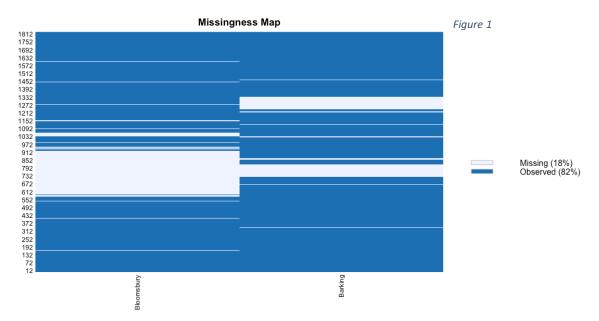
Assignment 2

1)



In Bloomsbury the average level of of PM10 pollution is 5.5, with a maximum of 77.7 and an average level of 22.09; there are 427 NA values in the Bloomsbury dataset. In terms of NA values by year in Bloomsbury, there are 12 in 2000 and 2001, 240 in 2002, 154 in 2003, and 9 in 2004. In Barking the average level of PM10 pollution is 21.53, with a minimum of 3.8, maximum of 71.8, and 232 NA values. By year, Barking has 3 NA values in 2000, 104 in 2001, 113 in 2002, 11 in 2003, and 1 in 2004. Bloomsbury has more missing values, with the NA values being very low for 2 years, rising suddenly in the next 2, before falling very low again in 2004. Barking starts very low also, and then rises quick for the next two years, before pollution falls very low for the last 2 years. Clearly, for both areas, the patterns of missing data change over time. This is shown by the missingess map in Figure 1, by the significant chunk of 2002 missing for Bloomsbury, and smaller chunks missing for Barking in 2001 and 2002.

Figure 2

2)

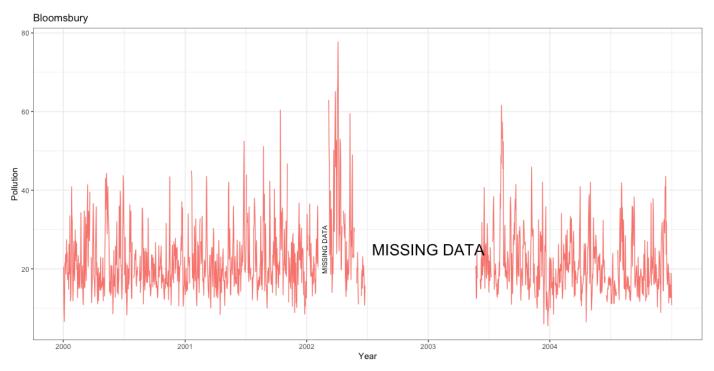


Figure 3

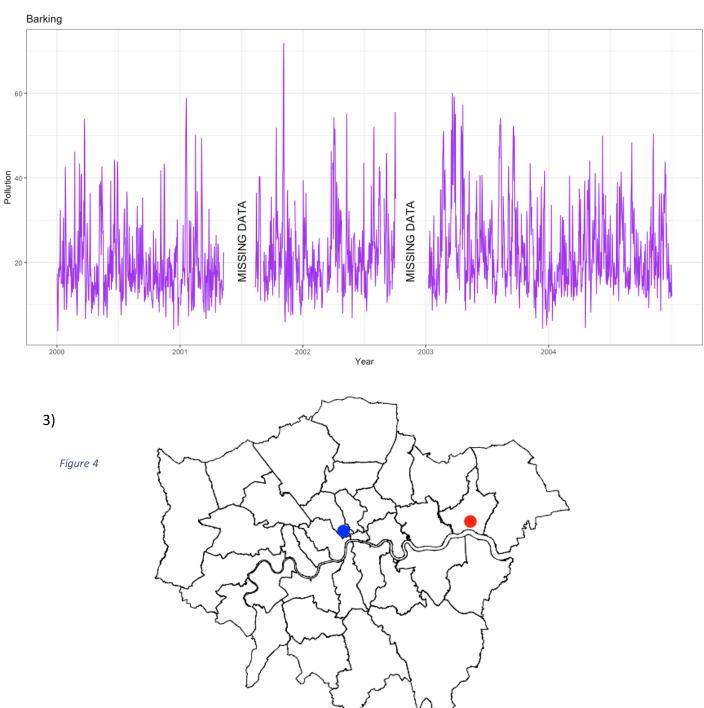


Figure 4 shows the locations of Barking and Bloomsbury on a map of London; Barking is red and Bloomsbury is blue. Bloomsbury is located in the West End, a very tourist heavy area, whilst Barking is in East London. Bloombury's higher average, minimum, and maximum pollution may be explained by the fact that it is a very tourist heavy area, and also has multiple universities and museums located there.

Figure 5



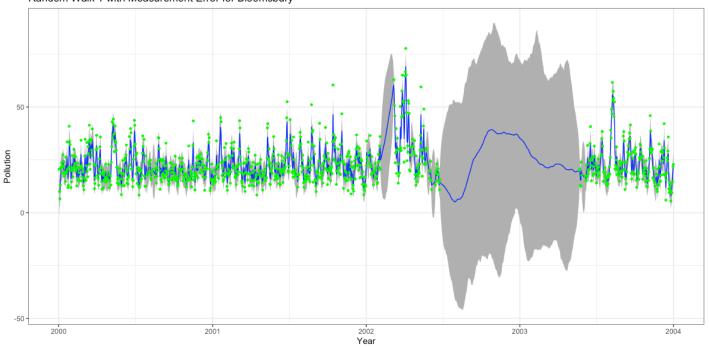
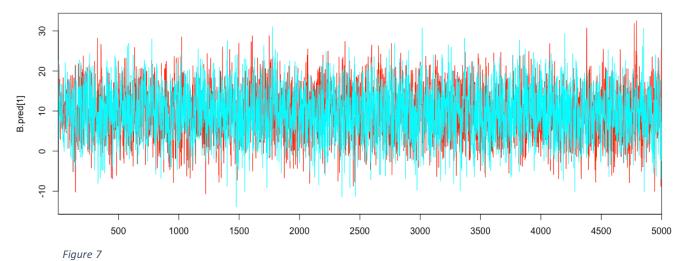
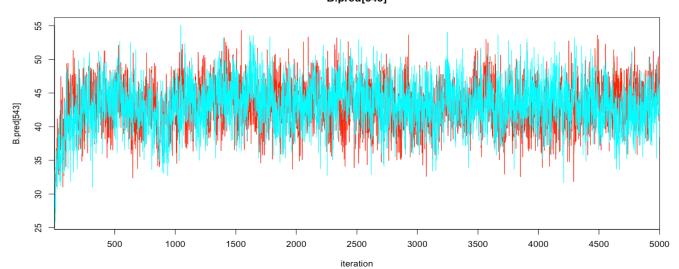


Figure 6 B.pred[1]



B.pred[543]



> Gelman Diagnostic for Bloomsbury Random Walk 1

	Point est.	Upper C.I.
B.pred[1]	0.9999728	1.0002011
B.pred[10]	1.0006330	1.0006331
B.pred[100]	0.9999436	1.0000567
B.pred[1000]	1.7289491	3.4612309
Bloomsbury[1000]	1.7079327	3.3559620
Bloomsbury[1001]	1.6929037	3.3987269
Bloomsbury[1002]	1.6772799	3.4128634
deviance	1.0051572	1.0085559
MSErw1	1.0046632	1.0071221
sigma.v2	1.0045029	1.0057244
sigma.w2	1.0070508	1.0129532
tau.v	1.0077037	1.0140151
tau.w	1.0071243	1.0071255

In terms of convergence in this model, the traceplots mostly seem to converge. Looking at the Gelman diagnostic is more helpful, and whilst the above only shows the Gelman values for a few parameters, looking through the whole output shows there are many parameters which are less than 1.1, but also many slightly above 1.1, which overall indicates a lack of overall model convergence, despite the converging traceplots. Figure 5 shows the RW process in blue, and the actual data points in green; the model seems to fit the actual data points very well.

