

Cost and time to diagnosis

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```
library(IDEAdectree)
library(treeSimR)
library(dplyr)

# cleaned IDEA patient data
proj_folder <- "C:/Users/ngreen1/Google Drive/TB/IDEA/R/packages/IDEAdectree"
load(paste0(proj_folder, "/data/TBdata_clinical_cleaned.RData"))

# test/procedure costs
load(paste0(proj_folder, "/data/COSTdistns_allerror.RData"))

# diagnosis times
times <- estimate_start_to_diag(data)

# total costs
cost_distns <- COST.distns.allerror

rcosts <- means_distributions(cost_distns)

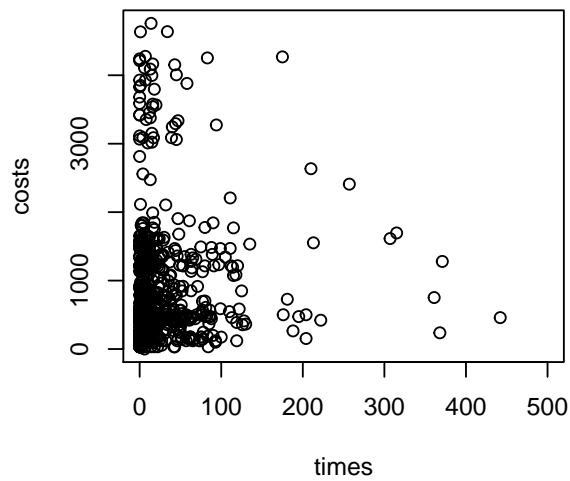
costs <- calcPatientCostofTests(data, COSTS = rcosts)
```

All patients using the estimated diagnosis time.

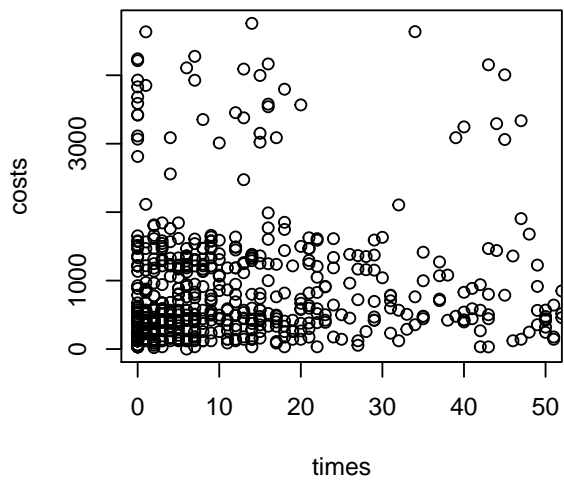
```
par(mfrow = c(2, 2))

plot(times, costs, xlim = c(0, 500))
plot(times, costs, xlim = c(0, 50))

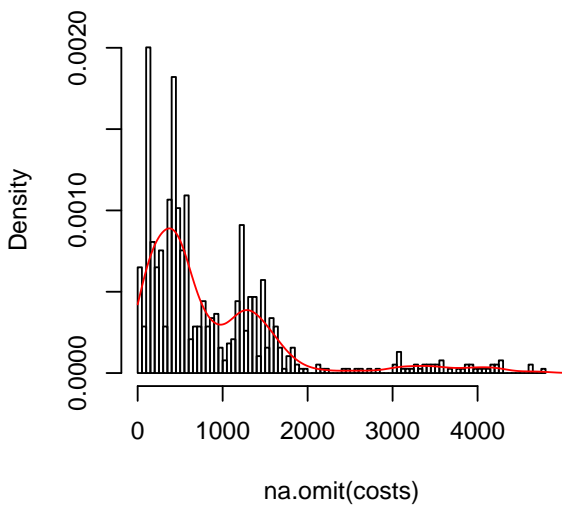
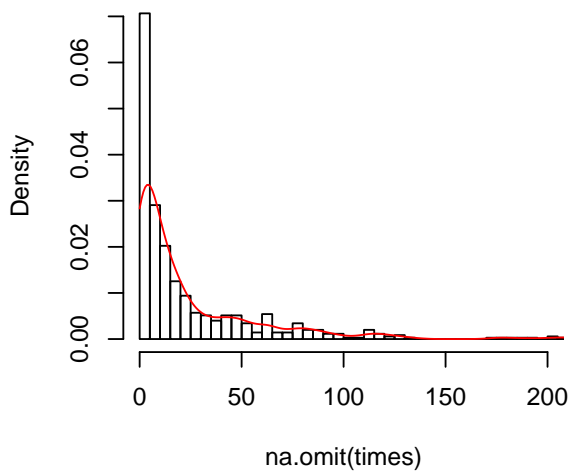
hist(na.omit(times), breaks = 80, freq = FALSE, xlim = c(0,200), main = "times")
lines(density(na.omit(times), kernel = "g", from = 0), col = "red")
hist(na.omit(costs), breaks = 100, freq = FALSE, main = "costs")
lines(density(na.omit(costs), from = 0), col = "red")#, width = 1000, kernel = "bi"))
```



times



costs



Dosanjh category 1 or 2 patients using time from first test to start on treatment.

