

# APPLICATIONS



OF DATA SCIENCE

# The Trees

## Applications of Data Science - Class 12

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# The Pros and Cons of Trees

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# Pros

- It's just a set of if-else statements my 7-8-9 y/o can get
- Highly interpretable (when tree is not large)
- Easy to implement
- Fast? (to predict)
- Little pre-processing of predictors needed
- Handle all types of predictors (continuous, categorical)
- Handle missing data, *predict* missing data
- Assumption free
- Feature selection built-in (but when predictors are correlated...)
- Low bias, in general

# Cons

- High variance, in general
- Rectangular predictor regions - not always a good thing
- Complexity of prediction limited in no. of leaves! (For a simple CART)
- Not so fast? (to train)
- Greedy
- Selection Bias of predictors with more distinct values?
- Variable Importance when predictors are correlated

# Detour: A Regression Problem

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# OKCupid: Predicting Annual Income

It won't be easy:

```
okcupid <- read_csv("~/okcupid.csv.zip")  
  
okcupid %>% count(income, sort = TRUE) %>% head(20)  
  
## # A tibble: 13 x 2  
##       income     n  
##       <dbl> <int>  
## 1      -1  48442  
## 2    20000   2952  
## 3   100000   1621  
## 4    80000   1111  
## 5    30000   1048  
## 6    40000   1005  
## 7    50000    975  
## 8    60000    736  
## 9    70000    707  
## 10   150000    631  
## 11  1000000    521  
## 12   250000    149  
## 13   500000     48
```

We will stick to non-NA (income) observations, and predict  $\log_{10}(income/100000)$ :

```
okupid2 <- okupid %>%
  mutate(income = ifelse(income == -1, NA, log10(income/100000)))
  drop_na(income)
```

In the vector `predictors` (see slides Rmd source) we have 42 continuous and categorical variables which may or may not be predictive to income:

```
okupid2 <- okupid2 %>%
  select(income, all_of(predictors)) %>%
  mutate(id = 1:n())
dim(okupid2)
```

```
## [1] 11504     44
```

```
glimpse(okcupid2)
```

```
## #> Rows: 11,504  
## #> Columns: 44  
## #> $ income <dbl> -0.09691001, -0.69897000, -0.39794001, -0...  
## #> $ age <dbl> 35, 23, 28, 30, 29, 40, 31, 22, 35, 31, 21...  
## #> $ height_cm <dbl> 177.80, 180.34, 182.88, 167.64, 157.48, 18...  
## #> $ sex <fct> m, m, m, f, f, m, f, m, m, f, m, m, f, m,...  
## #> $ body_type <fct> average, thin, average, skinny, thin, fit,...  
## #> $ body_type_not_perfect <fct> TRUE, FALSE, TRUE, FALSE, FALSE, FALSE, FA...  
## #> $ diet2 <fct> other, vegetarian, anything, anything, any...  
## #> $ drinks <fct> often, socially, socially, socially, social...  
## #> $ drugs <fct> sometimes, NA, never, never, never, NA, so...  
## #> $ religion2 <fct> atheist, NA, christian, christian, christi...  
## #> $ education2 <fct> other, student1, degree1, high_school, stu...  
## #> $ education_kind <fct> working, working, graduated, graduated, wo...  
## #> $ education_academic <fct> FALSE, FALSE, TRUE, FALSE, FALSE, TRUE, FA...  
## #> $ ethnicity2 <fct> white, white, white, white, other, white,...  
## #> $ part_black <fct> FALSE, FALSE, FALSE, FALSE, FALSE, FALSE,...  
## #> $ part_white <fct> TRUE, TRUE, TRUE, TRUE, TRUE, NA, FA...  
## #> $ part_asian <fct> FALSE, FALSE, FALSE, FALSE, FALSE, FALSE,...  
## #> $ part_hispanic <fct> FALSE, FALSE, FALSE, FALSE, TRUE, FALSE, NA...  
## #> $ job3 <fct> travel, student, financial, marketing, othe...  
## #> $ orientation <fct> straight, straight, straight, straight, stra...  
## #> $ pets_has_dogs <fct> FALSE, FALSE, FALSE, TRUE, FALSE, FALSE, NA...  
## #> $ pets_has_cats <fct> FALSE, FALSE, FALSE, FALSE, TRUE, FALSE, NA...  
## #> $ pets_likes_cats <fct> TRUE, TRUE, TRUE, TRUE, FALSE, FALSE, NA...  
## #> $ pets_likes_dogs <fct> TRUE, FALSE, FALSE, FALSE, TRUE, TRUE, NA...  
## #> $ sian_fun <fct> FALSE, FALSE, FALSE, NA, FALSE, TRUE, NA,
```

## We split the data into training, validation and test sets:

```
# test_idx <- sample(1:nrow(okcupid2), 2000, replace = FALSE)
# train_idx <- okcupid2 %>% filter(!id %in% test_idx) %>% slice_sample(2000)
# valid_idx <- okcupid2 %>% filter(!id %in% test_idx, !id %in% train_idx)
okcupid2 <- okcupid2 %>% select(-id)

idx <- read_rds("../data/okcupid2_idx.rda")
train_idx <- idx$train_idx
valid_idx <- idx$valid_idx
test_idx <- idx$test_idx

okcupid2_train <- okcupid2[train_idx, ]
okcupid2_valid <- okcupid2[valid_idx, ]
okcupid2_test <- okcupid2[test_idx, ]

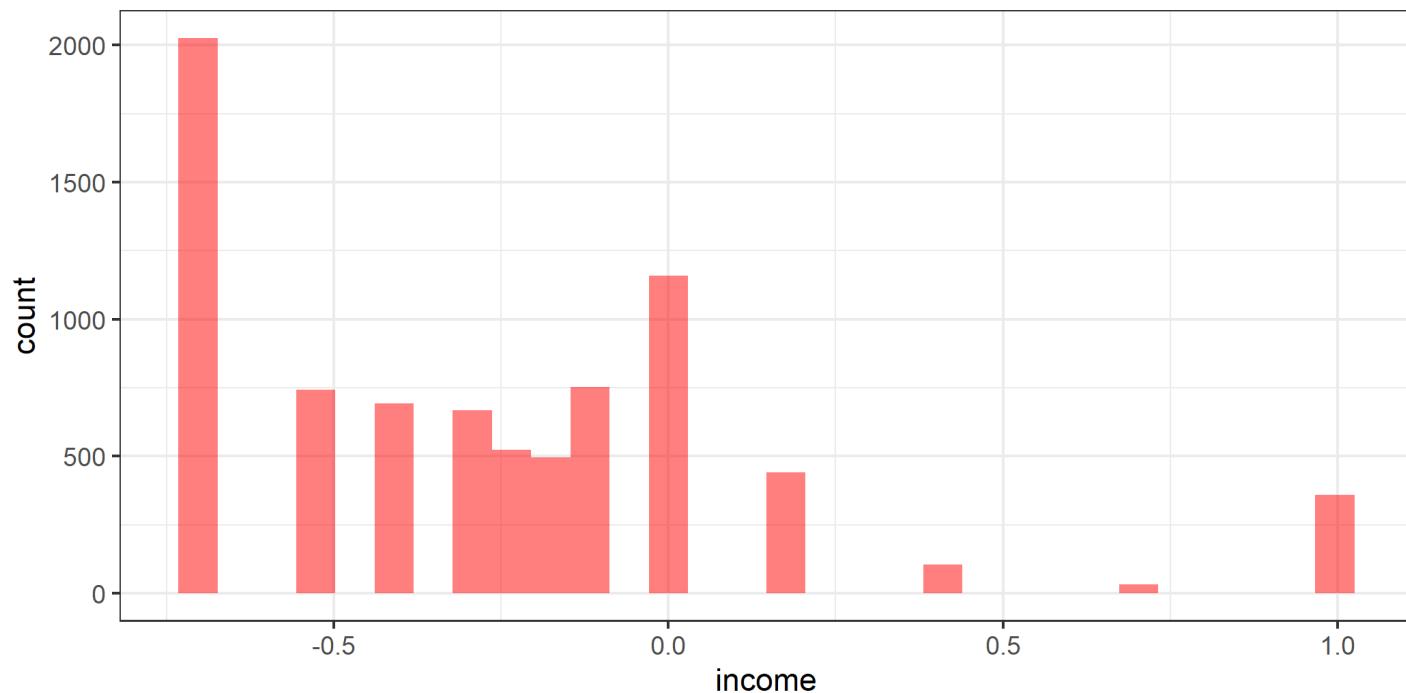
library(glue)
glue("train no. of rows: {nrow(okcupid2_train)}
      validation no. of rows: {nrow(okcupid2_valid)}
      test no. of rows: {nrow(okcupid2_test)}")
```

```
## train no. of rows: 8000
## validation no. of rows: 1504
## test no. of rows: 2000
```

Our transformed income dependent variable behaves "ok":

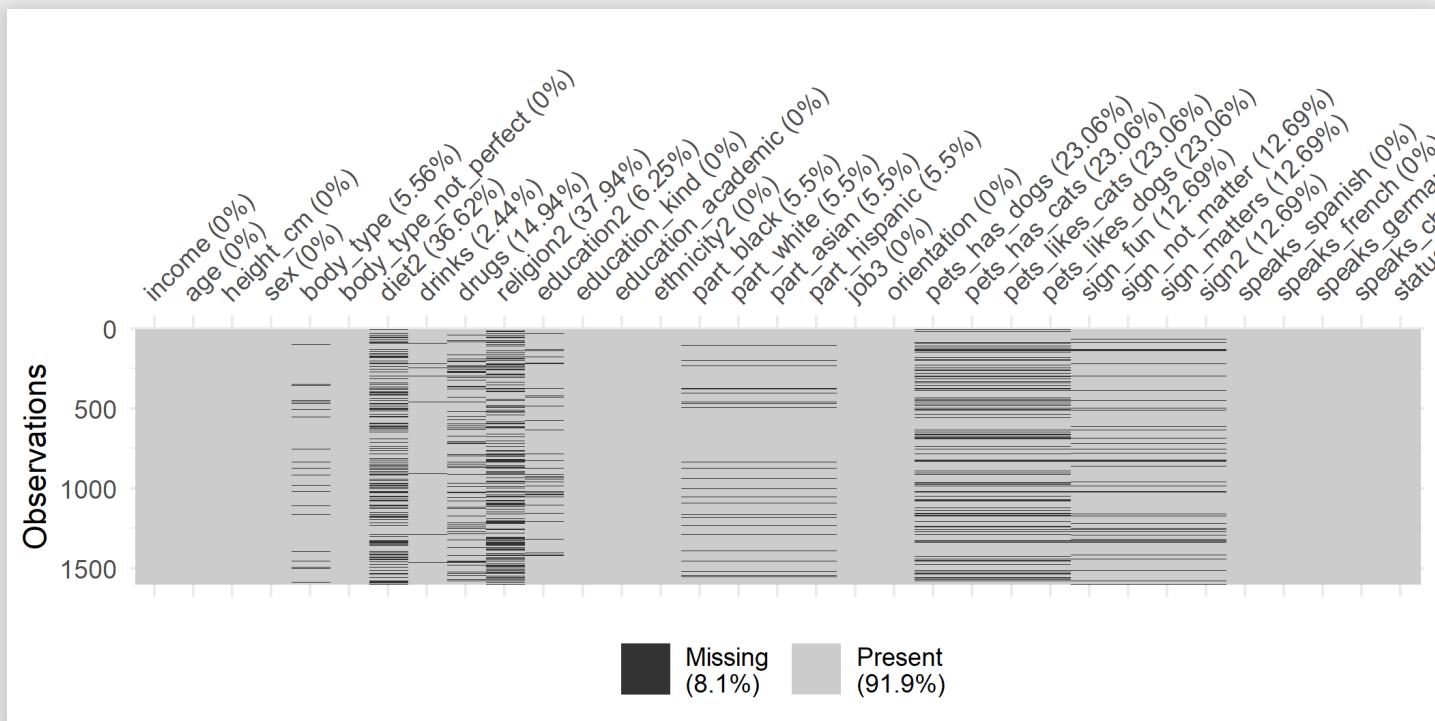
```
ggplot(okcupid2_train, aes(income)) +  
  geom_histogram(fill = "red", alpha = 0.5) +  
  theme_bw()
```



We can quickly see percentage of missing values with [naniar](#):

```
library(naniar)

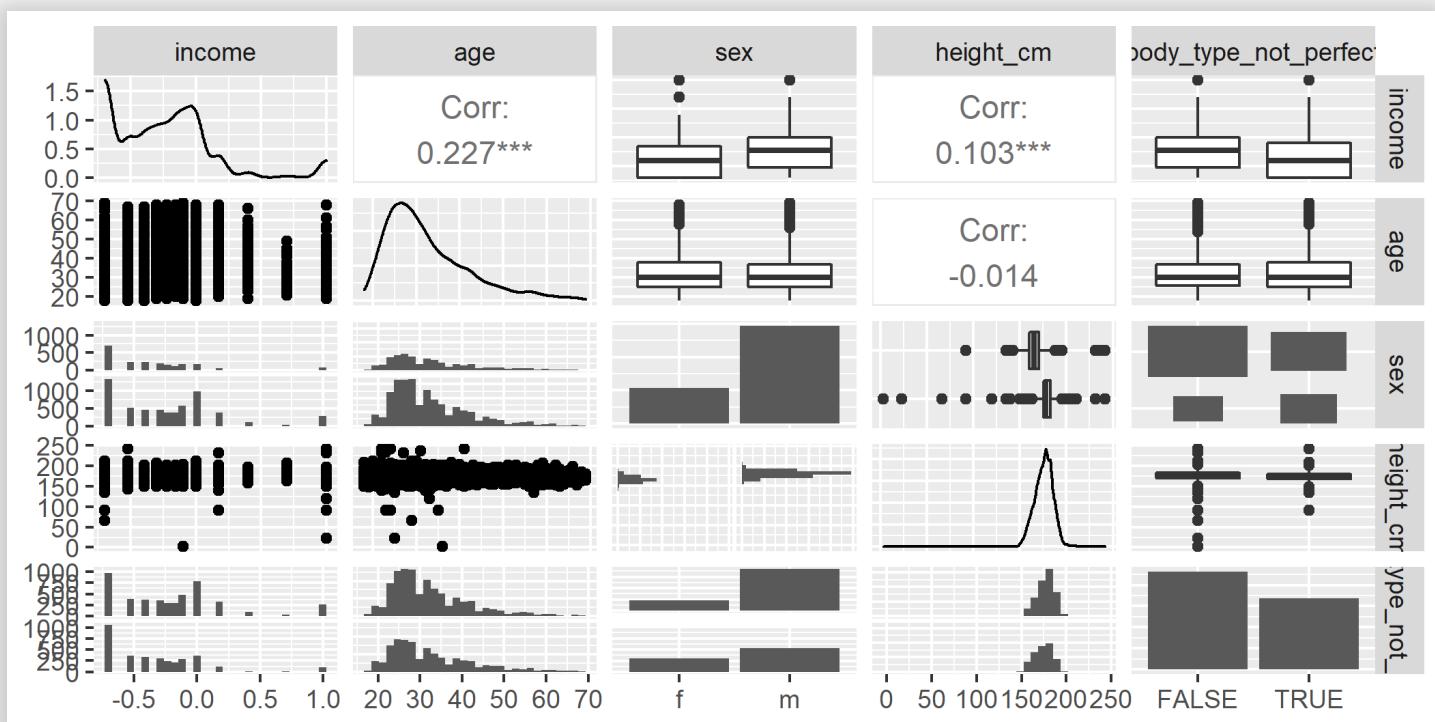
vis_miss(okcupid2_train %>%
          sample_frac(0.2) %>%
          select(-starts_with("essay")))
```



Also worth exploring some basic relations between predictors and income. You can use the work of others, e.g. [ggpairs](#):

```
library(GGally)
```

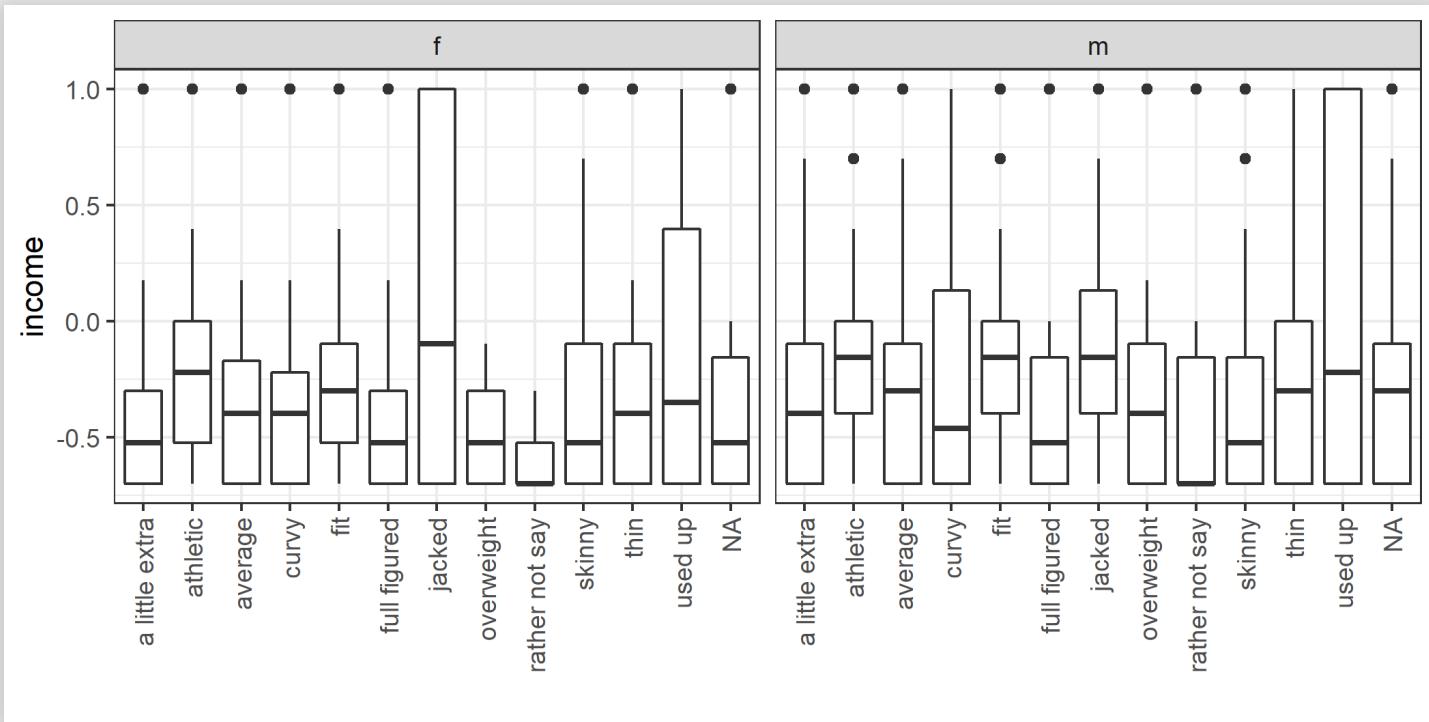
```
ggpairs(okcupid2_train %>%
           select(income, age, sex, height_cm, body_type_not_perfec
```



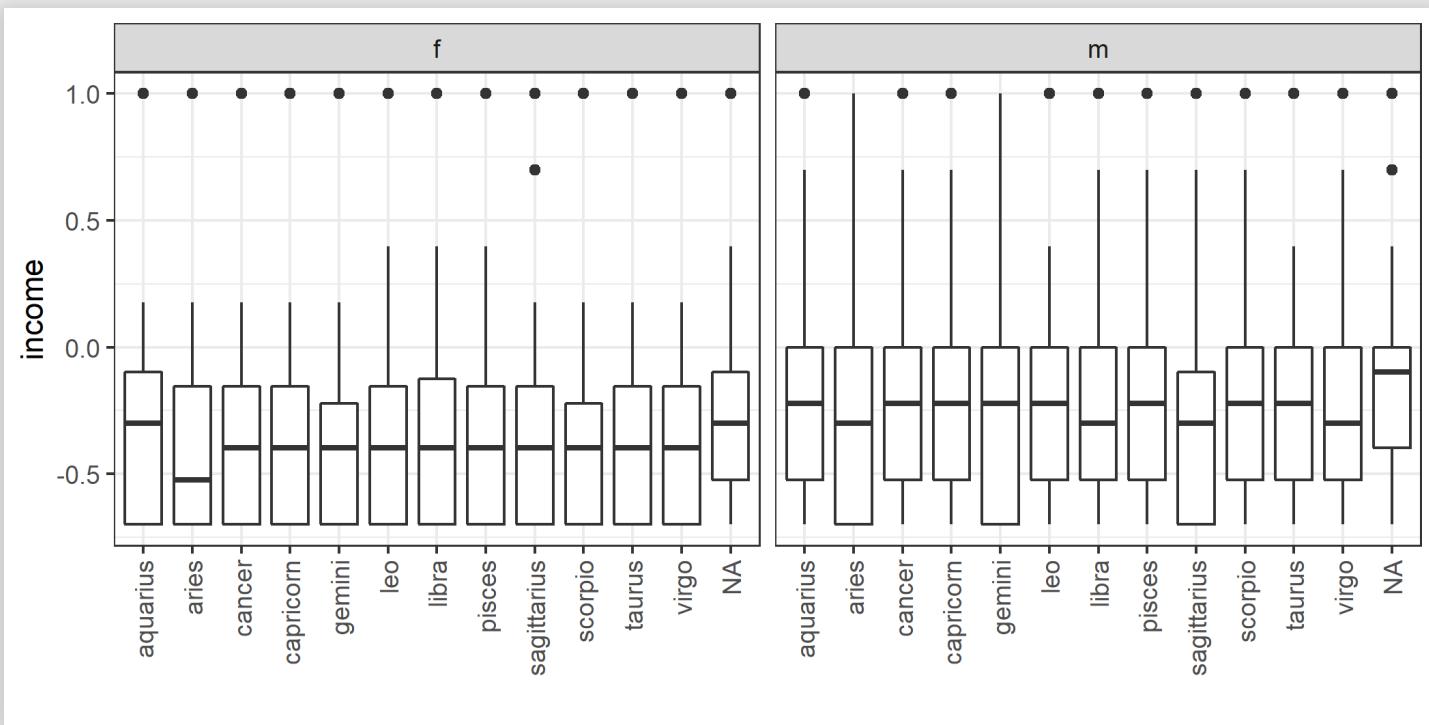
But don't be ashamed of simply exploring on your own:

```
var_vs_income_boxplot <- function(var) {  
  ggplot(okcupid2_train, aes({{var}}, income)) +  
  geom_boxplot() +  
  facet_wrap(~ sex) +  
  theme_bw() +  
  labs(x = "") +  
  theme(axis.text.x = element_text(angle = 90, hjust = 1, vjust =  
})
```