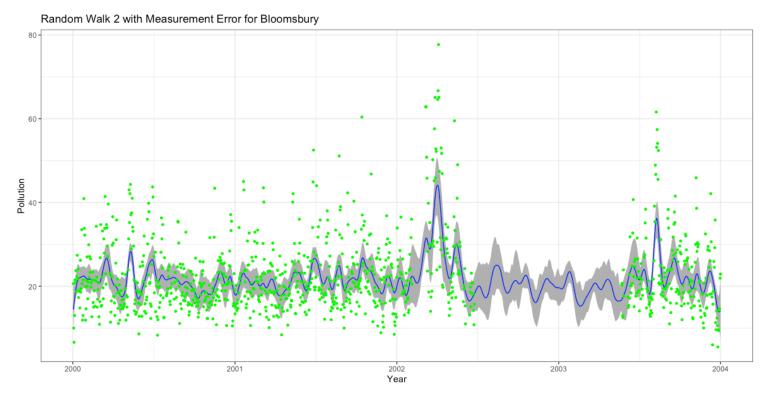
	mean	sd	2.5%	25%	50%	75%	97.5%	Rhat	n.eff
B.pred[1]	9.5351	6.0254	-	5.3859	9.5414	13.644	21.173	1.00	10000
	559	504	2.1767	104	994	7611	8745	0955	
			398						
B.pred[2]	9.7523	3.4333	2.9787	7.4256	9.7724	12.064	16.458	1.00	7700
	796	462	301	501	557	8285	5776	1093	
B.pred[3]	9.5674	3.0960	3.5317	7.5119	9.5547	11.593	15.707	1.00	3400
	463	575	300	024	174	6914	8534	1340	
B.pred[4]	13.808	3.0230	7.8204	11.808	13.769	15.810	19.855	1.00	8100
	5924	021	282	4694	9813	1845	3550	1084	
B.pred[5]	19.054	3.0514	13.052	17.003	19.065	21.087	24.930	1.00	5700
	2740	485	6078	3015	5769	0345	5802	1160	
MSErw1	4.2156	0.3718	3.5837	3.9836	4.2002	4.4180	4.8953	1.00	1600
	489	739	016	596	592	860	155	5011	
deviance	5943.3	177.73	5614.0	5834.7	5944.2	6047.0	6260.9	1.00	1600
	999698	38982	413316	302178	526998	802465	211786	5442	
sigma.v2	17.814	3.3864	12.596	15.717	17.485	19.452	24.072	1.00	1800
	2037	511	4655	8321	1787	4571	9475	4820	
sigma.w2	26.419	4.2013	18.384	24.015	26.576	29.119	34.002	1.00	3800
	7795	926	9628	0748	0261	0890	5284	7962	
tau.v	0.0579	0.0100	0.0415	0.0514	0.0571	0.0636	0.0793	1.00	1800
	196	791	404	074	913	220	873	4820	
tau.w	0.0393	0.0113	0.0294	0.0343	0.0376	0.0416	0.0543	1.00	3800
	427	523	096	417	279	405	923	7962	

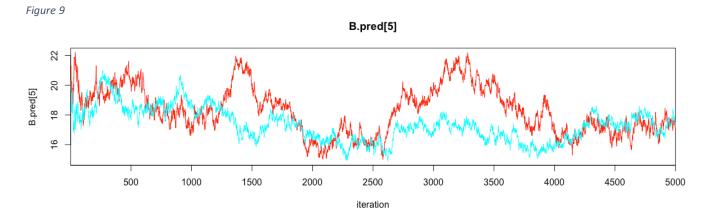
Summary of RW1 model for Bloomsbury

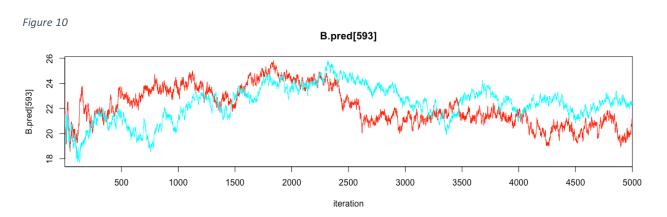
Lack of full model convergence is further seen through the Rhat values in the model summary shown above; in the full output, many Rhat values exceed 1.1, as in the Gelman diagnostic, thus inferring a lack of convergence. In terms of the credible interval widths for the missing data periods, their widths are far larger than for the periods that contain data, which makes sense as the model is predicting between which values the actual data would be. The credible widths also look like they broadly follow the trend of the missing data points.

7)

Figure 8







	Point est.	Upper C.I.		
B.pred[1]	0.9999728	1.0002011		
B.pred[10]	1.0006330	1.0006331		
B.pred[100]	0.9999436	1.0000567		
B.pred[1000]	1.7289491	3.4612309		
Bloomsbury[1000]	1.7079327	3.3559620		
Bloomsbury[1001]	1.6929037	3.3987269		
Bloomsbury[1002]	1.6772799	3.4128634		
deviance	1.0051572	1.0085559		
MSErw1	1.0046632	1.0071221		
sigma.v2	1.0045029	1.0057244		
sigma.w2	1.0070508	1.0129532		
tau.v	1.0077037	1.0140151		
tau.w	1.0071243	1.0071255		

Gelman Diagnostic for Bloomsbury Random Walk 2

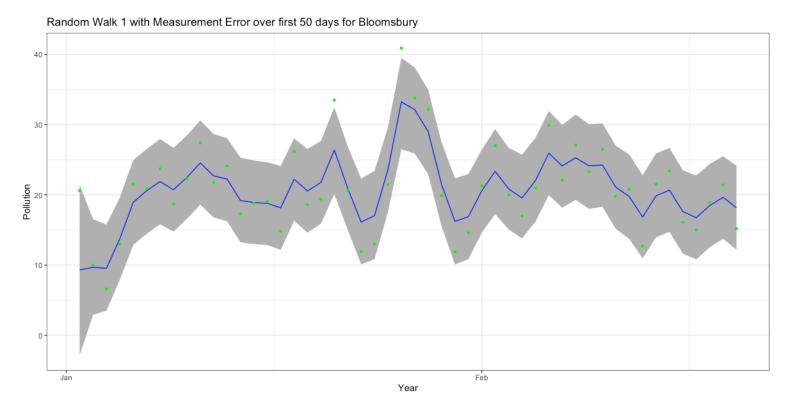
This model does not seem to fit the data as well as the RW1 model. In terms of convergence, none of the traceplots seem to converge, and the Gelman diagnostic and Rhat values shown in the summary table below, are mostly slightly or significantly greater than 1.1, futher indicating a lack of convergence. So the RW1 model seems a better fit for the data, and converges more than the RW2 model.

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	mean	sd	2.5%	25%	50%	75%	97.5%	Rhat	n.e ff
B.pre	14.4673	2.722	9.46505	12.6930	14.2740	16.1350	20.3280	1.00	10
d[1]	503	4623	16	016	632	976	528	5691	00 0
B.pre	15.3212	2.179	11.4502	13.8614	15.1195	16.6855	20.0830	1.00	21
d[2]	318	6168	964	416	607	362	207	8770	0
B.pre	16.1665	1.768	13.1173	14.8960	15.9934	17.2972	19.9037	1.04	44
d[3]	134	4078	384	099	570	689	572	0980	
B.pre	17.0024	1.528	14.4696	15.8605	16.8100	18.0165	20.3121	1.13	17
d[4]	204	4351	791	422	306	180	579	0271	
B.pre	17.8127	1.444	15.5602	16.7369	17.5978	18.6941	21.0668	1.26	10
d[5]	860	6502	723	574	077	486	192	5146	
MSEr	7.60619	0.151	7.32330	7.49902	7.60459	7.70825	7.91472	1.89	4
w1	03	6851	06	85	66	82	98	0807	
devi	7180.06	33.68	7119.37	7151.15	7183.60	7202.44	7248.86	2.54	3
ance	95875	52582	27176	89032	85238	83943	89546	3572	
sigm	57.8926	3.167	51.9866	55.6846	57.7883	60.0022	64.3152	1.40	7
a.v2	985	9594	721	304	274	295	132	6529	
sigm	0.09538	0.081	0.05038	0.06165	0.08138	0.10592	0.21692	1.70	5
a.w2	62	3685	16	23	25	92	58	9127	
tau.v	0.01732	0.000	0.01554	0.01666	0.01730	0.01795	0.01923	1.40	7
	50	9461	84	60	45	83	57	6529	
tau.	12.6361	4.197	4.60987	9.44027	12.2876	16.2199	19.8485	1.70	5
w	759	9588	22	20	472	884	051	9127	

