Circular Drift Difussion Model on JAGS: Full example

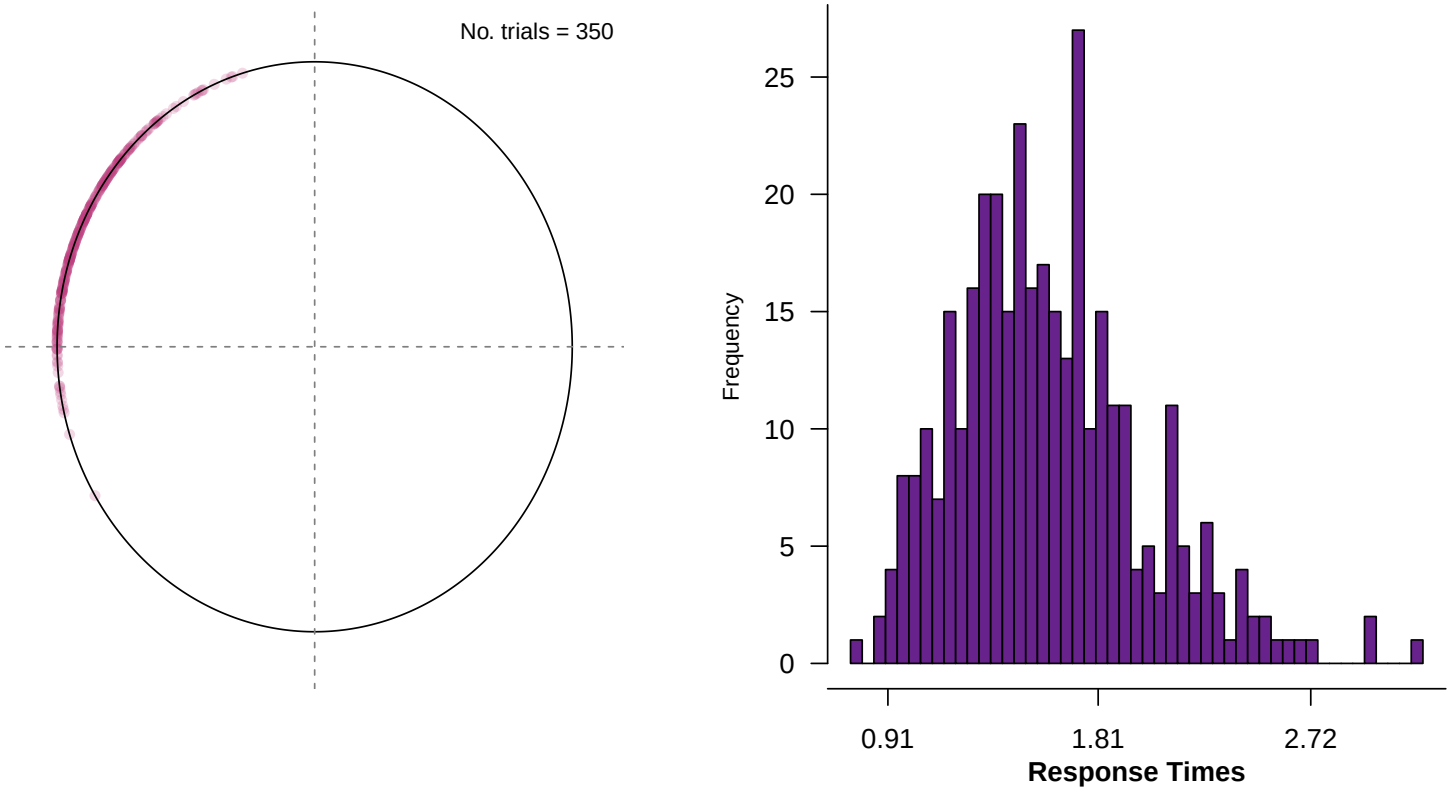
07 September, 2022

1. Generate/load simulated data

```
# Establish no. of trials
trials <- 350
# Call Rscript to generate simulated data / load it  if already existing
source("./getData.R")
head(data)
```

```
##   Choice     RT
## 1 2.4316 1.0805
## 2 2.6597 1.9685
## 3 2.5052 1.8530
## 4 3.1506 1.4555
## 5 2.0544 1.8920
## 6 2.8280 1.5275
```

```
# Plot data
cddm.plotData(data)
```




```
# Print parameter values used to generate this data
par
```

```
## true.theta0  true.drift  true.bound   true.ter0
##       2.685       2.870       3.990       0.230
```

