Problem_1

Problem 1: Predicting healthcare charges, in USD, using a patient's age and BMI as features

```r
library(readr)
library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 4.3.3
```

```r
library(tidyverse)
```

```
## -- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
## v dplyr     1.1.4     v stringr   1.5.1
## v forcats   1.0.0     v tibble    3.2.1
## v lubridate 1.9.3     v tidyr     1.3.0
## v purrr     1.0.2
## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
## i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become errors
```

```r
library(rpart) # this is what we use to make the decision tree
```

```
## Warning: package 'rpart' was built under R version 4.3.3
```

```r
library(rpart.plot)
```

```
## Warning: package 'rpart.plot' was built under R version 4.3.3
```

```r
library(dplyr)
```

```r
df <- read_csv("./insurance_charges.csv")
```

```
## Rows: 1338 Columns: 5
## -- Column specification --------------------------------------------------------
## Delimiter: ","
## dbl (5): age, bmi, charges, f_bmi, cardiovascular_care_cost
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```r
head(df)
```

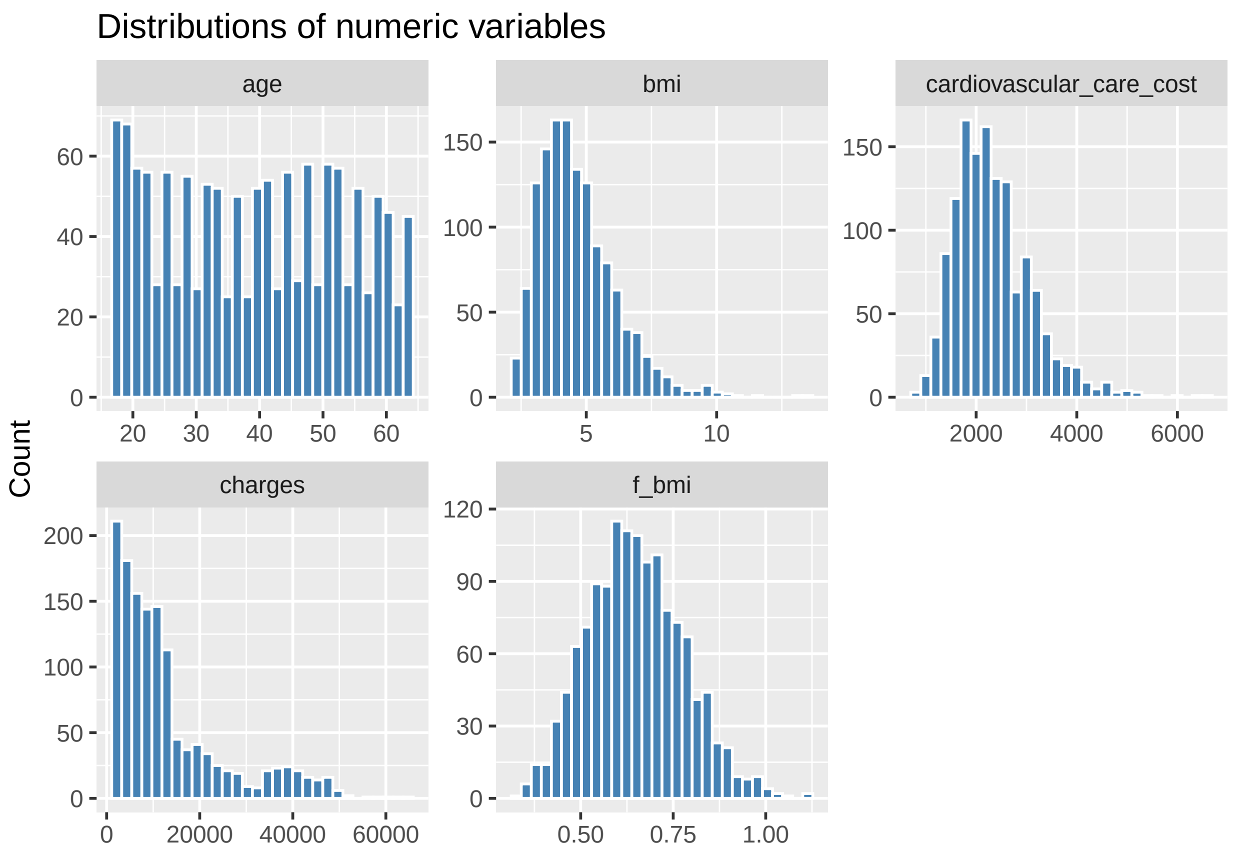
```
## # A tibble: 6 x 5
##     age   bmi charges f_bmi cardiovascular_care_cost
##   <dbl> <dbl>   <dbl> <dbl>                    <dbl>
## 1    19  3.90  16885. 0.591                    1876.
## 2    18  5.19   1726. 0.716                    2466.
## 3    28  5.00   4449. 0.699                    2473.
## 4    33  3.03  21984. 0.481                    1656.
## 5    32  4.09   3867. 0.612                    1933.
## 6    31  3.51   3757. 0.545                    1548.
```

```
summary(df)
```

