Circular Drift Difussion Model on JAGS: Full example

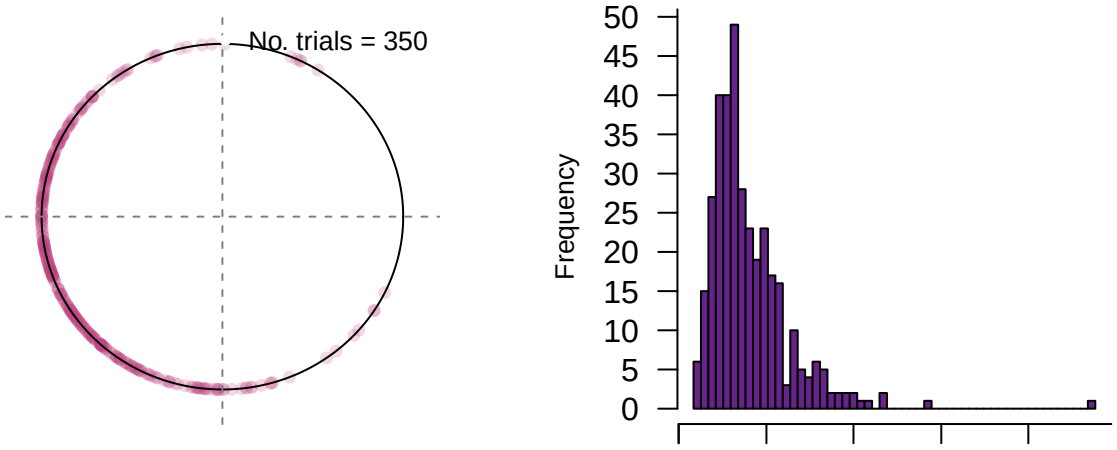
06 September, 2022

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")
dim(data)
```

```
## [1] 350   2
```

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




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