2. Write JAGS model

```
modelFile <- "cddm.bug"
write('
            model{
                  # Likelihood
                    for (i in 1:N) {
                         X[1:2,i] ~ dcddm(drift, bound, ter0, theta0)
                    }

                  # Priors
                    drift  ~ dnorm(0, 0.1)T(0,)
                    theta0 ~ dnorm(0, 0.1)T(-3.14, 3.14)
                    bound  ~ dgamma(3, 2)
                    ter0   ~ dexp(1)T(, tmin)
                  }',
      modelFile)
```

where:

- `drift` is the magnitude of the drift vector composed by the individual drift rates related to the average motion observed across the x and y axes, according to the CDDM.
- `bound` is the threshold (i.e. the radius of the circle)
- `ter0` is the non-decision time (a.k.a. "time for encoding and response")
- `theta0` is the direction of the drift vector, in radians.

Prepare Settings to be passed to JAGS

```
n.chains = 4
n.iter = 2500
n.burnin = 500
n.thin = 1
perParticipant = FALSE
perTask = FALSE

sampling.Settings <- list(n.chains,n.iter,n.burnin,n.thin,perParticipant,perTask)
names(sampling.Settings) <- c("n.chains","n.iter","n.burnin","n.thin","perParticipant","perTask")
```

Run JAGS model

```
# Load Rscript with main function to run jags CDDM model
source("../Functions/runCDDMjags.R")
```

```
samplesFile <- "samples.RData"

if(!file.exists(samplesFile)){
         myJAGSsampling.CDDM(sampling.Settings,modelFile,samplesFile,data)
  }

load(file=samplesFile)

if(file.exists(samplesFile)){
         samples
  }
```

```
## Inference for Bugs model at "cddm.bug", fit using jags,
##  4 chains, each with 2500 iterations (first 500 discarded)
##  n.sims = 8000 iterations saved
##           mu.vect sd.vect     2.5%      25%      50%      75%    97.5%  Rhat
```