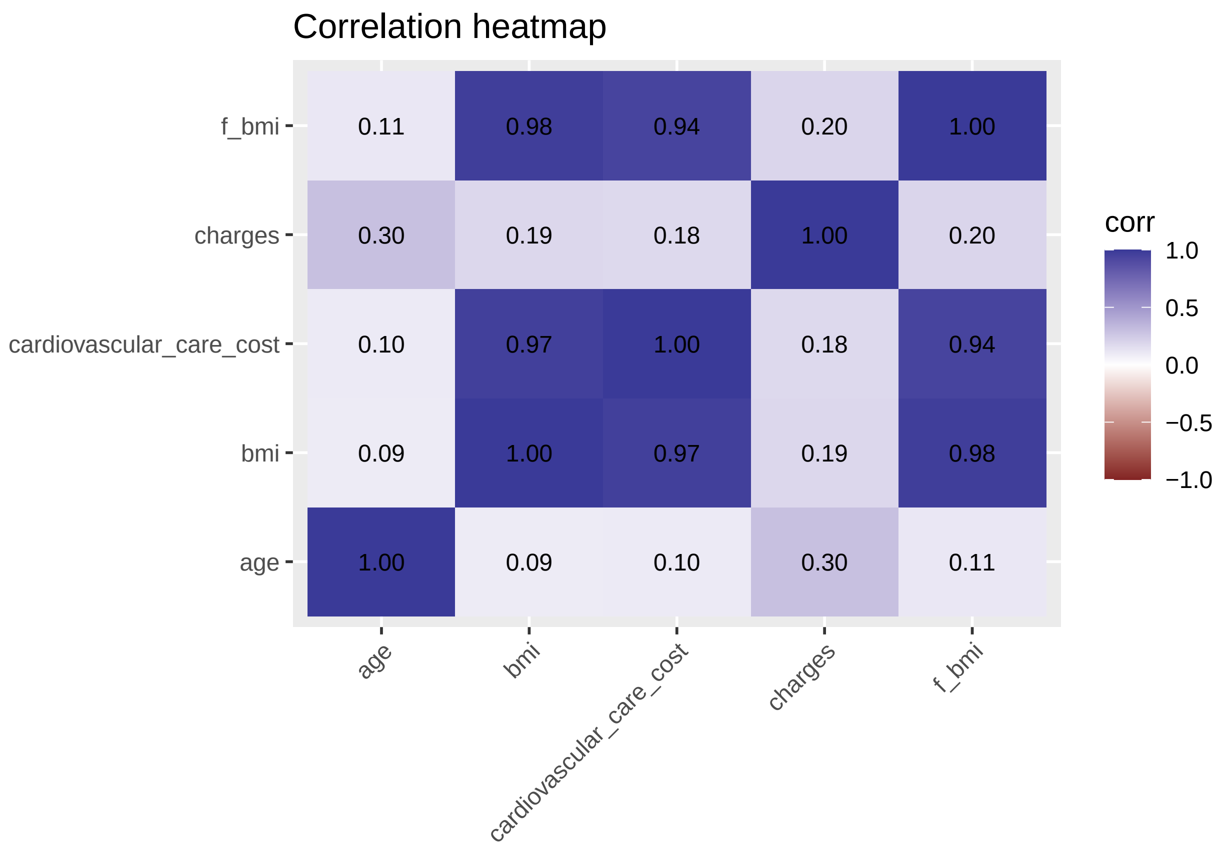
```
##       age             bmi            charges          f_bmi       
##  Min.   :18.00   Min.   : 2.179   Min.   : 1122   Min.   :0.3382  
##  1st Qu.:27.00   1st Qu.: 3.607   1st Qu.: 4740   1st Qu.:0.5572  
##  Median :39.00   Median : 4.407   Median : 9382   Median :0.6442  
##  Mean   :39.21   Mean   : 4.672   Mean   :13270   Mean   :0.6497  
##  3rd Qu.:51.00   3rd Qu.: 5.434   3rd Qu.:16640   3rd Qu.:0.7351  
##  Max.   :64.00   Max.   :13.359   Max.   :63770   Max.   :1.1258  
##  cardiovascular_care_cost
##  Min.   : 827.1          
##  1st Qu.:1784.1          
##  Median :2204.5          
##  Mean   :2338.0          
##  3rd Qu.:2720.7          
##  Max.   :6621.8          
```

Let us start with really basic exploratory data analysis to gain some understanding on our data.

```
# Distributions of the numeric columns
df |>
  select(where(is.numeric)) |>
  pivot_longer(everything(), names_to = "var", values_to = "val") |>
  ggplot(aes(val)) +
  geom_histogram(bins = 30, fill = "steelblue", color = "white") +
  facet_wrap(~ var, scales = "free") +
  labs(title = "Distributions of numeric variables", x = NULL, y = "Count")
```



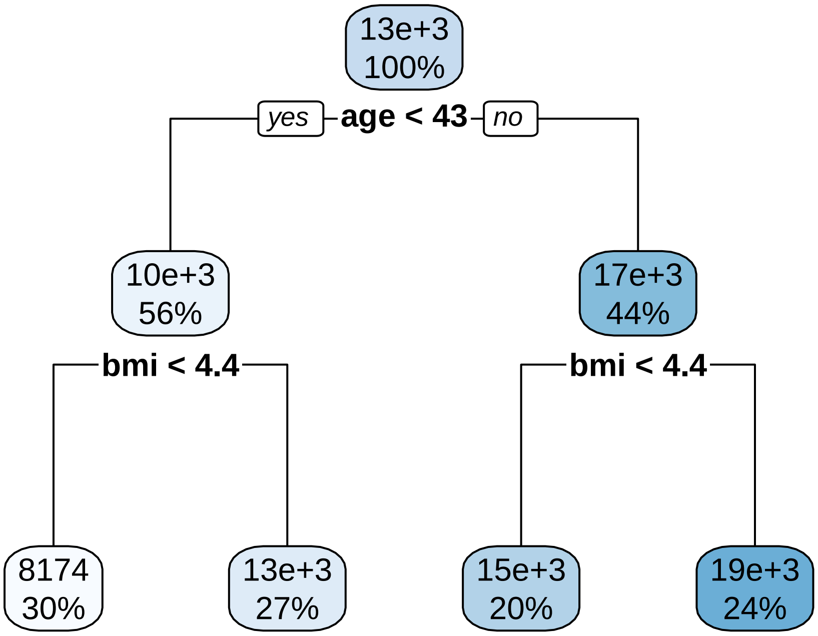
```r
# Correlation matrix heatmap
corr_mat <- cor(df |> select(where(is.numeric)), use = "pairwise.complete.obs")

corr_mat |>
  as.data.frame() |>
  tibble::rownames_to_column("var1") |>
  pivot_longer(-var1, names_to = "var2", values_to = "corr") |>
  ggplot(aes(var1, var2, fill = corr)) +
  geom_tile() +
  geom_text(aes(label = sprintf("%.2f", corr)), size = 3) +
  scale_fill_gradient2(limits = c(-1, 1)) +
  labs(title = "Correlation heatmap", x = NULL, y = NULL) +
  theme(axis.text.x = element_text(angle = 45, hjust = 1))
```



From the EDA, we can see that charges are right-skewed with a few high-cost outliers, while age is fairly uniform across the dataset. The correlation heatmap shows that BMI and f_bmi are almost perfectly correlated (~0.98), while their relationship to charges is only moderate. Because CART models split on orderings, monotone transforms like f_bmi usually yield nearly identical trees to BMI.

