Some Comparisons

Based on worked Bayesian examples with raw data. Classical analysis compared to Bayesian results.

Surgical Deaths (baby heart surgeries)

- 12 hospitals, record the number of deaths and the total number of surgeries.

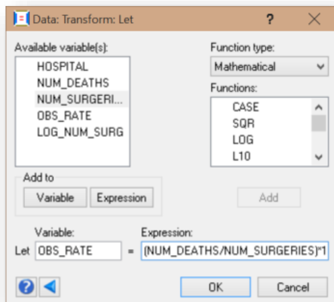
	A	B	C
1	Hospital	Deaths	Surgery
2	1	0	47
3	2	18	148
4	3	8	119
5	4	46	810
6	5	8	211
7	6	13	196
8	7	9	148
9	8	31	215
10	9	14	207
11	10	8	97
12	11	29	256
13	12	24	360

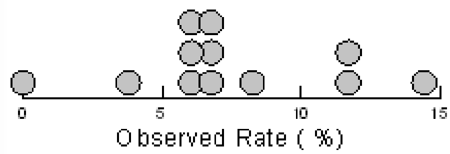
Estimate the mortality rate for baby heart surgery.

Approach 1 – Random sample of 12 hospitals

- One approach is to calculate the mortality rate at each hospital and use standard parametric statistics to describe the mean and SD.

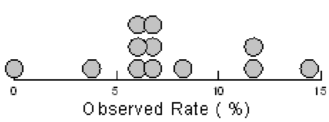
	A	B	C
1	Hospital	Deaths	Surgery
2	1	0	47
3	2	18	148
4	3	8	119
5	4	46	810
6	5	8	211
7	6	13	196
8	7	9	148
9	8	31	215
10	9	14	207
11	10	8	97
12	11	29	256
13	12	24	360

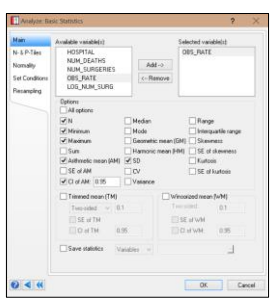




Approach 1 – Random sample of 12 hospitals

- One approach is to calculate the mortality rate at each hospital and use standard parametric statistics to describe the mean and SD.





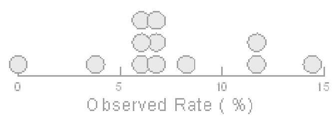
▼Descriptive Statistics

	OBS_RATE
N of Cases	12
Minimum	0.000
Maximum	14.419
Arithmetic Mean	7.374
95.0% LCL of Arithmetic Mean	4.932
95.0% UCL of Arithmetic Mean	9.817
Standard Deviation	3.844

Arithmetic Mean	7.374
95.0% LCL of Ar:	4.932
95.0% UCL of Ar:	9.817

Approach 1 – Random sample of 12 hospitals

- **Problem:** It treats all hospitals equally, even though we have 810 surgeries at one hospital and 47 at another.



▼Descriptive Statistics

```
                              ¦ OBS_RATE
------------------------------+----------
N of Cases                    ¦       12
Minimum                       ¦    0.000
Maximum                       ¦   14.419
Arithmetic Mean               ¦    7.374
95.0% LCL of Arithmetic Mean  ¦    4.932
95.0% UCL of Arithmetic Mean  ¦    9.817
Standard Deviation            ¦    3.844
```

	A	B	C
1	Hospital	Deaths	Surgery
2	1	0	47
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9	8	31	215
10	9	14	207
11	10	8	97
12	11	29	256
13	12	24	360

Approach 2 – Sum of all data

- If we sum the mortality from all hospitals and divide by the total surgeries, we get an estimate of the mortality rate (this is the MLE).

Hospital	Deaths	Surgery	
1	0	47	
2	18	148	
3	8	119	
4	46	810	
5	8	211	
6	13	196	
7	9	148	
8	31	215	
9	14	207	
10	8	97	
11	29	256	
12	24	360	
	208	2814	7.39%

How do we calculate a STD and CI for this single number??

If we assume that mortality rate is constant across hospitals (and thus all 2814 surgeries are independent and identical), we can use the Binomial Distribution!

Approach 2 – Sum of all data

Hospital	Deaths	Surgery	
1	0	47	
2	18	148	
3	8	119	
4	46	810	
5	8	211	
6	13	196	
7	9	148	
8	31	215	
9	14	207	
10	8	97	
11	29	256	
12	24	360	
	208	2814	7.39%

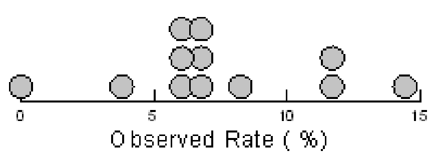
Binomial Distribution

SE = SQRT { ((p* (1 – p))/ n) }
SE = 0.49%

Estimate = 7.39%
L95 = 6.42%
U95 = 8.36%

$$SE = \sqrt{\frac{p(1-p)}{n}}$$

Comparison:



Arithmetic Mean	7.374
95.0% LCL of Ar	4.932
95.0% UCL of Ar	9.817

Hospital	Deaths	Surgery	
1	0	47	
2	18	148	
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11	29	256	
12	24	360	
	208	2814	7.39%

Estimate = 7.39%
L95 = 6.42%
U95 = 8.36%

Comment: We could do some math to calculate extra-binomial variability

Comparison:

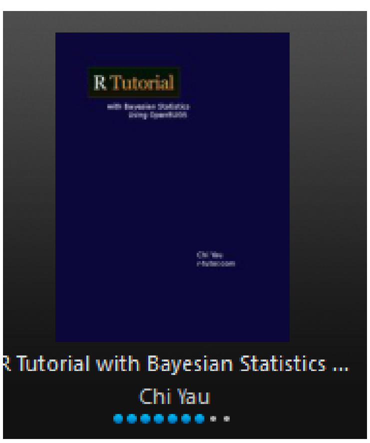
Arithmetic Mean	7.374
95.0% LCL of Ar:	4.932
95.0% UCL of Ar:	9.817

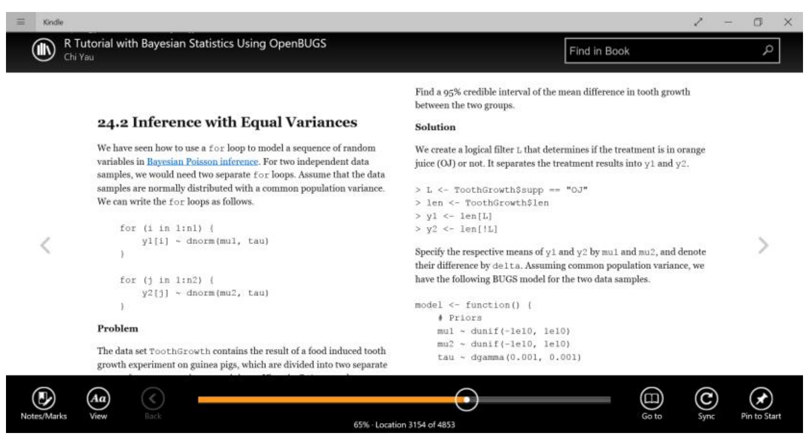
Estimate = 7.39%
L95 = 6.42%
U95 = 8.36%

Hospital	Deaths	Surgery	Rate		SE	L95	U95	OUTSIDE		Z
1	0	47	0.0%		3.8%	-0.1%	14.9%	~		-1.94
2	18	148	12.2%		2.2%	3.2%	11.6%	***		2.22
3	8	119	6.7%		2.4%	2.7%	12.1%			-0.28
4	46	810	5.7%		0.9%	5.6%	9.2%	~		-1.86
5	8	211	3.8%		1.8%	3.9%	10.9%	***		-2.00
6	13	196	6.6%		1.9%	3.7%	11.1%			-0.41
7	9	148	6.1%		2.2%	3.2%	11.6%			-0.61
8	31	215	14.4%		1.8%	3.9%	10.9%	***		3.94
9	14	207	6.8%		1.8%	3.8%	11.0%			-0.35
10	8	97	8.2%		2.7%	2.2%	12.6%			0.32
11	29	256	11.3%		1.6%	4.2%	10.6%	***		2.41
12	24	360	6.7%		1.4%	4.7%	10.1%			-0.53

Hospital	Deaths	Surgery	
1	0	47	
2	18	148	
3	8	119	
4	46	810	
5	8	211	
6	13	196	
7	9	148	
8	31	215	
9	14	207	
10	8	97	
11	29	256	
12	24	360	
	208	2814	7.39%

kindle



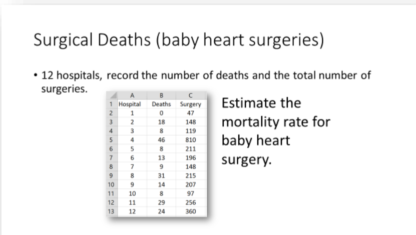


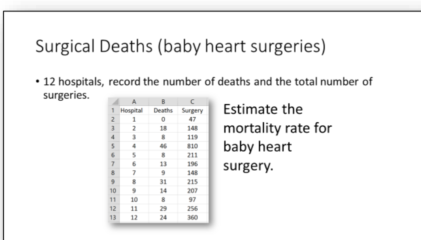
Solution

We can relate the logit of the expected mortality rate `pbar` with the mean of the random effect `mu` via a logical expression.