```
times <- as.numeric(data$testDrug_diff)

Dosanjh1 <- data$DosanjhGrouped == 1
Dosanjh12 <- data$DosanjhGrouped %in% c(1,2)

par(mfrow = c(2,2))

plot(times[Dosanjh1],
      costs[Dosanjh1], main = "Cat 1")
```

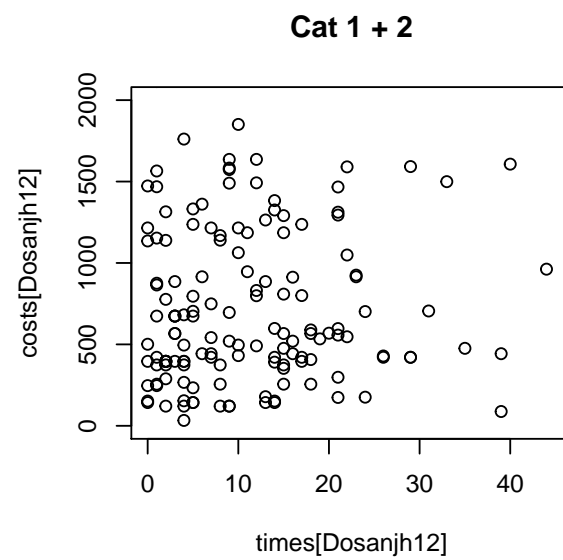
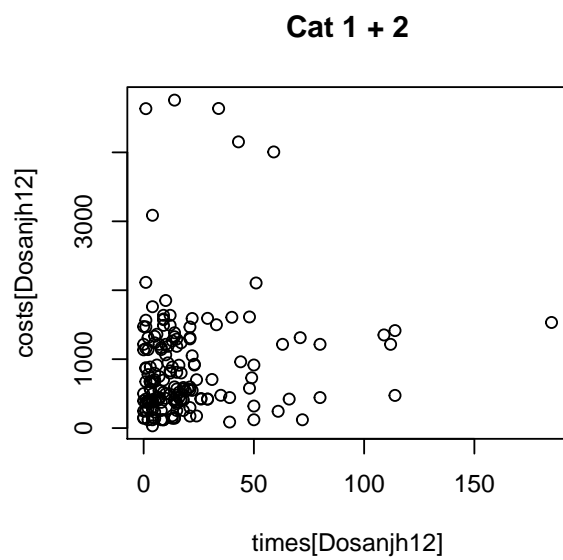
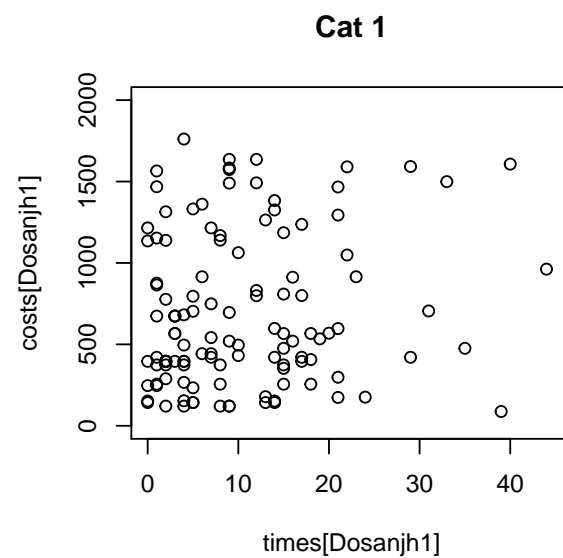
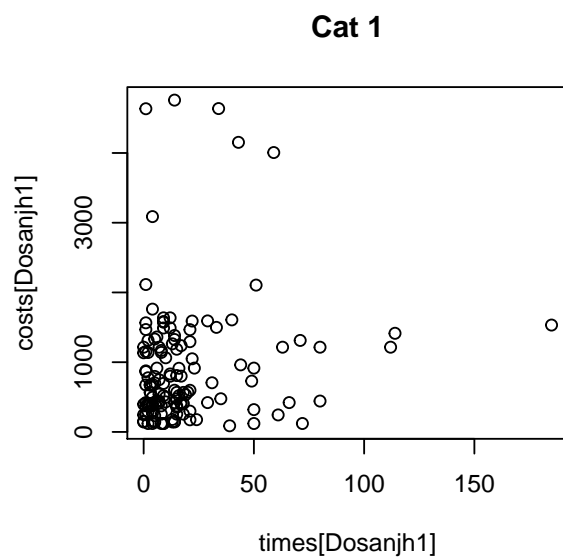
```