a)

```r
# Decision tree predicting charges based on bmi and age.
model1 <- rpart(charges ~ age + bmi, data = df)

# Plots the decision tree
rpart.plot(model1)
```



```
# Returns a summary of the model
summary(model1)
```

```
## Call:
## rpart(formula = charges ~ age + bmi, data = df)
##   n= 1338
##
##           CP nsplit rel error    xerror       xstd
## 1 0.07793137      0 1.0000000 1.0025356 0.05189781
## 2 0.01920458      1 0.9220686 0.9289775 0.04950382
## 3 0.01507422      2 0.9028640 0.9435374 0.04787011
## 4 0.01000000      3 0.8877898 0.9264762 0.04549575
##
## Variable importance
## age bmi
##  68  32
##
## Node number 1: 1338 observations,    complexity param=0.07793137
##   mean=13270.42, MSE=1.465428e+08
##   left son=2 (755 obs) right son=3 (583 obs)
##   Primary splits:
##       age < 42.5     to the left,  improve=0.07793137, (0 missing)
##       bmi < 4.357944 to the left,  improve=0.04212369, (0 missing)
##   Surrogate splits:
##       bmi < 5.728587 to the left,  agree=0.582, adj=0.041, (0 split)
##
```

```
## Node number 2: 755 observations,    complexity param=0.01920458
##   mean=10300.81, MSE=1.313497e+08
##   left son=4 (396 obs) right son=5 (359 obs)
##   Primary splits:
##       bmi < 4.357944 to the left,  improve=0.03797077, (0 missing)
##       age < 26.5     to the left,  improve=0.01289901, (0 missing)
##   Surrogate splits:
##       age < 18.5     to the right, agree=0.534, adj=0.019, (0 split)
##
## Node number 3: 583 observations,    complexity param=0.01507422
##   mean=17116.14, MSE=1.400084e+08
##   left son=6 (262 obs) right son=7 (321 obs)
##   Primary splits:
##       bmi < 4.392632 to the left,  improve=0.03621035, (0 missing)
##       age < 58.5     to the left,  improve=0.03075757, (0 missing)
##   Surrogate splits:
##       age < 47.5     to the left,  agree=0.566, adj=0.034, (0 split)
##
## Node number 4: 396 observations
##   mean=8174.444, MSE=5.228144e+07
##
## Node number 5: 359 observations
##   mean=12646.34, MSE=2.080781e+08
##
## Node number 6: 262 observations
##   mean=14623.87, MSE=5.261606e+07
##
## Node number 7: 321 observations
##   mean=19150.33, MSE=2.021303e+08
```

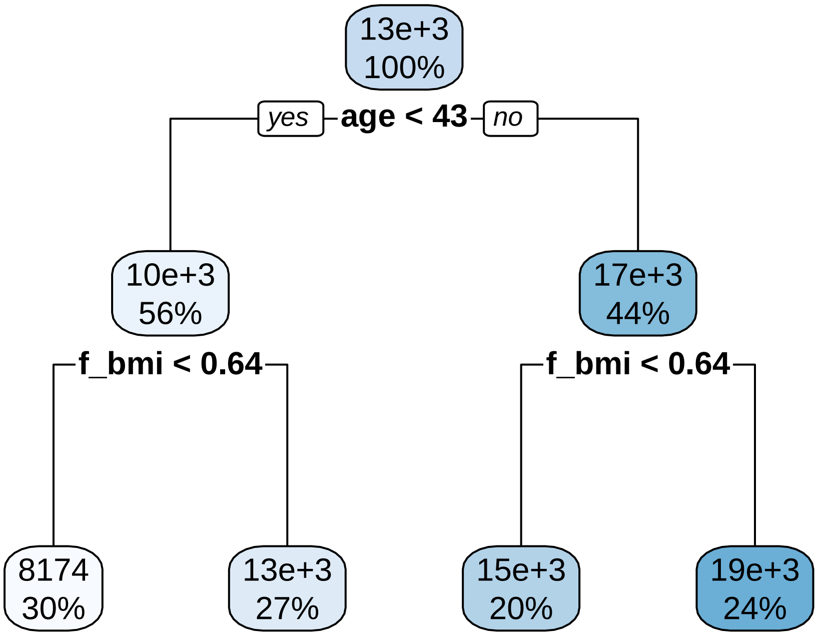
```r
# R-squared ( from training data)
pred <- predict(model1, df)
rss <- sum((df$charges - pred)^2)                # residual sum of squares
tss <- sum((df$charges - mean(df$charges))^2)   # total sum of squares
rsq <- 1 - rss/tss

cat("The Training R-squared is:", round(rsq, 3), "\n")
```

```
## The Training R-squared is: 0.112
```

The training R^2 is ~11.2%, and the cross-validated relative error from printcp is ~0.92, meaning the tree only modestly improves over predicting the mean. Age contributes most of the predictive power, with importance ~68 compared to 32 for BMI.

b)

```r
# Decision tree predicting charges based on f_bmi and age.
model2 <- rpart(charges ~ age + f_bmi, data = df)

# Plots the decision tree
rpart.plot(model2)
```



```
# Returns a summary of the model
summary(model2)
```

```
## Call:
## rpart(formula = charges ~ age + f_bmi, data = df)
##   n= 1338
##
##           CP nsplit rel error    xerror       xstd
## 1 0.07793137      0 1.0000000 1.0024098 0.05200392
## 2 0.01920458      1 0.9220686 0.9268229 0.04920849
## 3 0.01507422      2 0.9028640 0.9253720 0.04590948
## 4 0.01000000      3 0.8877898 0.9227373 0.04552839
##
## Variable importance
##   age f_bmi
##    68    32
##
## Node number 1: 1338 observations,    complexity param=0.07793137
##   mean=13270.42, MSE=1.465428e+08
##   left son=2 (755 obs) right son=3 (583 obs)
##   Primary splits:
##       age   < 42.5      to the left,  improve=0.07793137, (0 missing)
##       f_bmi < 0.6392812 to the left,  improve=0.04212369, (0 missing)
##   Surrogate splits:
##       f_bmi < 0.7580472 to the left,  agree=0.582, adj=0.041, (0 split)
##
```

```
## Node number 2: 755 observations,    complexity param=0.01920458
##   mean=10300.81, MSE=1.313497e+08
##   left son=4 (396 obs) right son=5 (359 obs)
##   Primary splits:
##       f_bmi < 0.6392812 to the left,  improve=0.03797077, (0 missing)
##       age   < 26.5      to the left,  improve=0.01289901, (0 missing)
##   Surrogate splits:
##       age < 18.5      to the right, agree=0.534, adj=0.019, (0 split)
##
## Node number 3: 583 observations,    complexity param=0.01507422
##   mean=17116.14, MSE=1.400084e+08
##   left son=6 (262 obs) right son=7 (321 obs)
##   Primary splits:
##       f_bmi < 0.6427244 to the left,  improve=0.03621035, (0 missing)
##       age   < 58.5      to the left,  improve=0.03075757, (0 missing)
##   Surrogate splits:
##       age < 47.5      to the left,  agree=0.566, adj=0.034, (0 split)
##
## Node number 4: 396 observations
##   mean=8174.444, MSE=5.228144e+07
##
## Node number 5: 359 observations
##   mean=12646.34, MSE=2.080781e+08
##
## Node number 6: 262 observations
##   mean=14623.87, MSE=5.261606e+07
##
## Node number 7: 321 observations
##   mean=19150.33, MSE=2.021303e+08
```

```r
# R-squared ( from training data)
pred <- predict(model2, df)
rss <- sum((df$charges - pred)^2)                # residual sum of squares
tss <- sum((df$charges - mean(df$charges))^2)   # total sum of squares
rsq <- 1 - rss/tss

cat("The Training R-squared is:", round(rsq, 3), "\n")
```

```
## The Training R-squared is: 0.112
```