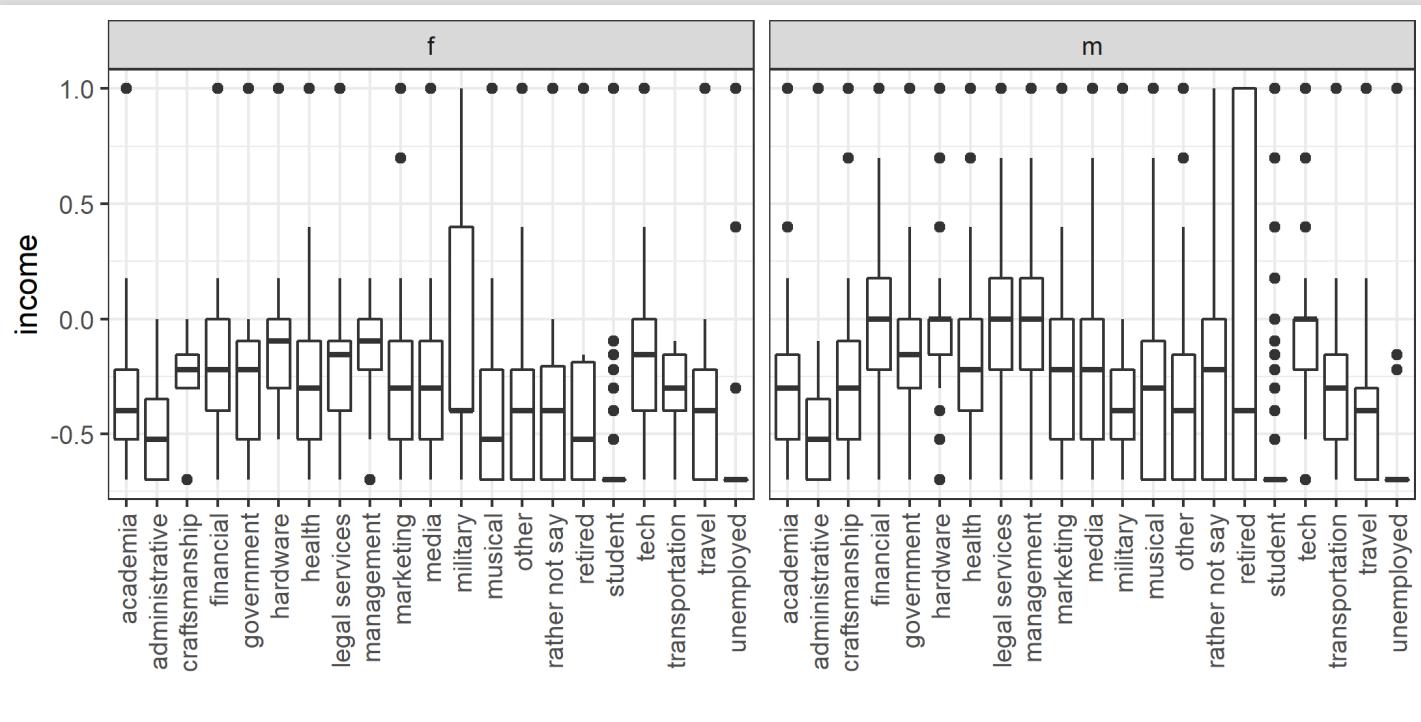
```
var_vs_income_boxplot(body_type)
```



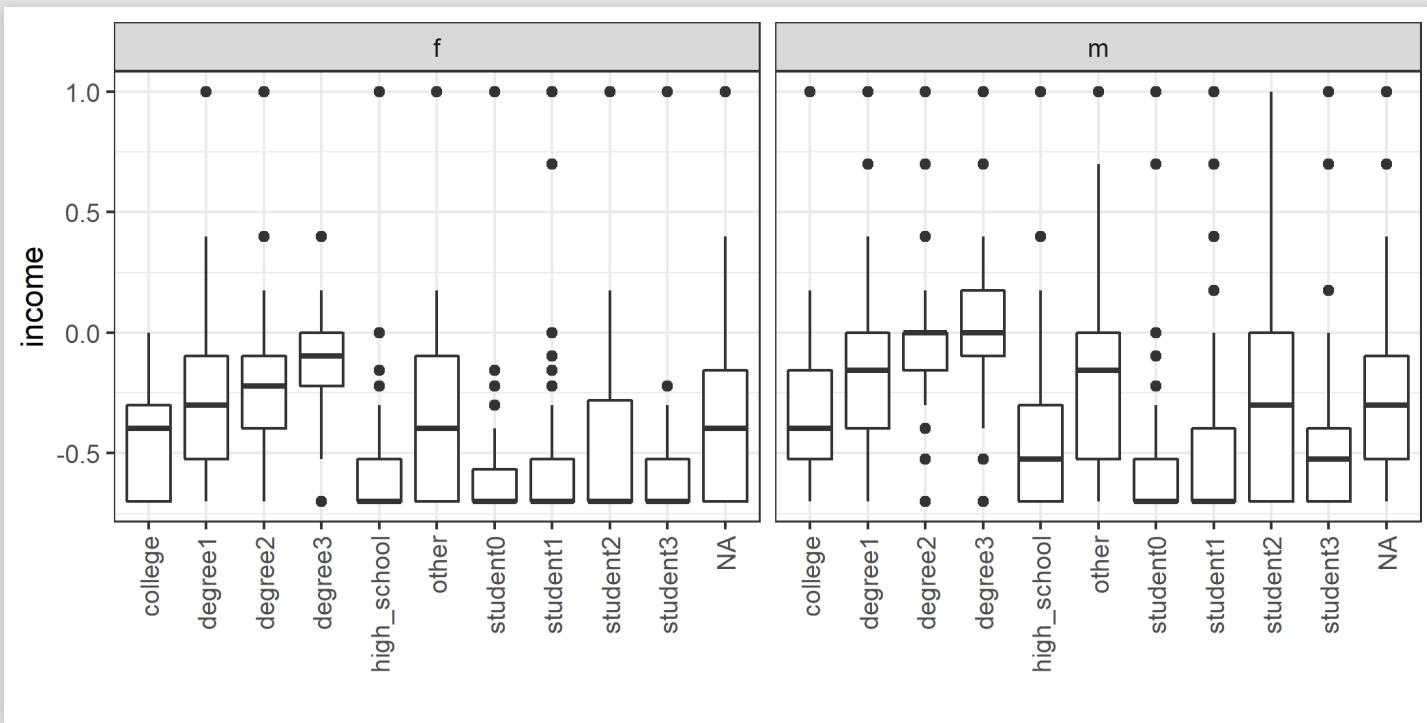
```
var_vs_income_boxplot(sign2)
```



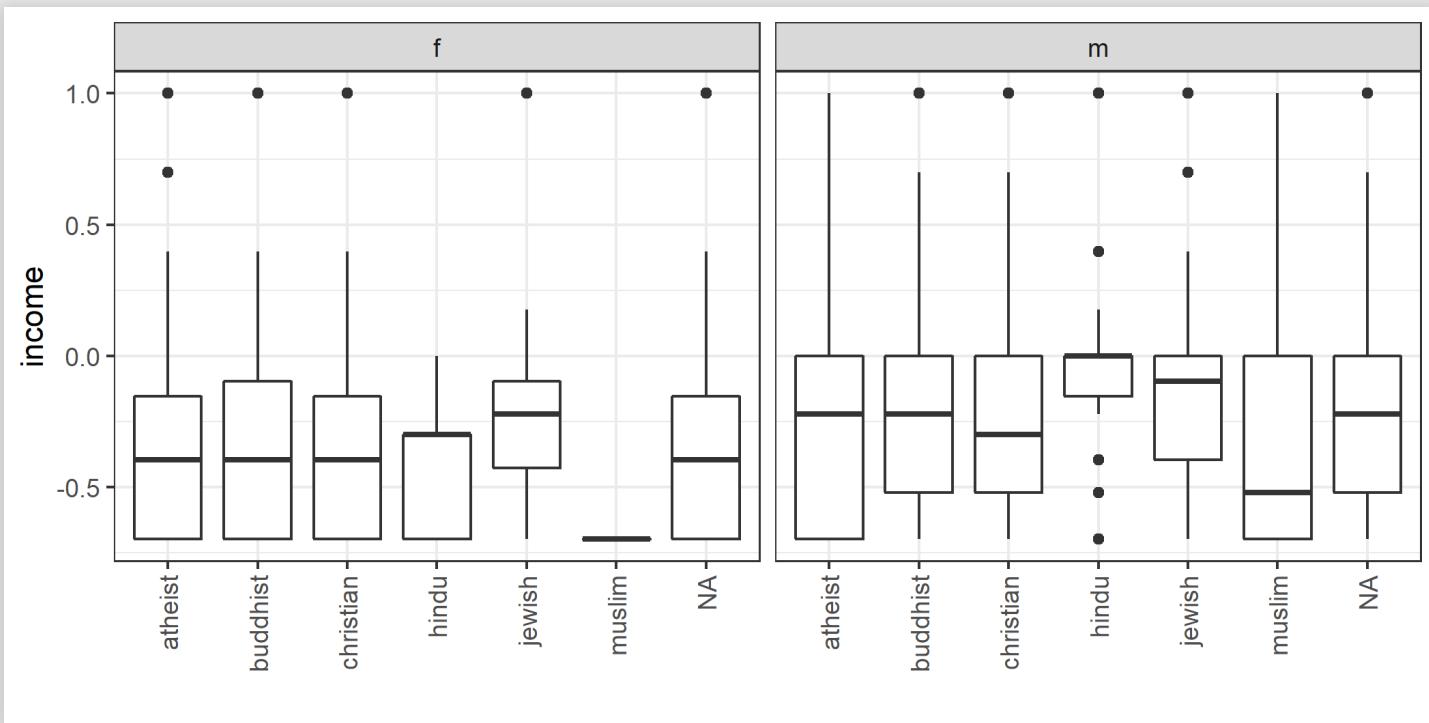
```
var_vs_income_boxplot(job3)
```



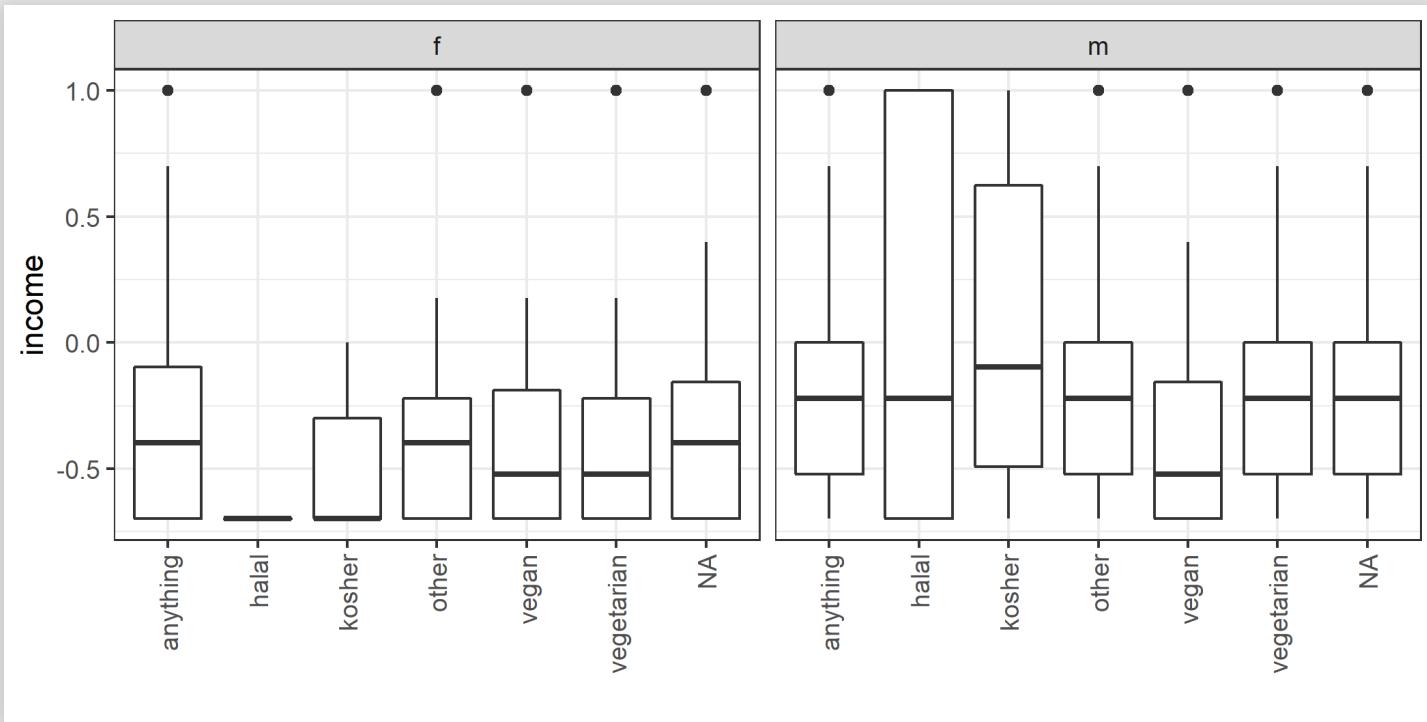
```
var_vs_income_boxplot(education2)
```



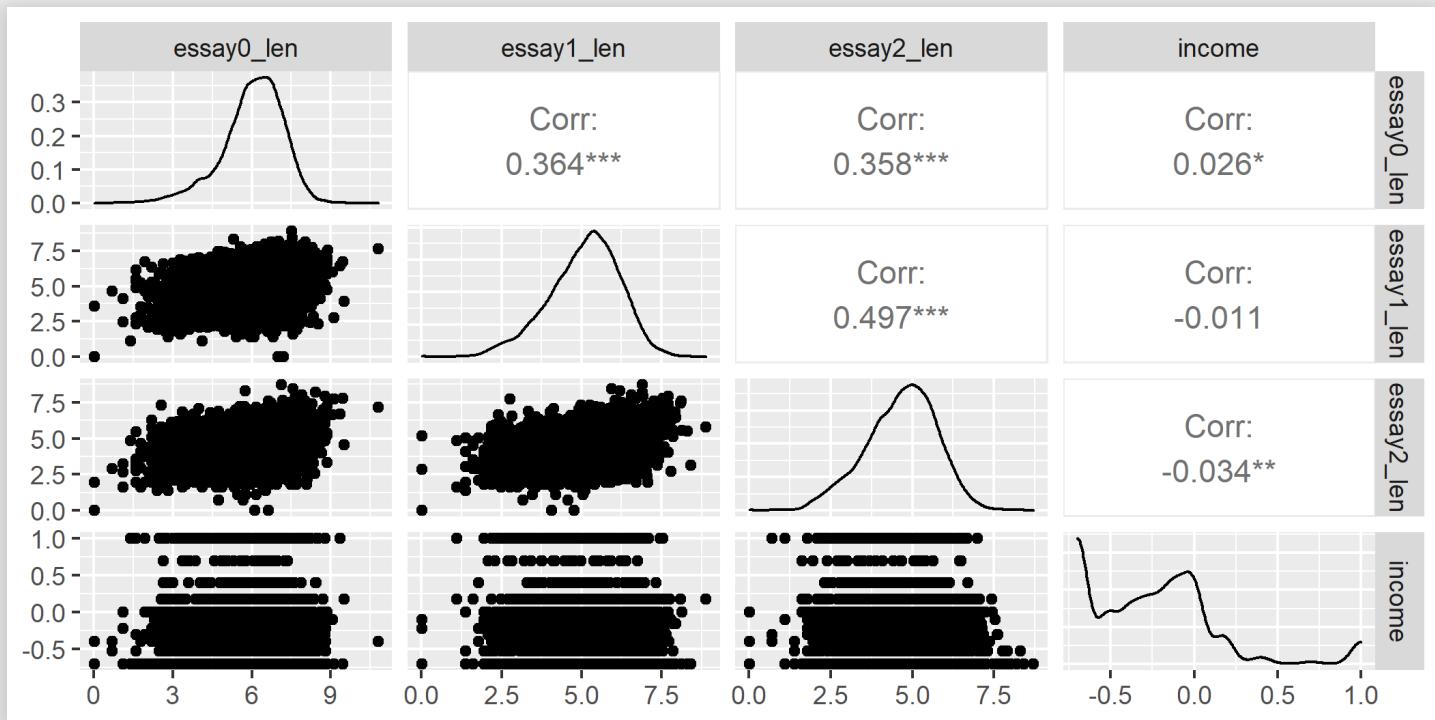
```
var_vs_income_boxplot(religion2)
```



```
var_vs_income_boxplot(diet2)
```



```
ggpairs(okcupid2_train %>%
         select(essay0_len:essay2_len, income))
```



# Baseline: Linear Regression

R's `lm` function does not take NA values.

