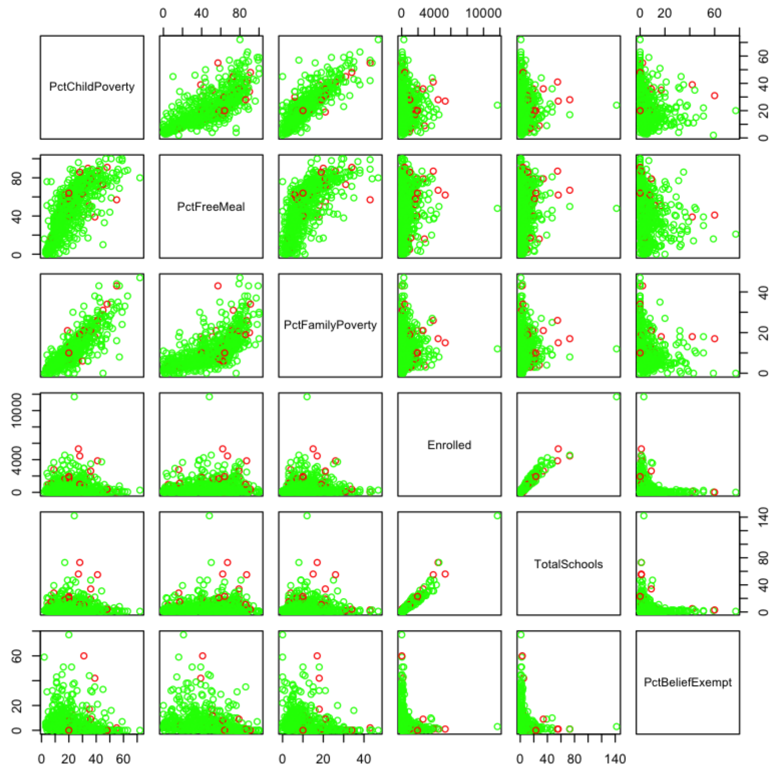


In [395…

```
pairs(districts[, append(pred_cols, c(pred_col))], col=cols)
cor(districts[,append(pred_cols, c(pred_col))])
```

A matrix: 6 × 6 of type dbl

	PctChildPoverty	PctFreeMeal	PctFamilyPoverty	Enrolled	TotalSchools	Pct
PctChildPoverty	1.00000000	0.75187546	0.85101699	-0.01439864	-0.02409280	
PctFreeMeal	0.75187546	1.00000000	0.71644320	0.08390907	0.06661373	
PctFamilyPoverty	0.85101699	0.71644320	1.00000000	0.04084347	0.02580181	
Enrolled	-0.01439864	0.08390907	0.04084347	1.00000000	0.97015737	
TotalSchools	-0.02409280	0.06661373	0.02580181	0.97015737	1.00000000	
PctBeliefExempt	-0.16611109	-0.28440060	-0.22760030	-0.19595735	-0.16336972	



GSM with Logistic Regression

Linear Regression for Collinearity Frequentist

In [405…

```
formula_str = paste(pred_col, ' ~ PctChildPoverty + PctFreeMeal + PctFamilyPover
lmOut <- lm(formula_str, data=districts)
summary(lmOut)
confint(lmOut)
coef(lmOut)
```

```
Call:
lm(formula = formula_str, data = districts)

Residuals:
    Min      1Q  Median      3Q     Max 
-12.778  -4.188  -2.029   1.356  65.288 

Coefficients:
                  Estimate Std. Error t value Pr(>|t|)    
(Intercept)      10.409240   0.760733  13.683  < 2e-16 ***
PctChildPoverty   0.163897   0.055108   2.974 0.003041 ** 
PctFreeMeal      -0.106588   0.020288  -5.254 1.99e-07 ***
PctFamilyPoverty -0.216453   0.077435  -2.795 0.005329 ** 
Enrolled         -0.005280   0.001481  -3.565 0.000389 ***
TotalSchools      0.331600   0.129837   2.554 0.010863 *  
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 8.311 on 693 degrees of freedom
Multiple R-squared:  0.132,	Adjusted R-squared:  0.1257 
F-statistic: 21.08 on 5 and 693 DF,  p-value: < 2.2e-16
```