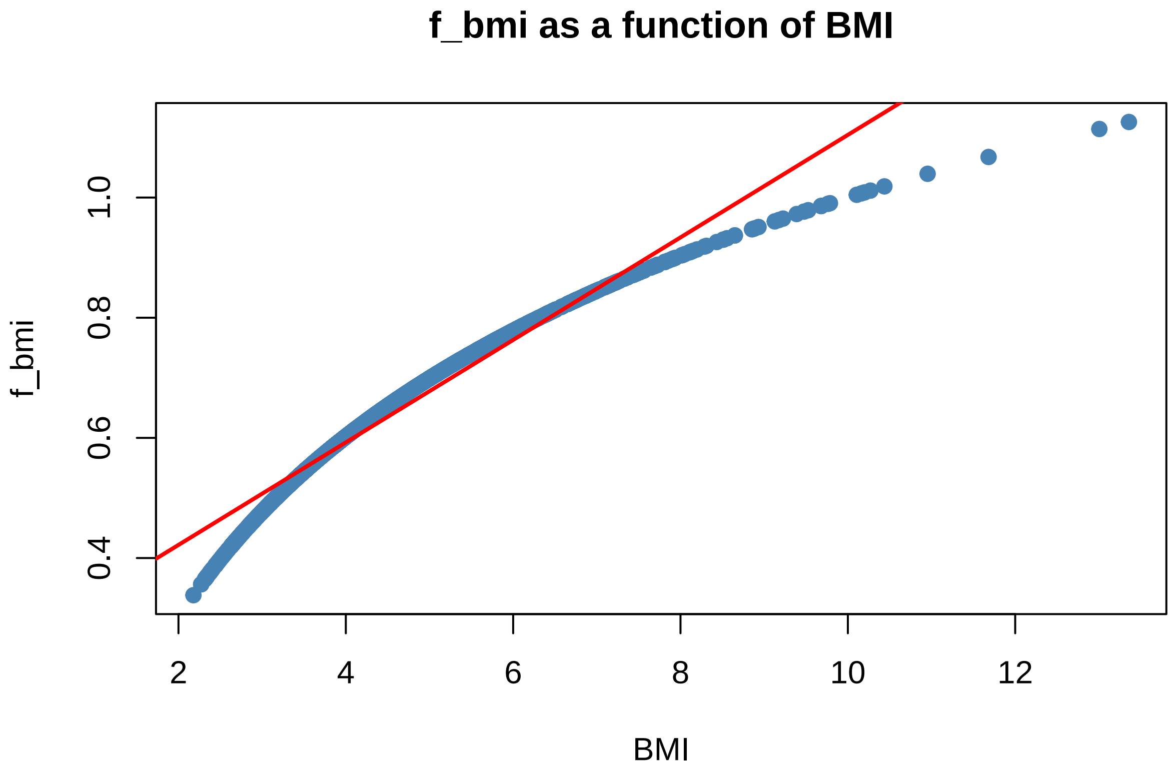
The training R² is again ~11.2%. The tree structure and splits are almost identical to model (a), which is expected since f_bmi is a monotone transform of BMI. Age still dominates in variable importance (~68 vs 32)

c)

Both trees have nearly identical splits (root split on age < 42.5, secondary splits on BMI ~ 4.36 or f_bmi ~ 0.64). Their training R² values are essentially the same (~11.2%). This outcome is expected because f_bmi is a near-monotone transform of BMI (correlation ~0.98), which preserves ordering. CART models base splits on order thresholds, so any monotone transform will yield similar partitions and performance.

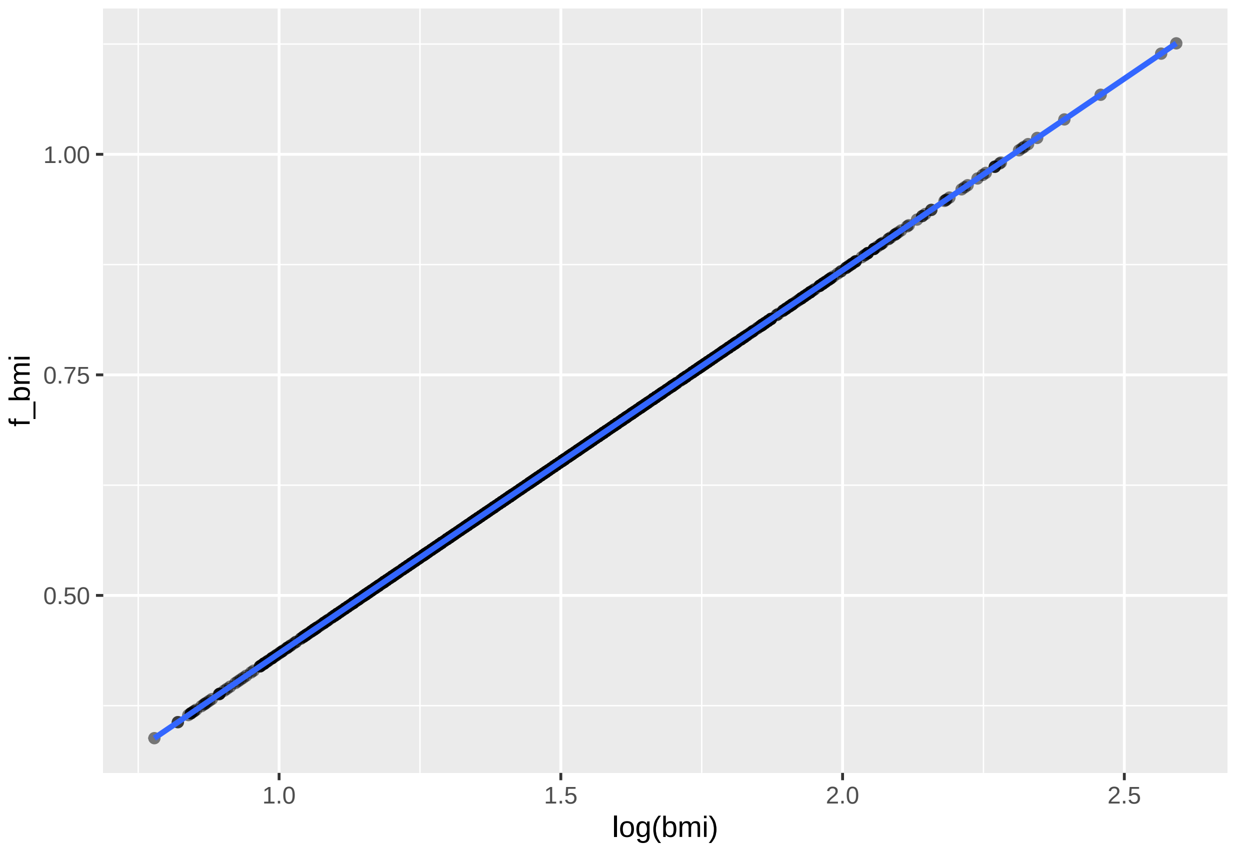
```r
# Plot f_bmi as a function of bmi
plot(df$bmi, df$f_bmi,
     xlab = "BMI",
     ylab = "f_bmi",
     main = "f_bmi as a function of BMI",
     pch = 19, col = "steelblue")
```

```
abline(lm(f_bmi ~ bmi, data = df), col = "red", lwd = 2)
```



```
ggplot(df, aes(log(bmi), f_bmi)) + geom_point(alpha=0.5) + geom_smooth()
```

```
## `geom_smooth()` using method = 'gam' and formula = 'y ~ s(x, bs = "cs")'
```