One strategy is to impute these values using a "common" value such as the median for continuous variables and mode for categorical variables. This can easily be achieved with `naniar`:

```
okcupid2_imp <- naniar::impute_median_all(okcupid2)
okcupid2_imp_train <- okcupid2_imp[train_idx, ]
okcupid2_imp_valid <- okcupid2_imp[valid_idx, ]

mod_lm <- lm(income ~ ., data = okcupid2_imp_train)
pred_lm <- predict(mod_lm, okcupid2_imp_valid)

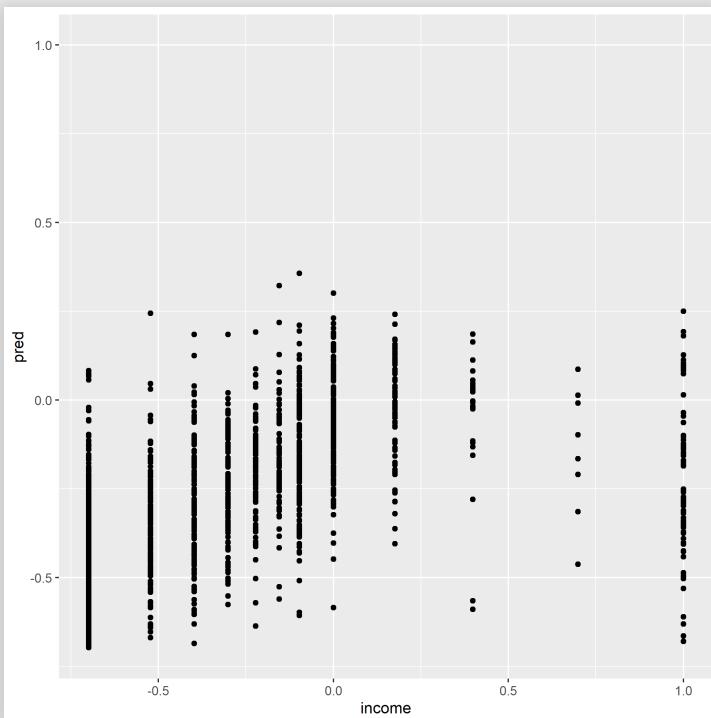
rmse <- function(obs, pred) sqrt(mean((obs - pred)^2))

report_rmse_and_cor <- function(obs, pred) {
  RMSE <- rmse(obs, pred)
  CORR <- cor(obs, pred)
  glue("RMSE: {format(RMSE, digits = 3)}\n      CORR: {format(CORR, digits = 3)}")
}
```

```
report_rmse_and_cor(okcupid2_valid$income, pred_lm)
```

```
## RMSE: 0.352  
## CORR: 0.501
```

```
tibble(income = okcupid2_valid$income, pred = pred_lm) %>%  
  ggplot(aes(income, pred)) + geom_point() + ylim(range(okcupid2_`
```



A more intelligent strategy for imputing missing values would be to *predict* them using whatever data is not missing. This can be done quite seamlessly with the [mice](#) package:

```
# library(mice)
# mice_obj <- mice(okcupid2, m = 1, maxit = 10, seed = 42)
# okcupid2_imp_mice <- complete(mice_obj)

okcupid2_imp_mice <- read_rds("../data/okcupid2_imp_mice.rds")
okcupid2_imp_mice_train <- okcupid2_imp_mice[train_idx, ]
okcupid2_imp_mice_valid <- okcupid2_imp_mice[valid_idx, ]

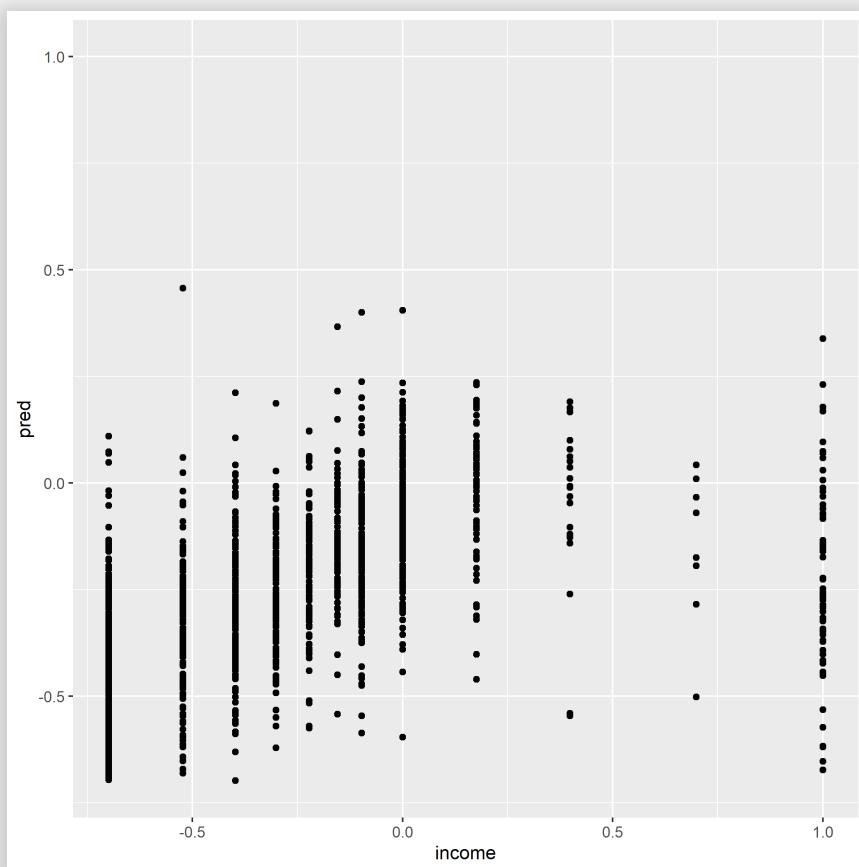
mod_lm_mice <- lm(income ~ ., data = okcupid2_imp_mice_train)
pred_lm_mice <- predict(mod_lm_mice, okcupid2_imp_mice_valid)

report_rmse_and_cor(okcupid2_valid$income, pred_lm_mice)

## RMSE: 0.351
## CORR: 0.504
```

 Can you think of other imputation strategies?

```
tibble(income = okcupid2_valid$income, pred = pred_lm_mice) %>%
  ggplot(aes(income, pred)) +
  geom_point() +
  ylim(range(okcupid2_valid$income))
```



# Baseline: Ridge Regression

```
library(glmnet)

okcupid2_imp_mat_train <- model.matrix(~ ., okcupid2_imp_mice_train)
okcupid2_imp_mat_valid <- model.matrix(~ ., okcupid2_imp_mice_valid)

ridge_cv <- cv.glmnet(x = okcupid2_imp_mat_train,
                      y = okcupid2_train$income, alpha = 0)

best_lambda <- ridge_cv$lambda.min

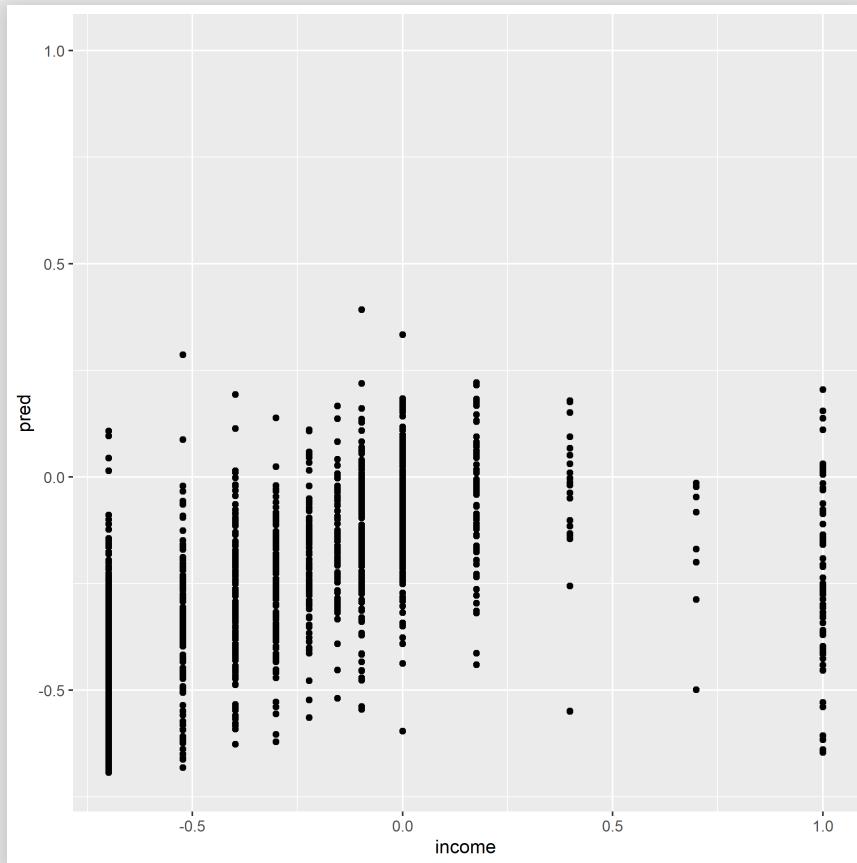
mod_lm_ridge <- glmnet(x = okcupid2_imp_mat_train,
                        y = okcupid2_train$income, alpha = 0,
                        lambda = best_lambda)

pred_lm_ridge <- predict(mod_lm_ridge, okcupid2_imp_mat_valid)

report_rmse_and_cor(okcupid2_valid$income, pred_lm_ridge)

## RMSE: 0.351
## CORR: 0.505
```

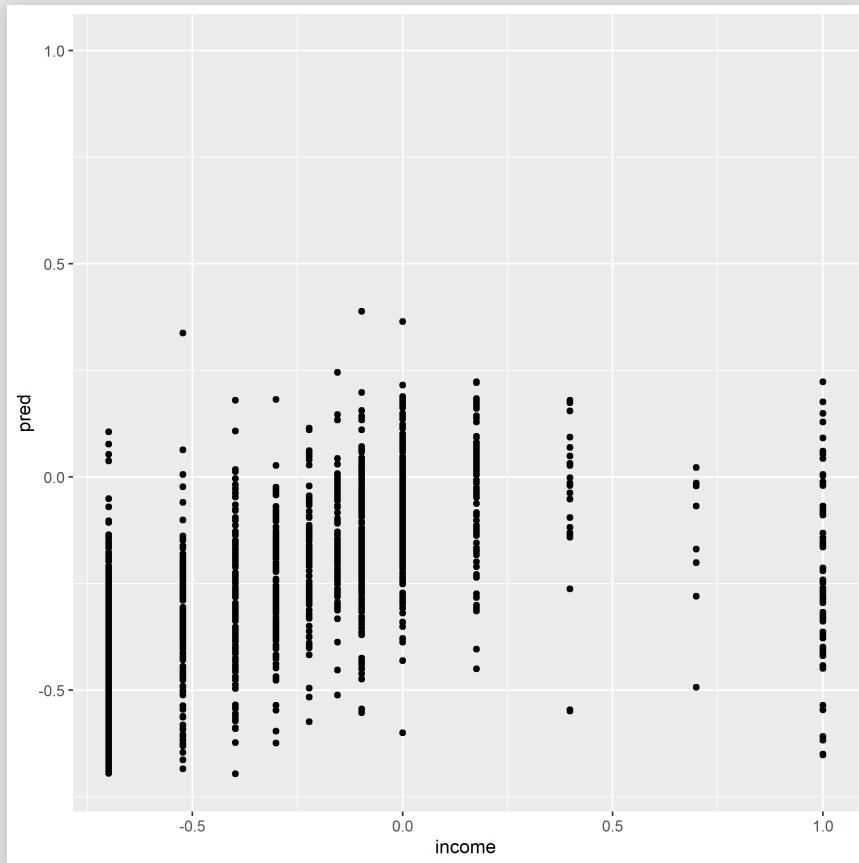
```
tibble(income = okcupid2_valid$income, pred = pred_lm_ridge) %>%
  ggplot(aes(income, pred)) +
  geom_point() +
  ylim(range(okcupid2_valid$income))
```



# Baseline: Lasso Regression

```
lasso_cv <- cv.glmnet(x = okupid2_imp_mat_train,  
                      y = okupid2_imp_train$income, alpha = 1)  
  
best_lambda <- lasso_cv$lambda.min  
  
mod_lm_lasso <- glmnet(x = okupid2_imp_mat_train,  
                        y = okupid2_train$income, alpha = 1,  
                        lambda = best_lambda)  
  
pred_lm_lasso <- predict(mod_lm_lasso, okupid2_imp_mat_valid)  
  
report_rmse_and_cor(okupid2_valid$income, pred_lm_lasso)  
  
## RMSE: 0.351  
## CORR: 0.506
```

```
tibble(income = okcupid2_valid$income, pred = pred_lm_lasso) %>%
  ggplot(aes(income, pred)) +
  geom_point() +
  ylim(range(okcupid2_valid$income))
```



# End of Detour

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# The CART (Regression)

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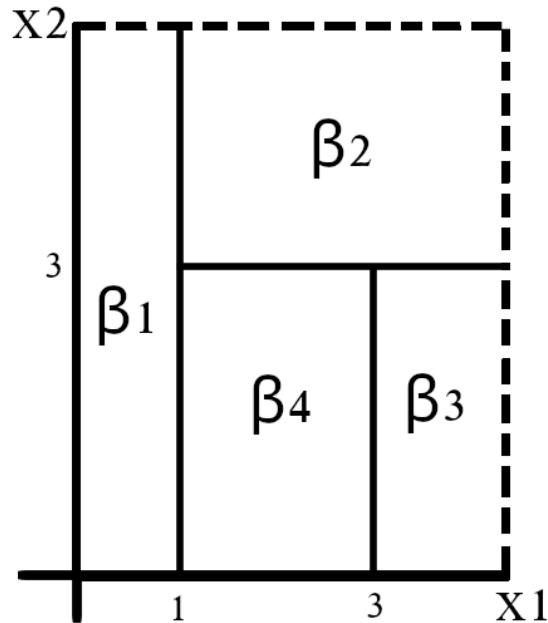
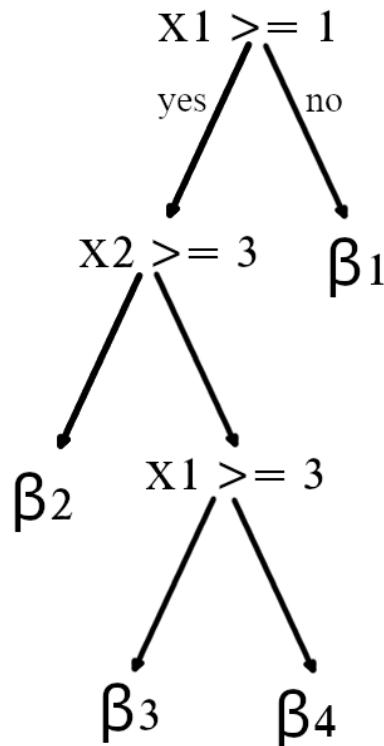
# The OG CART

1. Find the predictor to (binary) split on and the value of the split, by  $SSE$  criterion
2. For each resulting node if  $n_{node} > 20$  go to 1
3. Once full tree has been grown, perform pruning using the *cost-complexity parameter*  $c_p$  and the  $SSE_{c_p}$  criterion
4. Predict the average value at each terminal node
  - For each split *surrogate splits* are saved for future NAs
  - An alternative criterion for complexity could be tree maximum depth (sklearn)
  - One can also reduce all tree's unique paths to a set of rules
  - Variables can be ranked by "importance"



What if the best split isn't binary?

# Why *Rectangular* Regions?



💡 Does this remind you of anything?

# The $SSE$ criterion - continuous predictor

- $y$  is the continuous dependent variable
- a continuous predictor  $v$  is nominated for splitting the current node
- with splitting value  $l$
- such that  $S_1$  is the set of observations for which  $v_i \leq l$
- and  $S_2$  is the set of observations for which  $v_i > l$
- $\bar{y}_1$  is the average of  $y$  in set  $S_1$

$$SSE = \sum_{i \in S_1} (y_i - \bar{y}_1)^2 + \sum_{i \in S_2} (y_i - \bar{y}_2)^2$$

For example if `age` is candidate in splitting `income`:

```

library(patchwork)

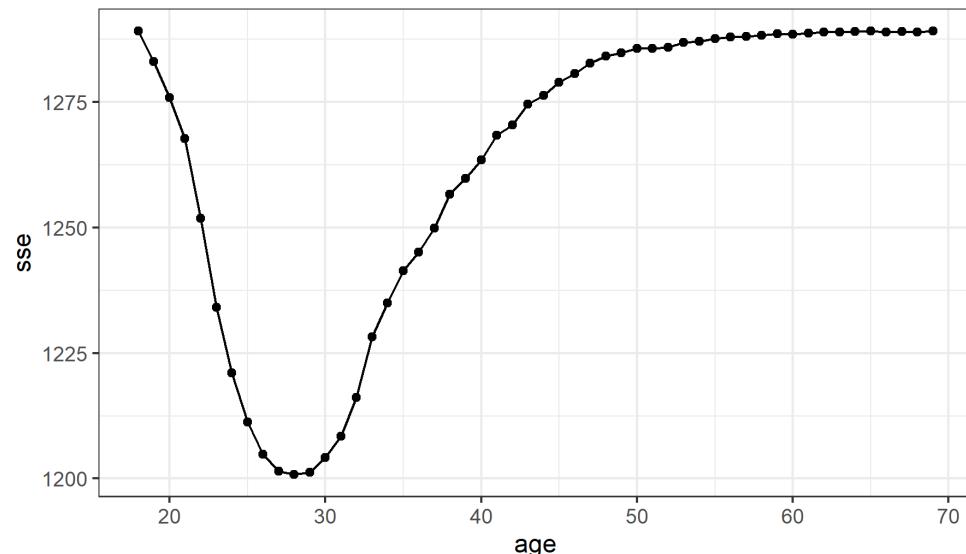
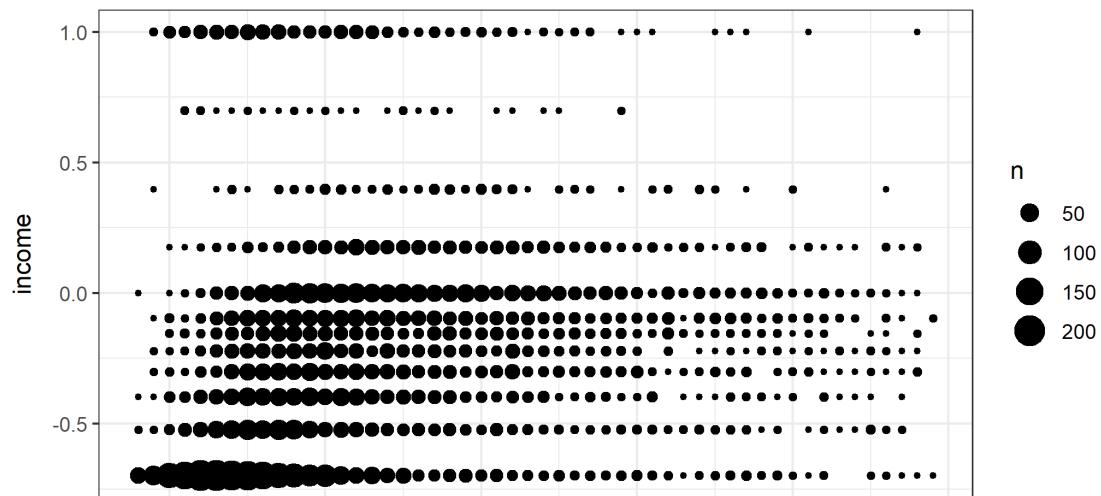
sse <- function(l, df, v) {
  income_above <- df %>% filter({{v}} >= l) %>% pull(income)
  income_below <- df %>% filter({{v}} < l) %>% pull(income)
  sse_above <- sum((income_above - mean(income_above))^2)
  sse_below <- sum((income_below - mean(income_below))^2)
  return(sse_above + sse_below)
}
age <- seq(18, 69, 1)
sse_age <- map_dbl(age, sse, df = okcupid2_train, v = age)

p1 <- okcupid2_train %>%
  count(age, income) %>%
  ggplot(aes(age, income)) +
  geom_point(aes(size = n)) +
  theme_bw() +
  labs(x = "") +
  theme(axis.text.x = element_blank())

p2 <- tibble(age = age, sse = sse_age) %>%
  ggplot(aes(age, sse)) +
  geom_line() +
  geom_point() +
  theme_bw()

p1 / p2

```



# The *SSE* criterion - categorical predictor

💡 What could be an issue with a categorical variable with many levels?

- a categorical predictor  $l$  is nominated for splitting the current node
  - option 1: use dummy variables, turning each level into a 2-level 0/1 category variable
  - option 2: order levels by some criterion like  $\bar{y}_j$  and treat  $l$  as continuous from here on

For example if `job3` is candidate in splitting `income`:

```

mean_income_vs_job <- okcupid2_train %>%
  group_by(job3) %>%
  summarise(mean_income = mean(income)) %>%
  arrange(mean_income)
jobs_levels_sorted <- as.character(mean_income_vs_job$job3)
okcupid2_train_job_sorted <- okcupid2_train %>%
  mutate(job_ordered = fct_relevel(job3, jobs_levels_sorted),
         job_ordered_n = as.numeric(job_ordered))

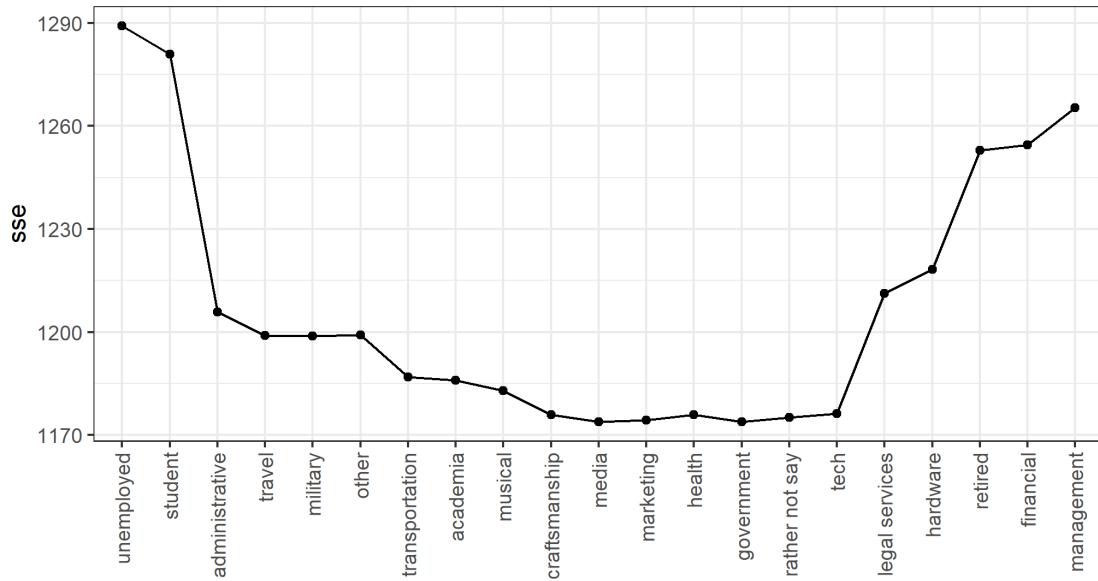
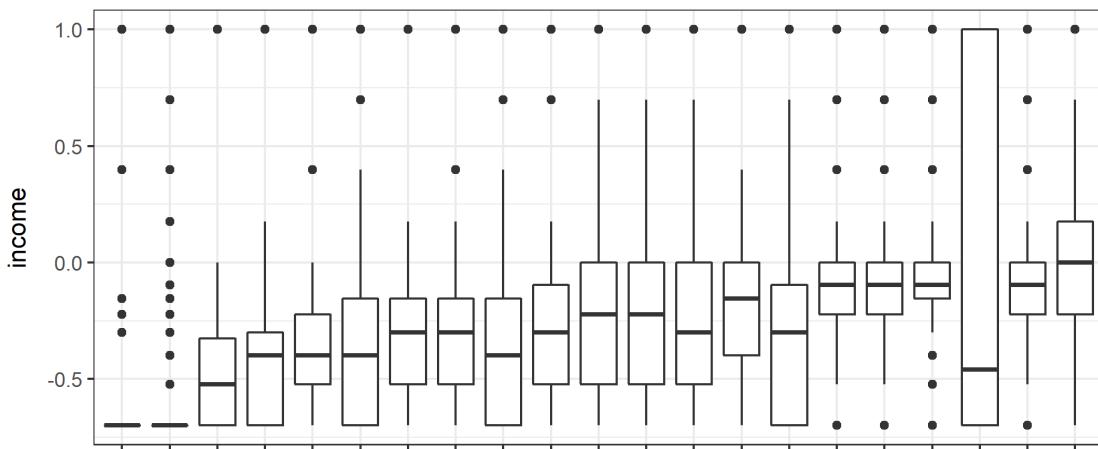
job_rank <- seq(1, length(jobs_levels_sorted), 1)
sse_job <- map_dbl(job_rank, sse, df = okcupid2_train_job_sorted,

p1 <- okcupid2_train_job_sorted %>%
  ggplot(aes(job_ordered, income)) +
  geom_boxplot() +
  theme_bw() + labs(x = "") +
  theme(axis.text.x = element_blank())

p2 <- tibble(job = factor(jobs_levels_sorted, levels = jobs_levels_sorted),
             sse, group = 1)) +
  geom_line() +
  geom_point() +
  theme_bw() +
  labs(x = "") +
  theme(axis.text.x = element_text(angle = 90, hjust = 1, vjust = 0))

p1 / p2

```



# Pruning: The $SSE_{c_p}$ criterion

The "right-sized" tree should not be too deep to avoid overfitting.