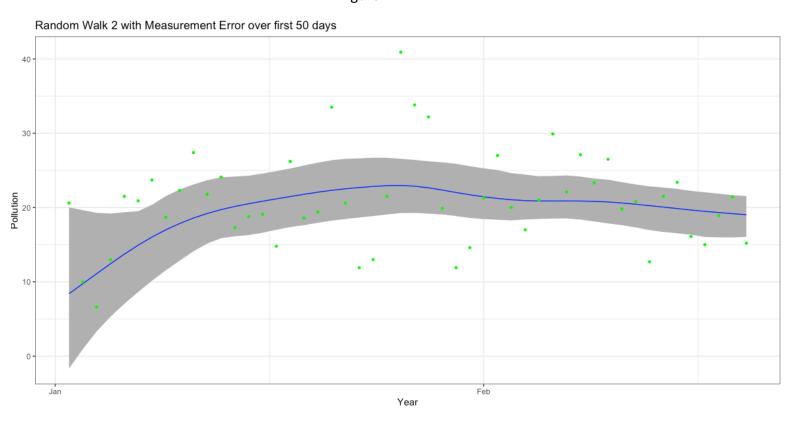
Summary of RW2 model for Bloomsbury

Figure 11



Comparing the first 50 days for each model shows that RW2 has a far greater smoothing effect than RW1

Figure 12



8/9) Figure 13

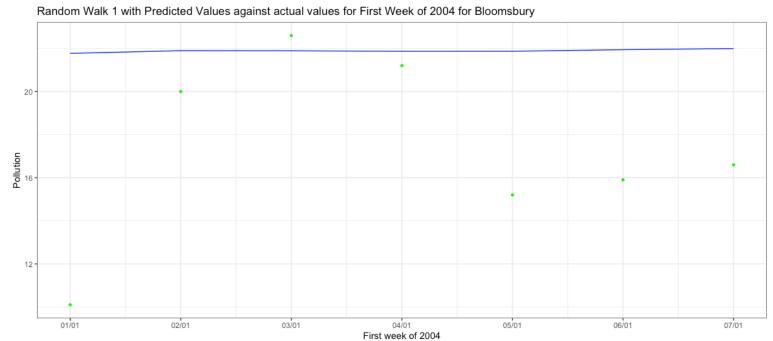
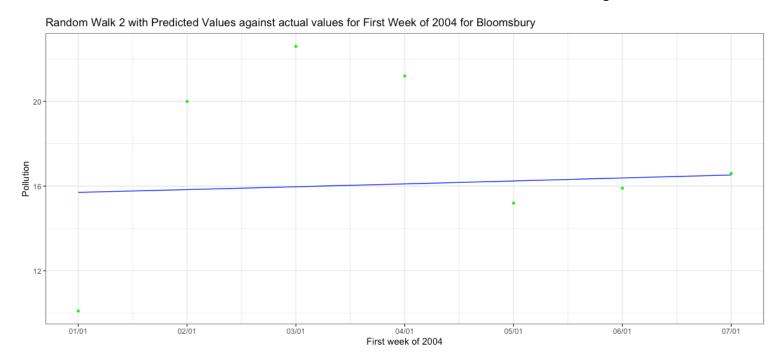
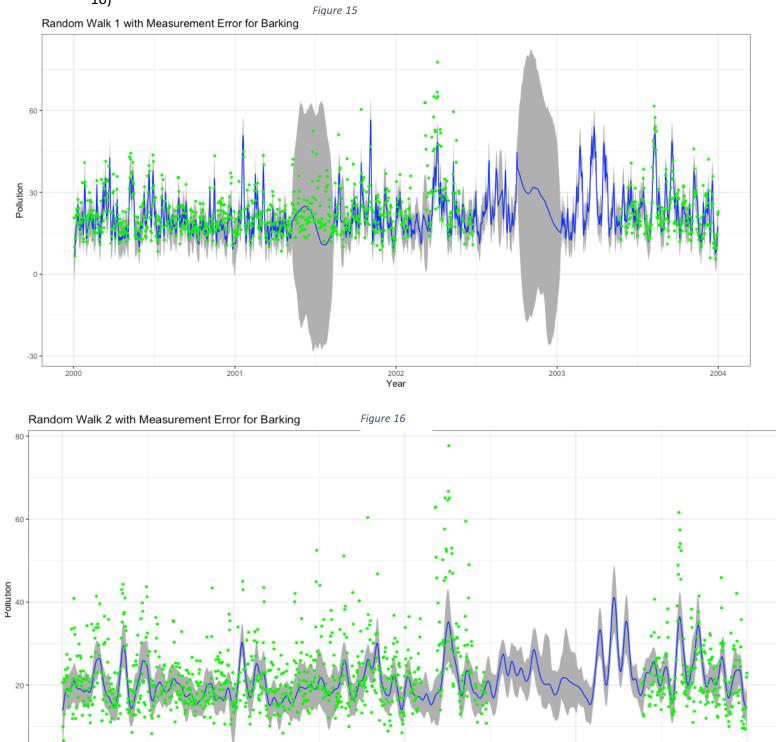


Figure 14



Looking at figures 13 and 14 above, RW2 appears to be closer to 3 of the actual data points than the 3 that RW1 is close to. Yet the mean squared error of RW 1 is 4.25, compared to 7.75 for RW2, suggesting that the RW1 model is better at forecasting. Perhaps more than 7 days are needed to judge if the forecasts are accurate.

10)



Similarly to the Bloomsbury models, the traceplots show that RW1 for Barking has mostly converged, but for RW2 the traceplots don't converge; these patterns are further confirmed when comparing the Gelman diagnostic values between the two models. In terms of model fit, as for Bloomsbury, RW1 fits the data better than RW2.

2002 Year

2001

2003

Figure 17

Bloomsbury Model RW 1, Posterior of tau.w

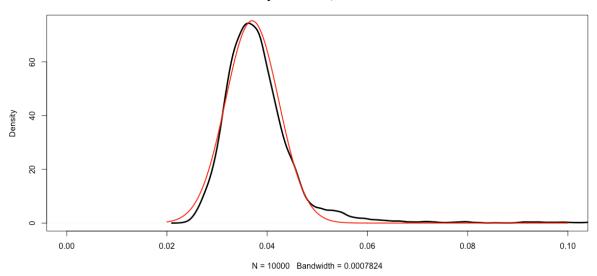


Figure 18

Bloomsbury Model RW 1, Posterior of tau.v

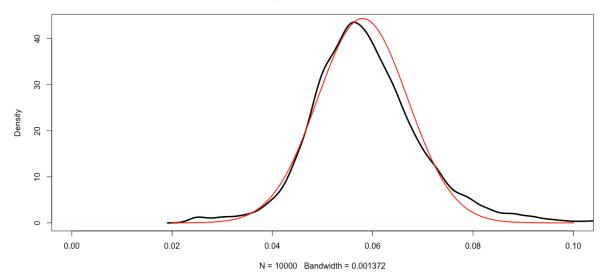
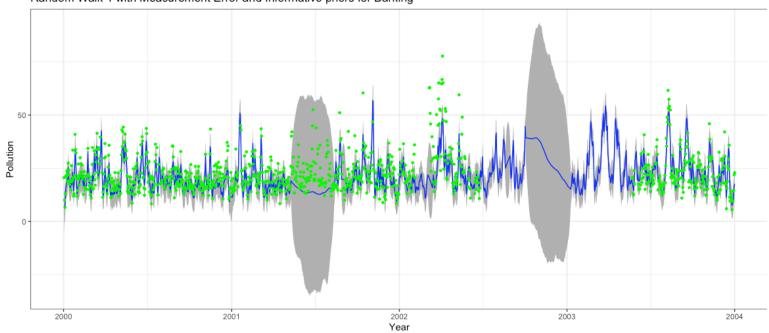


Figure 19





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Figures 17 and 18 show the distributions of tau w and tau v for RW 1, and the red line is adjusting the mean and standard deviations to fit these distributions as closely as possible. Using these distributions and thus informative priors to re run Barking for RW1, is shown in Figure 19. Compared to RW1 with non-informative priors in Figure 15, they both seem to fit the data equally well, but differ more in the missing data trend line, although only slightly, but this also means the credible intervals are slightly different between the two models. In terms of convergence, the RW1 informative priors model's traceplots almost all converge, as they did for the non informative priors RW1 model for Barking. Again, this convergence pattern is indicated by the gelman diagnostic and rhat values in the model summary, which shows that most values are less than 1.1.