> Here we can see that bmi vs f_bmi is related as f_bmi is a monotonic transform of bmi(scaling, log, square), therefore the trees will have similar R^2 (0.1122102) and comparable split logic although at different threshold values due to the difference in the scaling. Structural differences (number/depth of splits) may be minor; performance tends to stay close because decision trees rely primarily on ordering of values.

d)

> If f_bmi = g(bmi) where g is strictly monotone, then bmi_i < bmi_j <=> g(bmi_i) < g(bmi_j)
>
> CART chooses split thresholds by sorting a feature and scanning cut points; only the order matters. A strictly monotonic transform preserves that order, so the same partitions of the data are available (just at transformed thresholds). Hence training fit and structure remain essentially unchanged (up to ties/rounding). The entropy or impurity of the partitions remain the same as the proportion of points in each bucket doesnt change.

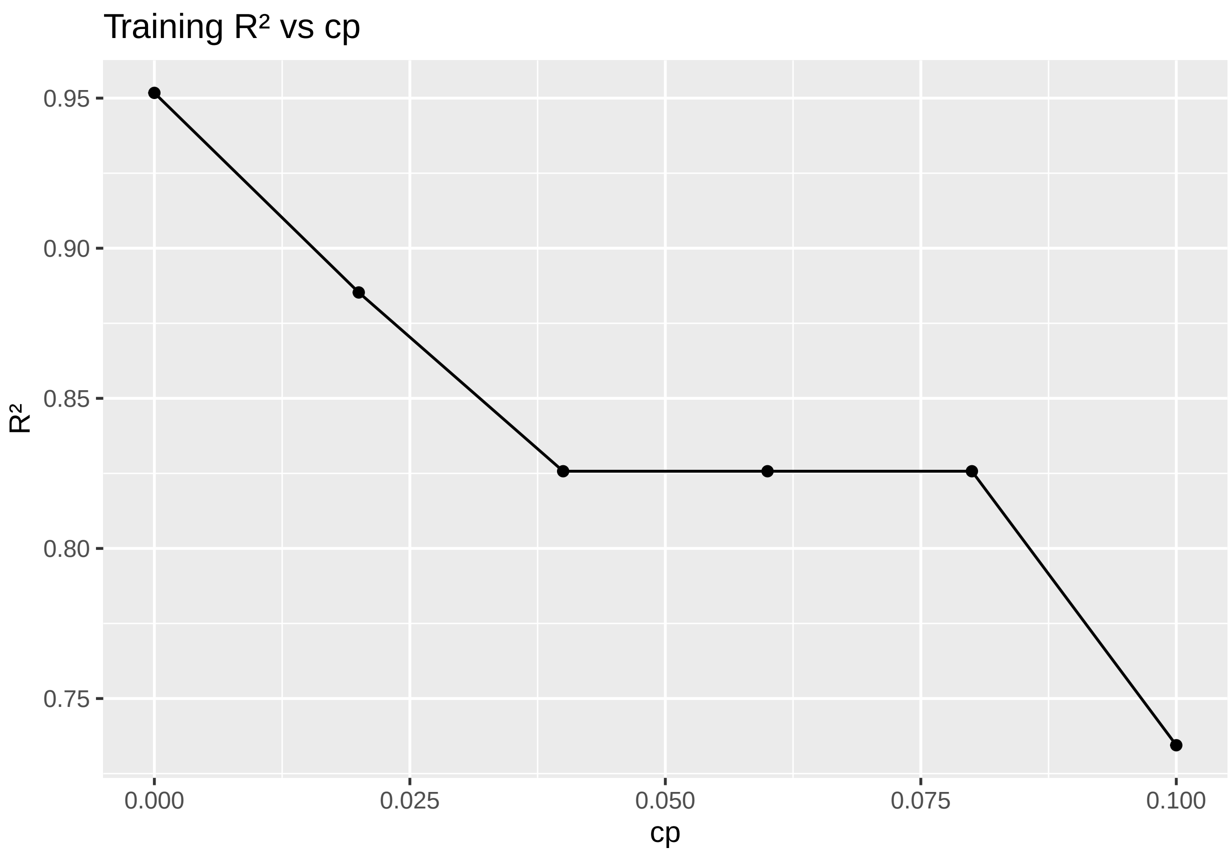
e)

Firstly, we should define clearly which dependent variables we would like to keep. We will not use bmi since it is highly correlated to f_bmi, as shown above. We will keep age, and add charges, since it is not a value we aim to predict anymore.