The model then becomes:

```
    # Derived
    logit(pbar) <- mu

model <- function() {
    # Priors

    mu ~ dnorm(0, 0.001)
    tau ~ dgamma(0.001, 0.001)

    # Likelihood
    for (i in 1:k) {
        y[i] ~ dbin(prob[i], n[i])
        logit(prob[i]) <- x[i]
        x[i] ~ dnorm(mu, tau)
    }

    # Derived
    logit(pbar) <- mu
}
```





Denote the number of surgical deaths by `y`, and the number of operations by `n`. From the data in the Surgical example of OpenBUGS, we have

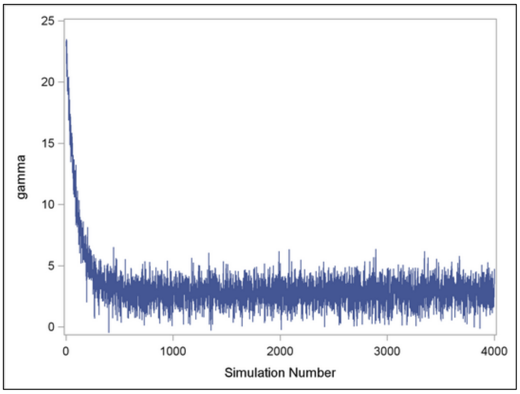
```
y <- c( 0, 18,  8, 46,  8, 13,
        9, 31, 14,  8, 29, 24)
n <- c( 47, 148, 119, 810, 211, 196,
       148, 215, 207,  97, 256, 360)
```

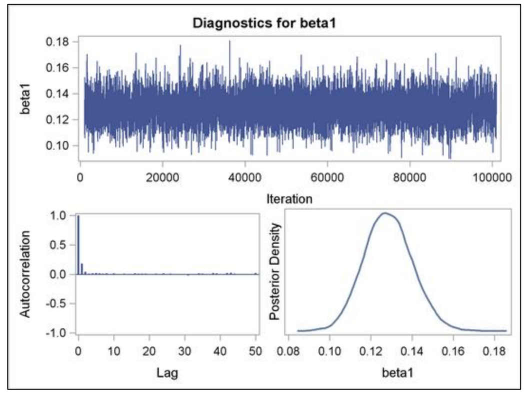
Then we define the data and initialization parameters.

```
k <- 12
data <- list("y", "n", "k")
params <- c("mu", "pbar")
inits <- function() {
    list(mu=0, tau=1, x=numeric(k))
}
```

After the simulation, the `xyplot` shows no obvious upward or downward trends in the trace plot.

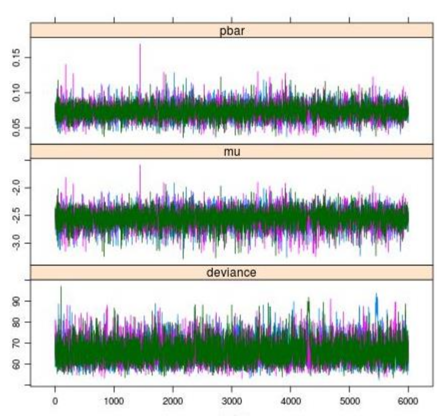
General MCMC Diagnostics





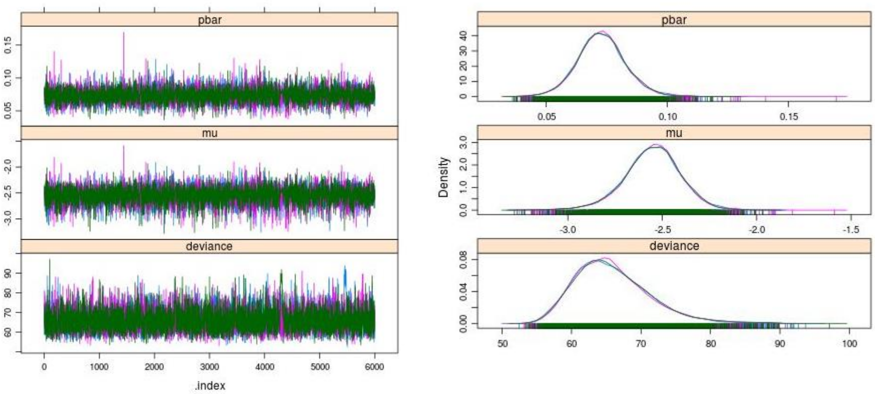

```
params <- c("mu", "pbar")
inits <- function() {
    list(mu=0, tau=1, x=numeric(k))
}
```

After the simulation, the *xyplot* shows no obvious upward or downward trends in the trace plot.