Figure 20

Bloomsbury Model RW 2, Posterior of tau.w

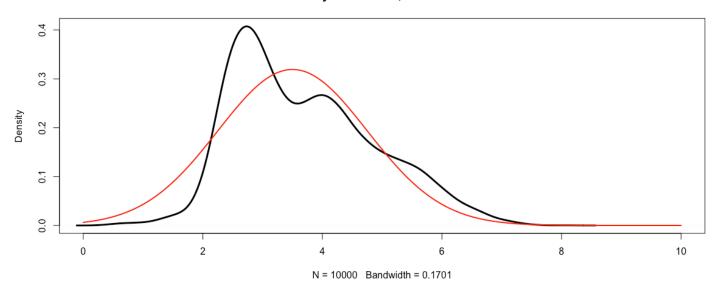


Figure 21

Bloomsbury Model RW 2, Posterior of tau.v

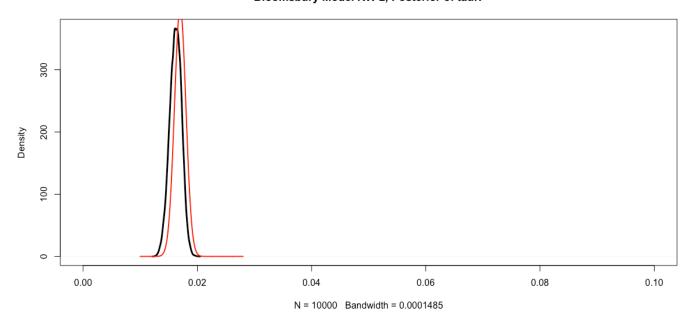
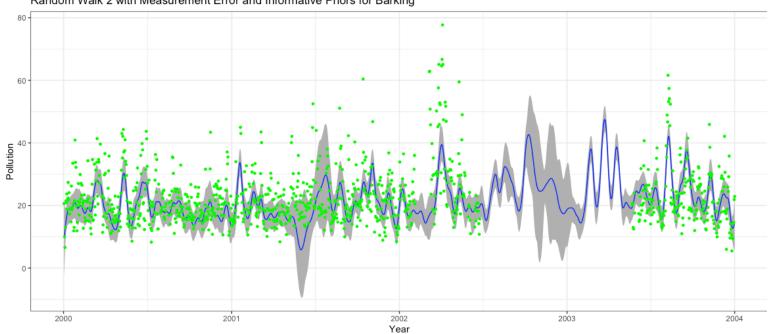


Figure 22

Random Walk 2 with Measurement Error and Informative Priors for Barking



Figures 20 and 21 show the same as Figures 17 and 18, but for RW2. Using informative priors for RW2 results in Figure 22, which also looks fairly similar to the non informative priors RW2 in Figure 16. The periods of missing data differ between the models to a greater extent than they did for RW1, and so the credible intervals are also more different. It could be argued the missing data blue line in Figure 22 is perhaps more expected than that in Figure 16, based on the data points. In terms of convergence, as seen before, the traceplots do not converge, the same as for RW2 non informative priors for Barking and Bloomsbury. And again, this lack of convergence is seen in the gelman diagnostic values and Rhat values in the model summary.

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Code Appendix

```
#Advanced Topics Assignment 2
library(ggplot2)
library(tidyverse)
library(fivethirtyeight)
library(VIM)
library(Amelia)
library(rqdal)
library(coda)
library(rjags)
library(R2jags)
library(coda)
library(dvmisc)
library(kableExtra)
set.seed(1000)
London <- read.csv('London_Pollution.csv')</pre>
summary(London)
#Bloomsbury pollution minimum is 5.5, average of 22.09, maximum of 77.7
#427 NA values
#Barking minimum is 3.8, average of 21.53, maximum of 71.8
#232 NA values
Bloomsbury<- London[,1:2]
summary(Bloomsbury)
y2k <- Bloomsbury[1:366,]
y2001 <- Bloomsbury[367:731,]
y2002 <- Bloomsbury[732:1096,]
y2003 <- Bloomsbury[1097:1461,]
y2004 <- Bloomsbury[1462:1827,]
sum(is.na(y2k$Bloomsbury))
#12 NA values in 2000 in Bloomsbury
sum(is.na(y2001$Bloomsbury))
#12 NA values in 2001
sum(is.na(y2002$Bloomsbury))
#240 NA values in 2002
sum(is.na(y2003$Bloomsbury))
#154 NA values in 2003
sum(is.na(y2004$Bloomsbury))
#9 NA values in 2004
Barking<- London[,2:3]</pre>
summary(Barking)
y2k <- Barking[1:366,]
```

```
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y2001 <- Barking[367:731,]
y2002 <- Barking[732:1096,]
y2003 <- Barking[1097:1461,]
y2004 <- Barking[1462:1827,]
sum(is.na(y2k$Barking))
#3 NA values in 2000
sum(is.na(y2001$Barking))
#104 NA values in 2001
sum(is.na(y2002$Barking))
#113 NA values in 2002
sum(is.na(y2003$Barking))
#11 NA values in 2003
sum(is.na(y2004$Barking))
#1 NA value in 2004
#missingness for both increases from 2000 to peak in 2002, falls in 2003
#and then falls dramatically in 2004
London <- London[,2:3]
matrixplot(London)
spineMiss(London)
missmap(London)
#2
qgplot(Bloomsbury, aes(x = c(1:1827), y = Bloomsbury, col='RED')) +
geom\_line(group=1) + theme\_bw()+scale\_x\_continuous(breaks = c(0, 366, 731,
1096, 1461), labels = c('2000', '2001', '2002', '2003', '2004')) +
 ggtitle("Bloomsbury") +
  annotate('text', x=1096, y=25, label='MISSING DATA', size=7)+
  annotate('text', x=785, y=25, label='MISSING DATA', angle = 90, size=3)+
  labs(y='Pollution', x='Year') +theme(legend.position = 'none')
ggplot() + geom_line(Barking, mapping=aes(x = c(1:1827), y = Barking),
col='purple') + theme_bw()+scale_x_continuous(breaks = c(0, 366, 731,
1096, 1461), labels = c('2000', '2001', '2002', '2003', '2004'))+
ggtitle("Barking") +
  labs(y='Pollution', x='Year') +
  annotate('text', x=550, y=25, label='MISSING DATA', angle=90, size=5)+
  annotate('text', x=1050, y=25, label='MISSING DATA', angle = 90, size=5)+
  theme(legend.position = 'none')
#3
London <- readOGR(dsn = '.', layer = 'London')</pre>
plot(London) #map of London
```