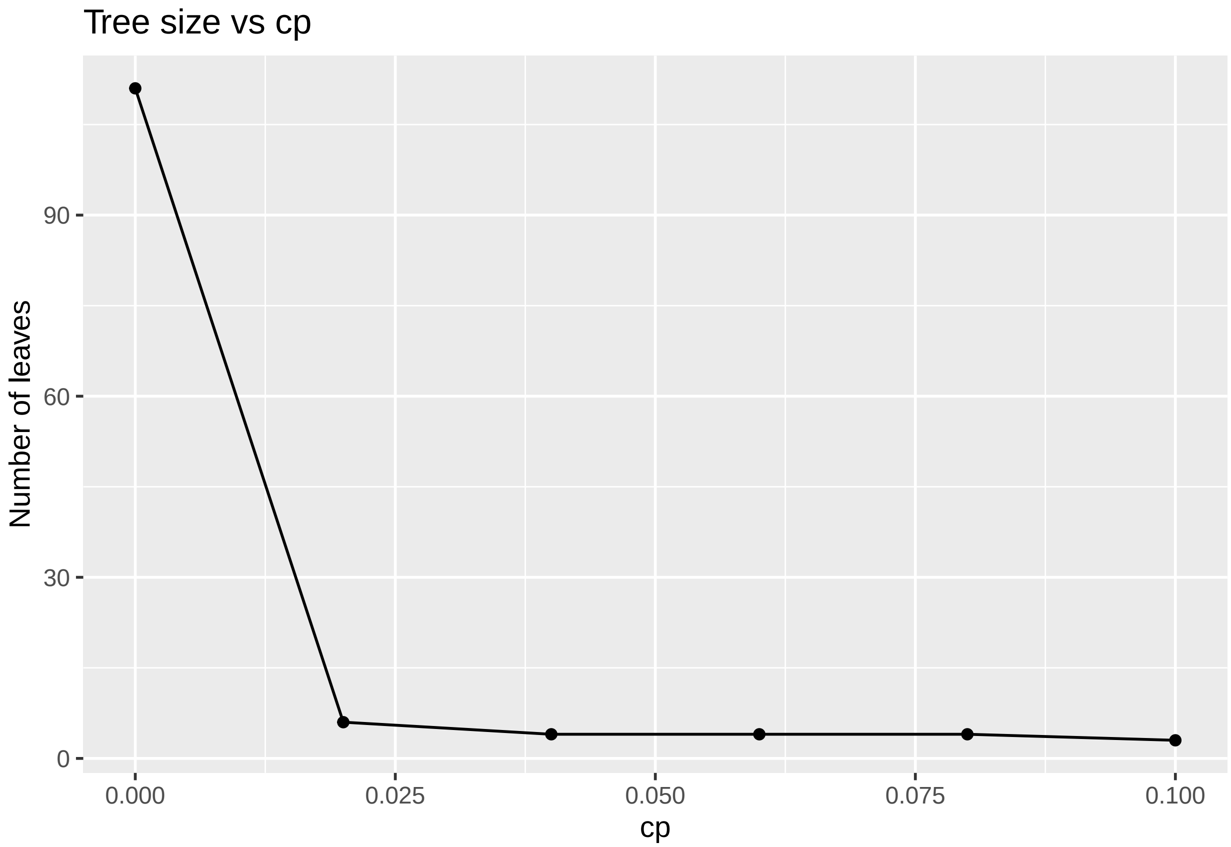
```r
# Grid of cp values
cps <- c(0, 0.02, 0.04, 0.06, 0.08, 0.1)

# Fit tree at a given cp and compute training metrics
fit_one <- function(cp) {

  fit <- rpart(cardiovascular_care_cost ~ age + f_bmi + charges,
               data = df,
               control = rpart.control(cp = cp))  # keep other defaults

  y <- df$cardiovascular_care_cost
  pred <- predict(fit, df)
  rss <- sum((y - pred)^2); tss <- sum((y - mean(y))^2)
  r2  <- 1 - rss/tss
  rmse <- sqrt(mean((y - pred)^2))

  leaves <- sum(fit$frame$var == "<leaf>")

  depth <- max(rpart:::tree.depth(as.numeric(row.names(fit$frame))))

  tibble(cp = cp, R2 = r2, RMSE = rmse, Leaves = leaves, Depth = depth, model = list(fit))
}

# Run fits
res <- bind_rows(lapply(cps, fit_one))

# Show summary table (metrics only)
res %>% select(cp, R2, RMSE, Leaves, Depth)
```

```
## # A tibble: 6 x 5
##      cp    R2  RMSE Leaves Depth
##   <dbl> <dbl> <dbl>  <int> <dbl>
## 1  0    0.952  169.    111    12
## 2  0.02 0.885  261.      6     3
## 3  0.04 0.826  321.      4     2
## 4  0.06 0.826  321.      4     2
## 5  0.08 0.826  321.      4     2
## 6  0.1  0.734  397.      3     2
```

```
# Plots how fit and complexity change with cp
ggplot(res, aes(cp, R2)) + geom_line() + geom_point() +
  labs(title = "Training R² vs cp", x = "cp", y = "R²")
```



```r
ggplot(res, aes(cp, Leaves)) + geom_line() + geom_point() +
  labs(title = "Tree size vs cp", x = "cp", y = "Number of leaves")
```

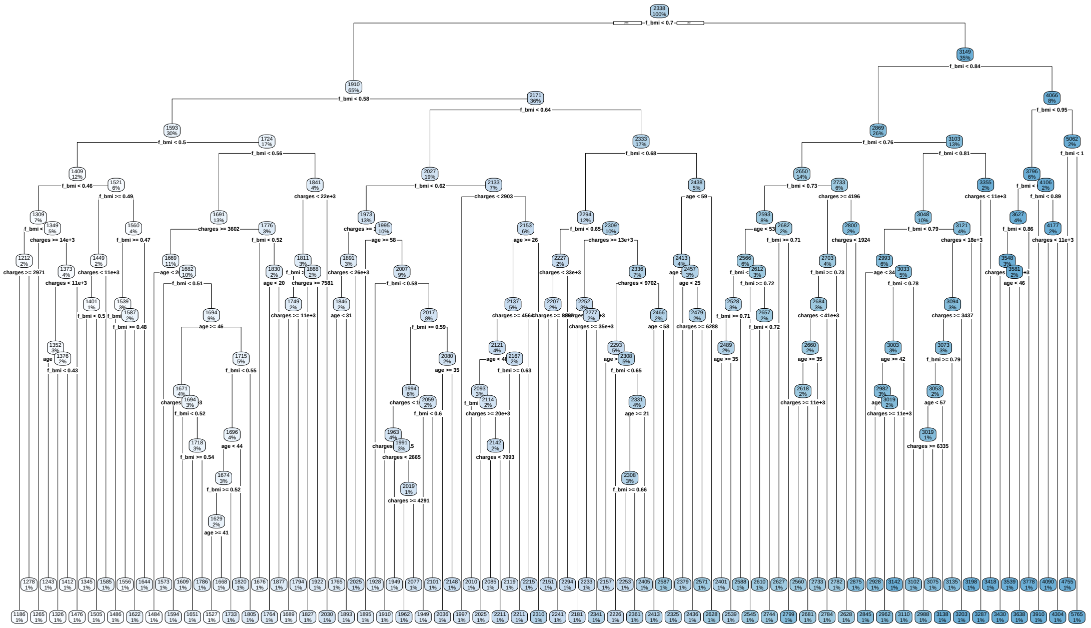


```
# Plot each tree (one after another)
for (i in seq_len(nrow(res))) {
  cat("\n\n## cp =", res$cp[i], "\n")
  rpart.plot(res$model[[i]],
             main = paste0("CART: cardiovascular_care_cost (cp = ", res$cp[i], ")"))
}
```