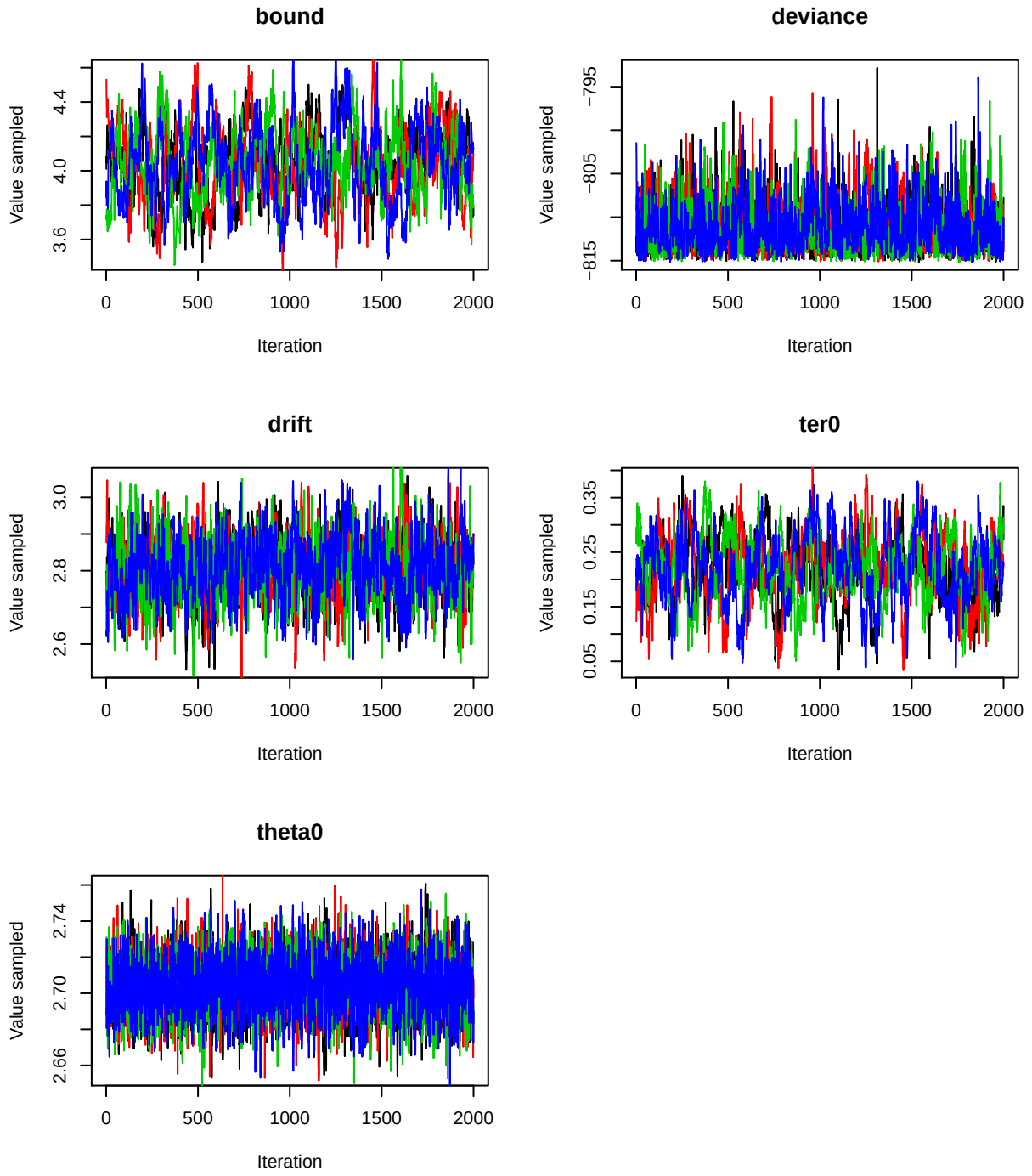
```
## bound       4.042   0.207    3.654    3.899    4.037    4.186    4.444 1.003
## drift       2.805   0.085    2.637    2.747    2.805    2.861    2.977 1.001
## ter0        0.221   0.060    0.094    0.183    0.224    0.262    0.333 1.003
## theta0      2.704   0.016    2.673    2.693    2.704    2.715    2.736 1.001
## deviance -811.210   2.838 -814.754 -813.315 -811.850 -809.825 -803.833 1.001
##          n.eff
## bound     1700
## drift     4400
## ter0      5200
## theta0    8000
## deviance  6700
##
## For each parameter, n.eff is a crude measure of effective sample size,
## and Rhat is the potential scale reduction factor (at convergence, Rhat=1).
##
## DIC info (using the rule, pD = var(deviance)/2)
## pD = 4.0 and DIC = -807.2
## DIC is an estimate of expected predictive error (lower deviance is better).
```

```
source("../Functions/processJAGSsamples.R")
drift  <- myJAGSsampling.extractSamples("drift",samples)
bound  <- myJAGSsampling.extractSamples("bound",samples)
ter0   <- myJAGSsampling.extractSamples("ter0",samples)
theta0 <- myJAGSsampling.extractSamples("theta0",samples)
```

```
# Get descriptive statistics for posterior samples
##########################################################
map.theta0 <- JAGSoutput.maxDensity(theta0)
map.drift <- JAGSoutput.maxDensity(drift)
map.bound <- JAGSoutput.maxDensity(bound)
map.ter0 <- JAGSoutput.maxDensity(ter0)
MAPS <- c(map.theta0,map.drift,map.bound,map.ter0)
names(MAPS) <- c("map.theta0","map.drift","map.bound","map.ter0")

mean.theta0 <- mean(theta0)
mean.drift <- mean(drift)
mean.bound <- mean(bound)
mean.ter0 <- mean(ter0)
means <- c(mean.theta0,mean.drift,mean.bound,mean.ter0)
names(means) <- c("mean.theta0","mean.drift","mean.bound","mean.ter0")
```

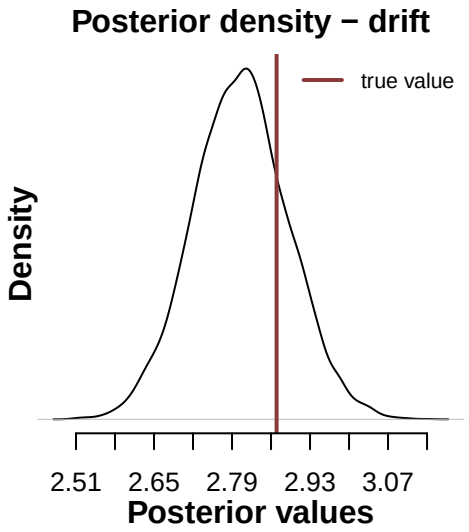
```
source("../Functions/plotJAGSsamples.R")
par(mfrow = c(3,2))
plot.ShowAllChains(samples)
```