A matrix: 6 × 2 of type dbl

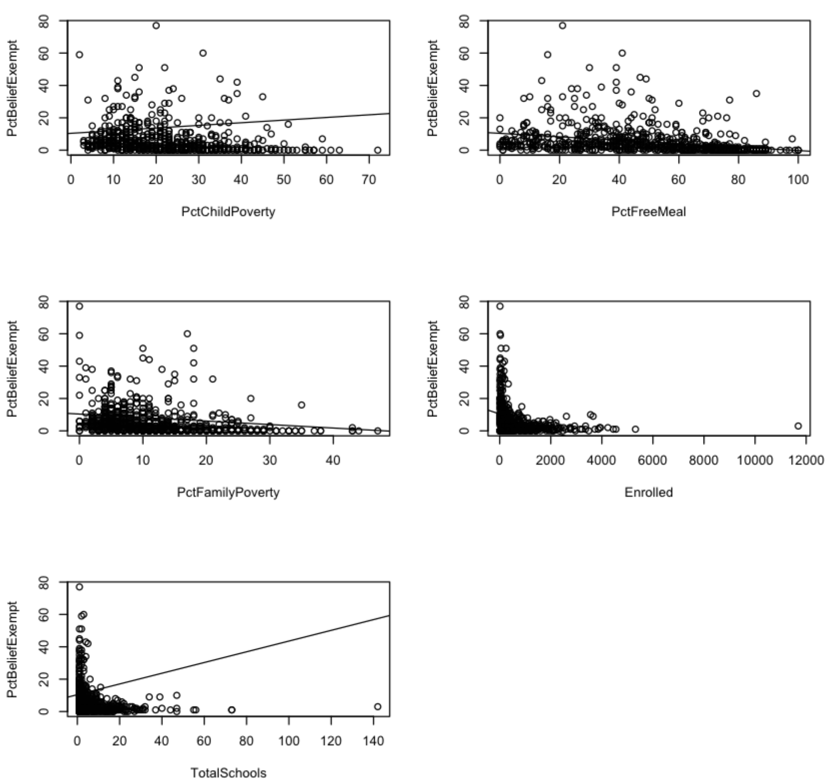
	2.5 %	**97.5 %**

	2.5 %	97.5 %
(Intercept)	8.915623322	11.902857619
PctChildPoverty	0.055697752	0.272096864
PctFreeMeal	-0.146421528	-0.066755394
PctFamilyPoverty	-0.368488320	-0.064417536
Enrolled	-0.008187741	-0.002371884
TotalSchools	0.076678425	0.586520983

(Intercept): 10.4092404707735 **PctChildPoverty:** 0.163897308353196 **PctFreeMeal:** -0.10658846107995 **PctFamilyPoverty:** -0.216452928319036 **Enrolled:** -0.00527981265898942 **TotalSchools:** 0.331599703902863

In [398…

```
par(mfrow = c(3,2))
for (x in pred_cols){
    plot(districts[, x], districts[, pred_col], xlab=x, ylab=pred_col)
    abline(lmOut$coefficients[c('(Intercept)', x)], col = "black")
}
```



Linear Regression for Collinearity Bayesian

In [401…

```
formula_str = paste(pred_col, '~ PctChildPoverty + PctFreeMeal + PctFamilyPovert
regOutMCMC <- lmBF(as.formula(formula_str), data=districts, posterior=TRUE, iter
regOutBF <- lmBF(as.formula(formula_str), data=districts)
summary(regOutMCMC)
summary(regOutMCMC)$statistics[, 'Mean']
regOutBF
```

```
Iterations = 1:10000
Thinning interval = 1
Number of chains = 1
Sample size per chain = 10000

1. Empirical mean and standard deviation for each variable,
   plus standard error of the mean:

                      Mean       SD  Naive SE Time-series SE
mu                 5.71002 0.313963 3.140e-03      3.240e-03
PctChildPoverty    0.15979 0.054123 5.412e-04      5.412e-04
PctFreeMeal       -0.10365 0.020285 2.029e-04      2.029e-04
PctFamilyPoverty -0.21044 0.076133 7.613e-04      7.613e-04
Enrolled          -0.00513 0.001471 1.471e-05      1.471e-05
TotalSchools       0.32241 0.129086 1.291e-03      1.291e-03
sig2              69.08373 3.693309 3.693e-02      3.649e-02
g                  0.06755 0.065002 6.500e-04      6.472e-04

2. Quantiles for each variable:

                       2.5%       25%      50%       75%     97.5%
mu                 5.101558  5.497042  5.71019  5.921093  6.330966
PctChildPoverty    0.054028  0.122814  0.15996  0.195722  0.265154
PctFreeMeal       -0.143785 -0.117211 -0.10323 -0.089981 -0.064310
PctFamilyPoverty -0.357898 -0.262313 -0.21180 -0.159199 -0.060390
Enrolled          -0.008026 -0.006118 -0.00514 -0.004139 -0.002258
TotalSchools       0.069583  0.235113  0.32260  0.409676  0.570590
sig2              62.255911 66.565504 68.98035 71.511723 76.743113
g                  0.018487  0.034716  0.05088  0.078244  0.212934
```