Once the full tree is grown, we check for each split:

$$SSE_{c_p} = SSE_{tot} + c_p \cdot \#\text{terminal nodes}$$

Where  $c_p$  is a penalty or regularization parameter usually chosen by cross validation.

And we choose the smallest pruned tree with the minimum  $SSE_{c_p}$ .

# CART with rpart

Growing the full tree (for a numeric (y) rpart will guess this is Regression):

```
library(rpart)  
  
mod_tree <- rpart(income ~ ., data = okcupid2_train)
```

Pruning with some  $c_p$ :

```
mod_tree <- prune(mod_tree, cp = 0.05)
```

⚠ There is a  $c_p$  parameter you can pass to rpart while training like so:

```
rpart(income ~ ., data = okcupid2_train, control =  
rpart.control(cp = 0.05))
```

But this will only make rpart consider this  $c_p$  at each split as a minimum criterion *while growing the unpruned tree*. In fact the default of this parameter is 0.01!

So, in order to train a true unpruned tree you would need to pass  $c_p = 0$ :

```
mod_tree <- rpart(income ~ ., data = okcupid2_train,  
control = rpart.control(cp = 0))
```

Now, `rpart` by default will perform 10-fold Cross Validation on each split, resulting in this `cptable`:

```
head(mod_tree$cptable)
```

```
##          CP nsplit rel_error xerror      xstd  
## 1 0.113597498    0 1.0000000 1.0000930 0.02237966  
## 2 0.048179174    1 0.8864025 0.8895296 0.02276700  
## 3 0.013140594    2 0.8382233 0.8449979 0.02358206  
## 4 0.010043056    3 0.8250827 0.8335388 0.02366560  
## 5 0.009147817    4 0.8150397 0.8264539 0.02378065  
## 6 0.005634308    5 0.8058919 0.8149773 0.02394991
```

The nature of the `xerror` is unclear from the [docs](#) (SSE/n ?) except that it is relative to the error in the root node.

You can either use it like so:

```
best_cp <- mod_tree$cptable[which.min(mod_tree$cptable[, "xerror"])]
mod_tree <- prune(mod_tree, cp = best_cp)
```

Or you can perform CV on your own, passing at each stage a parameter for `rpart` to not perform CV:

```
mod_tree <- rpart(income ~ ., data = okcupid2_train,
control = rpart.control(cp = 0), xval = 1)
```

Let's tune  $c_p$  for our data using a 5-fold (manual) Cross Validation.  
The criterion to maximize would be RMSE.

```
n_cv <- 5; cp_seq <- seq(0, 0.02, 0.001)

okupid2_train_val <- okupid2_train %>%
  mutate(val = sample(1:n_cv, n(), replace = TRUE))

get_validation_set_rmse <- function(i, .cp) {
  ok_tr <- okupid2_train_val %>% filter(val != i) %>% select(-val)
  ok_val <- okupid2_train_val %>% filter(val == i) %>% select(-val)
  mod <- rpart(income ~ ., data = ok_tr,
               control = rpart.control(cp = 0, xval = 1))
  mod <- prune(mod, cp = .cp)
  pred <- predict(mod, ok_val)
  rmse(ok_val$income, pred)
}

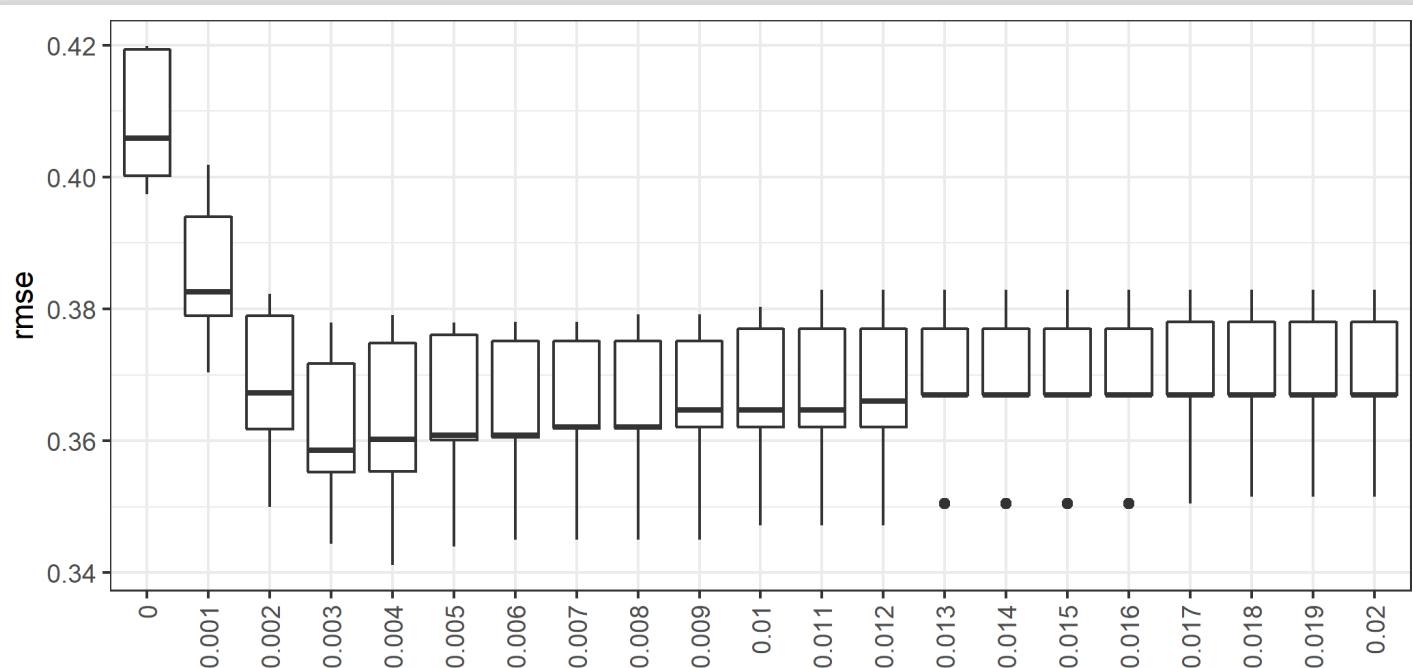
get_cv_rmse <- function(.cp) {
  tibble(cp = rep(.cp, n_cv),
        rmse = map_dbl(1:n_cv, get_validation_set_rmse, .cp = .cp)
}
```

```

cv_table <- map_dfr(cp_seq, get_cv_rmse)

cv_table %>%
  mutate(cp = factor(cp)) %>%
  ggplot(aes(cp, rmse)) +
  geom_boxplot() +
  theme_bw() +
  labs(x = "") +
  theme(axis.text.x = element_text(angle = 90, hjust = 1, vjust =

```



## Training on the entire training set:

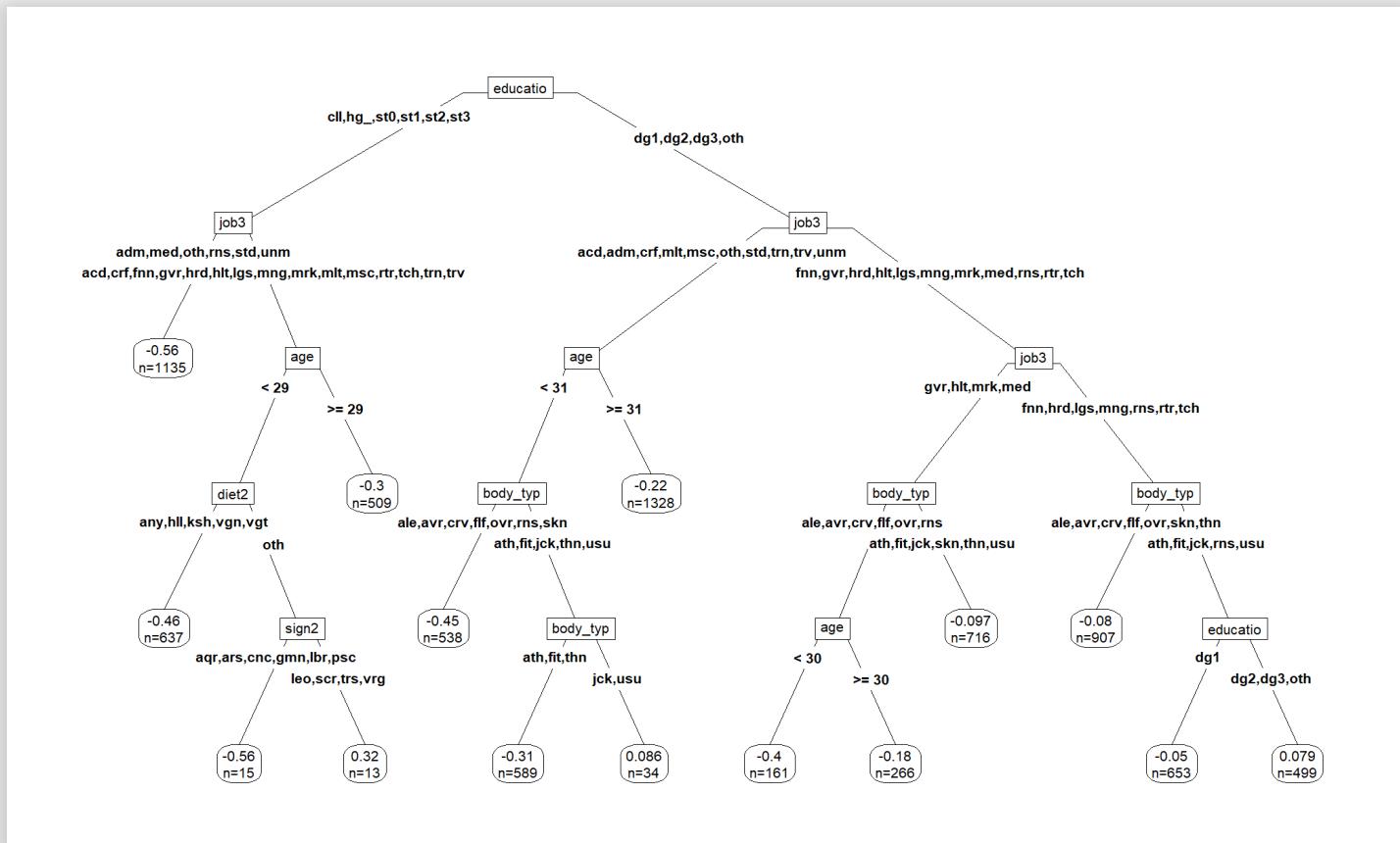
```
mod_tree_na <- rpart(income ~ ., data = okcupid2_train,  
                      control = rpart.control(cp = 0, xval = 1))  
mod_tree_na <- prune(mod_tree_na, cp = 0.003)
```

You can plot the tree using `rpart`, but...

```
plot(mod_tree_na)  
text(mod_tree_na, pretty = 1, use.n = TRUE)
```

The plotting function in the `rpart.plot` package is slightly nicer:

```
library(rpart.plot)
prp(mod_tree_na, type = 5, extra = 1)
```

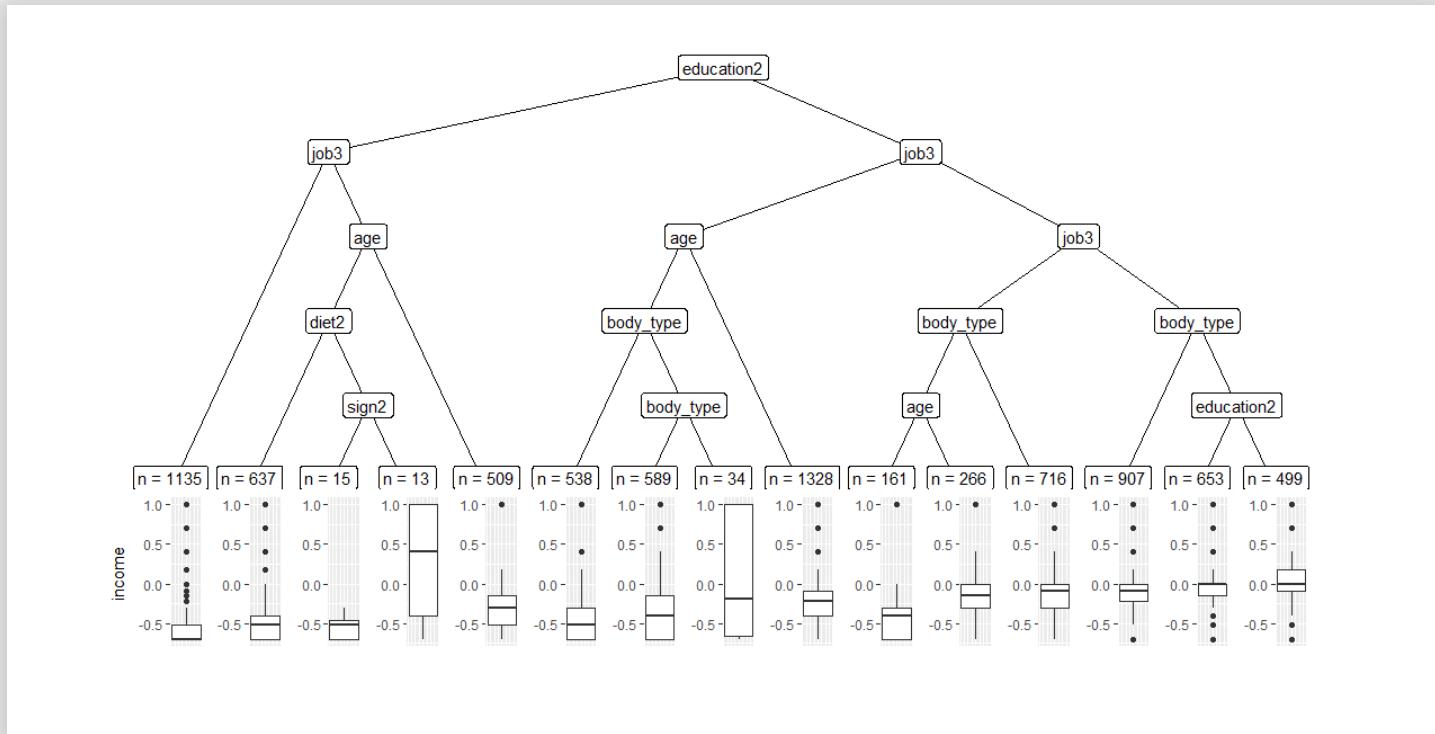


You can go fancy and use partykit and/or ggparty:

```
library(ggparty)

party_obj <- as.party(mod_tree_na)

ggparty(party_obj) +
  geom_edge() +
  # geom_edge_label() +
  geom_node_label(aes(label = splitvar), ids = "inner") +
  geom_node_label(aes(label = str_c("n = ", nodesize)),
                  ids = "terminal", nudge_y = 0.02) +
  geom_node_plot(gglist = list(geom_boxplot(aes(y = income)),
                               theme(axis.text.x=element_blank(),
                                     axis.ticks.x=element_blank,
                                     shared_axis_labels=TRUE))
```



# Or you can just print the tree and see what is going on:

```
print(party_obj)
```

```
Fitted party:
[1] root
[2] education2 in college, high_school, student0, student1, student2, student3
| [3] job3 in administrative, media, other, rather not say, student, unemployed: -0.555 (n = 1135, err = 126.9)
| [4] job3 in academia, craftsmanship, financial, government, hardware, health, legal services, management, marketing, military
| [5] age < 28.5
|   [6] diet2 in anything, halal, kosher, vegan, vegetarian: -0.460 (n = 637, err = 84.2)
|   [7] diet2 in other
|     [8] sign2 in aquarius, aries, cancer, gemini, libra, pisces: -0.559 (n = 15, err = 0.3)
|     [9] sign2 in leo, scorpio, taurus, virgo: 0.316 (n = 13, err = 5.9)
|   [10] age >= 28.5: -0.301 (n = 509, err = 53.0)
[11] education2 in degree1, degree2, degree3, other
[12] job3 in academia, administrative, craftsmanship, military, musical, other, student, transportation, travel, unemployed
| [13] age < 30.5
|   [14] body_type in a little extra, average, curvy, full figured, overweight, rather not say, skinny: -0.450 (n = 538,
|   [15] body_type in athletic, fit, jacked, thin, used up
|     [16] body_type in athletic, fit, thin: -0.314 (n = 589, err = 141.6)
|     [17] body_type in jacked, used up: 0.086 (n = 34, err = 16.1)
|   [18] age >= 30.5: -0.221 (n = 1328, err = 171.8)
[19] job3 in financial, government, hardware, health, legal services, management, marketing, media, rather not say, retired,
[20] job3 in government, health, marketing, media
| [21] body_type in a little extra, average, curvy, full figured, overweight, rather not say
|   [22] age < 29.5: -0.402 (n = 161, err = 13.7)
|   [23] age >= 29.5: -0.178 (n = 266, err = 17.3)
|     [24] body_type in athletic, fit, jacked, skinny, thin, used up: -0.097 (n = 716, err = 95.6)
[25] job3 in financial, hardware, legal services, management, rather not say, retired, tech
| [26] body_type in a little extra, average, curvy, full figured, overweight, skinny, thin: -0.080 (n = 907, err = 83.
|   [27] body_type in athletic, fit, jacked, rather not say, used up
|     [28] education2 in degree1: -0.050 (n = 653, err = 48.7)
|     [29] education2 in degree2, degree3, other: 0.079 (n = 499, err = 51.3)

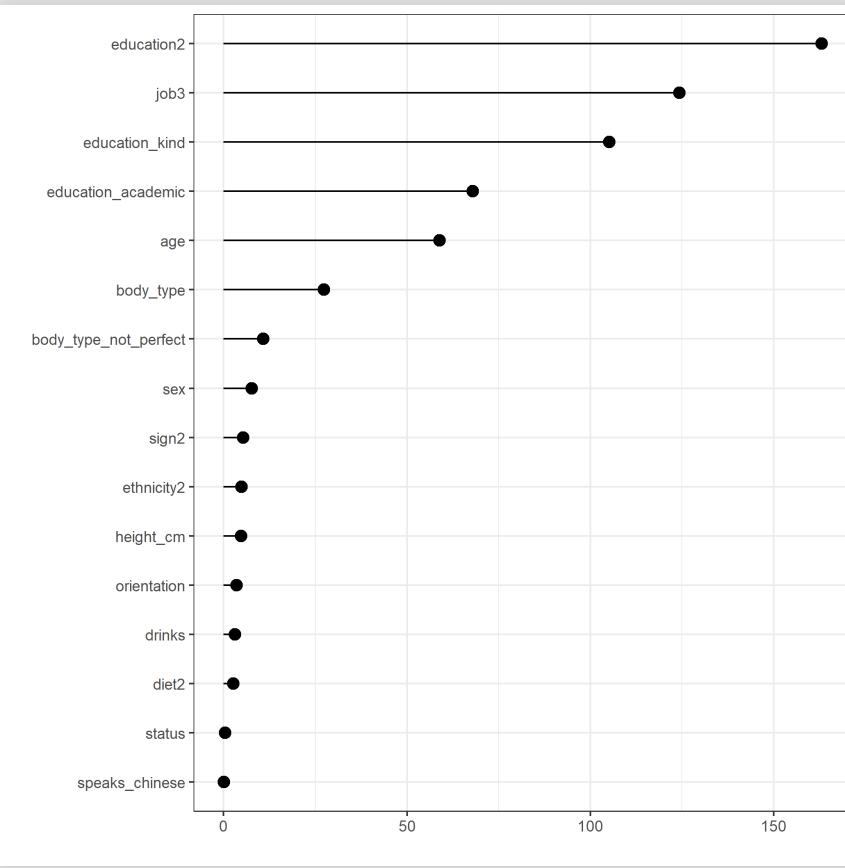
Number of inner nodes: 14
Number of terminal nodes: 15
```

# Variables Importance

Summing the reduction in  $SSE$  for each split variable, we can get a measure of importance.

Unfortunately in `rpart` the "potential" reduction in (SSE) for surrogate splits is also summed. You can either ignore or retrain with only the variables chosen by the model.

```
enframe(mod_tree_na$variable.importance) %>%
  arrange(value) %>%
  mutate(variable = as_factor(name)) %>%
  ggplot(aes(variable, value)) +
  geom_segment(aes(x = variable, xend = variable,
                    y = 0, yend = value)) +
  geom_point(size = 3) +
  theme_bw() +
  coord_flip() +
  labs(x = "", y = "")
```



💡 How would this profile look for a couple of very correlated predictors?