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```
par(mfrow=c(1,1))
points(548030, 183363, col='red', pch=19, cex=2) #Barking is red
points(530123, 182014, col='blue', pch=19, cex=2) #Bloomsbury is blue
#Bloomsbury has more missing values, but higher average pollution, higher
minimum pollution,
#and higher maximum pollution compared to Barking.
#This may be bc Bloomsbury is a tourism heavy area in the West End
#so has more air pollution
#4, 5, 6
#Model 1 corrected
BLOOM <- Bloomsbury[1:1461,]
jags.data <- list(Bloomsbury=BLOOM$Bloomsbury,N=1461)</pre>
jags.param <- c("Bloomsbury", "sigma.w2", "tau.w", "sigma.v2", "tau.v",</pre>
                 "B.pred", "MSErw1")
#'MSErw1'
# Initial values
miss.v <- is.na(jags.data)</pre>
b.init1 <- rep(1, times=1461)
b.init1[miss.v==FALSE] <- NA</pre>
b.init1[miss.v==TRUE] <- 22</pre>
b.init2 <- rep(1, times=1461)
b.init2[miss.v==FALSE] <- NA
b.init2[miss.v==TRUE] <- 20</pre>
B.pred.inits1 = rep(20, 1461)
B.pred.inits2 = rep(20, 1461)
inits1 <- list( "tau.w" = 1, "tau.v" = 1, "Bloomsbury" =</pre>
                   b.init1, "B.pred" = B.pred.inits1)
inits2 <- list( "tau.w" = 1, "tau.v" =
                   1, "Bloomsbury"=b.init2 , "B.pred" = B.pred.inits2)
jags.inits <- list(inits1, inits2)</pre>
potato <- function() {</pre>
  tau.w \sim dgamma(1,0.01)
  sigma.w2 <- 1/tau.w
  tau.v \sim dgamma(1,0.01)
  sigma.v2 <- 1/tau.v</pre>
  B.pred[1] \sim dnorm(0, 1.0E-3)
  for(i in 2:N) {
    Bloomsbury[i] ~ dnorm(B.pred[i],tau.v)
    B.pred[i] ~ dnorm(B.pred[i-1], tau.w)
  MSErw1 <- sqrt(sum((B.pred - Bloomsbury)^2)/N)</pre>
}
```

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```
mod.rw.intercept = jags(jags.data, parameters.to.save = jags.param, inits =
jags.inits,
                         n.chains = 2, model.file = potato, n.burnin = 5000,
n.thin = 1,
                         n.iter = 10000, DIC = TRUE)
#MSE
mod.rw.intercept$BUGSoutput$mean$MSErw1
#MSE of 4.25
traceplot(mod.rw.intercept)
#gelman and check convergence, needs to be saved as df, multivariate=False
mod.rw.interceptmc <- (as.mcmc(mod.rw.intercept))</pre>
gelmanbloomrw1 <- gelman.diag(mod.rw.interceptmc, multivariate = FALSE)</pre>
gelmanbloomrw1 <- as.data.frame(gelmanbloomrw1[["psrf"]])</pre>
kable(gelmanbloomrw1, 'html') %>%
  cat(., file = 'GelmanRW1.html')
#no convergence, as not all values are below 1.1
#plot of model
p <- as.data.frame(mod.rw.intercept$BUGSoutput$summary)</pre>
p <- p[1:1461,]
lower <- p$`2.5%`
upper <- p$\) 97.5%\
h \leftarrow qaplot(mappinq=aes(x=c(1:1461),
y=mod.rw.intercept$BUGSoutput$mean$B.pred))
h + geom_ribbon(aes(ymin = lower, ymax = upper), fill = "grey70") +
  geom_line(mapping=aes(x=c(1:1461),
y=mod.rw.intercept$BUGSoutput$mean$B.pred), colour='blue') +
theme_bw()+scale_x_continuous(breaks = c(0, 366, 731, 1096, 1461), labels
= c('2000', '2001', '2002', '2003', '2004')) +
 labs(y='Pollution', x='Year') +
  geom_point(mapping = aes(x=c(1:1461),
y=BLOOM$Bloomsbury), size=1, colour='green')+
  ggtitle('Random Walk 1 with Measurement Error for Bloomsbury')+
  theme(legend.position = 'none')
```

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```
p <- as.data.frame(mod.rw.intercept$BUGSoutput$summary)</pre>
kable(p, 'html') %>%
  cat(., file = 'SummaryBloomRW1.html')
#plot with first 50 days
p <- as.data.frame(mod.rw.intercept$BUGSoutput$summary)</pre>
p < -p[1:50,]
lower <- p$`2.5%`
upper <- p$\ 97.5%\
j <- as.data.frame(mod.rw.intercept$BUGSoutput$mean$B.pred)</pre>
j <- j[1:50,]
h \leftarrow qqplot(mappinq=aes(x=c(1:50), y=j))
h + geom_ribbon(aes(ymin = lower, ymax = upper), fill = "grey70") +
  geom_line(mapping=aes(x=c(1:50), y=j), colour='blue') +
theme_bw()+scale_x_continuous(breaks = c(0, 31), labels = c('Jan', 'Feb'))
  labs(y='Pollution', x='Year') +
  geom\_point(mapping = aes(x=c(1:50),
y=Bloomsbury$Bloomsbury[1:50]), size=1, colour='green')+
  ggtitle('Random Walk 1 with Measurement Error over first 50 days for
Bloomsbury')+
  theme(legend.position = 'none')
#7
#correct model 2
BLOOM <- Bloomsbury[1:1461,]
jags.data <- list(Bloomsbury=BLOOM$Bloomsbury,N=1461)</pre>
jags.param <- c("Bloomsbury", "sigma.w2", "tau.w", "sigma.v2", "tau.v",</pre>
                 "B.pred", 'MSErw1')
# Initial values
miss.v <- is.na(jags.data)</pre>
b.init1 <- rep(1, times=1461)
b.init1[miss.v==FALSE] <- NA</pre>
b.init1[miss.v==TRUE] <- 22</pre>
b.init2 <- rep(1, times=1461)
b.init2[miss.v==FALSE] <- NA
b.init2[miss.v==TRUE] <- 20
B.pred.inits1 = rep(20, 1461)
B.pred.inits2 = rep(20, 1461)
inits1 <- list( "tau.w" = 1, "tau.v" = 1, "Bloomsbury" =</pre>
                   b.init1, "B.pred" = B.pred.inits1)
inits2 <- list( "tau.w" = 1, "tau.v" =</pre>
```

```
Candidate Number: 124070
```

```
1, "Bloomsbury"=b.init2 , "B.pred" = B.pred.inits2)
jags.inits <- list(inits1, inits2)</pre>
potato3<-function() {</pre>
  B.pred[1] \sim dnorm(0, 1.0E-3)
  B.pred[2] \sim dnorm(0, 1.0E-3)
  for (i in 3 : N){
    Bloomsbury[i] ~ dnorm(B.pred[i],tau.v)
    B.pred[i] ~ dnorm(2 * B.pred[i-1] - B.pred[i-2],
                       tau.w)
  }
  MSErw1 <- sqrt(sum((B.pred - Bloomsbury)^2)/N)</pre>
  # priors
  tau.w \sim dgamma(1,0.01)
  sigma.w2 <- 1/tau.w</pre>
  tau.v \sim dgamma(1,0.01)
  sigma.v2 <- 1/tau.v</pre>
}
mod.rw.intercept = jags(jags.data, parameters.to.save = jags.param, inits =
jags.inits,
                         n.chains = 2, model.file = potato3, n.burnin =
5000, n.thin = 1,
                         n.iter = 10000, DIC = TRUE)
traceplot(mod.rw.intercept)
mod.rw.intercept$BUGSoutput$mean$MSErw1
#MSE is 7.75.
#gelman and check convergence, needs to be saved as df, multivariate=False
mod.rw.interceptmc <- (as.mcmc(mod.rw.intercept))</pre>
gelmanbloomrw2 <- gelman.diag(mod.rw.interceptmc, multivariate = FALSE)</pre>
gelmanbloomrw2 <- as.data.frame(gelmanbloomrw2[["psrf"]])</pre>
kable(gelmanbloomrw2, 'html') %>%
  cat(., file = 'GelmanRW2.html')
#model does not converge
#plot of model
p <- as.data.frame(mod.rw.intercept$BUGSoutput$summary)</pre>
```