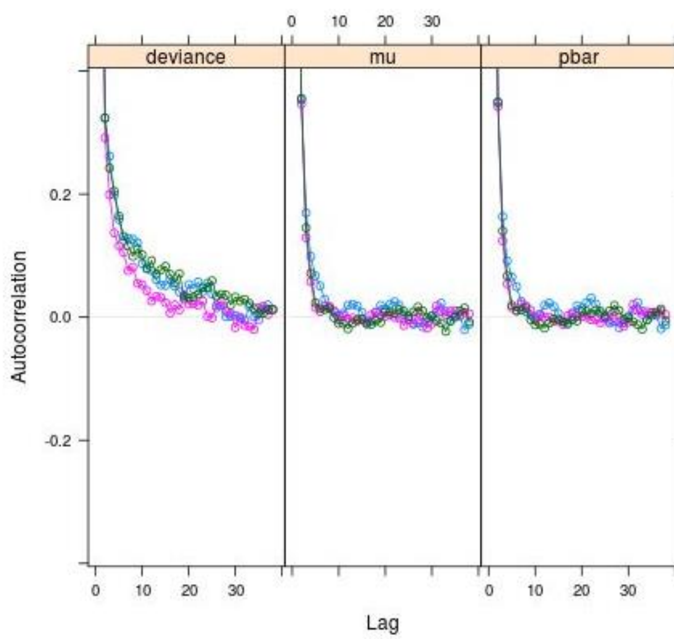


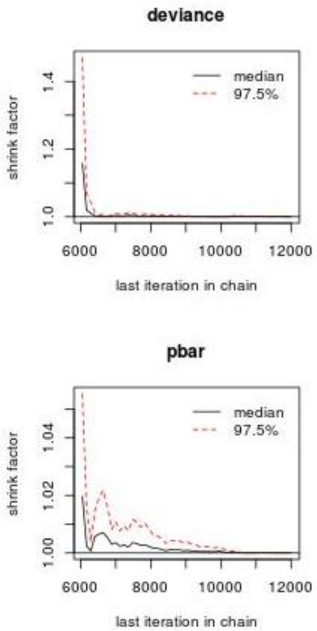
These are traces of the MCMC values. Typically the initial 1000 or 2000 are thrown away as a burn in period.

(We might talk about MCMC and the Metropolis Hastings a bit)



In addition, the *acfplot* shows that the auto-correlation converges to zero.





Assured convergence, we retrieve the expected mortality rate and its 95% credible interval.

```
library(coda)
xyplot(out.coda)
densityplot(out.coda)
acfplot(out.coda)

gelman.diag(out.coda)
gelman.plot(out.coda)

out.summary <- summary(out.coda,
    q=c(0.025, 0.975))
out.summary$stat["pbar",
    "Mean", drop=FALSE]
out.summary$q["pbar", ]
```

Surgical Deaths (baby heart surgeries)

- 12 hospitals, record the number of deaths and the total number of surgeries.

	A	B	C
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2	1	0	47
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11	10	8	97
12	11	29	256
13	12	24	360

Estimate the mortality rate for baby heart surgery.

```
+       q=c(0.025, 0.975))
> out.summary$stat["pbar",
+       "Mean", drop=FALSE]
          Mean
pbar 0.07292

> out.summary$q["pbar", ]
   2.5%    97.5%
0.05332 0.09401
```

Final Comparisons:

	Estimate	L95	U95
12 rates	7.37	4.93	9.82
Pooled Binomial	7.39	6.42	8.36
Bayesian Hierarchical	7.29	5.33	9.40

1-way ANOVA

	A	B	C	D
1	Item	Sales	TM2	TM3
2	1	22	1	0
3	1	42	1	0
4	1	44	1	0
5	1	52	1	0
6	1	45	1	0
7	1	37	1	0
8	2	52	0	1
9	2	33	0	1
10	2	8	0	1
11	2	47	0	1
12	2	43	0	1
13	2	32	0	1
14	3	16	0	0
15	3	24	0	0
16	3	19	0	0
17	3	18	0	0
18	3	34	0	0
19	3	39	0	0

1-Way ANOVA

Effects Coding

Estimates of Effects $B = (X'X)^{-1}X'Y$

Factor	Level	SALES
CONSTANT		33.722
GROUP	1	6.611
GROUP	2	2.111

Analysis of Variance

Source	Type III SS	df	Mean Squares	F-Ratio	p-Value
GROUP	745.444	2	372.722	2.541	0.112
Error	2,200.167	15	146.678		

Least Squares Means

Factor	Level	LS Mean	Standard Error	N
GROUP	1	40.333	4.944	6.000
GROUP	2	35.833	4.944	6.000
GROUP	3	25.000	4.944	6.000

Dummy Coding

Dependent Variable	SALES
N	18
Multiple R	0.503
Squared Multiple R	0.253

Estimates of Effects $B = (X'X)^{-1}X'Y$

Factor	Level	SALES
CONSTANT		25.000
GROUP	1	15.333
GROUP	2	10.833

Analysis of Variance

Source	Type III SS	df	Mean Squares	F-Ratio	p-Value
Regression	745.444	2	372.722	2.541	0.112
Residual	2,200.167	15	146.678		

Dummy Variable Regression

Regression Coefficients $B = (X'X)^{-1}X'Y$

Effect	Coefficient	Standard Error	Std. Coefficient	Tolerance	t	p-Value
CONSTANT	25.000	4.944	0.000	.	5.056	0.000
TM1	15.333	6.992	0.565	0.750	2.193	0.044
TM2	10.833	6.992	0.399	0.750	1.549	0.142

Confidence Interval for Regression Coefficients

Effect	Coefficient	95.0% Confidence Interval		VIF
		Lower	Upper	
CONSTANT	25.000	14.461	35.539	.
TM1	15.333	0.430	30.237	1.333
TM2	10.833	-4.070	25.737	1.333

Analysis of Variance

Source	SS	df	Mean Squares	F-Ratio	p-Value
Regression	745.444	2	372.722	2.541	0.112
Residual	2,200.167	15	146.678		