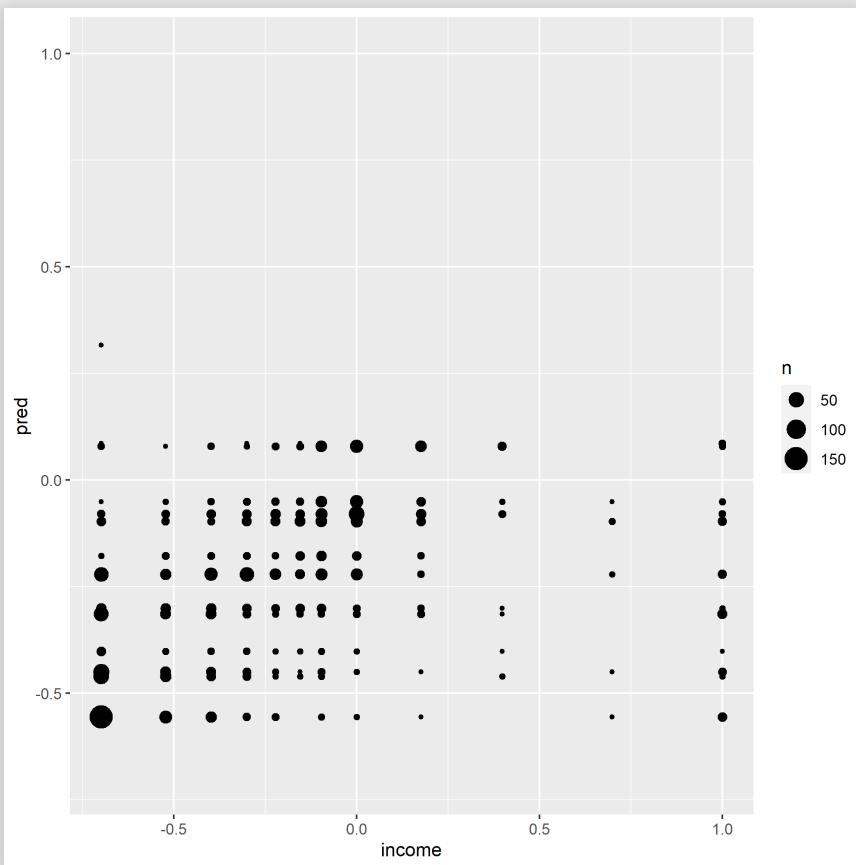
# Prediction

```
pred_tree_na <- predict(mod_tree_na, okcupid2_valid)  
report_rmse_and_cor(okcupid2_valid$income, pred_tree_na)  
  
## RMSE: 0.363  
## CORR: 0.449
```

As expected, far from impressive. Let's try using the imputed NA data:

```
mod_tree_imp <- rpart(income ~ ., data = okcupid2_imp_mice_train,  
                      control = rpart.control(cp = 0, xval = 1))  
mod_tree_imp <- prune(mod_tree_imp, cp = 0.003)  
pred_tree_imp <- predict(mod_tree_imp, okcupid2_imp_mice_valid)  
  
report_rmse_and_cor(okcupid2_valid$income, pred_tree_imp)  
  
## RMSE: 0.369  
## CORR: 0.424
```

```
tibble(income = okcupid2_valid$income, pred = pred_tree_na) %>%
  count(income, pred) %>%
  ggplot(aes(income, pred)) +
  geom_point(aes(size = n)) +
  ylim(range(okcupid2_valid$income))
```

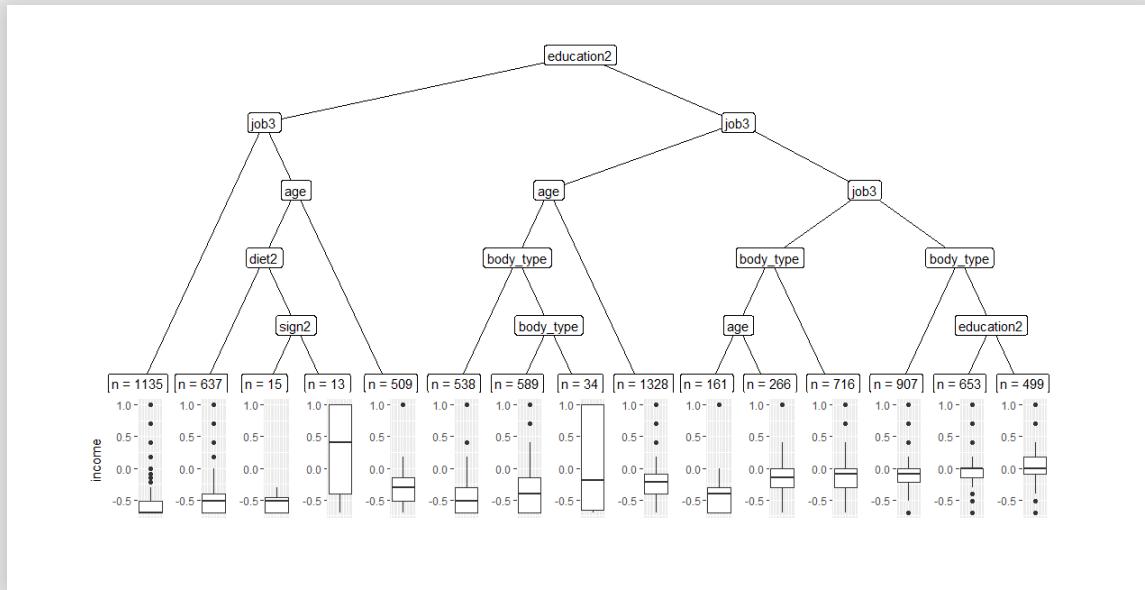


# The Others

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Looking at this one might wonder:

- Since when do we just split, how about a statistical test?
- Predicting a single value for each terminal node? Is that the best we can do?
- Many variables repeat in the same path, can we compact paths into simple rules?

# Conditional Inference Trees

[Hothorn et. al. \(2006\)](#) perform a statistical hypothesis test for each variable to decide whether it is related to  $y$  (including multiple comparisons adjustment).

If no variable passes test - stop. No pruning necessary.

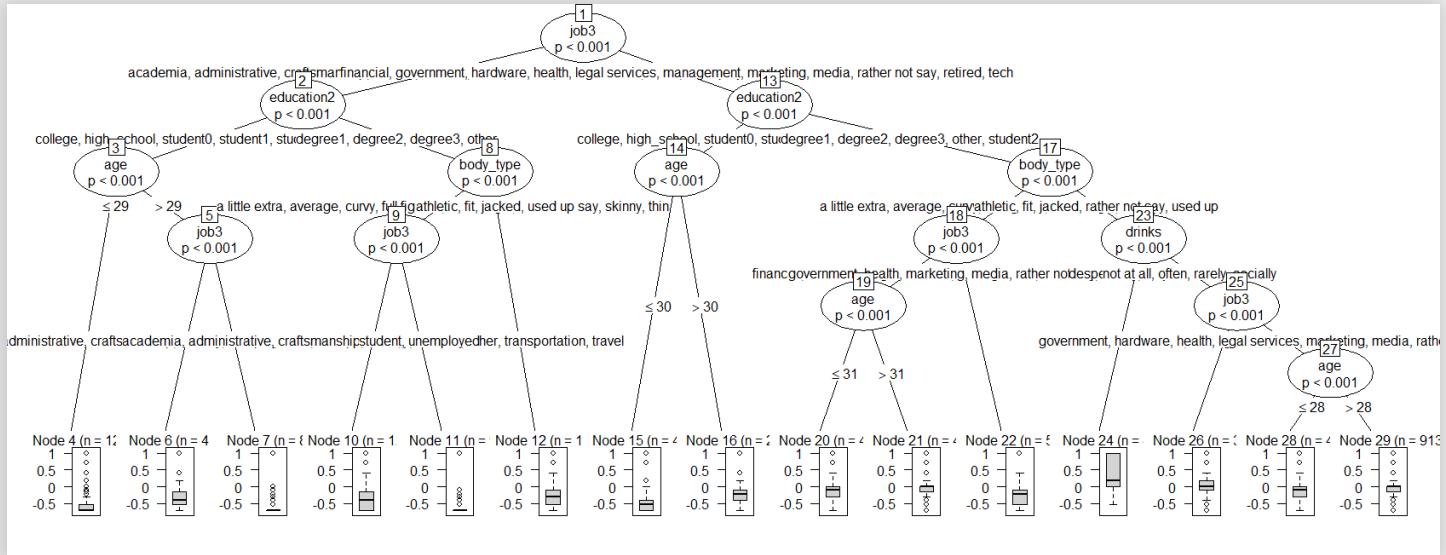
If a few variables pass - choose the most related, e.g. using a p-value.

```
library(partykit)

mod_ctree_na <- ctree(income ~ ., data = okcupid2_train, alpha = 0)
pred_ctree_na <- predict(mod_ctree_na, okcupid2_valid)
report_rmse_and_cor(okcupid2_valid$income, pred_ctree_na)

## RMSE: 0.365
## CORR: 0.442
```

```
plot(mod_ctree_na)
```



# Model Trees

[Quinlan \(1992\)](#) and later [Wang and Witten \(1997\)](#) made a few changes to the beloved CART:

- instead of single values at terminal nodes, M5 trees have *linear models*
- sort of a piecewise linear regression only the "pieces" can come from many variables
- can extrapolate to never before seen values (not necessarily good)

You can find an implementation in R in the `RWeka` package, function `M5P()`.

[Zeileis et. al. \(2008\)](#) approach is slightly simpler to grasp. It allows you to specify variables for splitting and variables for regression.

See `lmtree()` and `glmtree()` functions in the `partykit`

```

mod_lmtree_na <- lmtree(income ~ age | sex + job3 + education2, data = okupid2)

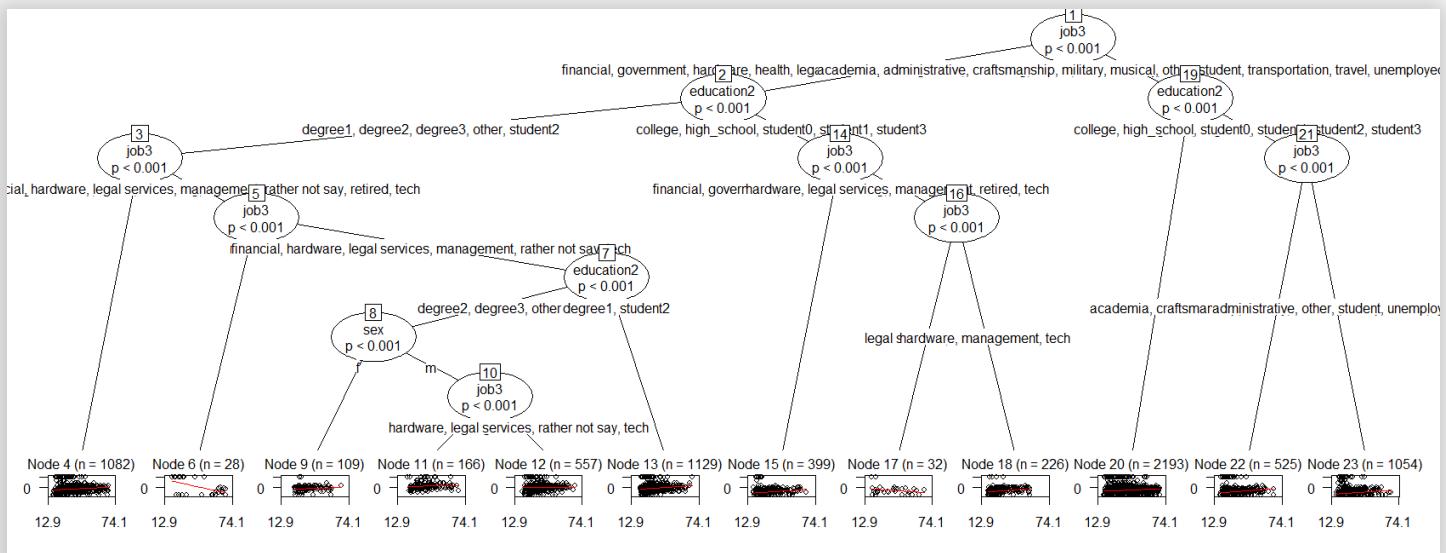
pred_lmtree_na <- predict(mod_lmtree_na, okupid2_valid)

report_rmse_and_cor(okupid2_valid$income, pred_lmtree_na)

plot(mod_lmtree_na)

```

## RMSE: 0.366  
## CORR: 0.437



# Rule-Based Trees

Holmes et. a. (1993) general approach:

1. Build a model tree (e.g. M5)
2. For each path compute the coverage (= % of relevant observations to that path)
3. Compact the path with largest coverage into a rule
4. Remove previous relevant observations and go back to 1 until all observations are accounted for.

```
library(RWeka)

# limiting predictors just for a nice print!
mod_m5rules_na <- M5Rules(income ~ ., data = okcupid2_train[, c("i
pred_m5rules_na <- predict(mod_m5rules_na, okcupid2_valid)
report_rmse_and_cor(okcupid2_valid$income, pred_m5rules_na)

## RMSE: 0.374
## CORR: 0.392
```

```
print(mod_m5rules_na)
```

```
M5 pruned model rules
(using smoothed linear models) :
Number of Rules : 2

Rule: 1
IF
    education2=student2,degree1,other,degree2,degree3 > 0.5
    age > 30.5
THEN
income =
    -0.0015 * age
    + 0.1123 * sex=m
    + 0.0003 * education2=student1,high_school,student3,college,student2,degree1,other,degree2,degree3
    + 0.0002 * education2=high_school,student3,college,student2,degree1,other,degree2,degree3
    + 0.0002 * education2=student2,degree1,other,degree2,degree3
    + 0.185 * education2=degree1,other,degree2,degree3
    + 0.0003 * education2=other,degree2,degree3
    + 0.0672 * education2=degree2,degree3
    + 0.0755 * education2=degree3
    - 0.3345 [2977/81.357%]

Rule: 2
income =
    0.009 * age
    + 0.1196 * sex=m
    + 0.0927 * education2=student1,high_school,student3,college,student2,degree1,other,degree2,degree3
    - 0.0384 * education2=high_school,student3,college,student2,degree1,other,degree2,degree3
    + 0.0505 * education2=student3,college,student2,degree1,other,degree2,degree3
    + 0.212 * education2=student2,degree1,other,degree2,degree3
    + 0.111 * education2=degree2,degree3
    - 0.8955 [4523/93.176%]
```

# Bagged Trees

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# Bagging: The Gist

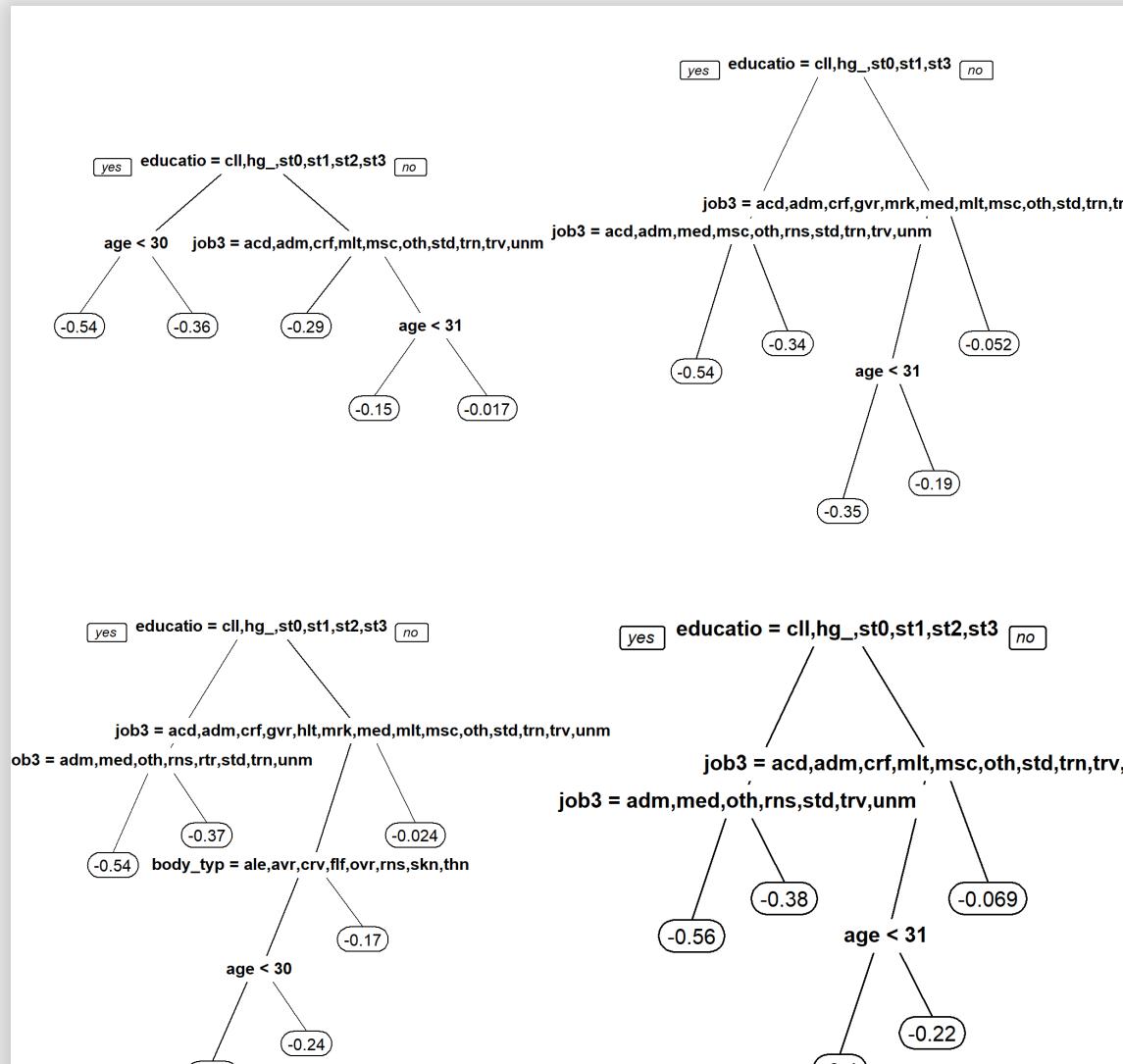
For  $j = 1$  to  $m$  do

- Generate a bootstrap sample of the original data
- Train an unpruned tree model on this sample

End.