```
## $driftAngle
## [1] 3.486
##
## $ndt
## [1] 0.08
##
## $driftLength
## [1] 1.46
##
## $thresh
## [1] 1.58
```

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, 1)
                    theta0 ~ dnorm(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

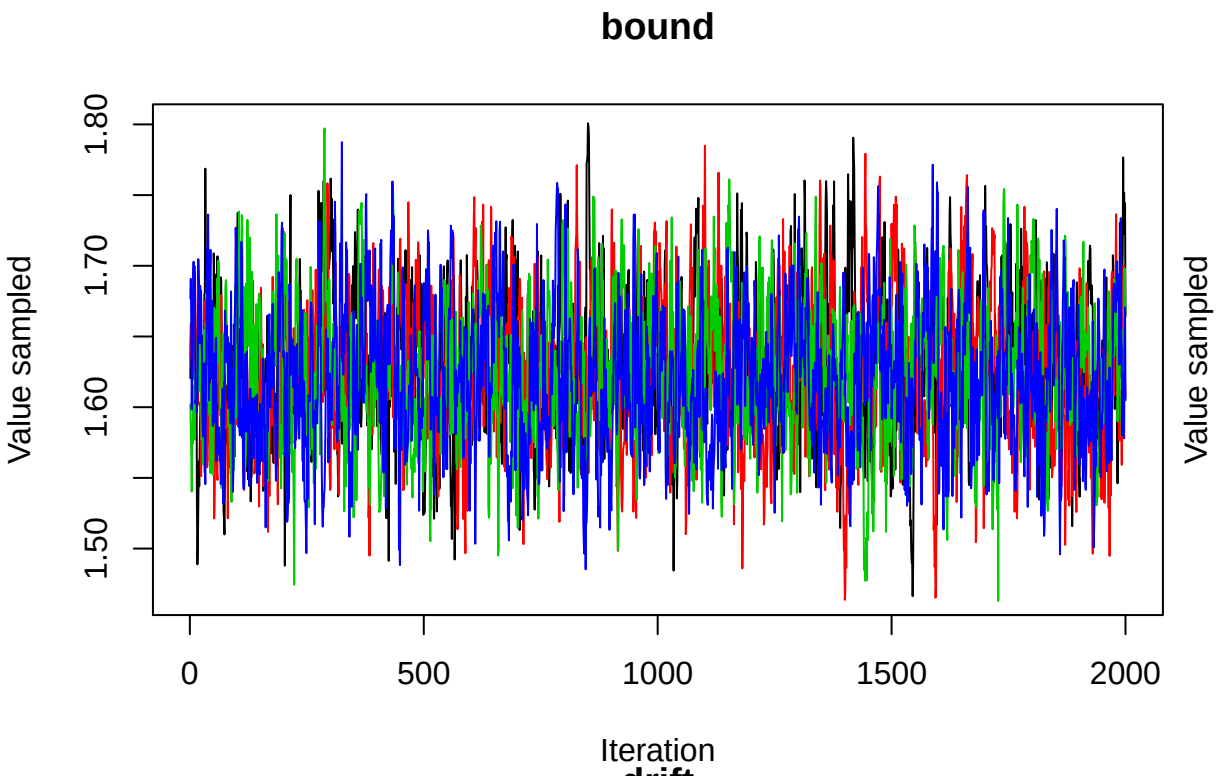
```
source("../Functions/runCDDMjags.R")
```

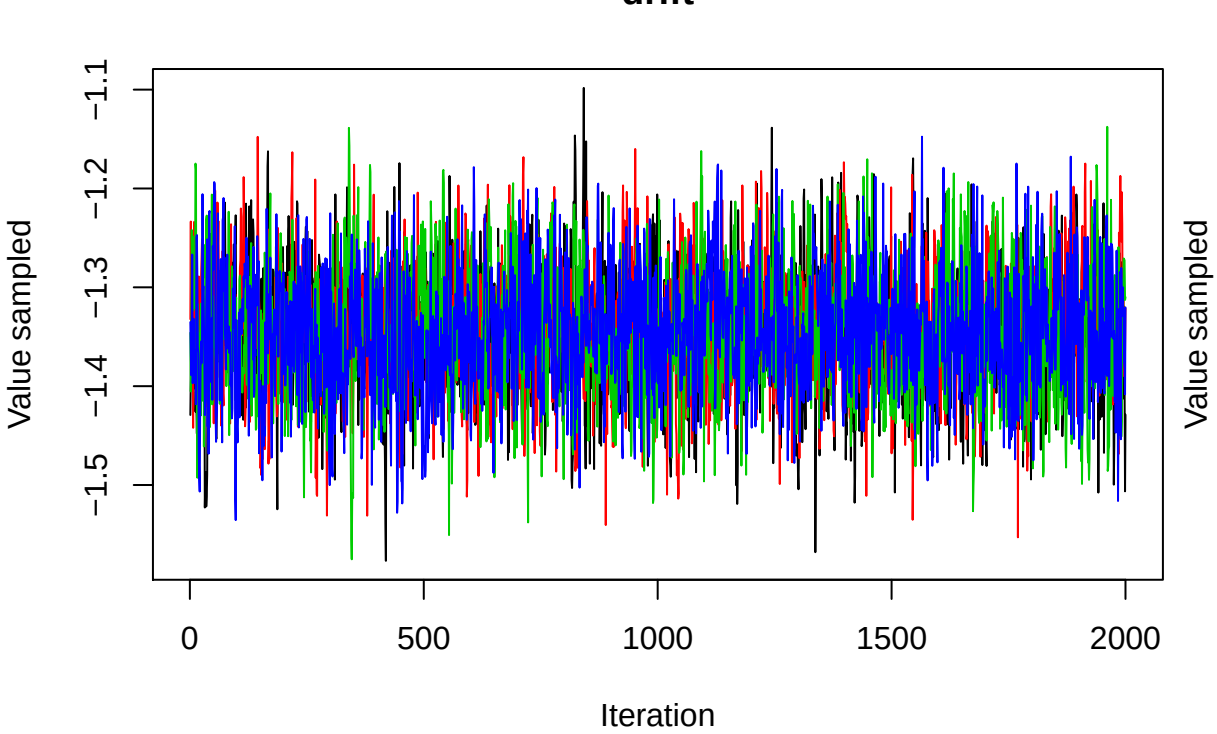
```
## Loading required package: rjags
## Loading required package: coda
## Linked to JAGS 4.3.0
## Loaded modules: basemod,bugs
##
## Attaching package: 'R2jags'
## The following object is masked from 'package:coda':
##
##     traceplot
## module cddm loaded
```