```
p \leftarrow p[1:1461,]
lower <- p$`2.5%`
upper <- p$`97.5%`
h \leftarrow qqplot(mapping=aes(x=c(1:1461),
y=mod.rw.intercept$BUGSoutput$mean$B.pred))
h + geom_ribbon(aes(ymin = lower, ymax = upper), fill = "grey70") +
  geom_line(mapping=aes(x=c(1:1461),
y=mod.rw.intercept$BUGSoutput$mean$B.pred), colour='blue') +
theme_bw()+scale_x_continuous(breaks = c(0, 366, 731, 1096, 1461), labels
= c('2000', '2001', '2002', '2003', '2004')) +
 labs(y='Pollution', x='Year') +
  geom\_point(mapping = aes(x=c(1:1461),
y=BLOOM$Bloomsbury), size=1, colour='green')+
  agtitle('Random Walk 2 with Measurement Error for Bloomsbury')+
  theme(legend.position = 'none')
p <- as.data.frame(mod.rw.intercept$BUGSoutput$summary)</pre>
kable(p, 'html') %>%
  cat(., file = 'SummaryBloomRW2.html')
#plot with first 50 days
p <- as.data.frame(mod.rw.intercept$BUGSoutput$summary)</pre>
p \leftarrow p[1:50,]
lower <- p$\cdot 2.5%\cdot
upper <- p$`97.5%`
j <- as.data.frame(mod.rw.intercept$BUGSoutput$mean$B.pred)</pre>
j < -j[1:50,]
h \leftarrow qaplot(mapping=aes(x=c(1:50), y=j))
h + geom_ribbon(aes(ymin = lower, ymax = upper), fill = "grey70") +
  geom_line(mapping=aes(x=c(1:50), y=j), colour='blue') +
theme_bw()+scale_x_continuous(breaks = c(0, 31), labels = c('Jan', 'Feb'))
  labs(y='Pollution', x='Year') +
  geom\_point(mapping = aes(x=c(1:50),
y=Bloomsbury$Bloomsbury[1:50]), size=1, colour='green')+
  ggtitle('Random Walk 2 with Measurement Error over first 50 days for
Bloomsbury')+
  theme(legend.position = 'none')
#first 50 days of each model shows that rw 2 has a much larger smoothing
```

```
effect than rw1
#8, model predictions
#RW 1 prediction, need to double check this
BLOOM <- Bloomsbury[1:1461,]</pre>
NA), N = (1461 + 7))
jags.param <- c("Bloomsbury", "sigma.w2", "tau.w", "sigma.v2", "tau.v",</pre>
                "B.pred")
# Initial values
miss.v <- is.na(jags.data)</pre>
b.init1 <- rep(1, times=1468)
b.init1[miss.v==FALSE] <- NA</pre>
b.init1[miss.v==TRUE] <- 22</pre>
b.init2 <- rep(1,times=1468)
b.init2[miss.v==FALSE] <- NA</pre>
b.init2[miss.v==TRUE] <- 20</pre>
B.pred.inits1 = rep(20, 1468)
B.pred.inits2 = rep(20, 1468)
inits1 <- list( "tau.w" = 1, "tau.v" = 1, "Bloomsbury" =</pre>
                  b.init1, "B.pred" = B.pred.inits1)
inits2 <- list( "tau.w" = 1, "tau.v" =</pre>
                   1, "Bloomsbury"=b.init2 , "B.pred" = B.pred.inits2)
jags.inits <- list(inits1, inits2)</pre>
potato <- function() {</pre>
  tau.w \sim dgamma(1,0.01)
  sigma.w2 <- 1/tau.w
  tau.v \sim dgamma(1,0.01)
  sigma.v2 <- 1/tau.v
  B.pred[1] \sim dnorm(0, 1.0E-3)
  for(i in 2:N) {
    Bloomsbury[i] ~ dnorm(B.pred[i],tau.v)
    B.pred[i] ~ dnorm(B.pred[i-1], tau.w)
  }
jags.param <- c("Bloomsbury", "sigma.w2", "tau.w", "sigma.v2", "tau.v",</pre>
                "B.pred")
mod_ss_forecast = jags(jags.data, parameters.to.save = jags.param, inits =
jags.inits,
                        model.file = potato, n.chains = 2, n.burnin = 5000,
n.thin = 1,
                        n.iter = 10000, DIC = TRUE)
oh <- as.data.frame(mod_ss_forecast$BUGSoutput$mean$B.pred)</pre>
```

```
#Predicted against actual
#RW1
h \leftarrow qqplot(mapping=aes(x=c(1462:1468),
y=oh$`mod_ss_forecast$BUGSoutput$mean$B.pred`))
h + geom_line(mapping=aes(x=c(1462:1468),
y=oh$`mod_ss_forecast$BUGSoutput$mean$B.pred`[1462:1468]), colour='blue')
+ theme_bw()+scale_x_continuous(breaks = c(1462, 1463, 1464, 1465, 1466,
1467, 1468), labels = c("01/01", "02/01", "03/01", "04/01", "05/01",
"06/01", "07/01")) +
 labs(y='Pollution', x='First week of 2004') +
  geom_point(mapping = aes(x=c(1462:1468),
y=Bloomsbury$Bloomsbury[1462:1468]), size=1, colour='green')+
  ggtitle('Random Walk 1 with Predicted Values against actual values for
First Week of 2004 for Bloomsbury')+
 theme(legend.position = 'none')
 #RW 2 Prediction
BLOOM <- Bloomsbury[1:1461,]
jags.data <- list(Bloomsbury=c(BLOOM$Bloomsbury, NA, NA, NA, NA, NA, NA,</pre>
NA), N = (1461 + 7))
jags.param <- c("Bloomsbury", "sigma.w2", "tau.w", "sigma.v2", "tau.v",</pre>
                 "B.pred")
# Initial values
miss.v <- is.na(jags.data)</pre>
b.init1 <- rep(1,times=1468)
b.init1[miss.v==FALSE] <- NA</pre>
b.init1[miss.v==TRUE] <- 22
b.init2 <- rep(1,times=1468)
b.init2[miss.v==FALSE] <- NA</pre>
b.init2[miss.v==TRUE] <- 20</pre>
B.pred.inits1 = rep(20, 1468)
B.pred.inits2 = rep(20, 1468)
inits1 <- list( "tau.w" = 1, "tau.v" = 1, "Bloomsbury" =</pre>
                   b.init1, "B.pred" = B.pred.inits1)
inits2 <- list( "tau.w" = 1, "tau.v" =
                   1, "Bloomsbury"=b.init2 , "B.pred" = B.pred.inits2)
jags.inits <- list(inits1, inits2)</pre>
potato3<-function() {</pre>
  B.pred[1] \sim dnorm(0, 1.0E-3)
  B.pred[2] \sim dnorm(0, 1.0E-3)
  for (i in 3 : N){
    Bloomsbury[i] ~ dnorm(B.pred[i],tau.v)
    B.pred[i] \sim dnorm(2 * B.pred[i-1] - B.pred[i-2],
```

```
tau.w)
  }
  # priors
  tau.w \sim dgamma(1,0.01)
  sigma.w2 <- 1/tau.w</pre>
  tau.v \sim dgamma(1,0.01)
  sigma.v2 <- 1/tau.v
}
 mod_ss_forecast = jags(jags.data, parameters.to.save = jags.param, inits =
jags.inits,
                         model.file = potato3, n.chains = 2, n.burnin =
5000, n.thin = 1,
                         n.iter = 10000, DIC = TRUE)
 oh <- as.data.frame(mod_ss_forecast$BUGSoutput$mean$B.pred)</pre>
#Predicted against actual
#RW2
 h \leftarrow qqplot(mapping=aes(x=c(1462:1468),
y=oh$`mod_ss_forecast$BUGSoutput$mean$B.pred`))
 h + geom\_line(mapping=aes(x=c(1462:1468),
y=oh\`mod_ss_forecast\BUGSoutput\mean\B.pred`[1462:1468]), colour='blue')
+ theme_bw()+scale_x_continuous(breaks = c(1462, 1463, 1464, 1465, 1466,
1467, 1468), labels = c("01/01", "02/01", "03/01", "04/01", "05/01",
"06/01", "07/01")) +
   labs(y='Pollution', x='First week of 2004') +
   geom\_point(mapping = aes(x=c(1462:1468),
y=Bloomsbury$Bloomsbury[1462:1468]), size=1, colour='green')+
   ggtitle('Random Walk 2 with Predicted Values against actual values for
First Week of 2004 for Bloomsbury')+
   theme(legend.position = 'none')
#9
#MSE
# Model one has MSE of 4.25
# Model 2 has MSE of 7.75
#Model 1 must be better at forecasting due to lower MSE
#But model 2 seems to have better predictions
#10
```

