## Bart-Based Born-Again Trees

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Load requiered packages

Load the Bayesian data generation function

```
gendata_bay <- function(data, PPD, n_gen){
   if(nrow(data) != ncol(PPD)){stop("Amount of observations in PPD is different from data")}
   index_gen <- sample.int(n = nrow(data), size = n_gen, replace = TRUE)
   x_gen <- data[index_gen,]
   y_gen <- sapply(index_gen, function(i) sample(x = PPD[,i], size = 1))
   # y_gen <- sapply(index_gen, function(i) sample(x = PPD[,i][PPD[,i] >= quantile(PPD[,i], probs = .40)
   return(cbind(x_gen, y_gen))
}
```

Load the Smearing data generation function

```
gendata_smr <- function(data, palt = 0.5, n_gen){

if(palt < 0 | palt > 1){stop("palt must be bound between between 0 and 1")}

index_gen <- sample.int(n = nrow(data), size = n_gen, replace = TRUE)
gen_data <- data[index_gen,]

if(palt != 0){
    for(i in 1:nrow(gen_data)){

        for(j in 1:ncol(gen_data)){

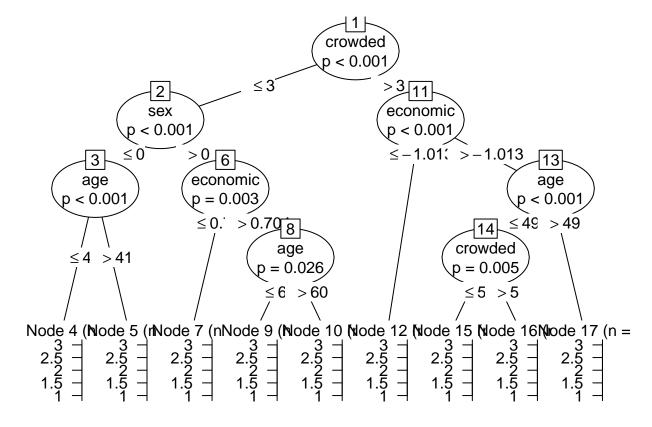
            if(runif(1) <= palt){gen_data[i,j] <- sample(x = data[,j], size = 1)}
        }
    }
    return(gen_data)
}</pre>
```

Load Safety data

```
set.seed(42)
data = read_sav(file.path(here(), "Project David", "Safety.sav"))
```

```
set.seed(42)
sample <- sample.int(n = nrow(data), size = floor(.75*nrow(data)), replace = F)
traindat <- data[sample, ]
testdat <- data[-sample, ]</pre>
```

Single GLMM tree



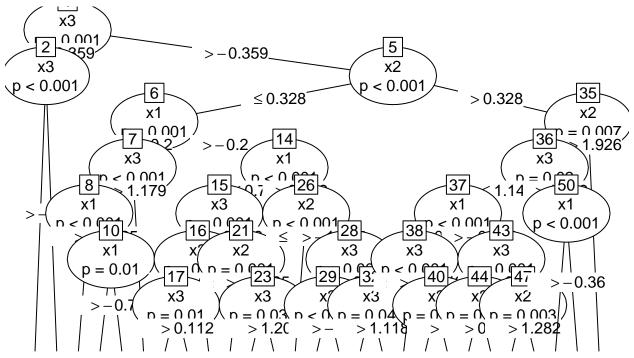
Multilevel bart model

```
PPD_mlbart <- predict(Mbart, newdata = testdat, type = "ppd",</pre>
                   group.by = testdat$street, combineChains = TRUE)
# Predicted Values
pred_mlbart <- fitted(object = Mbart, type = "ppd", sample = "test")</pre>
MSE_mlbart <- mean((pred_mlbart - testdat$unsafe)^2)</pre>
Born-again lmertree (Multilevel BART)
set.seed(42)
PPD_mlbart_train <- predict(Mbart, newdata = traindat, type = "ppd",</pre>
                       group.by = traindat$street, combineChains = TRUE)
surr_mlbart <- gendata_bay(traindat, PPD_mlbart_train, 2 * nrow(traindat))</pre>
babart <- lmertree(y_gen ~ 1 | (1|street) | age + sex + economic + crowded,
                        data = surr_mlbart)
pred_babart <- predict(babart, newdata = testdat)</pre>
MSE_ba <- mean((pred_babart - testdat$unsafe)^2)</pre>
Test the model accuracies
var(testdat$unsafe)
## [1] 0.6025542
MSE_mlbart
## [1] 0.449172
MSE_glmtree
## [1] 0.4844973
MSE ba
## [1] 0.6980035
Simulate Data
set.seed(42)
N <- 999 \#sample\ size
nG <- 20 #anount of groups
```

G <- factor(sample(1:nG, N, replace=T)) #grouping variable

```
# level 1 coefs
beta1 <- 1
beta2 <- -2
beta3 <- 3
beta4 <- -4
beta5 <- -1
beta6 <- 2
beta7 <- 3
# level 2 coefs
beta_12 <- 2
# level 1 vars
x1 <- rnorm(N)
x2 \leftarrow rnorm(N)
x3 <- rnorm(N)
err1 <- rnorm(N)</pre>
# level 2 vars
tmp <- rnorm(nG)#generate 20 random numbers, m = 0, sd = 1</pre>
group <- sapply(G, function(i) tmp[i]) #all units in 12 have the same value
tmp <- rnorm(nG) #error term for level 2</pre>
err2 <- sapply(G, function(i) tmp[i]) #all units in 12 have the same value
y \leftarrow beta1*x1 + beta2*x2 + beta3*x3 +
  beta4*x1*x2 + beta5*x2*x3 + beta6*x1*x3 + beta7*x1*x2*x3 +
  beta_12*group +
  err1 + err2
#putting it all together
data <- data.frame(y, group, x1, x2, x3)</pre>
sample <- sample.int(n = nrow(data), size = floor(.75*nrow(data)), replace = F)</pre>
traindat <- data[sample, ]</pre>
testdat <- data[-sample, ]</pre>
```

Single GLMM tree



Multilevel bart model

Born-again lmertree (Multilevel BART)

```
data = surr_mlbart)
pred_babart <- predict(babart, newdata = testdat)

MSE_ba <- mean((pred_babart - testdat$y)^2)</pre>
```

Test the model accuracies

var(testdat\$y)

## [1] 41.67231

 ${\tt MSE\_mlbart}$ 

## [1] 3.251631

 ${\tt MSE\_glmtree}$ 

## [1] 22.13857

MSE\_ba

## [1] 118.2236