- Predict average through all  $m$  trees (or %vote for each class in classification)
- What you get: better prediction,  $OOB$  error estimates
- What you lose: interpretability, speed (but bagging can be paralleled)

# Why does Bagging work?



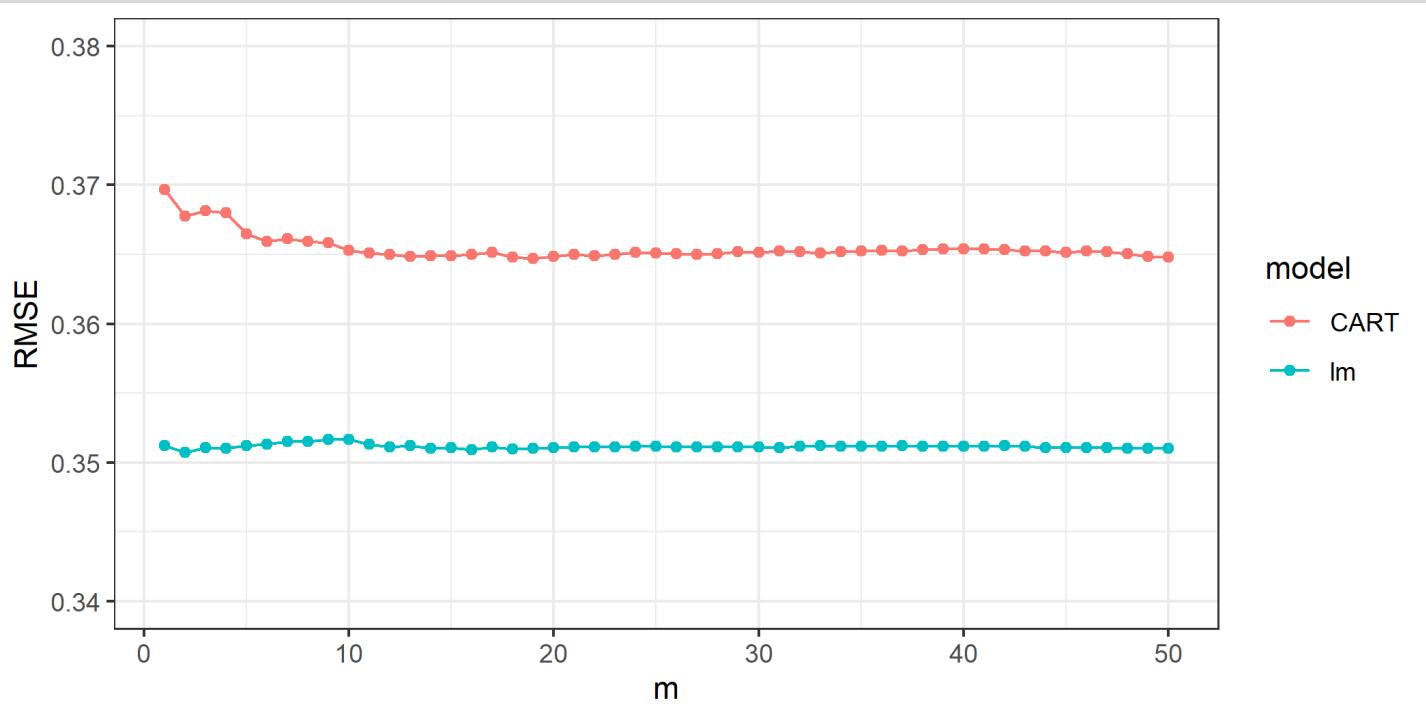
# Which models are likely to benefit from bagging?

```
train_lm <- function(i, .n) {  
  samp <- sample(1:n, .n, replace = TRUE)  
  lm(income ~ ., data = okcupid2_imp_mice_train[samp, ])  
}  
  
train_tree <- function(i, .n) {  
  samp <- sample(1:n, .n, replace = TRUE)  
  rpart(income ~ ., data = okcupid2_imp_mice_train[samp, ])  
}  
  
predict_mod <- function(mod) {  
  tibble(pred = predict(mod, okcupid2_imp_mice_valid))  
}  
  
rmse_m_models <- function(m, .preds) {  
  rmse(okcupid2_imp_mice_valid$income, rowMeans(.preds[, 1:m]))  
}  
  
n <- nrow(okcupid2_imp_mice_train)  
m_max <- 50  
  
mod_lms <- map(1:m_max, train_lm, .n = n)  
mod_trees <- map(1:m_max, train_tree, .n = n)  
  
preds_lm <- map_dfc(mod_lms, predict_mod)  
preds_tree <- map_dfc(mod_trees, predict_mod)
```

```

rmse_lm <- map_dbl(1:m_max, rmse_m_models, .preds = preds_lm)
rmse_tree <- map_dbl(1:m_max, rmse_m_models, .preds = preds_tree)
tibble(m = rep(1:m_max, 2),
       model = c(rep("lm", m_max), rep("CART", m_max)),
       RMSE = c(rmse_lm, rmse_tree)) %>%
  ggplot(aes(m, RMSE, color = model)) +
  ylim(c(0.34, 0.38)) +
  geom_line() + geom_point() +
  theme_bw()

```



# Bagging with ipred

```
library(ipred)

mod_bag_na <- bagging(income ~ ., data = okcupid2_train, nbagg = 5)
pred_bag_na <- predict(mod_bag_na, okcupid2_valid)
report_rmse_and_cor(okcupid2_valid$income, pred_bag_na)
```

```
## RMSE: 0.366
## CORR: 0.438
```

```
mod_bag_mice <- bagging(income ~ ., data = okcupid2_imp_mice_train)
pred_bag_mice <- predict(mod_bag_na, okcupid2_imp_mice_valid)
report_rmse_and_cor(okcupid2_valid$income, pred_bag_mice)
```

```
## RMSE: 0.364
## CORR: 0.443
```

# Random Forests

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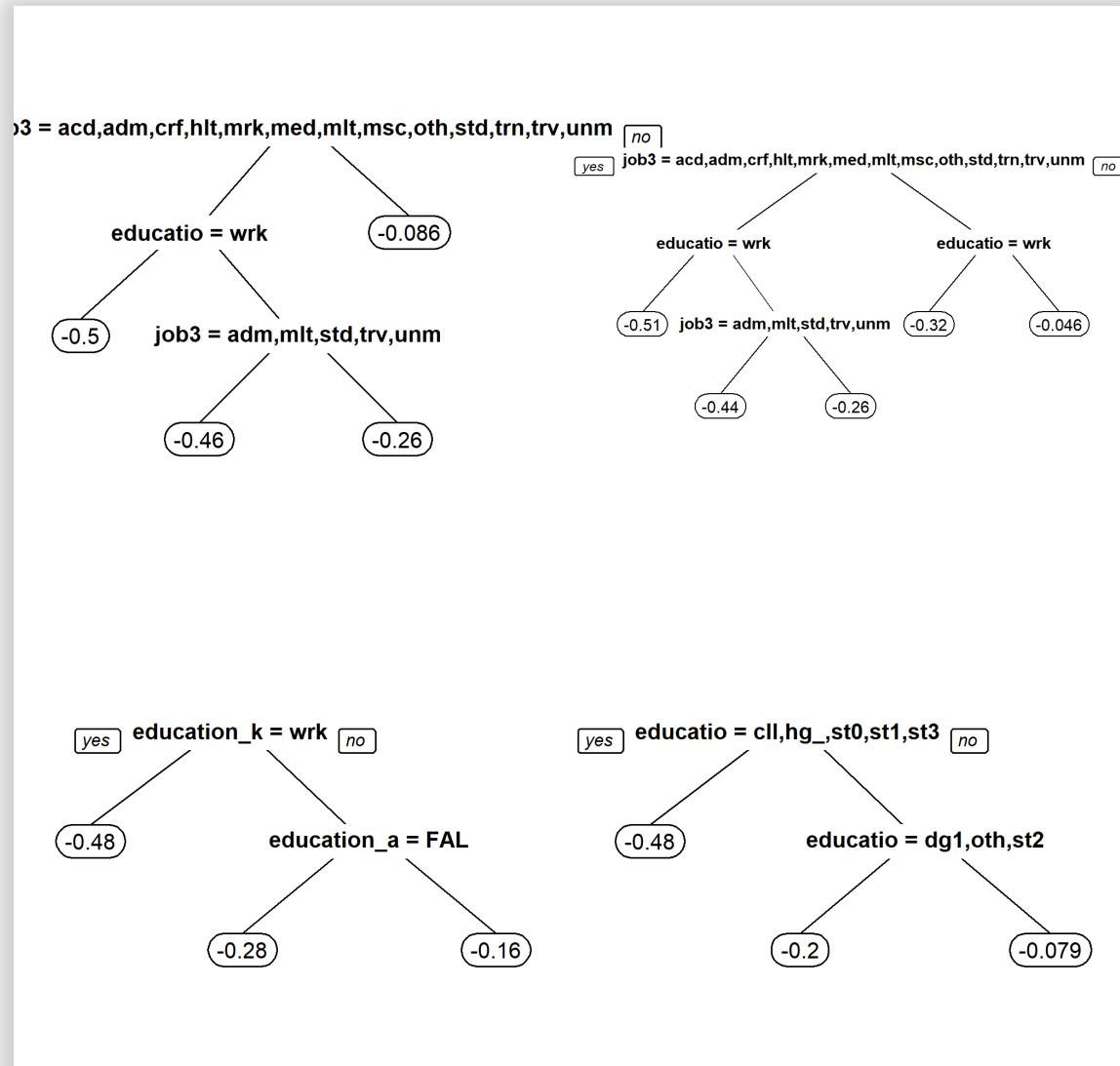
# Random Forests: The Gist

For  $j = 1$  to  $m$  do

- Generate a bootstrap sample of the original data
- Train an unpruned tree model on this sample
- For each split:
  - Randomly select  $m_{try}$  predictors
  - Select best predictor for split in this subset only

End.

# What does RF add on top of Bagging?



# RF with randomForest

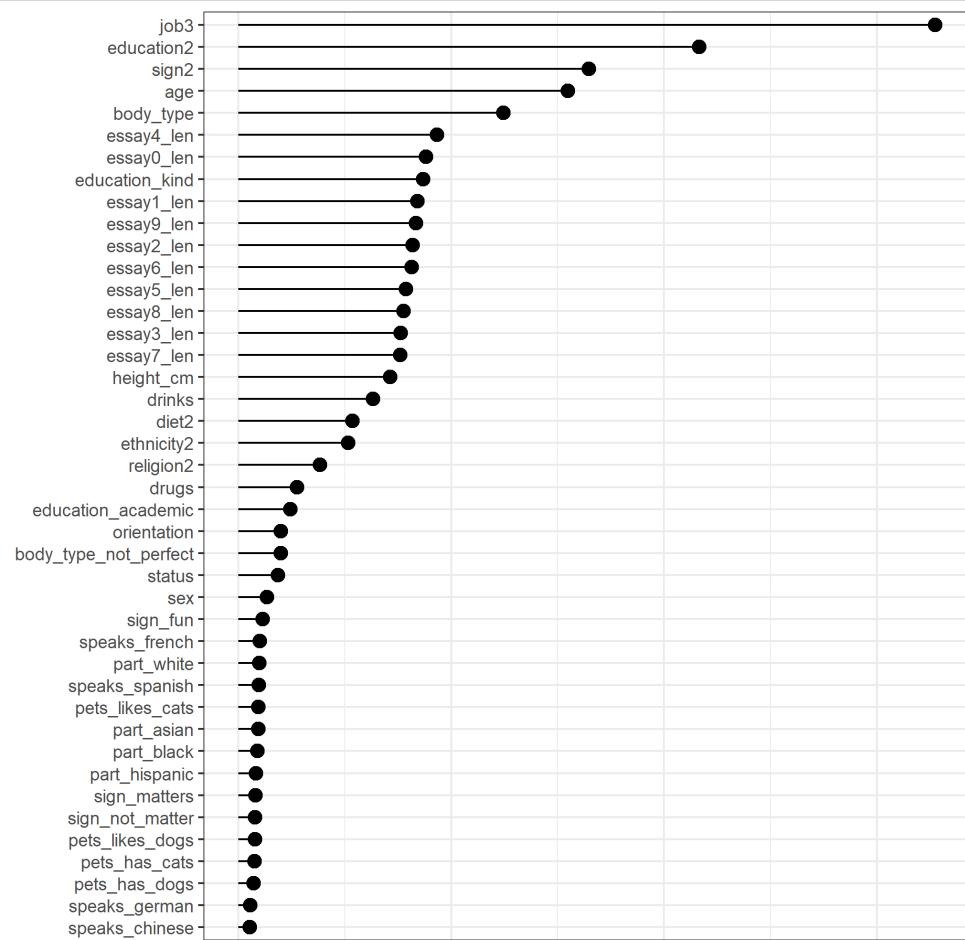
For some reason this implementation of RF won't accept missing values:

```
library(randomForest)

mod_rf_mice <- randomForest(income ~ ., data = okcupid2_imp_mice_t
                           mtry = 10, ntree = 50, importance = TRUE)
pred_rf_mice <- predict(mod_rf_mice, okcupid2_imp_mice_valid)
report_rmse_and_cor(okcupid2_valid$income, pred_rf_mice)

## RMSE: 0.354
## CORR: 0.491
```

For variable importance check out the `importance` field of the RF object:

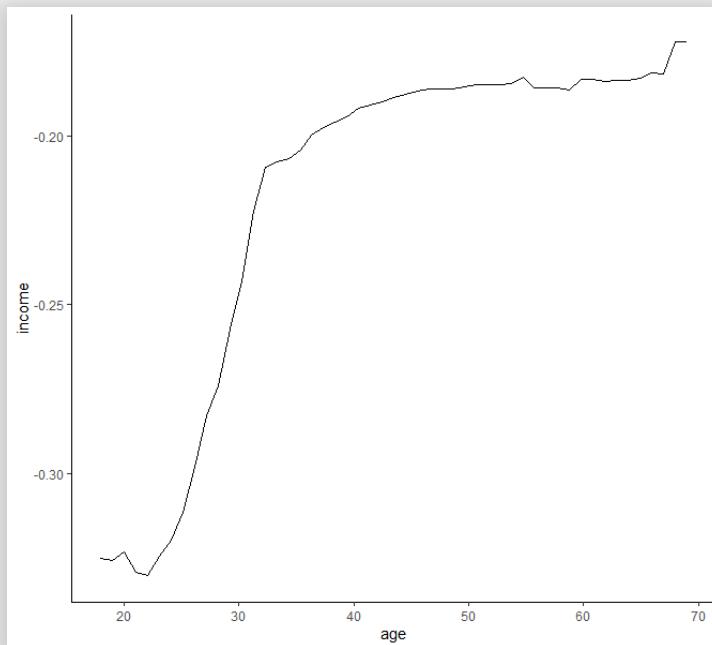


💡 What is troubling about variable importance?

# Partial Dependency Plots

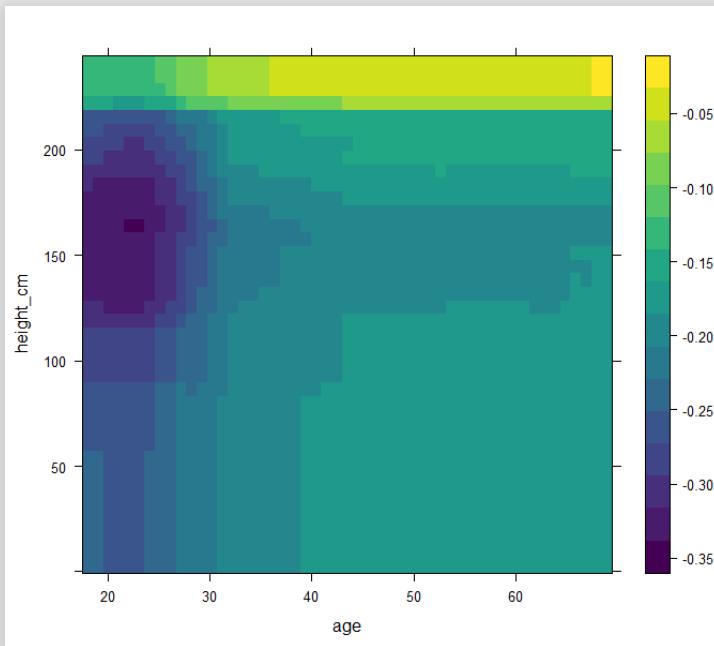
1. Select a subset  $X_s$  of variables (usually 1-2) you wish to know the relation to the dependent variable  $y$
2. For each possible permutation of  $X_s$  run the model on the original data imputing this specific permutation instead of the values of  $X_s$
3. Average predictions of  $y$
4. Plot  $y$  vs.  $X_s$

```
partial(mod_rf_mice, pred.var = "age",
       plot = TRUE, plot.engine = "ggplot2") +
  labs(y = "income") +
  theme_classic()
```



Let's see this for age and height\_cm together (takes some time!):

```
partial(mod_rf_mice, pred.var = c("age", "height_cm"), plot = TRUE)
```



# Gradient Boosted Trees

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# Boosting: The Gist

Compute the average response  $\bar{y}$ , and use this as the initial predicted value for each sample

For  $j = 1$  to  $m$  do

- Compute the residual for each observation
- Sample a fraction of the original data
- Fit a regression tree of a certain "*interaction depth*" using the residual as response
- Predict each sample using this tree
- Update the predicted value of each sample by adding the previous iteration's value to current predicted value X *learning rate* or *shrinkage* parameter

End.

What you end up with:

$$\hat{y}_i = \bar{y} + \sum_{j=1}^m \lambda \cdot tree_j(\mathbf{x}_i)$$

That is why GBT (or GBM) in general is called an additive model.

💡 Where does "Gradient" come from?

- The added random sampling of the data was added later, this version is called *Stochastic* Gradient Boosting, the default for the parameter often called "bagging fraction" is 0.5
- The shrinkage  $\lambda$  can be turned into  $\lambda_j$ , a unique weight for each added tree
- Note the **many** tuning parameters here. Do you know how to tune multiple params?
- Not so parallel now, eh?

# GBT with gbm

```
library(gbm)

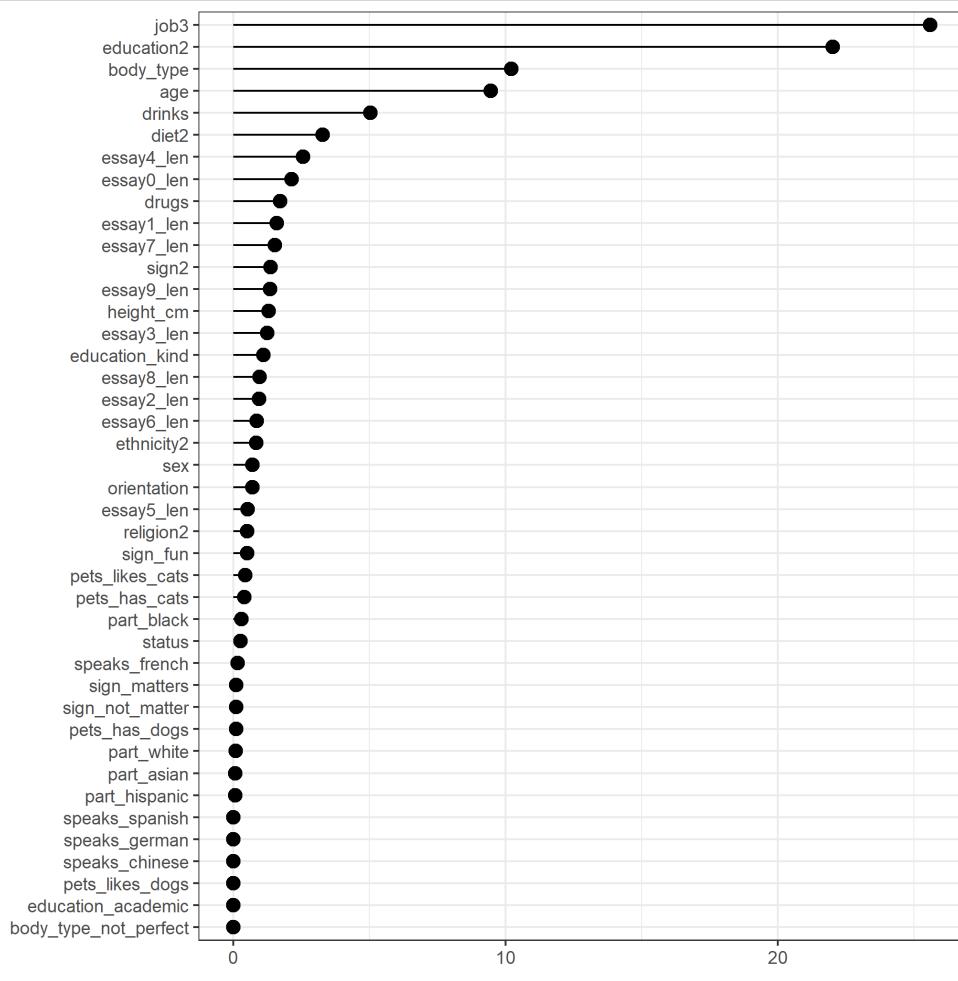
mod_gbm_na <- gbm(income ~ ., data = okupid2_train,
                     distribution = "gaussian",
                     n.trees = 500, shrinkage = 0.1, bag.fraction = (
pred_gbm_na <- predict(mod_gbm_na, okupid2_valid, n.trees = 500)
report_rmse_and_cor(okupid2_valid$income, pred_gbm_na)
```

```
## RMSE: 0.351
## CORR: 0.505
```

```
mod_gbm_mice <- gbm(income ~ ., data = okupid2_imp_mice_train,
                      distribution = "gaussian", n.trees = 500, shrinkage =
pred_gbm_mice <- predict(mod_gbm_na, okupid2_imp_mice_valid, n.trees = 500)
report_rmse_and_cor(okupid2_valid$income, pred_gbm_mice)
```

```
## RMSE: 0.353
## CORR: 0.496
```

For variables importance see the `summary` function:



Do you see the difference in the profile of importance between RF and GBT?

