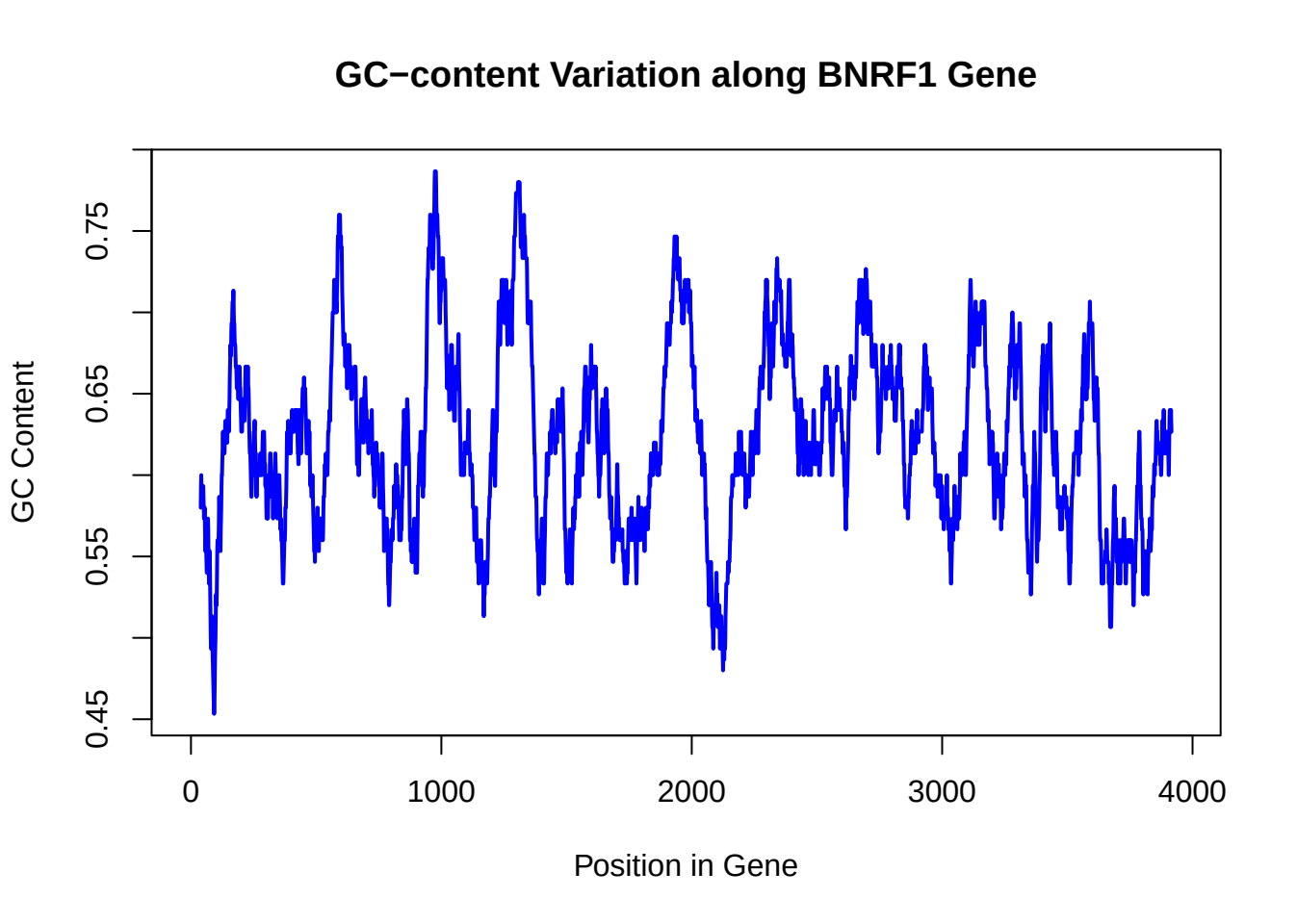
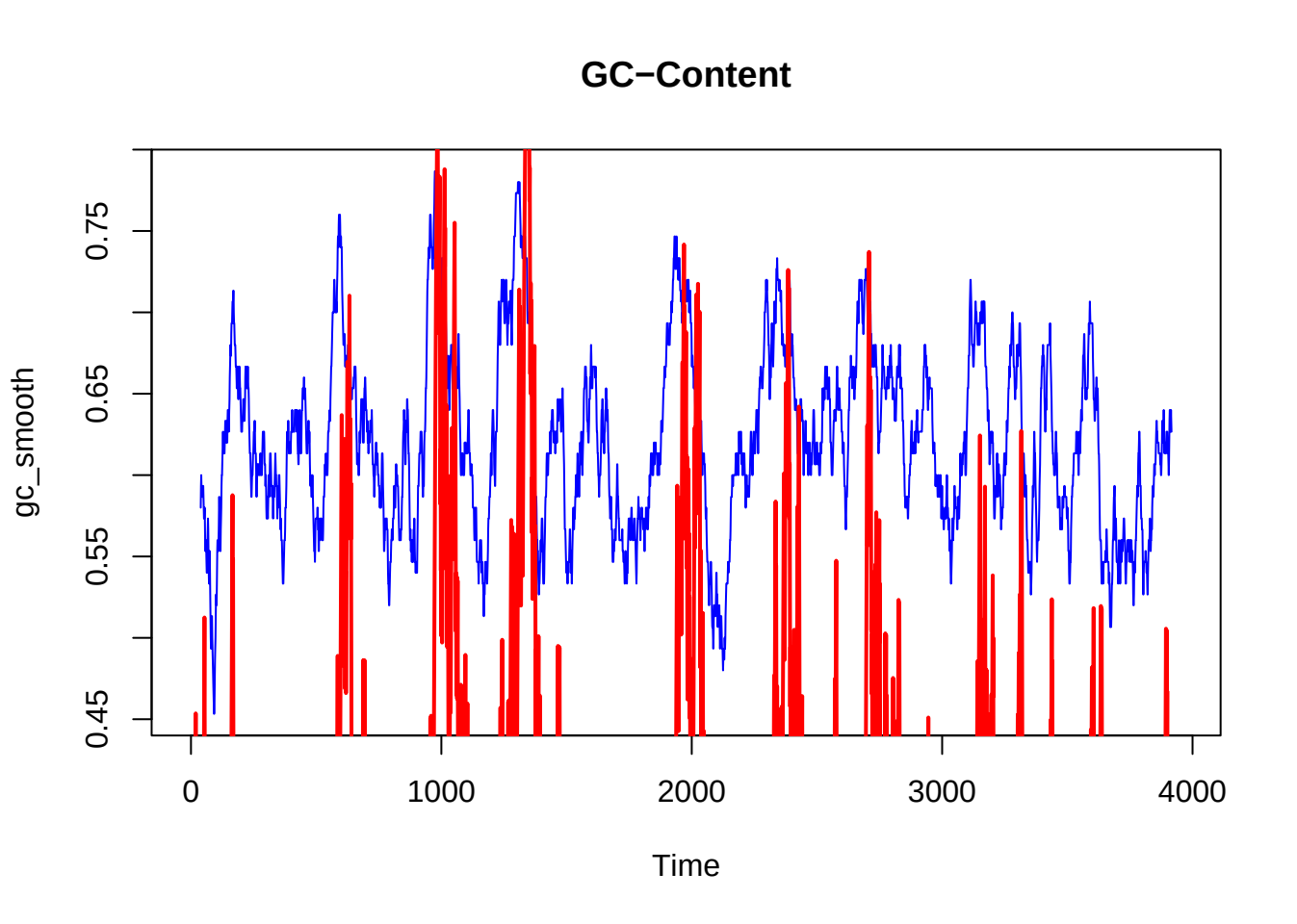
```
library(astsa)
dna = bnrf1ebv # the BNRF1 gene of EBV
head(dna)
gcTF = (dna==2)|(dna==3)
gc = gcTF*1
head(gc)
length(gc)
mean(gc)

# Apply a moving average filter (window size = 100)
window_size = 75
gc_smooth = filter(gc, c(1/(2*window_size), rep(1/window_size, window_size), 1/(2*window_size)), sides=2)

# Plot the GC-content variation along the gene
plot(gc_smooth, type='l', col='blue', lwd=2, xlab="Position",
    ylab="GC", main="GC Variation")



# Define transition matrix based on expected segment lengths
P = matrix(c(0.995, 0.005,  # Typical -> GC-rich
             0.01,  0.99),  # GC-rich -> Typical
           ncol=2, byrow=TRUE)

# Define emission probabilities (Bernoulli model)
hmmFilter = function(P, l)
  function(f, y) {
    fNew = (f %*% P) * l(y)
    fNew / sum(fNew)
  }

advance = hmmFilter(
  P,
  function(y) c(dbinom(y, 1, 0.6), dbinom(y, 1, 0.7))  # Bernoulli emissions
)