```
#Repeating RW1 and RW2 but with Barking
 #RW 1
 BARK <- Barking[1:1461,]
 jags.data <- list(Barking=BARK$Barking,N=1461)</pre>
 jags.param <- c("Barking","sigma.w2","tau.w","sigma.v2","tau.v",</pre>
                  "B.pred")
 miss.v <- is.na(jags.data)</pre>
 b.init1 <- rep(1, times=1461)
 b.init1[miss.v==FALSE] <- NA
 b.init1[miss.v==TRUE] <- 22</pre>
 b.init2 <- rep(1, times=1461)
 b.init2[miss.v==FALSE] <- NA
 b.init2[miss.v==TRUE] <- 20</pre>
 B.pred.inits1 = rep(20, 1461)
 B.pred.inits2 = rep(20, 1461)
 inits1 <- list( "tau.w" = 1, "tau.v" = 1, "Barking" =</pre>
                    b.init1, "B.pred" = B.pred.inits1)
 inits2 <- list( "tau.w" = 1, "tau.v" =</pre>
                    1, "Barking"=b.init2, "B.pred" = B.pred.inits2)
 jags.inits <- list(inits1, inits2)</pre>
 potato <- function() {</pre>
   tau.w \sim dgamma(1,0.01)
   sigma.w2 <- 1/tau.w
   tau.v \sim dgamma(1,0.01)
   sigma.v2 <- 1/tau.v
   B.pred[1] \sim dnorm(0, 1.0E-3)
   for(i in 2:N) {
     Barking[i] ~ dnorm(B.pred[i],tau.v)
     B.pred[i] ~ dnorm(B.pred[i-1], tau.w)
   }
 }
 mod.rw.intercept = jags(jags.data, parameters.to.save = jags.param, inits
= jags.inits,
                           n.chains = 2, model.file = potato, n.burnin =
5000, n.thin = 1,
                          n.iter = 10000, DIC = TRUE)
 traceplot(mod.rw.intercept)
 #gelman and check convergence, needs to be saved as df, multivariate=False
mod.rw.interceptmc <- as.mcmc(mod.rw.intercept)</pre>
gelmanbarkrw1 <- gelman.diag(mod.rw.interceptmc, multivariate = FALSE)</pre>
```

```
gelmanbarkrw1 <- as.data.frame(gelmanbarkrw1['psrf'])</pre>
kable(gelmanbarkrw1, 'html') %>%
  cat(., file = 'GelmanBarkRW1.html')
#model does not converge
 #plot of model
 p <- as.data.frame(mod.rw.intercept$BUGSoutput$summary)</pre>
 p < -p[1:1461,]
 lower <- p$\cdot2.5%\cdot
 upper <- p$`97.5%`
 h <- ggplot(mapping=aes(x=c(1:1461),
y=mod.rw.intercept$BUGSoutput$mean$B.pred))
 h + geom_ribbon(aes(ymin = lower, ymax = upper), fill = "arey70") +
   geom_line(mapping=aes(x=c(1:1461),
y=mod.rw.intercept$BUGSoutput$mean$B.pred), colour='blue') +
theme_bw()+scale_x_continuous(breaks = c(0, 366, 731, 1096, 1461), labels
= c('2000', '2001', '2002', '2003', '2004')) +
   labs(y='Pollution', x='Year') +
   geom\_point(mapping = aes(x=c(1:1461),
y=BLOOM$Bloomsbury), size=1, colour='green')+
   ggtitle('Random Walk 1 with Measurement Error for Barking')+
   theme(legend.position = 'none')
 p <- as.data.frame(mod.rw.intercept$BUGSoutput$summary)</pre>
 kable(p, 'html') %>%
   cat(., file = 'SummaryBarkRW1.html')
 #RW 2
 BARK <- Barking[1:1461,]
 jags.data <- list(Barking=BARK$Barking,N=1461)</pre>
 jags.param <- c("Barking","sigma.w2","tau.w","sigma.v2","tau.v",</pre>
                  "B.pred")
 miss.v <- is.na(jags.data)
 b.init1 <- rep(1, times=1461)
 b.init1[miss.v==FALSE] <- NA</pre>
 b.init1[miss.v==TRUE] <- 22
 b.init2 <- rep(1,times=1461)
 b.init2[miss.v==FALSE] <- NA</pre>
 b.init2[miss.v==TRUE] <- 20</pre>
```

```
B.pred.inits1 = rep(20, 1461)
 B.pred.inits2 = rep(20, 1461)
 inits1 <- list( "tau.w" = 1, "tau.v" = 1, "Barking" =</pre>
                    b.init1, "B.pred" = B.pred.inits1)
 inits2 <- list( "tau.w" = 1, "tau.v" =</pre>
                    1, "Barking"=b.init2, "B.pred" = B.pred.inits2)
 jags.inits <- list(inits1, inits2)</pre>
 potato3<-function() {</pre>
   B.pred[1] \sim dnorm(0, 1.0E-3)
   B.pred[2] \sim dnorm(0, 1.0E-3)
   for (i in 3 : N){
     Barking[i] ~ dnorm(B.pred[i],tau.v)
     B.pred[i] \sim dnorm(2 * B.pred[i-1] - B.pred[i-2],
                        tau.w)
   }
   # priors
   tau.w \sim dgamma(1,0.01)
   sigma.w2 <- 1/tau.w</pre>
   tau.v \sim dgamma(1,0.01)
   siama.v2 <- 1/tau.v
 }
 mod.rw.intercept = jags(jags.data, parameters.to.save = jags.param, inits
= jags.inits,
                           n.chains = 2, model.file = potato3, n.burnin =
5000, n.thin = 1,
                           n.iter = 10000, DIC = TRUE)
 traceplot(mod.rw.intercept)
 #gelman and check convergence, needs to be saved as df, multivariate=False
mod.rw.interceptmc <- as.mcmc(mod.rw.intercept)</pre>
gelmanbarkrw2 <- gelman.diag(mod.rw.interceptmc, multivariate = FALSE)</pre>
gelmanbarkrw2 <- as.data.frame(gelmanbarkrw2['psrf'])</pre>
kable(gelmanbarkrw2, 'html') %>%
  cat(., file = 'GelmanBarkRW2.html')
#model also does not converge...
 #plot of model
 p <- as.data.frame(mod.rw.intercept$BUGSoutput$summary)</pre>
 p \leftarrow p[1:1461,]
```

```
lower <- p$\\ 2.5\%\\\
 upper <- p$`97.5%`
 h \leftarrow ggplot(mapping=aes(x=c(1:1461).
y=mod.rw.intercept$BUGSoutput$mean$B.pred))
 h + geom_ribbon(aes(ymin = lower, ymax = upper), fill = "grey70") +
   qeom_line(mapping=aes(x=c(1:1461),
y=mod.rw.intercept$BUGSoutput$mean$B.pred), colour='blue') +
theme_bw()+scale_x_continuous(breaks = c(0, 366, 731, 1096, 1461), labels
= c('2000', '2001', '2002', '2003', '2004')) +
   labs(y='Pollution', x='Year') +
   qeom_point(mapping = aes(x=c(1:1461),
y=BLOOM$Bloomsbury), size=1, colour='green')+
   ggtitle('Random Walk 2 with Measurement Error for Barking')+
   theme(legend.position = 'none')
 p <- as.data.frame(mod.rw.intercept$BUGSoutput$summary)</pre>
 kable(p, 'html') %>%
   cat(., file = 'SummaryBarkRW2.html')
#11
#Finding distributions that fit these density plots
 #RW1
 plot(density(mod.rw.intercept[["BUGSoutput"]][["sims.list"]][["tau.w"]]),
      main = "Bloomsbury Model RW 1, Posterior of tau.w", lwd = 3, xlim =
c(0, 0.1)
 x \leftarrow seq(0.02, 0.10, length = 1000)
 y \leftarrow dnorm(x, mean = 0.0370, sd = 0.0053)
 lines(x, y, type = "l", lwd = 2, col = "red")
 plot(density(mod.rw.intercept[["BUGSoutput"]][["sims.list"]][["tau.v"]]),
      main = "Bloomsbury Model RW 1, Posterior of tau.v", lwd = 3, xlim =
c(0, 0.10)
 x \leftarrow seq(0.02, 0.10, length = 1000)
 y \leftarrow dnorm(x, mean = 0.058, sd = 0.009)
 lines(x, y, type = "l", lwd = 2, col = "red")
 #RW2
 plot(density(mod.rw.intercept[["BUGSoutput"]][["sims.list"]][["tau.w"]]),
      main = "Bloomsbury Model RW 2, Posterior of tau.w", lwd = 3, xlim =
c(0, 0.1)
```