# GBT with xgboost

xgboost is faster and has some additional features, e.g. the ability to train with a validation set until it shows no improvement, similar to neural networks.

```
library(xgboost)

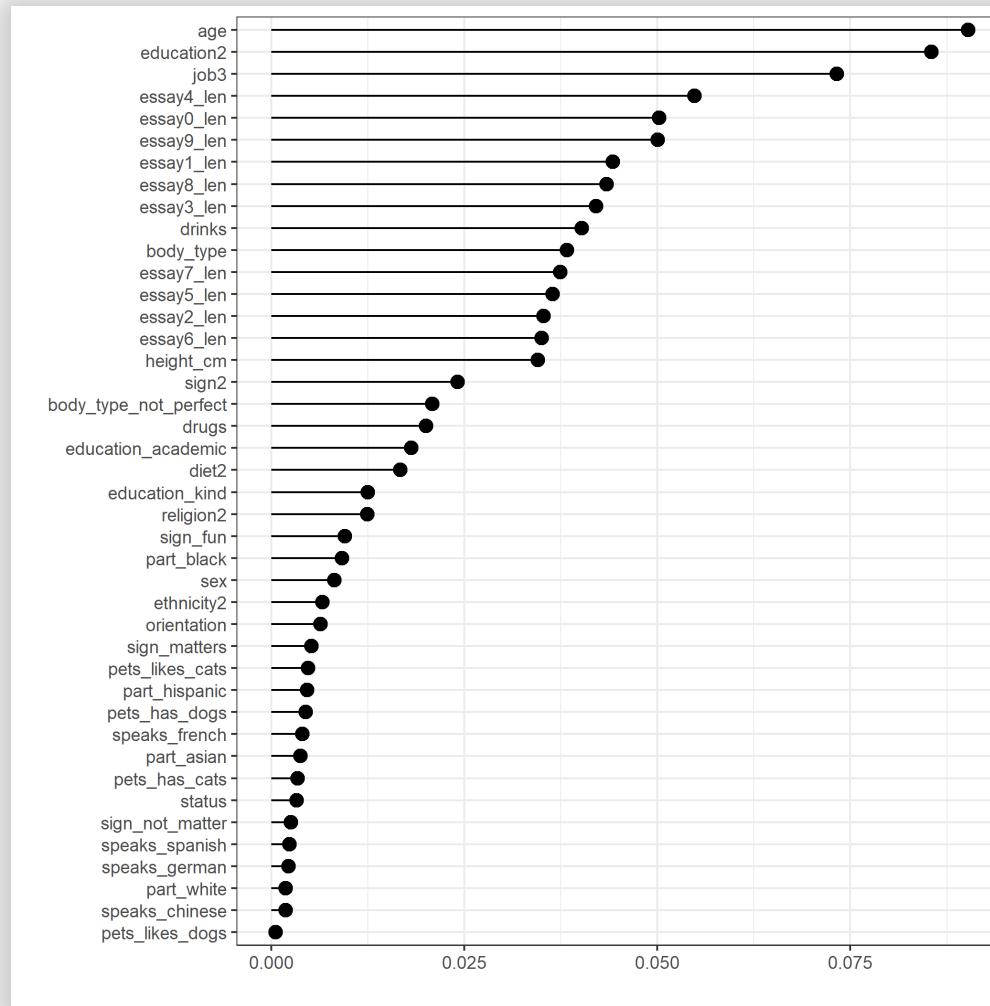
dtrain <- xgb.DMatrix(data = data.matrix(okcupid2_train[, predictors],
                                         label = okcupid2_train$income)
dval <- xgb.DMatrix(data = data.matrix(okcupid2_valid[, predictors],
                                         label=okcupid2_valid$income))
watchlist <- list(train=dtrain, test=dval)

mod_xgboost_na <- xgb.train(data = dtrain, watchlist=watchlist,
                               objective = "reg:squarederror", nrounds = 100,
                               eta = 0.1, subsample = 0.5,
                               early_stopping_rounds = 10, verbose = TRUE)

pred_xgboost_na <- predict(mod_xgboost_na, dval)
report_rmse_and_cor(okcupid2_valid$income, pred_xgboost_na)
```

```
## RMSE: 0.358
## CORR: 0.477
```

For variables importance see the `xgb.importance` function:



# The CART (Classification)

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# Detour: A Classification Problem

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# OKCupid: Predicting Dogs or Cats People

It won't be easy:

```
okcupid %>% count(pets)

## # A tibble: 16 x 2
##   pets                  n
##   <chr>                <int>
## 1 dislikes cats          122
## 2 dislikes dogs           44
## 3 dislikes dogs and dislikes cats 196
## 4 dislikes dogs and has cats     81
## 5 dislikes dogs and likes cats   240
## 6 has cats                1406
## 7 has dogs                 4134
## 8 has dogs and dislikes cats   552
## 9 has dogs and has cats      1474
## 10 has dogs and likes cats    2333
## 11 likes cats               1063
## 12 likes dogs                7224
## 13 likes dogs and dislikes cats 2029
## 14 likes dogs and has cats     4313
## 15 likes dogs and likes cats   14814
## 16 <NA>                   19921
```

We will define cats/dogs people in the following way and stick to non-NA observations:

```
cats_categories <- c("has cats", "likes cats", "dislikes dogs and  
                      "dislikes dogs and likes cats")  
dogs_categories <- c("has dogs", "likes dogs", "has dogs and dislikes dogs",  
                      "likes dogs and dislikes cats")  
okcupid3 <- okcupid %>%  
  mutate(pets = case_when(  
    pets %in% cats_categories ~ "cats",  
    pets %in% dogs_categories ~ "dogs",  
    TRUE ~ NA_character_)) %>%  
  drop_na(pets)  
  
okcupid3 %>% count(pets)
```

```
## # A tibble: 2 x 2  
##   pets      n  
##   <chr> <int>  
## 1 cats     2790  
## 2 dogs    13939
```

Notice the classes are very unbalanced, with roughly 5 dogs people to every 1 cats person.

As before in the vector predictors we have 37 continuous and categorical variables which may or may not be predictive to being a cats/dogs person:

```
okcupid3 <- okcupid3 %>%
  select(pets, all_of(predictors)) %>%
  mutate(id = 1:n())

dim(okcupid3)

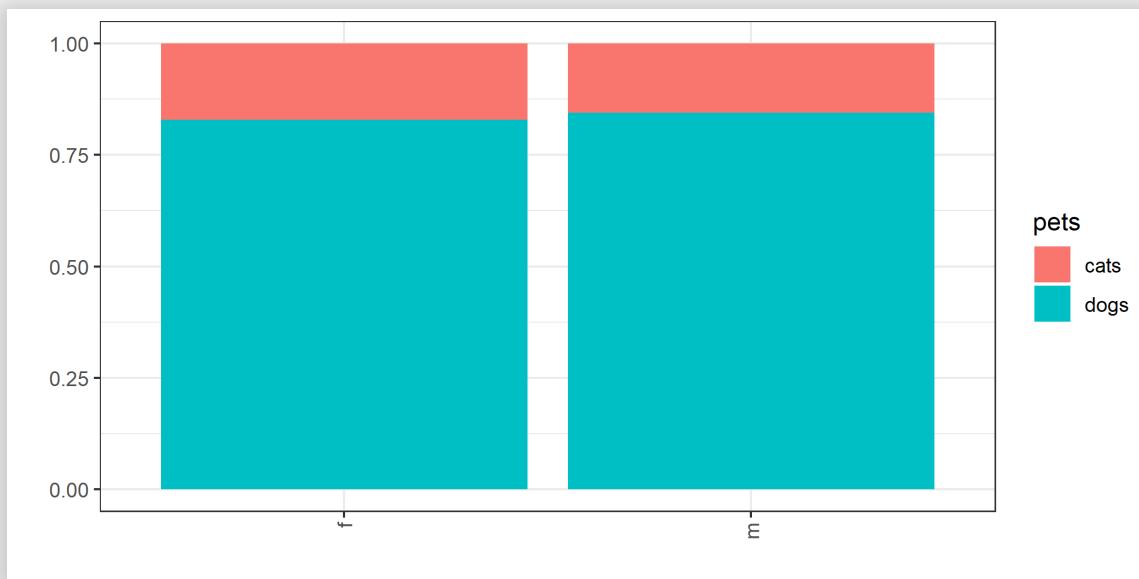
## [1] 16729     39
```

And as before we split the data into training, test and validation sets, not shown here:

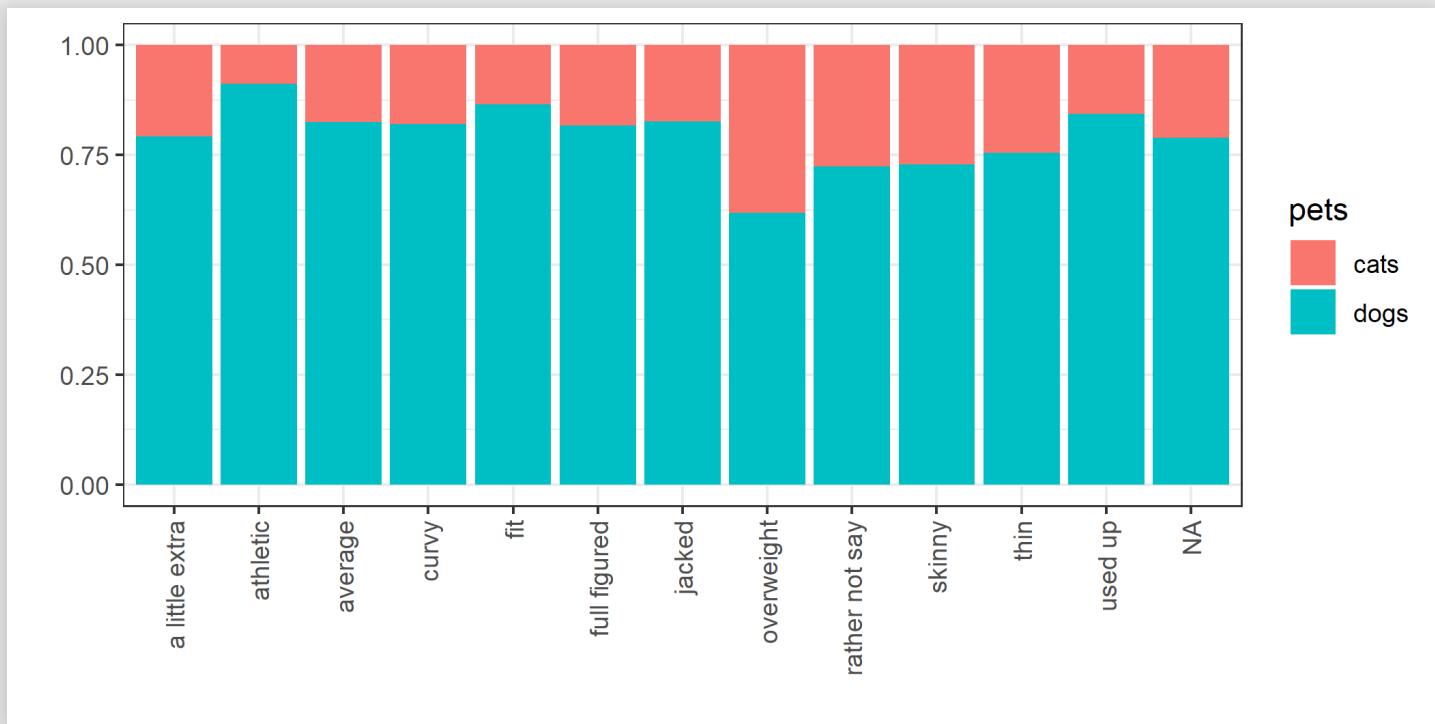
```
## train no. of rows: 10000
## validation no. of rows: 2729
## test no. of rows: 4000
```

Worth exploring relations between predictors and being a cats/dogs person:

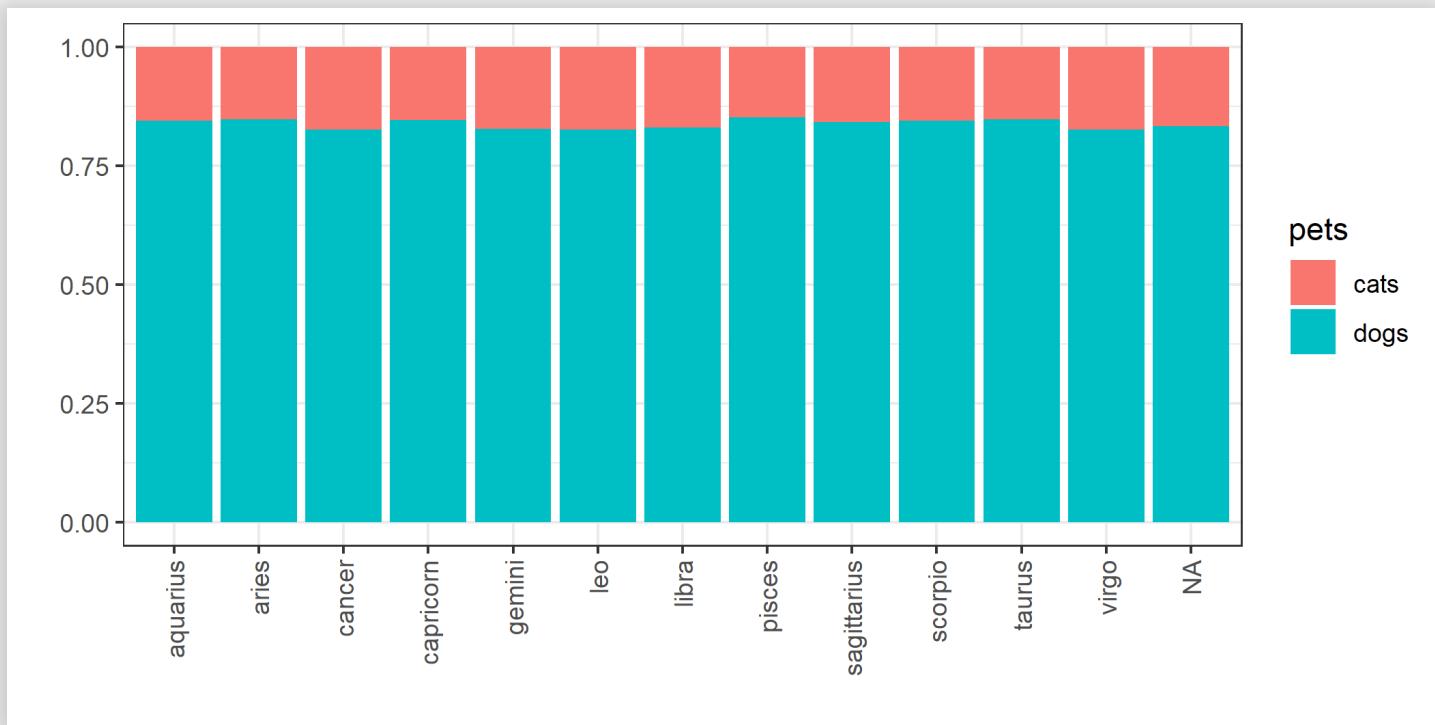
```
var_vs_pets_stackedbar <- function(var) {  
  ggplot(okcupid3_train, aes({{var}}, fill = pets)) +  
  geom_bar(position = "fill") +  
  theme_bw() +  
  labs(x = "", y = "") +  
  theme(axis.text.x = element_text(angle = 90, hjust = 1, vjust =  
})  
  
var_vs_pets_stackedbar(sex)
```



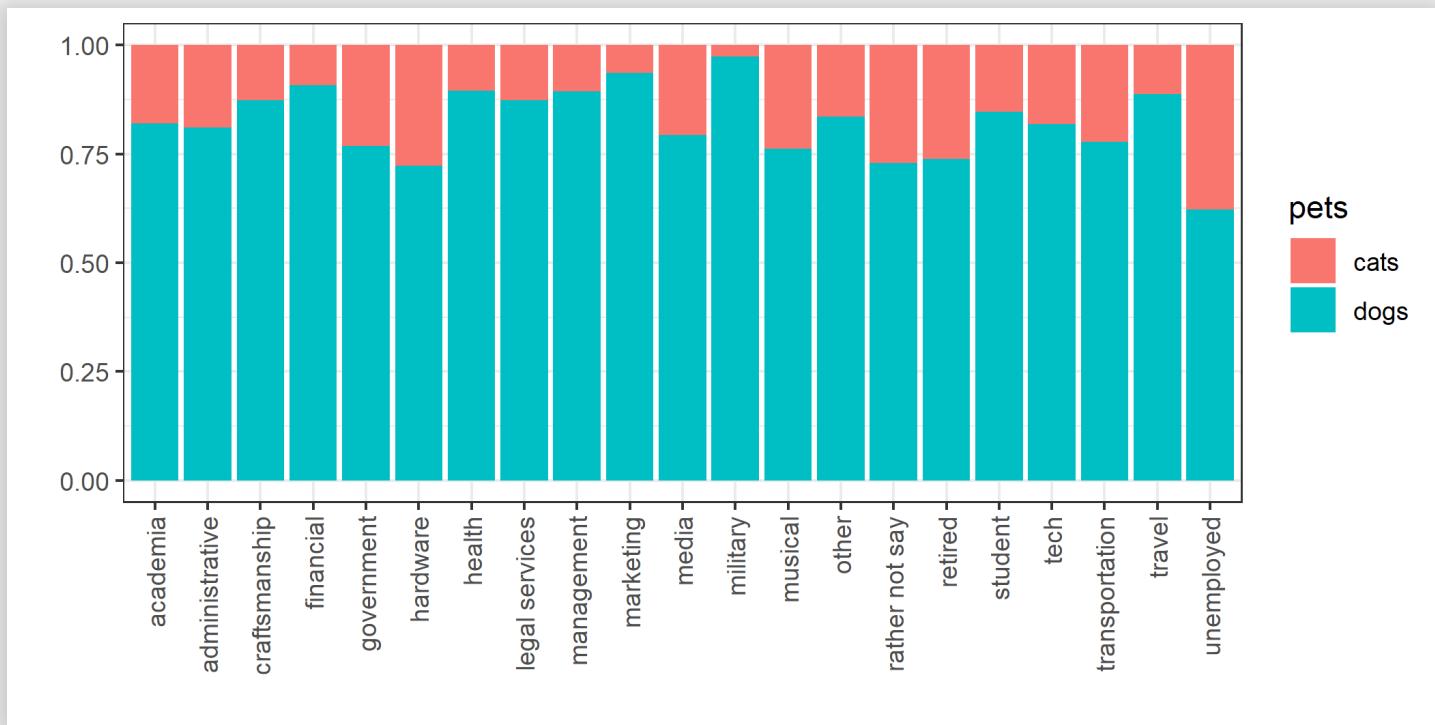
```
var_vs_pets_stackedbar(body_type)
```