# Forward filtering
fpList = Reduce(advance, gc, c(0.5, 0.5), acc=TRUE)
fpMat = sapply(fpList, cbind)
```

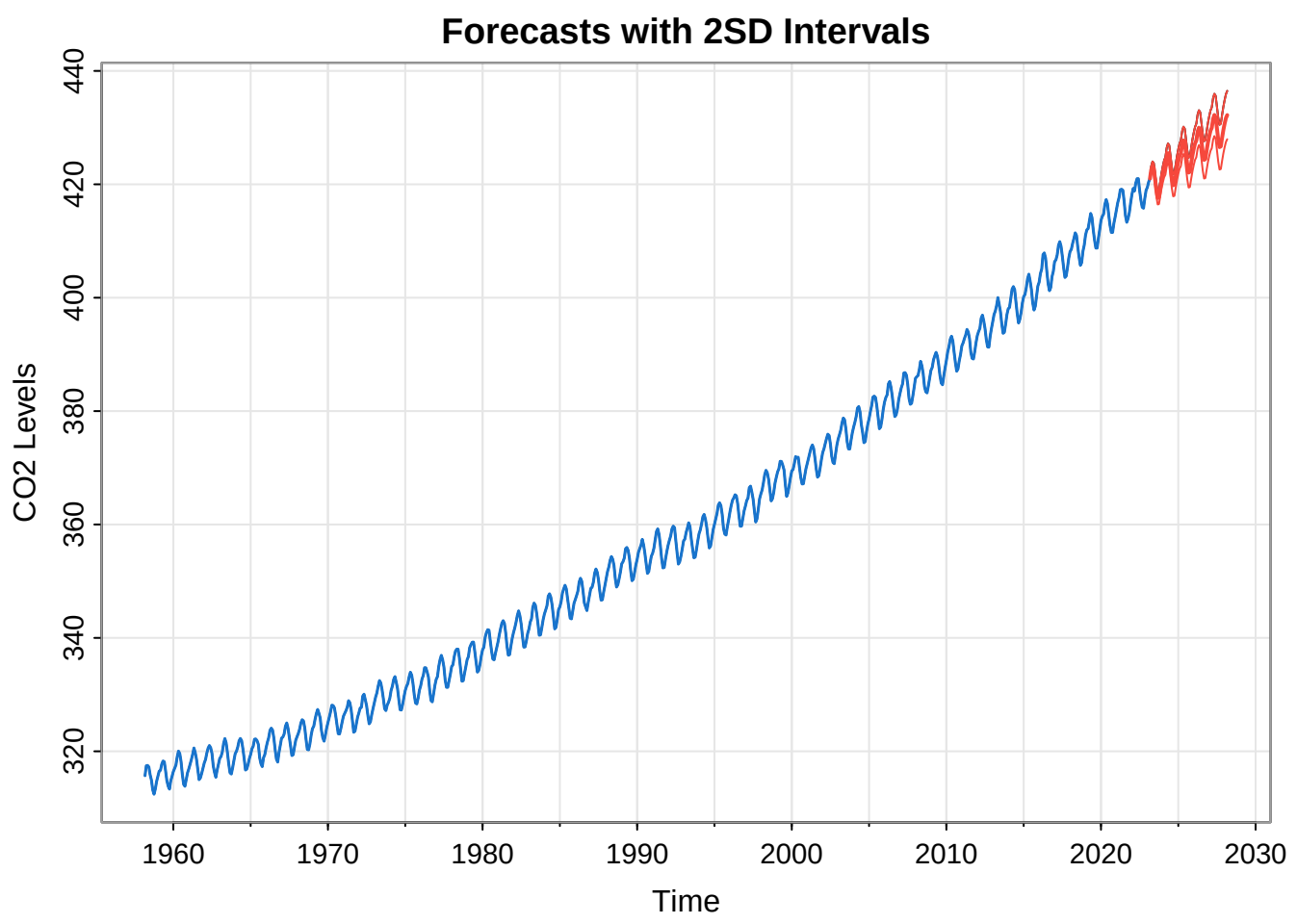
```
fp2Ts = ts(fpMat[2, -1], start=start(gc), freq=frequency(gc))

# Plot GC-content with filtered probabilities
plot(gc_smooth, type='l', col='blue', main="GC-Content")
lines(fp2Ts, col='red', lwd=2)
abline(h=mean(gc), col="black", lty=2)



hmmSmoother = function(P)
  function(fp, sp) {
    fp * ((sp / (fp %*% P)) %*% t(P))
  }

backStep = hmmSmoother(P)

spList = Reduce(backStep, fpList, right=TRUE, acc=TRUE)
spMat = sapply(spList, cbind)
sp2Ts = ts(spMat[2, -1], start=start(gc), freq=frequency(gc))

# Plot GC-content with smoothed probabilities
plot(gc_smooth, type='l', col='blue', main="GC-Content with HMM Smoothed Probability")
lines(sp2Ts, col='red', lwd=2)
abline(h=mean(gc), col="black", lty=2)

tsplot(cardox, col=4, lwd=1.5,
       main="Monthly carbon dioxide levels")
library(dlm)



buildMod <- function(lwv) {

  # Observation variance
  V <- exp(lwv[1])