Bayesian

```
model <- function() {
    # Priors
    alpha ~ dunif(-1e10, 1e10)

    beta[1] <- 0
    for (k in 2:ngroup) {
        beta[k] ~ dunif(-1e10, 1e10)
    }

    tau ~ dgamma(0.001, 0.001)

    # Likelihood
    for (i in 1:N) {
```

```
        y[i] ~ dnorm(mu[i], tau)
        mu[i] <- alpha + beta[tm[i]]
    }

    # Derived
    eff <- beta[2] - beta[3]
}
```

While we define `beta[1]` to be zero in the BUGS model, we set it as `NA` during the initialization.

```
inits <- function() {
    beta <- numeric(ngroup)
    beta[1] <- NA

    list(alpha=0, beta=beta, tau=1)
}
```

Bayesian

After the simulation, we can retrieve the 95% credible intervals of the contrast parameters `beta[2]`, `beta[3]`, and `eff`. Only `beta[3]` manages to exclude the zero value.

```
> cbind(unlist(out$mean[params]))
          [,1]
alpha   40.353
beta1   -4.475
beta2  -15.369
eff     10.895
```

```
> out$summary[,  c("2.5%", "97.5%")]
            2.5%     97.5%
alpha     30.160   51.0302
beta[2]  -19.760    9.5546
beta[3]  -30.550   -0.7822
eff       -4.064   25.5602
deviance 138.100  150.6000
```

Linear Model in R

```
> fastfood.lm <- lm(y ~ tm)
> anova(fastfood.lm)
Analysis of Variance Table

Response: y
          Df Sum Sq Mean Sq F value Pr(>F)
tm         2    745     373    2.54   0.11
Residuals 15   2200     147
```

Compare

However, the following shows almost identical parameter estimates with the classical linear model. As added bonus, we managed to estimate the contrast between the second and third treatment levels without extra effort using OpenBUGS.

```
> cbind(unlist(out$mean[params]))
         [,1]
alpha  40.353
beta1  -4.475
beta2 -15.369
eff    10.895

> cbind(coefficients(fastfood.lm))
              [,1]
(Intercept)  40.33
tm2          -4.50
tm3         -15.33
```

Final Comparison:

Systat Linear Model

	Estimate	L95	U95
Alpha	40.33	27.62	53.04
Beta2	-15.33	-30.24	-0.43
Beta3	-10.83	-4.07	25.74

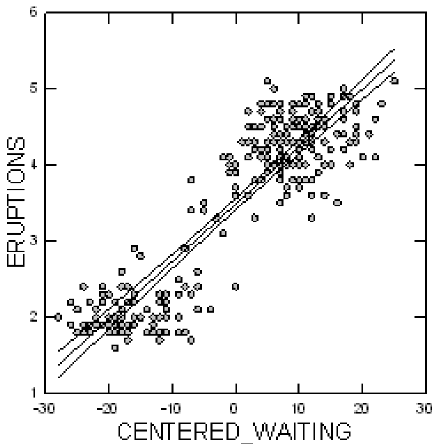
Bayesian in R

	Estimate	L95	U95
Alpha	40.35	30.16	51.03
Beta2	-15.37	-30.55	-0.78
Beta3	-10.90	-4.06	25.56

Linear Regression

	A	B	C
1	Eruption (y)	Wait (x)	Centered Wait
2	3.6	79	8.10
3	1.8	54	-16.90
4	3.3	74	3.10
5	2.3	62	-8.90
6	4.5	85	14.10
7	2.9	55	-15.90
8	4.7	88	17.10
9	3.6	85	14.10
10	2	51	-19.90
269	4.1	81	10.10
270	2.1	46	-24.90
271	4.4	90	19.10
272	1.8	46	-24.90
273	4.5	74	3.10

Linear Regression



Dependent Variable	ERUPTIONS
N	272
Multiple R	0.901
Squared Multiple R	0.812
Adjusted Squared Multiple R	0.811
Standard Error of Estimate	0.495

Regression Coefficients $B = (X'X)^{-1}X'Y$

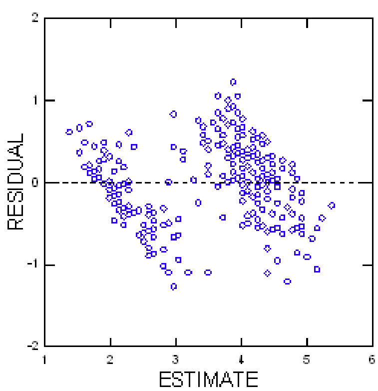
Effect	Coefficient	Standard Error	Std. Coefficient	Toler
CONSTANT	3.491	0.030	0.000	
CENTERED_WAITING	0.075	0.002	0.901	1

Confidence Interval for Regression Coefficients

Effect	Coefficient	95.0% Confidence Interval		VIF
		Lower	Upper	
CONSTANT	3.491	3.432	3.550	.
CENTERED_WAITING	0.075	0.071	0.080	1.000