plot(times[Dosanjh1],
     costs[Dosanjh1],
     xlim = c(0, 45), ylim = c(0, 2000),
     main = "Cat 1")

plot(times[Dosanjh12],
     costs[Dosanjh12], main = "Cat 1 + 2")

plot(times[Dosanjh12],
     costs[Dosanjh12],
     xlim = c(0, 45), ylim = c(0, 2000),
     main = "Cat 1 + 2")

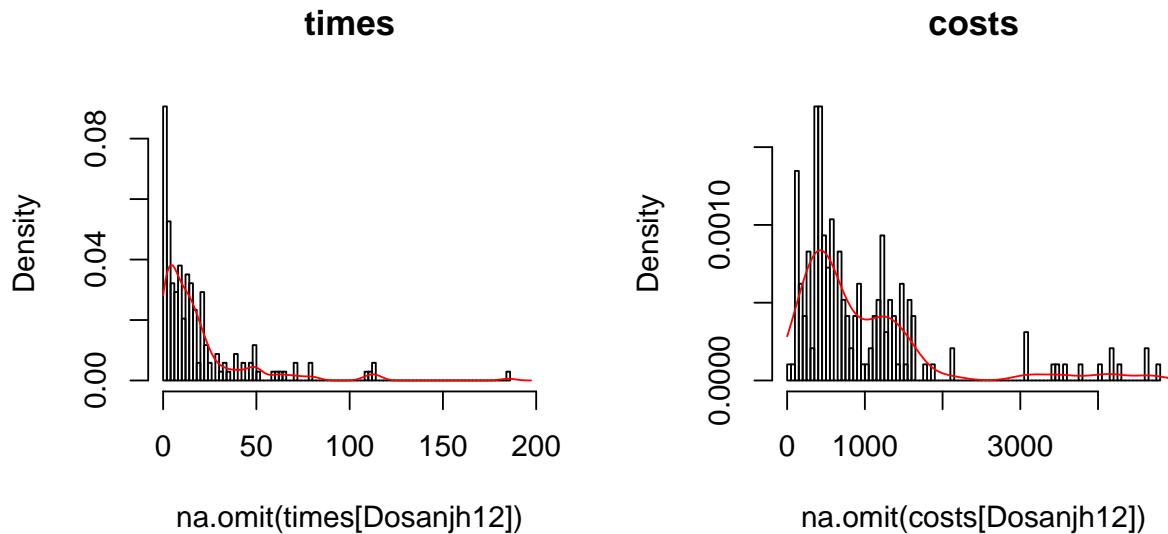
```



```

par(mfrow=c(1,2))
hist(na.omit(times[Dosanjh12]), breaks = 80, freq = FALSE, xlim = c(0,200), main = "times")
lines(density(na.omit(times[Dosanjh12]), kernel = "g", from = 0), col = "red")
hist(na.omit(costs[Dosanjh12]), breaks = 100, freq = FALSE, main = "costs")
lines(density(na.omit(costs[Dosanjh12]), from = 0), col = "red")#, width = 1000, kernel = "bi"))

```



First test to TB culture.

```

times <- as.numeric(data$start.to.TBcultorig)

par(mfrow = c(2,2))