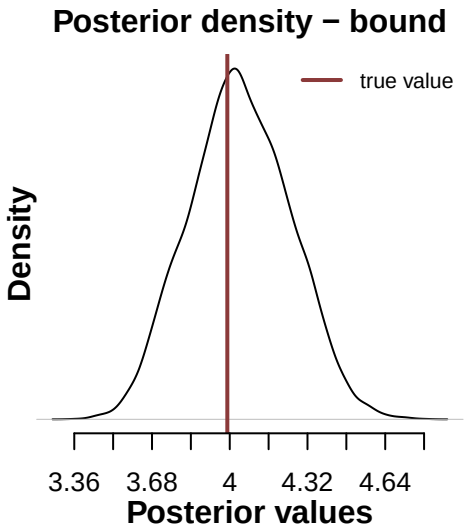


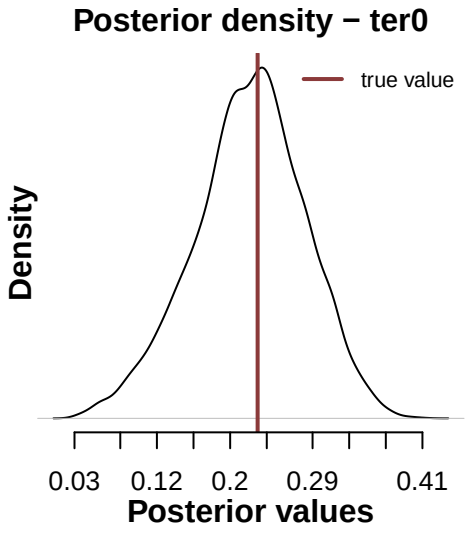

```
source("../Functions/processJAGSsamples.R")
myJAGSsampling.Rhat.max(samples)
```

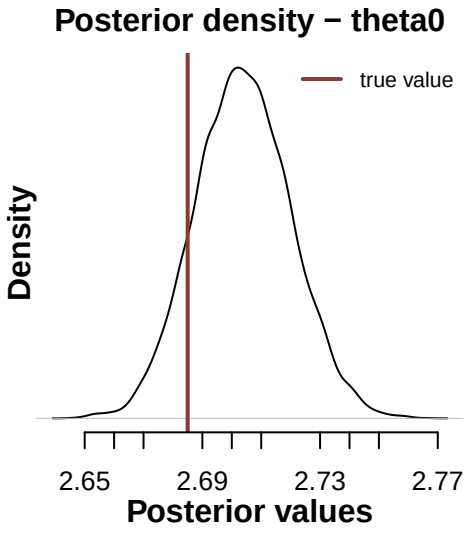
```
## [1] "The maximum value of Rhat observed was  1.0132  which corresponds to:  ter0"
```

```
par(mfrow = c(2,2))
plot.PosteriorDensity(drift,par["true.drift"])
plot.PosteriorDensity(bound,par["true.bound"])
plot.PosteriorDensity(ter0,par["true.ter0"])
plot.PosteriorDensity(theta0,par["true.theta0"])
```









Check against EZ-estimates

```
source("../Functions/ezcdm.R")
EZ <- ezcdm.fit(data$Choice,data$RT)


## First, compare EZ estimates against true parameter values
EZ
```

```
## EZ.theta0  EZ.drift  EZ.bound   EZ.ter0
## 2.7043808 2.8427654 4.0235061 0.2442079
```

```
par
```

```
## true.theta0  true.drift  true.bound   true.ter0
##       2.685       2.870       3.990       0.230
```

```
# Then, compare against point descriptors for posterior samples
#############################################################################
MAPS
```

```
## map.theta0  map.drift  map.bound   map.ter0
##      2.702      2.815      4.021      0.235
```

```
means
```

```
## mean.theta0  mean.drift  mean.bound   mean.ter0
##   2.7038419   2.8053794   4.0417243   0.2209097
```