Linear Regression

Plot of Residuals vs. Predicted Values



Analysis of Variance

Source	SS	df	Mean Squares	F-Ratio	p-Value
Regression	285.128	1	285.128	1,162.719	0.000
Residual	66.211	270	0.245		

Durbin-Watson D-Statistic	2.548
First Order Autocorrelation	-0.281

Bayesian Linear Regression

In a simple linear regression model, for a given value of x, the response data y is a random variable with expected value $E(y)$. We can break up the model into two parts. The first equation below denotes a *stochastic component* that expresses y as a normally distributed random variable, and the second equation denotes a *deterministic component* that expresses the expected value $E(y)$ linearly in terms of x.

$$\begin{aligned} y &= E(y) + \epsilon \\ E(y) &= \alpha + \beta x \end{aligned}$$

Hence, for a sequence of observations, we can write the following.

```
for (i in 1:n) {
    y[i] ~ dnorm(mu[i], tau)
    mu[i] <- alpha + beta*x[i]
}
```

Bayesian Linear Regression

We define the BUGS model as follows. Here, we use the vague prior `dnorm(0, 0.001)` for `alpha` and `beta`.

```
model <- function() {
    # Priors
    alpha ~ dnorm(0, 0.001)
    beta ~ dnorm(0, 0.001)
    tau ~ dgamma(0.001, 0.001)

    # Likelihood
    for (i in 1:n) {
        y[i] ~ dnorm(mu[i], tau)
        mu[i] <- alpha + beta*x[i]
    }
}
```

Bayesian Linear Regression

Source Listing

```
waiting <- faithful$waiting
x.m <- mean(waiting)

x <- waiting - x.m
y <- faithful$eruptions
n <- length(waiting)

data <- list("x", "y", "n")
```

```
params <- c("alpha", "beta", "mu")
inits <- function() {
    list(alpha=0, beta=0, tau=1)
}

library(R2OpenBUGS)
model.file <- file.path(tempdir(),
    "model.txt")
write.model(model, model.file)
out <- bugs(data, inits, params,
    model.file, n.iter=5000)
all(out$summary[,"Rhat"] < 1.1)

# fitting the model
cbind(unlist(out$mean[
    c("alpha", "beta")]))

# credible intervals
out$summary[c("alpha", "beta"),
    c("2.5%", "97.5%")]
```

Bayesian Linear Regression

```
+     c("alpha", "beta")]))

         [,1]
alpha 3.48693
beta  0.07565
```

The 95% credible intervals of the model coefficients are

```
> out$summary[c("alpha", "beta"),
+     c("2.5%", "97.5%")]

         2.5%   97.5%
alpha 3.42700 3.54600
beta  0.07118 0.08007
```

Bayesian Linear Regression

```
+     c("alpha", "beta")]))

         [,1]
alpha 3.48693
beta  0.07565
```

The 95% credible intervals of the model coefficients are

```
> out$summary[c("alpha", "beta"),
+     c("2.5%", "97.5%")]

         2.5%   97.5%
alpha 3.42700 3.54600
beta  0.07118 0.08007
```

Final Comparison:

Systat Linear Model

	Estimate	L95	U95
Alpha	3.491	3.432	3.550
Beta	.0754	.0711	.0798

Bayesian in R

	Estimate	L95	U95
Alpha	3.487	3.427	3.546
Beta	.0757	.0712	.0801

Note 1

The point estimates of the coefficients are almost identical to the classical linear parameters.

Sarah’s PhD research

The parameter estimates for nest success, juvenile mortality, and adult mortality were estimated with a beta-binomial mixture model, with one sample per study. The beta distribution constrained the estimates between 0 and 1, which was an important component of the realism of these estimates.