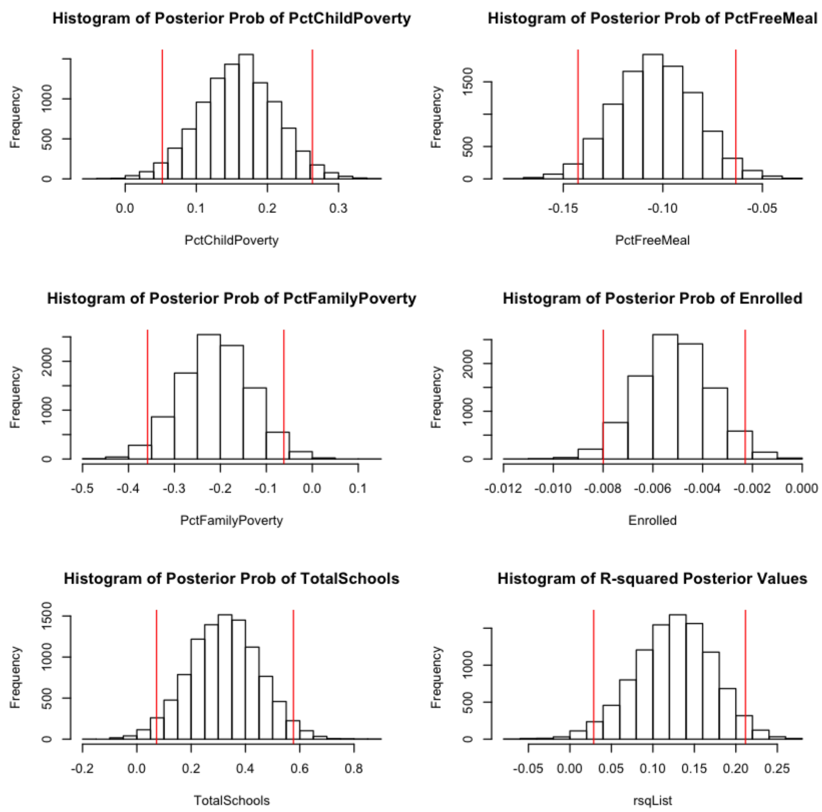
mu: 5.71002098987882 **PctChildPoverty:** 0.159791689656807 **PctFreeMeal:** -0.103650553167902 **PctFamilyPoverty:** -0.210443510444678 **Enrolled:** -0.00513033310454265 **TotalSchools:** 0.322407607904344 **sig2:** 69.0837299253517 **g:** 0.0675516141555137

```
Bayes factor analysis
--------------
[1] PctChildPoverty + PctFreeMeal + PctFamilyPoverty + Enrolled + TotalSchools :
2.349465e+16 ±0%

Against denominator:
  Intercept only
---
Bayes factor type: BFlinearModel, JZS
```

In [400…

```
rsqList <- 1 - (regOutMCMC[,"sig2"] / var(districts[, pred_col])) # sig2 from lm

par(mfrow = c(3,2))

for (x in pred_cols){
    hist(regOutMCMC[,x], xlab=x, main=paste('Histogram of Posterior Prob of', x)
    abline(v=quantile(regOutMCMC[,x],c(0.025)), col="red")
    abline(v=quantile(regOutMCMC[,x],c(0.975)), col="red")
}

mean(rsqList) # Overall mean R-squared is 0.75
hist(rsqList, main='Histogram of R-squared Posterior Values') # Show a histogram
# Lower bound of the 95% HDI
abline(v=quantile(rsqList,c(0.025)), col="red")
# Upper bound of the 95% HDI
abline(v=quantile(rsqList,c(0.975)), col="red")
```

0.125354576751932



Question 8

1. What's the big picture, based on all of the foregoing analyses? The staff member in the state legislator's office is interested to know how to allocate financial assistance to school districts to improve both their vaccination rates and their reporting compliance. What have you learned from the data and analyses that might inform this question?

```
In [ ]:
```