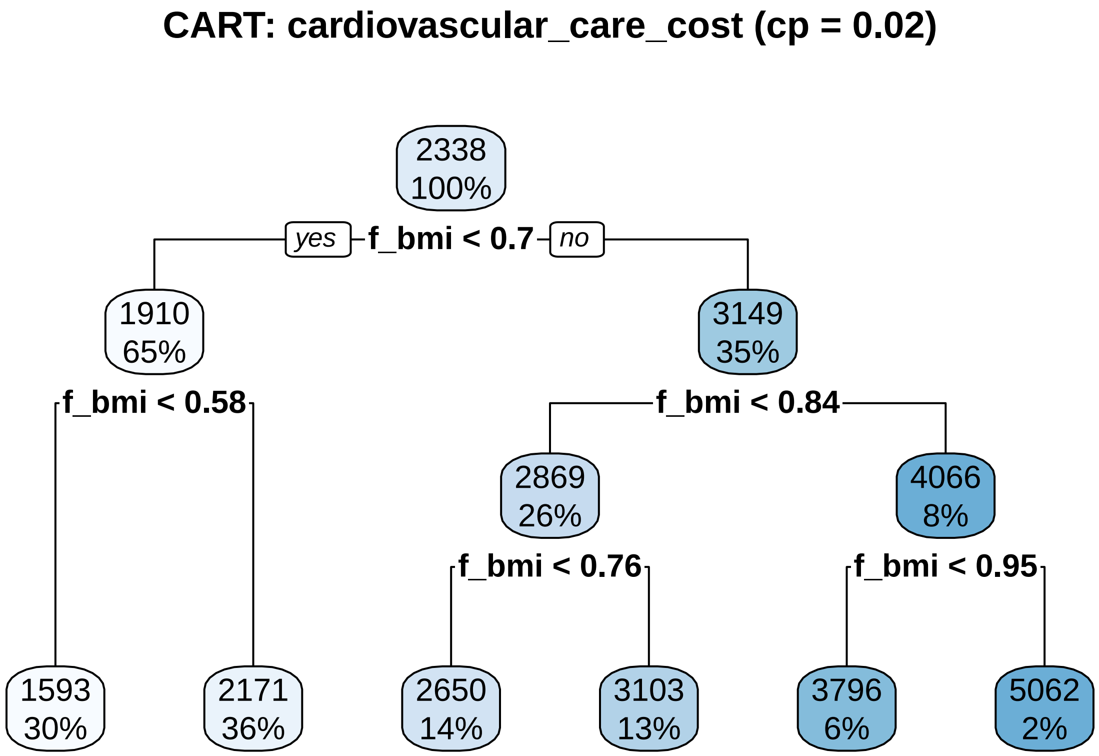
```
##
##
## ## cp = 0
```

```
## Warning: labs do not fit even at cex 0.15, there may be some overplotting
```

CART: cardiovascular_care_cost (cp = 0)

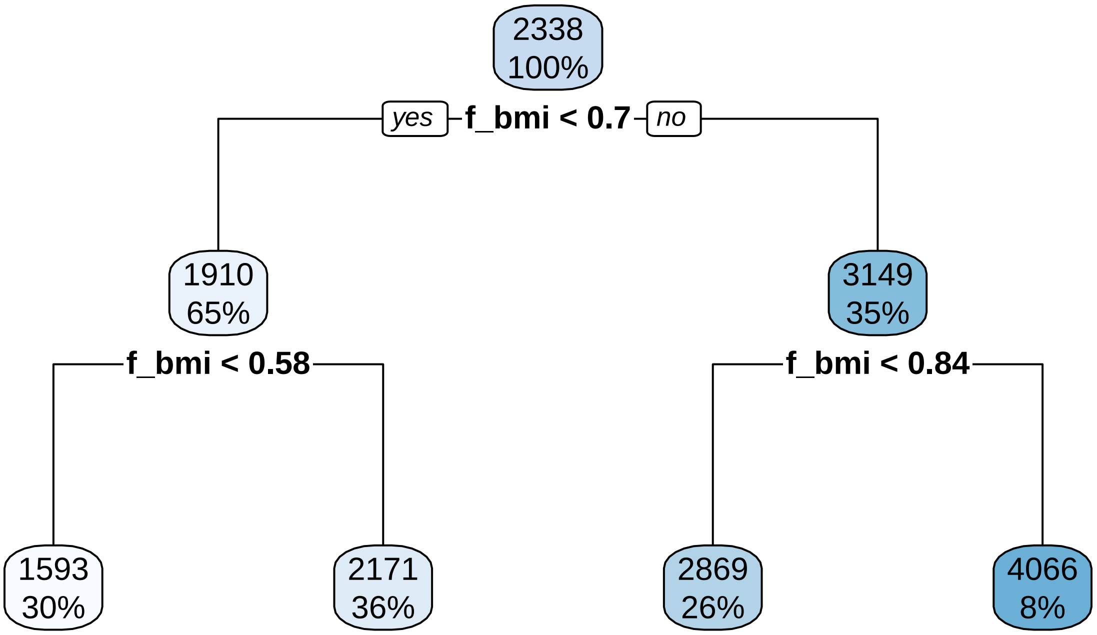


```
##
##
## ## cp = 0.02
```



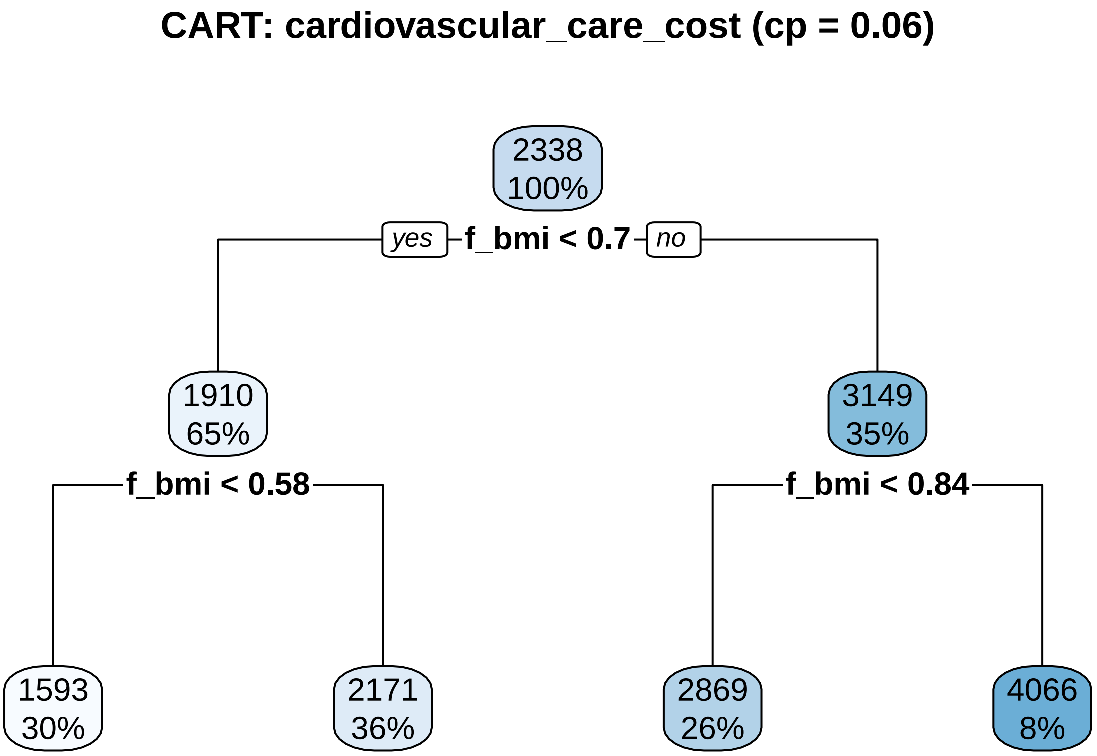
CART: cardiovascular_care_cost (cp = 0.02)

```
##
##
## ## cp = 0.04
```