(Eq 2) $X_{ij} \sim \text{Binomial}(n_i, p_i)$

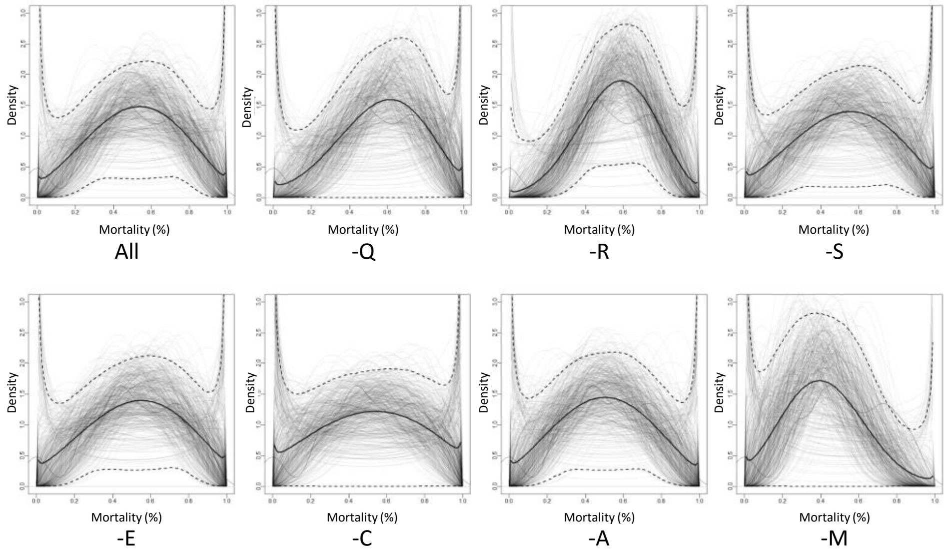
$p_i \sim \text{Beta}(\alpha,\beta)$

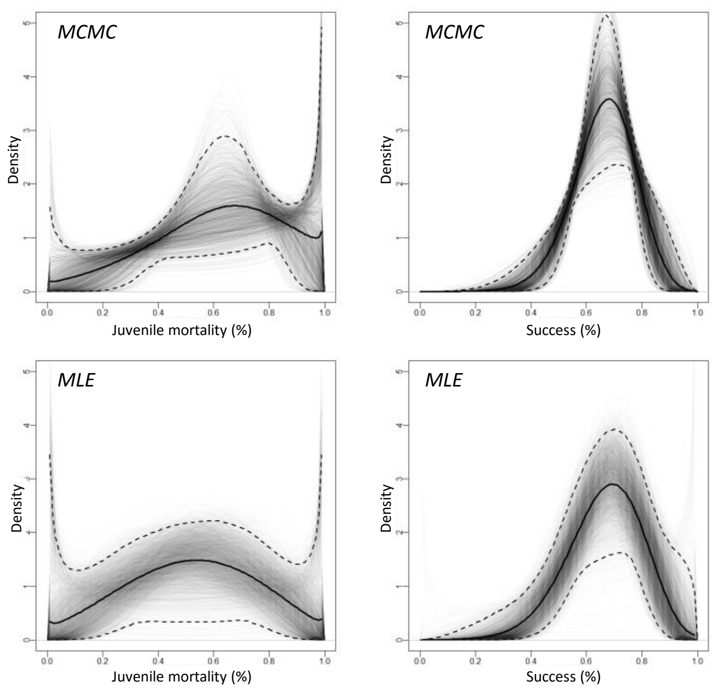
Parameter estimates were computed using the Metropolis Hastings algorithm for Markov Chain Monte Carlo (MCMC) estimation. The Metropolis Hastings algorithm enables nonsymmetric proposals for each parameter, which is needed when estimating non-Gaussian distributions. Gibbs sampling was utilized to increase sampling efficiency. For the poisson gamma model, MCMC estimated the α and β parameters of the gamma distribution. For the beta-binomial models, MCMC estimated the α and β parameters of the beta distribution. The conjugate prior utilized for all models was a weak gamma prior (0.001, 0.001).

The starting point for the beta-binomial chain was α=18 and β=7. The chain ran 5000 iterations, of which the first 1000 iterations were discarded as the burn-in period. The remaining 4000 iterations comprised the posterior distribution and were used to create 95% credible intervals that represent 95% of the probability distribution. Histograms representing 1000 random samples from each beta and gamma model fit were created using the rgamma function based on mean estimate values for alpha and beta.