```
x < - seq(0, 1, length = 1000)
y \leftarrow dnorm(x, mean = 3.5, sd = 1.25)
lines(x, y, type = "l", lwd = 2, col = "red")
 plot(density(mod.rw.intercept[["BUGSoutput"]][["sims.list"]][["tau.v"]]),
      main = "Bloomsbury Model RW 2, Posterior of tau.v", lwd = 3, xlim =
c(0, 0.10)
x \leftarrow seq(0.01, 0.028, length = 1000)
y \leftarrow dnorm(x, mean = 0.017, sd = 0.001)
lines(x, y, type = "l", lwd = 2, col = "red")
#using these distributions as priors in new models for Barking
#RW 1
BARK <- Barking[1:1461,]
 jags.data <- list(Barking=BARK$Barking,N=1461)</pre>
 jags.param <- c("Barking","sigma.w2","tau.w","sigma.v2","tau.v",</pre>
                  "B.pred")
miss.v <- is.na(jaas.data)
b.init1 <- rep(1, times=1461)
b.init1[miss.v==FALSE] <- NA
b.init1[miss.v==TRUE] <- 22
b.init2 <- rep(1, times=1461)
b.init2[miss.v==FALSE] <- NA</pre>
b.init2[miss.v==TRUE] <- 20</pre>
 B.pred.inits1 = rep(20, 1461)
 B.pred.inits2 = rep(20, 1461)
 inits1 <- list( "tau.w" = 1, "tau.v" = 1, "Barking" =</pre>
                    b.init1, "B.pred" = B.pred.inits1)
 inits2 <- list( "tau.w" = 1, "tau.v" =
                    1, "Barking"=b.init2 , "B.pred" = B.pred.inits2)
 jags.inits <- list(inits1, inits2)</pre>
potato <- function() {</pre>
  tau.w \sim dnorm(0.0370, 0.0053)
   sigma.w2 <- 1/tau.w
   tau.v \sim dnorm(0.058, 0.009)
   siama.v2 <- 1/tau.v
   B.pred[1] \sim dnorm(0, 1.0E-3)
  for(i in 2:N) {
     Barking[i] ~ dnorm(B.pred[i],tau.v)
     B.pred[i] ~ dnorm(B.pred[i-1], tau.w)
   }
 }
mod.rw.intercept = jags(jags.data, parameters.to.save = jags.param, inits
= jags.inits,
```

```
n.chains = 2, model.file = potato, n.burnin =
5000, n.thin = 1,
                          n.iter = 10000, DIC = TRUE)
p <- as.data.frame(mod.rw.intercept$BUGSoutput$summary)</pre>
p <- p[1:1461,]
lower <- p$\\ 2.5\%\\\
upper <- p$`97.5%`
h \leftarrow applot(mapping=aes(x=c(1:1461),
y=mod.rw.intercept$BUGSoutput$mean$B.pred))
h + geom_ribbon(aes(ymin = lower, ymax = upper), fill = "grey70") +
   geom\_line(mapping=aes(x=c(1:1461),
y=mod.rw.intercept$BUGSoutput$mean$B.pred), colour='blue') +
theme_bw()+scale_x_continuous(breaks = c(0, 366, 731, 1096, 1461), labels
= c('2000', '2001', '2002', '2003', '2004')) +
   labs(y='Pollution', x='Year') +
   qeom_point(mapping = aes(x=c(1:1461),
y=BLOOM$Bloomsbury), size=1, colour='green')+
   ggtitle('Random Walk 1 with Measurement Error and Informative priors for
Barking')+
   theme(legend.position = 'none')
p <- as.data.frame(mod.rw.intercept$BUGSoutput$summary)</pre>
 kable(p, 'html') %>%
   cat(., file = 'infSummaryBarkRW1.html')
 traceplot(mod.rw.intercept)
 #gelman and check convergence, needs to be saved as df, multivariate=False
mod.rw.interceptmc <- as.mcmc(mod.rw.intercept)</pre>
 infgelmanbarkrw1 <- gelman.diag(mod.rw.interceptmc, multivariate = FALSE)</pre>
 infgelmanbarkrw1 <- as.data.frame(infgelmanbarkrw1['psrf'])</pre>
 kable(infgelmanbarkrw1, 'html') %>%
   cat(., file = 'infGelmanBarkRW1.html')
#RW 2
BARK <- Barking[1:1461,]
 jags.data <- list(Barking=BARK$Barking,N=1461)</pre>
 jags.param <- c("Barking","sigma.w2","tau.w","sigma.v2","tau.v",</pre>
                  "B.pred")
```

```
miss.v <- is.na(jags.data)</pre>
b.init1 <- rep(1, times=1461)
b.init1[miss.v==FALSE] <- NA</pre>
b.init1[miss.v==TRUE] <- 22</pre>
b.init2 \leftarrow rep(1,times=1461)
b.init2[miss.v==FALSE] <- NA</pre>
b.init2[miss.v==TRUE] <- 20
B.pred.inits1 = rep(20, 1461)
B.pred.inits2 = rep(20, 1461)
inits1 <- list( "tau.w" = 1, "tau.v" = 1, "Barking" =</pre>
                    b.init1, "B.pred" = B.pred.inits1)
inits2 <- list( "tau.w" = 1, "tau.v" =
                    1, "Barking"=b.init2, "B.pred" = B.pred.inits2)
jags.inits <- list(inits1, inits2)</pre>
potato3<-function() {</pre>
  B.pred[1] \sim dnorm(0, 1.0E-3)
  B.pred[2] \sim dnorm(0, 1.0E-3)
  for (i in 3 : N){
    Barking[i] ~ dnorm(B.pred[i],tau.v)
    B.pred[i] \sim dnorm(2 * B.pred[i-1] - B.pred[i-2],
                        tau.w)
  }
  # priors
  tau.w \sim dnorm(3.5, 1.25)
  sigma.w2 <- 1/tau.w
  tau.v \sim dnorm(0.017, 0.001)
  sigma.v2 <- 1/tau.v
}
mod.rw.intercept = jags(jags.data, parameters.to.save = jags.param, inits
= jags.inits,
                          n.chains = 2, model.file = potato3, n.burnin =
5000, n.thin = 1,
                          n.iter = 10000, DIC = TRUE)
p <- as.data.frame(mod.rw.intercept$BUGSoutput$summary)</pre>
p \leftarrow p[1:1461,]
lower <- p^2.5\%
upper <- p$^97.5%
h <- ggplot(mapping=aes(x=c(1:1461),
y=mod.rw.intercept$BUGSoutput$mean$B.pred))
h + geom_ribbon(aes(ymin = lower, ymax = upper), fill = "grey70") +
geom_line(mapping=aes(x=c(1:1461),
```

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```
y=mod.rw.intercept$BUGSoutput$mean$B.pred), colour='blue') +
theme_bw()+scale_x_continuous(breaks = c(0, 366, 731, 1096, 1461), labels
= c('2000', '2001', '2002', '2003', '2004')) +
  labs(y='Pollution', x='Year') +
  qeom_point(mapping = aes(x=c(1:1461),
y=BLOOM$Bloomsbury), size=1, colour='green')+
  ggtitle('Random Walk 2 with Measurement Error and Informative Priors for
Barking')+
  theme(legend.position = 'none')
p <- as.data.frame(mod.rw.intercept$BUGSoutput$summary)</pre>
kable(p, 'html') %>%
  cat(., file = 'infSummaryBarkRW2.html')
traceplot(mod.rw.intercept)
#gelman and check convergence, needs to be saved as df, multivariate=False
mod.rw.interceptmc <- as.mcmc(mod.rw.intercept)</pre>
infgelmanbarkrw2 <- gelman.diag(mod.rw.interceptmc, multivariate = FALSE)</pre>
infgelmanbarkrw2 <- as.data.frame(infgelmanbarkrw2['psrf'])</pre>
kable(infgelmanbarkrw2, 'html') %>%
  cat(., file = 'infgelmanBarkRW2.html')
```