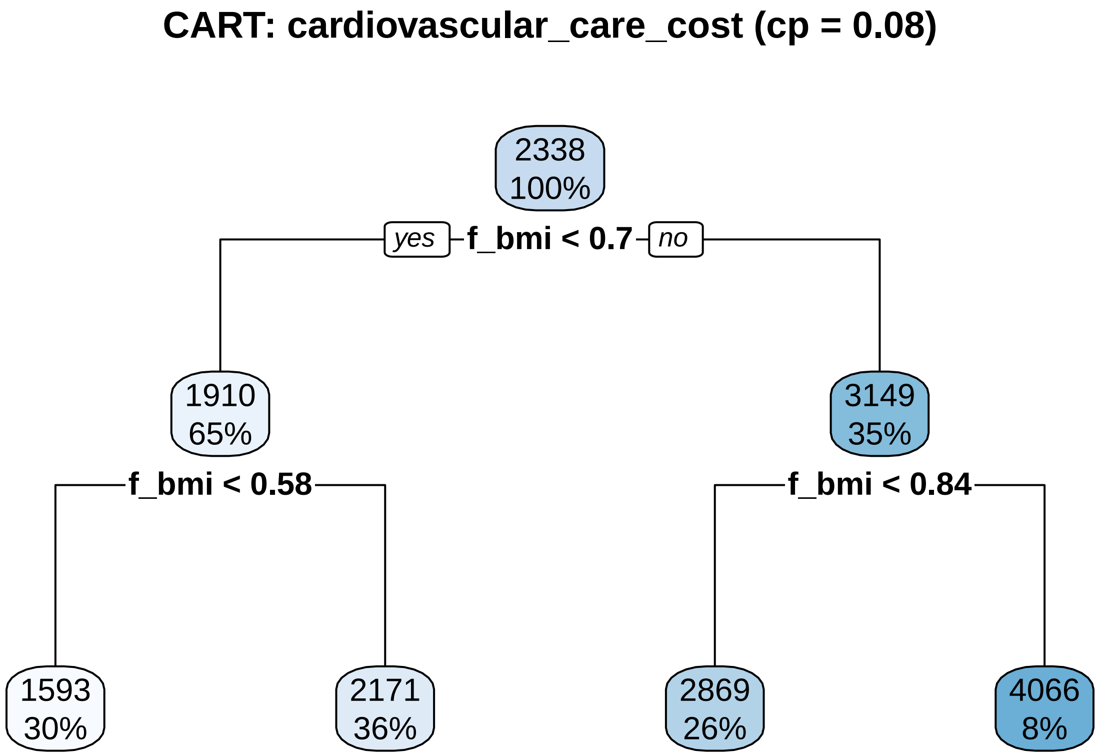
CART: cardiovascular_care_cost (cp = 0.04)

```
##
##
## ## cp = 0.06
```

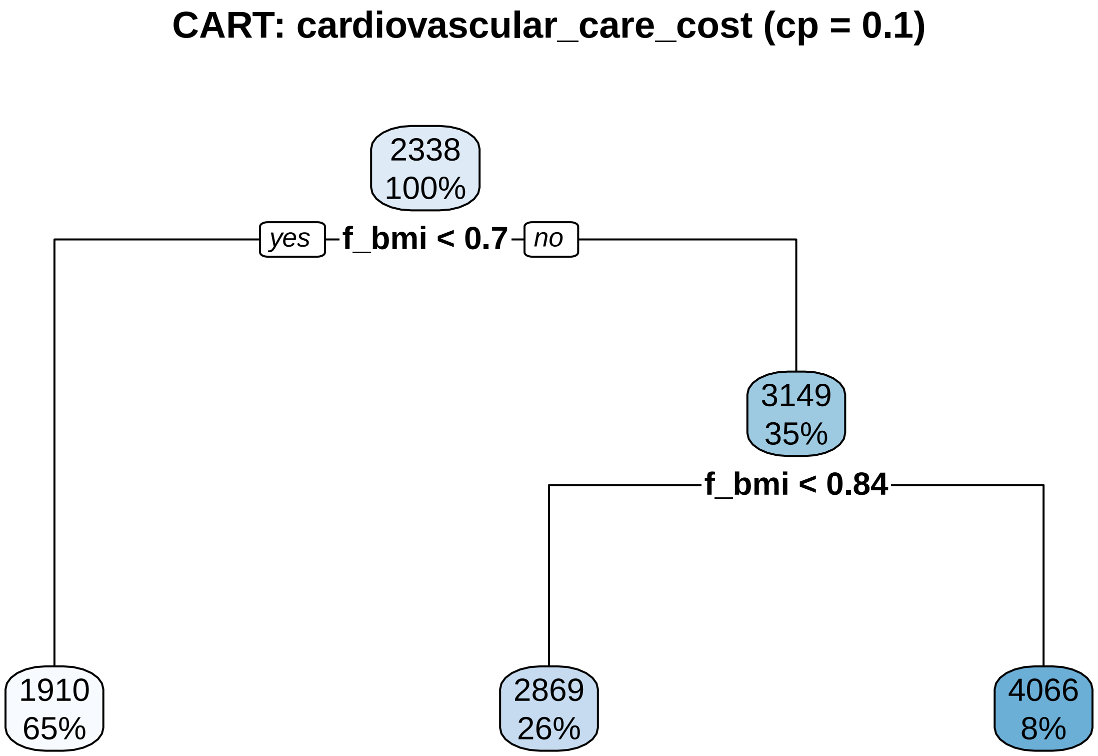


CART: cardiovascular_care_cost (cp = 0.06)

```
##
##
## ## cp = 0.08
```


CART: cardiovascular_care_cost (cp = 0.08)
2338
100%
yes
f_bmi < 0.7
no
1910
65%
3149
35%
f_bmi < 0.58
f_bmi < 0.84
1593
30%
2171
36%
2869
26%
4066
8%

```
##
##
## ## cp = 0.1
```



When cp = 0, the tree grows very deep (12 levels, 111 leaves), leading to extremely high training R^2 (~0.95) but clear overfitting, as seen in the highly complex structure. Increasing cp prunes the tree aggressively: at cp = 0.02, the tree shrinks to just 6 leaves and R^2 drops to ~0.89. For cp = 0.04–0.08, the tree stabilizes with 4 leaves and depth 2, achieving R^2 around 0.83, which indicates a simpler but still reasonable fit. Finally, at cp = 0.10, the tree becomes even smaller (3 leaves, depth 2) and the R^2 falls further to ~0.73, showing underfitting.

In summary, smaller cp values allow deeper trees with very high training R^2 (~0.95) but clear overfitting, while larger cp values prune the tree aggressively, reducing variance but increasing bias. The appropriate cp should be chosen by cross-validated error using the 1-SE rule. In this case, cp around 0.04–0.06 yields a shallow tree (4 leaves, depth 2) with R^2 ~0.83 — a balance between interpretability and reasonable fit.