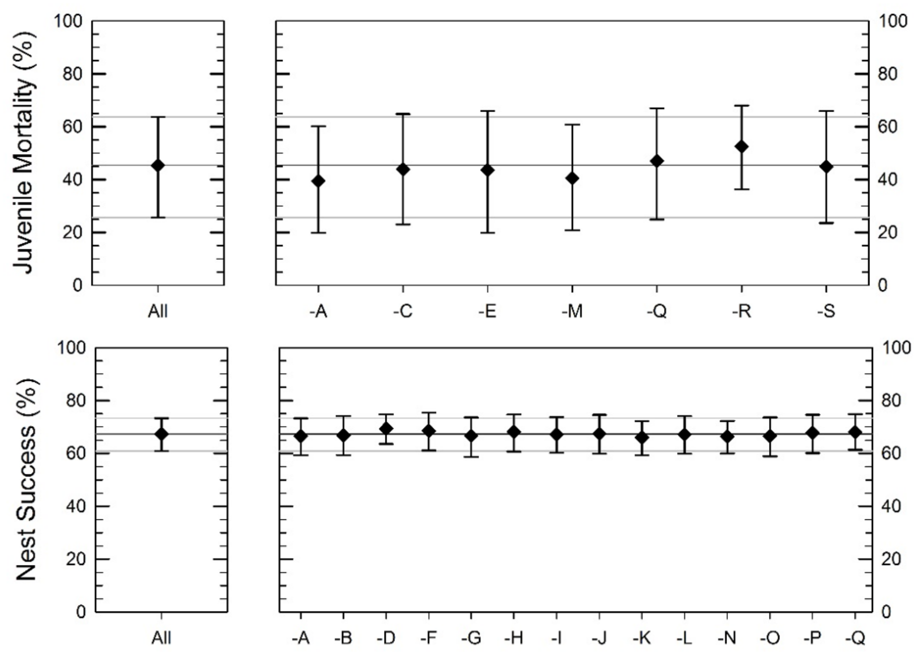
Table X. Data summary from literature

Study ID	Study	Site	Habitat	Fossorial Mammal	Burrow type	Method	Year	Juvenile Mortality	n juv.	Adult mortality	n adult	Nest Success	n nest	Productivity	SE	n
A	Barclay et al 2011	California	Airport	CA ground squirrels	Both	observations	1990-2007	0.74	656	0.46	23	0.79	342			
B	Berardelli et al 2010	New Mexico	urban/ grassland	Rock squirrel	both	observations	2000-01					0.74	144	3.47	0.21	106
C	Clayton and Schmutz 1999	Alberta Saskatchewan	pasture	NA	NA	Radiotelemetry	1995-1996	0.53	46	0.43	30					
D	Conway et al 2006	Washington	Urban/ agriculture	badger, marmot, ground squirrel	natural	observations	2000-2004					0.46	1088	3.15	0.13	500
E	Davies and Restani 2006	North Dakota	grassland	Prairie dogs	Natural	Radiotelemetry	2003-4	0.45	40							
F	Green & Anthony 1989	Oregon	Grassland shrubland	badger	natural	observations	1980-1					0.53	139			
G	Griebel and Savidge 2007	South Dakota	Grassland	Prairie dogs	natural	observations	1999-2000					0.76	274	3.5		207
H	Holmes et al 2003	Oregon	Grassland	Badger	natural	observations	1995-1997					0.57	99			
I	Lantz & Conway 2009	Wyoming	grassland	Prairie dogs	natural	observations	2003-4					0.71	77			
J	Lehman et al 1998	Idaho	Shrub steppe			observations	1992-1994					0.64	108			
K	Lutz and Plumpton 1999	Colorado	Grassland	Prairie dogs	natural	Banding, observations	1990-1994					0.82	167			
L	Millsap & Bear 2000	Florida	suburban	Owls	natural	observations	1987-90					0.7	736	2.9	0.1	512
M	Millsap 2002	Florida	suburban	Owls	natural	Banding, observations	1987-1991	0.7	310	0.33	271					
N	Restani et al. 2001	Montana	Grassland	Prairie dogs	Natural	observations	1998					0.92	13			
O	Rosenberg & Haley 2004	Imperial County, CA	agricultural	CA Ground Squirrel	Natural artificial	Banding, observations	1997-2000			0.36	295	0.79	78	3.09		62
P	Rosenberg et al 2007	California	several	CA ground squirrel	natural	observations	1997-2003					0.62	419	3.38	0.43	297
Q	Thomsen 1971	California	Airport	Ca ground squirrels	Natural	Banding, observations	1965-6	0.27	71	0.19	21	0.54	24	4.4		13
R	Todd 2001	Saskatchewan	Pasture	NA	Artificial	Radiotelemetry	1997	0	12							
S	Todd et al. 2003	Saskatchewan	Pasture	Richardson’s ground squirrels	Mostly artificial	Radiotelemetry, banding	1998-2000	0.55	64							


Density
Mortality (%)
All
-Q
-R
-S
-E
-C
-A
-M


MCMC
MLE
Density
Juvenile mortality (%)
Success (%)

Parameter	Mean ± SD	CV	95% credible interval
Juvenile mortality	0.45 ± 0.21	0.47	0.257 – 0.637
Adult mortality	0.35 ± 0.03	0.09	0.295 – 0.401
Nest success	0.67 ± 0.02	0.03	0.609 – 0.733
Productivity	3.3 ± 0.32	0.10	3.0 – 3.6



24.1 Inference for Two Matched Samples

When we have two matched samples from repeated measurements in the same experiment, say y1 and y2, we can pair up the data and calculate their difference.

```
y <- y1 -y2
```

Therefore, comparing the population means of two matched samples is the same as finding the population mean of their difference, and we can apply one of our previous models for this purpose.

Problem

The data set immer contains the yield data of six barley fields in years 1931 and 1932. The 1931 yield is in Y1, and the 1932 yield is in Y2. Assuming the data to be normally distributed, find a 95% credible interval of the difference in population means between Y1 and Y2.

Solution

We denote the two barley yield data as y1 and y2. With matched samples, we can denote their difference as y.

```
> library(MASS)
> y1 <- immer$Y1
> y2 <- immer$Y2

> y <- y1 - y2
> n <- length(y)
```

We then investigate the expected value of y using our previous model for the mean of a normal distribution.

```
model <- function() {
    # Priors
    mu ~ dunif(-1e10, 1e10)
    tau ~ dgamma(0.001, 0.001)

    # Likelihood
    for (i in 1:n) {
        y[i] ~ dnorm(mu, tau)
    }
}
```

Then we define similar data and initial parameters.

```
> data <- list("y", "n")
> params <- c("mu")
> inits <- function() {
```

```
> unlist(out$mean[params])
   mu
15.88

> out$summary[params,
+      c("2.5%", "97.5%")]
  2.5%   97.5%
 6.076 25.550
```

Variable	Mean Difference	95.00% Confidence Interval	
		Lower Limit	Upper Limit
VAR(1)	15.9133	6.1220	25.7047
VAR(2)			

t	df	p-Value
3.3240	29.0000	0.0024