  # System variances
  W_level <- exp(lwv[2])
  W_slope <- exp(lwv[3])
  W_seasonal <- exp(lwv[4])
```

```
  # Locally linear trend components
  trend <- dlmModPoly(order = 2, dV = V, dW = c(W_level, W_slope))

  # Monthly seasonal component (12 months)
  seasonal <- dlmModSeas(frequency = 12, dV = 0, dW = c(W_seasonal, rep(0, 10)))

  # Combine the components
  mod <- trend + seasonal
  return(mod)
}



# Initial parameter guesses (log-transformed variances)
init_params <- c(log(1), log(1), log(1), log(1))  # Corresponding to V, W_level, W_slope, W_seasonal

# Optimize the parameters
opt <- dlmMLE(cardox, parm = init_params, build = buildMod)
opt

optimized_variances <- exp(opt$par)
optimized_variances
# 2.884121e-02 3.891608e-02 5.705924e-06 1.206646e-03

final_mod <- buildMod(opt$par)
fit <- dlmFilter(cardox, final_mod)
fore <- dlmForecast(fit, nAhead = 60)  # Forecast 60 months
# Forecasted values
pred <- ts(c(tail(cardox, 1), fore$f),
          start = end(cardox), frequency = frequency(cardox))

# Upper and lower bounds (2 standard deviations)
upper <- ts(c(tail(cardox, 1), fore$f + 2 * sqrt(unlist(fore$Q))),
           start = end(cardox), frequency = frequency(cardox))
lower <- ts(c(tail(cardox, 1), fore$f - 2 * sqrt(unlist(fore$Q))),
           start = end(cardox), frequency = frequency(cardox))
all <- ts(c(cardox, upper[-1]), start = start(cardox),
          frequency = frequency(cardox))
```

```
tsplot(all, ylab = "CO2 Levels",
      main = "Forecasts with 2SD Intervals")
lines(cardox, col = 4, lwd = 1.5)  # Original data
lines(pred, col = 2, lwd = 2)      # Forecasted values
lines(upper, col = 2)              # Upper bound
lines(lower, col = 2)              # Lower bound
```


GC−content Variation along BNRF1 Gene
GC Content
0.45
0.55
0.65
0.75
0
1000
2000
3000
4000
Position in Gene


GC−Content
gc_smooth
0.45
0.55
0.65
0.75
0
1000
2000
3000
4000
Time


Forecasts with 2SD Intervals
CO2 Levels
Time
320
340
360
380
400
420
440
1960
1970
1980
1990
2000
2010
2020
2030