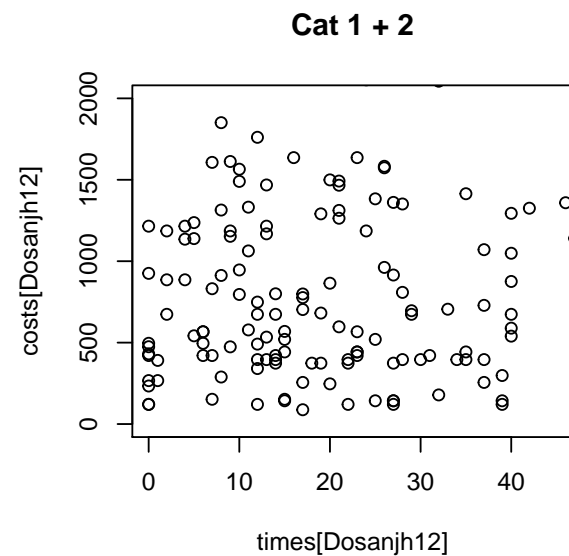
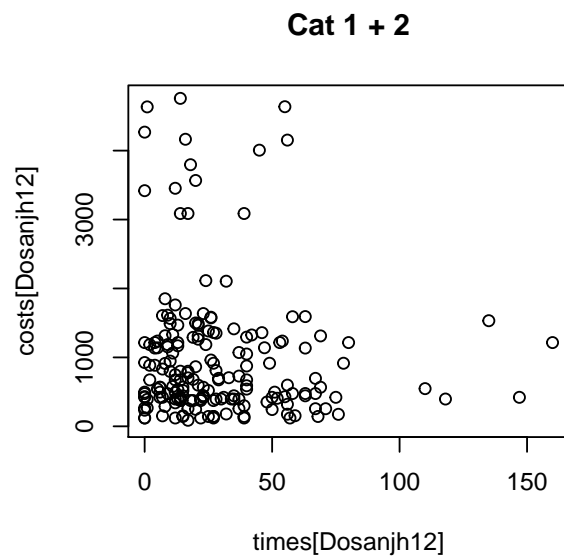
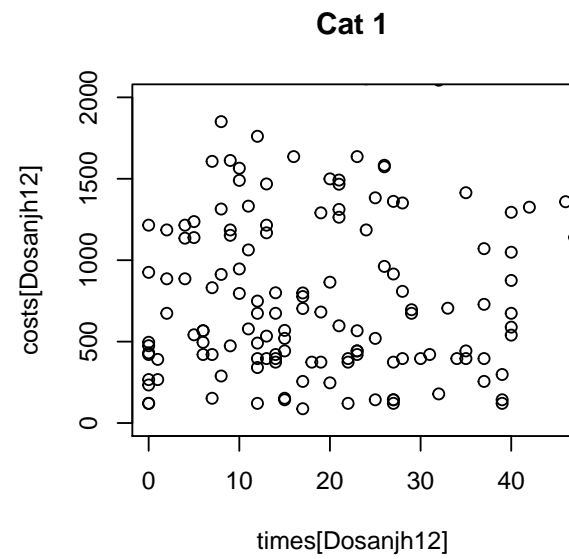
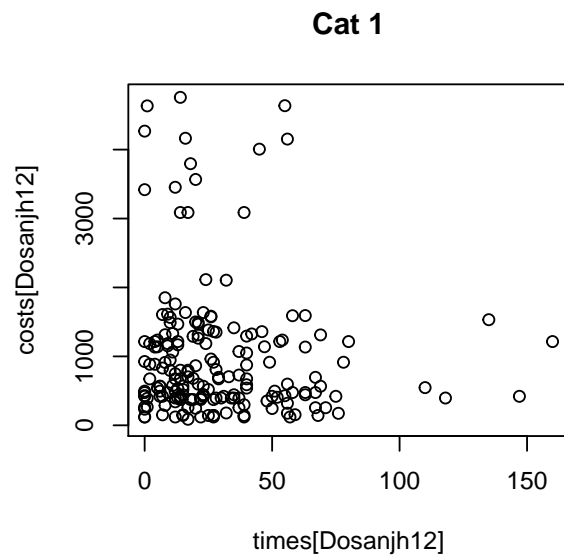
plot(times[Dosanjh12],
      costs[Dosanjh12], main = "Cat 1")

plot(times[Dosanjh12],
      costs[Dosanjh12],
      xlim = c(0, 45), ylim = c(0, 2000),
      main = "Cat 1")

plot(times[Dosanjh12],
      costs[Dosanjh12], main = "Cat 1 + 2")

plot(times[Dosanjh12],
      costs[Dosanjh12],
      xlim = c(0, 45), ylim = c(0, 2000),
      main = "Cat 1 + 2")

```



```
par(mfrow=c(1,2))
hist(na.omit(times[Dosanjh12]), breaks = 80, freq = FALSE, xlim = c(0,200), main = "times")
lines(density(na.omit(times[Dosanjh12]), kernel = "g", from = 0), col = "red")
hist(na.omit(costs[Dosanjh12]), breaks = 100, freq = FALSE, main = "costs")
lines(density(na.omit(costs[Dosanjh12]), from = 0), col = "red")#, width = 1000, kernel = "bi"))
```