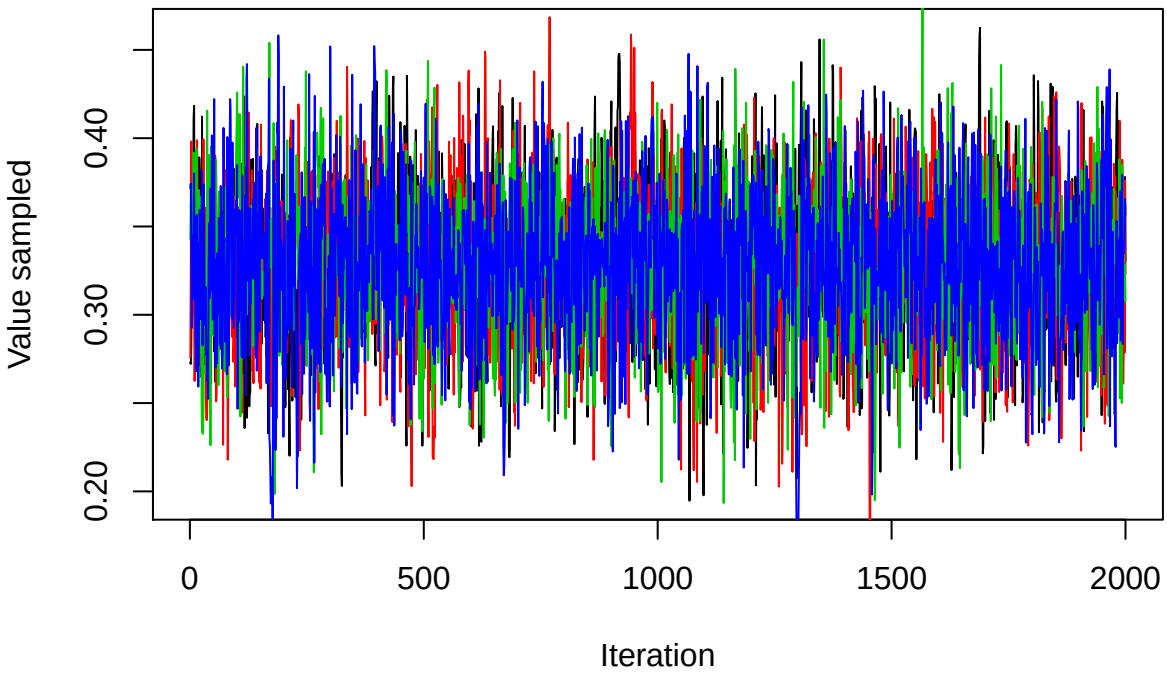
```
samplesFile <- "samples.RData"

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

```
   load(file=samplesFile)
}else{
   myJAGSsampling.CDDM(sampling.Settings,modelFile,samplesFile,data)}
```

```
source("../Functions/plotJAGSsamples.R")
plot.ShowAllChains(samples)
```








```
source("../Functions/processJAGSsamples.R")
```

```
## This is posterior version 1.3.0
```

```
##
## Attaching package: 'posterior'
```

```
## The following objects are masked from 'package:stats':
##
##     mad, sd, var
```

```
myJAGSsampling.Rhat.max(samples)
```

```
## [1] "The maximum value of Rhat observed was  1.0034  which corresponds to:  bound"
```