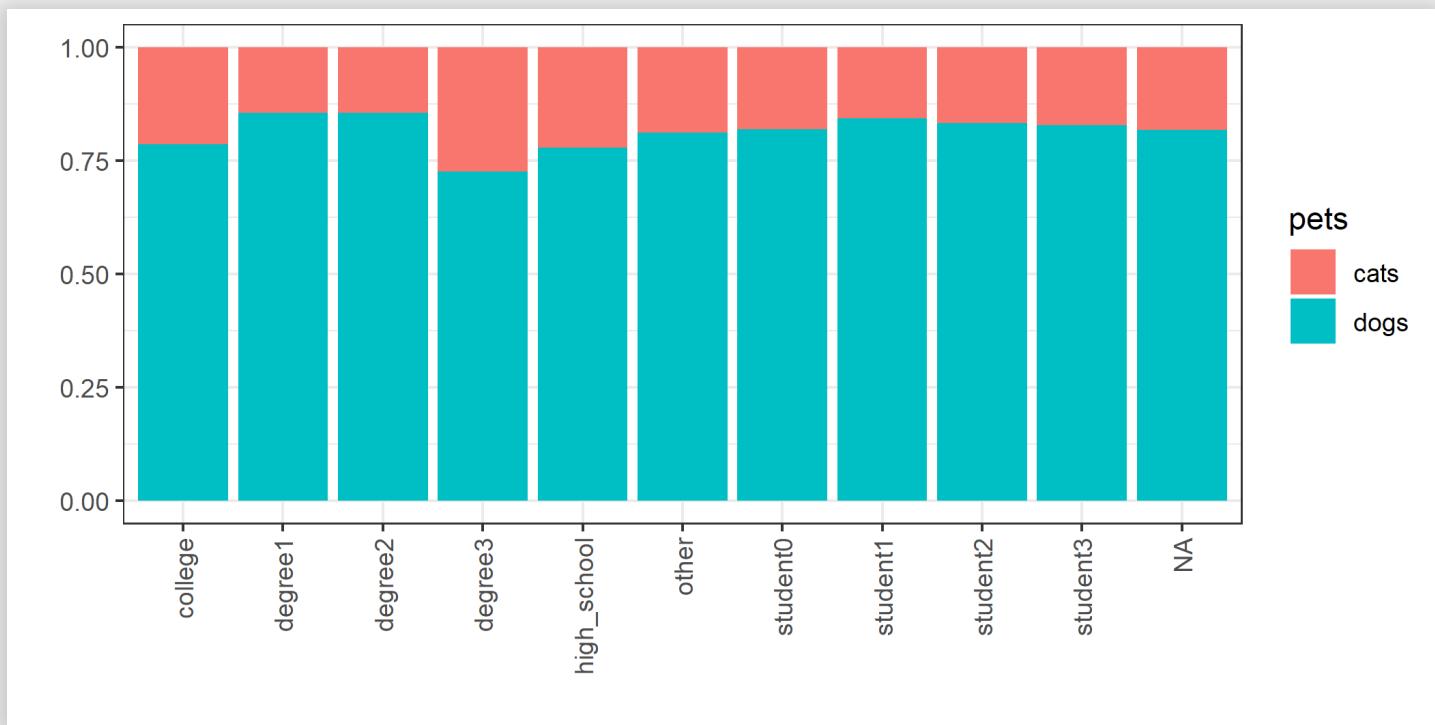
```
var_vs_pets_stackedbar(sign2)
```



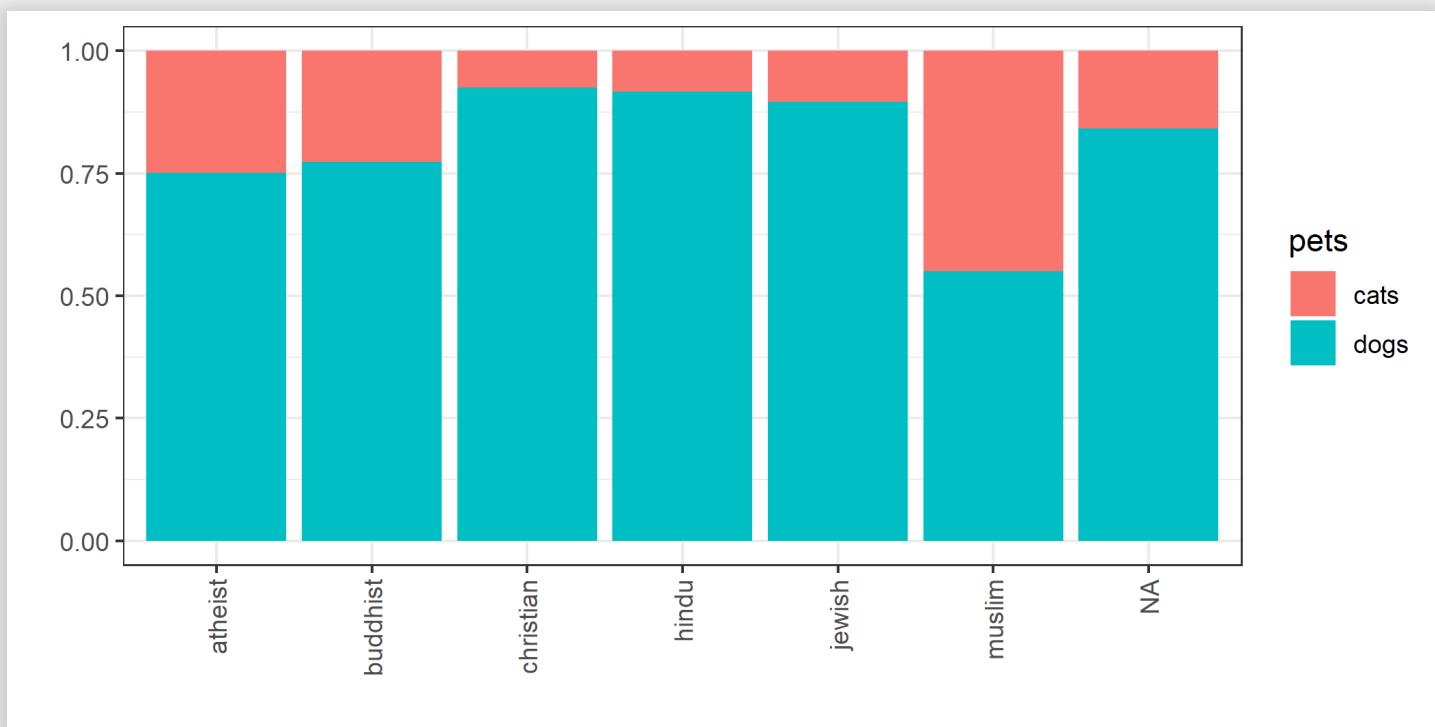
```
var_vs_pets_stackedbar(job3)
```



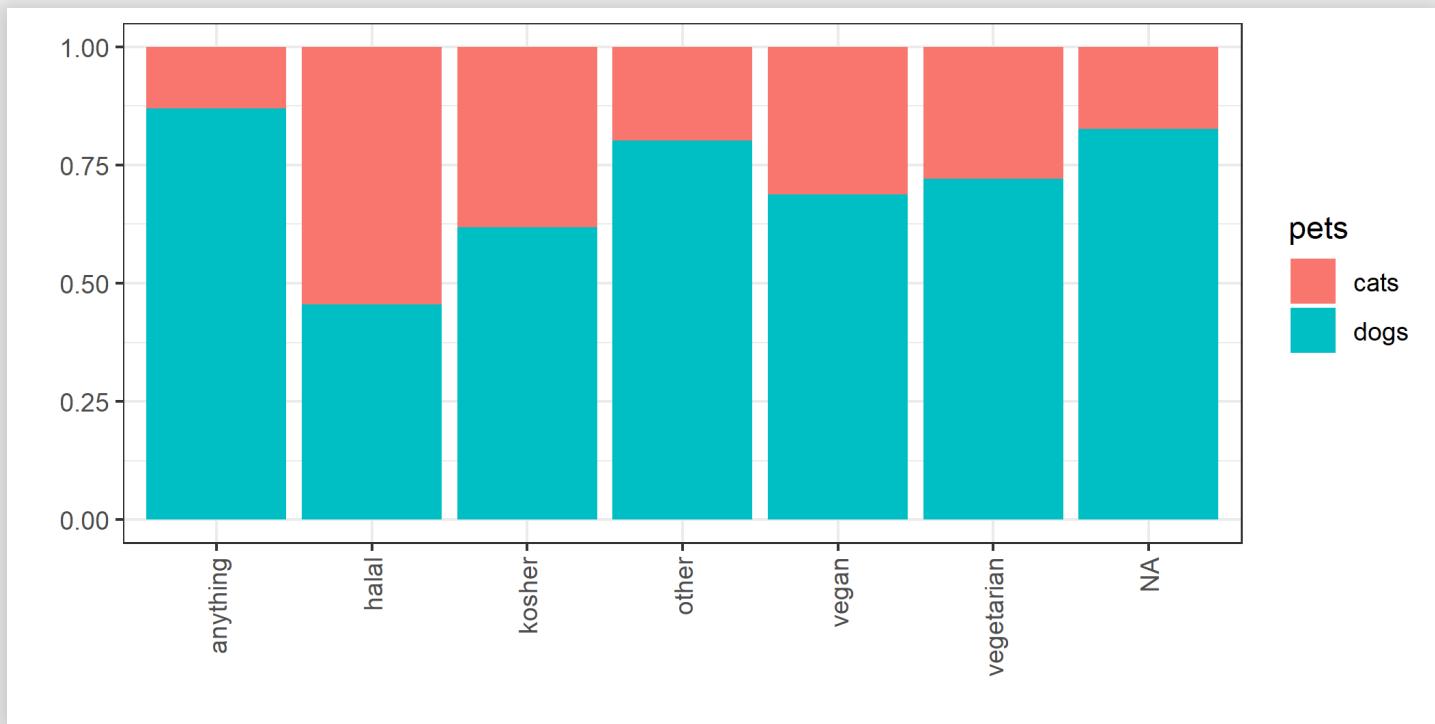
```
var_vs_pets_stackedbar(education2)
```



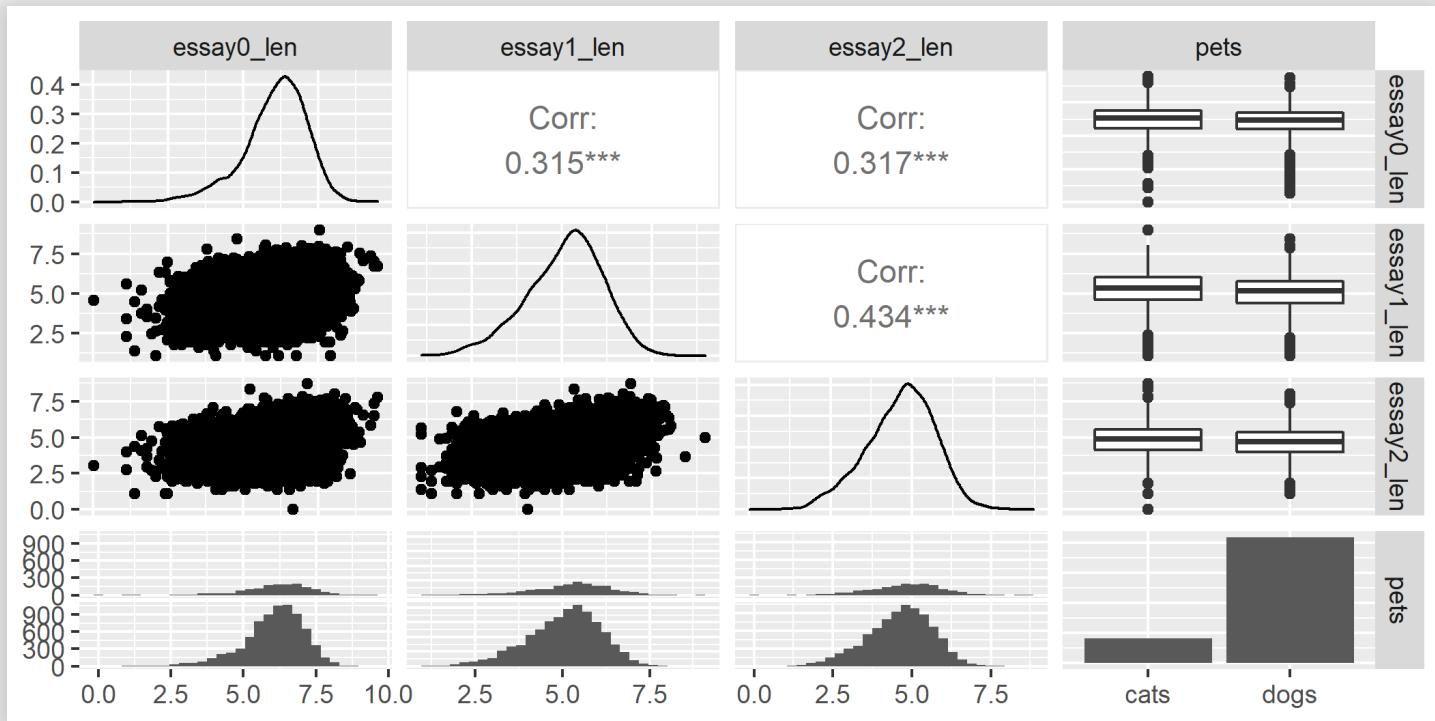
```
var_vs_pets_stackedbar(religion2)
```



```
var_vs_pets_stackedbar(diet2)
```



```
ggpairs(okcupid3_train %>%
         select(essay0_len:essay2_len, pets))
```



# Baseline: Logistic Regression

As in `lm`, it is better to impute missing values than to lose these observations:

```
# library(mice)
# mice_obj <- mice(okcupid3, m = 1, maxit = 10, seed = 42)
# okcupid3_imp_mice <- complete(mice_obj)

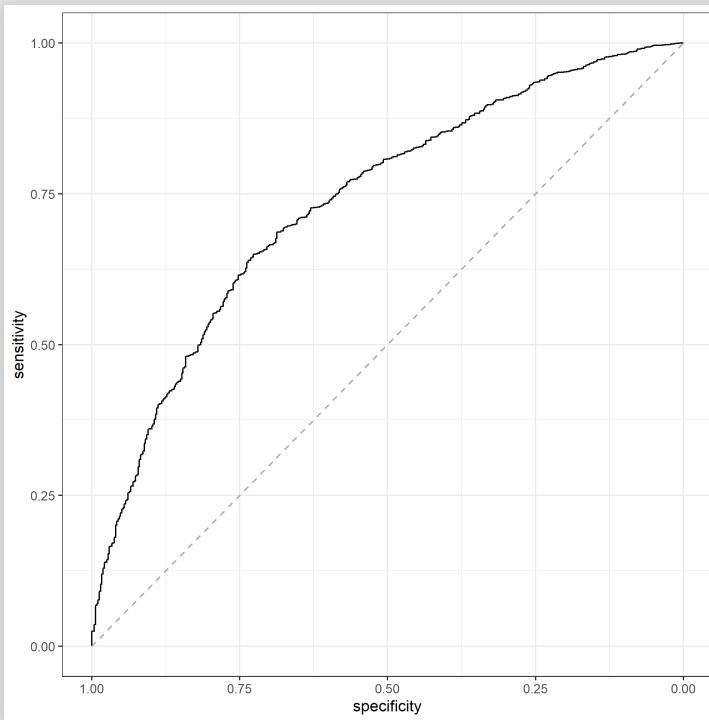
okcupid3_imp_mice <- read_rds("../data/okcupid3_imp_mice.rds")
okcupid3_imp_mice_train <- okcupid3_imp_mice[train_idx, ]
okcupid3_imp_mice_valid <- okcupid3_imp_mice[valid_idx, ]

mod_glm_mice <- glm(pets ~ ., data = okcupid3_imp_mice_train, family = "binomial")
pred_glm_mice <- predict(mod_glm_mice, okcupid3_imp_mice_valid, type = "response")
```

Let's plot the ROC curve:

```
library(pROC)
roc_obj <- roc(okcupid3_valid$pets, pred_glm_mice)

ggroc(roc_obj) +
  theme_bw() +
  geom_segment(aes(x = 1, xend = 0, y = 0, yend = 1), color="darkgrey")
```



Choosing a specific cutoff, the proportion of dogs people in the training sample (the "positive" class), 0.84, let's look at the confusion matrix:

```
cutoff <- mean(okcupid3_train$pets == "dogs")
pred_class <- ifelse(pred_glm_mice > cutoff, "dogs", "cats")
true_class <- okcupid3_valid$pets

table(true_class, pred_class)

##           pred_class
## true_class  cats  dogs
##       cats    313   160
##       dogs    679  1577
```

💡 What would be the accuracy? Recall (sensitivity, specificity)? Precision (PPV, NPV)?

We would like to know the model's AUC, accuracy for a given score cutoff, recall and precision:

```
report_accuracy_and_auc <- function(obs, pred, cutoff = mean(okcupy$pet_type == "Dogs")) {  
  roc_obj <- roc(obs, pred)  
  AUC <- as.numeric(auc(roc_obj))  
  res <- coords(roc_obj, x = cutoff,  
                ret = c("accuracy", "recall", "precision", "specificity"),  
                transpose = TRUE)  
  glue("AUC: {format(AUC, digits = 3)}  
ACC: {format(res['accuracy'], digits = 3)}  
Dogs: Recall: {format(res['recall'], digits = 3)}  
      Precision: {format(res['precision'], digits = 3)}  
Cats: Recall: {format(res['specificity'], digits = 3)}  
      Precision: {format(res['npv'], digits = 3)}")  
}  
  
report_accuracy_and_auc(okcupid3_valid$pets, pred_glm_mice)  
  
## AUC: 0.736  
## ACC: 0.693  
## Dogs: Recall: 0.699  
##           Precision: 0.908  
## Cats: Recall: 0.662  
##           Precision: 0.316
```

## Baseline: GLMNET: Penalized Logistic Regression

```
okcupid3_imp_mat_train <- model.matrix(~ ., okcupid3_imp_mice_train)
okcupid3_imp_mat_valid <- model.matrix(~ ., okcupid3_imp_mice_validation)

glmnet_cv <- cv.glmnet(x = okcupid3_imp_mat_train,
                        y = okcupid3_train$pets, family = "binomial")

best_lambda <- glmnet_cv$lambda.min

mod_glm_glmnet <- glmnet(x = okcupid3_imp_mat_train,
                           y = okcupid3_train$pets,
                           family = "binomial", lambda = best_lambda)
pred_glm_glmnet <- predict(mod_glm_glmnet, okcupid3_imp_mat_valid,
                           type = "response")

report_accuracy_and_auc(okcupid3_valid$pets, pred_glm_glmnet[, 1])

## AUC: 0.738
## ACC: 0.687
## Dogs: Recall: 0.691
##           Precision: 0.91
## Cats: Recall: 0.672
##           Precision: 0.313
```

# End of Detour

APPLICATIONS



OF DATA SCIENCE

# The OG CART

1. Find the predictor to (binary) split on and the value of the split, by *Gini* (a.k.a impurity) criterion
2. For each resulting node if  $n_{node} > 20$  go to 1
3. Once full tree has been grown, perform pruning using the *cost-complexity parameter*  $c_p$  and the  $Gini_{c_p}$  criterion
4. Predict the proportion of each class at each terminal node, or most common class

# The *Gini* criterion

- $y$  is the discrete dependent variable with  $J$  classes
- The  $Gini_{parent}$  at a parent node is:  
$$\sum_{j=1}^J P(y = j)[1 - P(y = j)] = \sum_j p_j(1 - p_j)$$
- a continuous predictor  $v$  is nominated for splitting the current node with splitting value  $l$
- such that  $S_1$  is the set of observations for which  $v_i \leq l$
- and  $S_2$  is the set of observations for which  $v_i > l$
- $p_{1j}$  is the (observed) probability of  $y$  equals class  $j$  in set  $S_1$

$$Gini_{split} = \frac{\#\text{obs node1}}{\#\text{obs parent}} Gini_{node1} + \frac{\#\text{obs node2}}{\#\text{obs parent}} Gini_{node2} = \\ \frac{\#\text{obs node1}}{\#\text{obs parent}} \sum_j p_{1j}(1 - p_{1j}) + \frac{\#\text{obs node2}}{\#\text{obs parent}} \sum_j p_{2j}(1 - p_{2j})$$

And we find  $l$  for which  $\Delta G = Gini_{parent} - Gini_{split}$  is greatest.

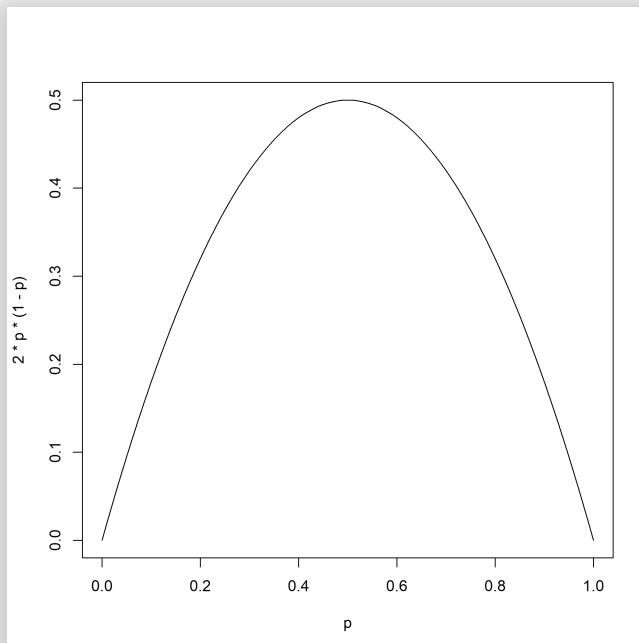
## Why Gini?

For  $J = 2$  classes this means:

$$p_1(1 - p_1) + p_2(1 - p_2) = 2p_1(1 - p_1)$$

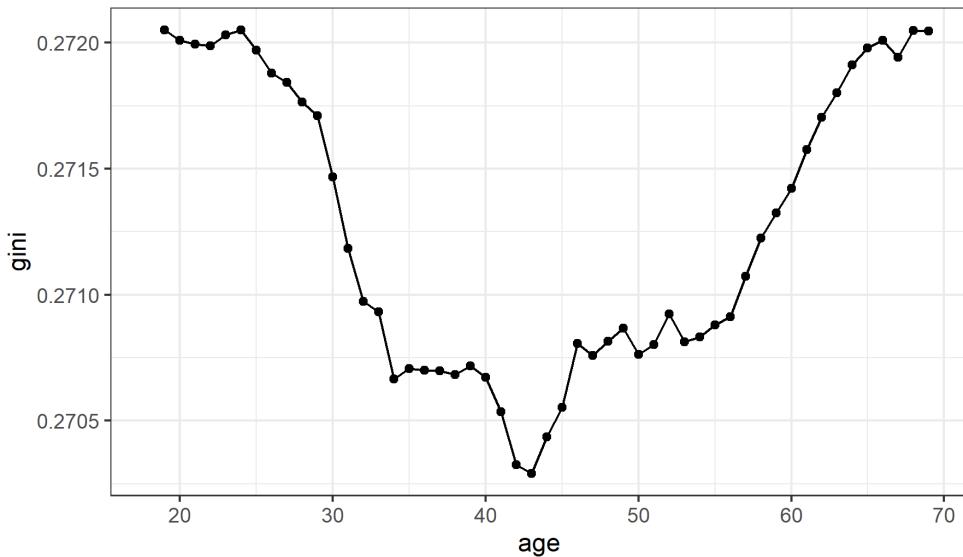
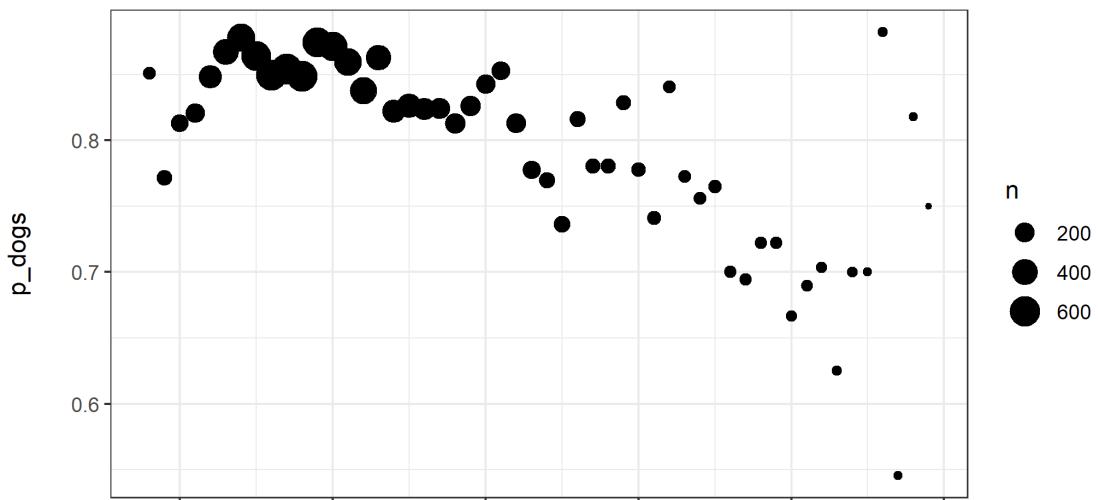
The more "impure" the node, the higher this metric:

```
p <- seq(0, 1, 0.01)
plot(p, 2 * p * (1 - p), type = "l")
```



For example if age is candidate in splitting pets:

```
gini <- function(l, df, v) {  
  pets_above <- df %>% filter({{v}} >= l) %>% pull(pets)  
  pets_below <- df %>% filter({{v}} < l) %>% pull(pets)  
  p_dogs_above <- mean(pets_above == "dogs")  
  gini_above <- 2 * p_dogs_above * (1 - p_dogs_above)  
  p_dogs_below <- mean(pets_below == "dogs")  
  gini_below <- 2 * p_dogs_below * (1 - p_dogs_below)  
  gini_weighted <- (length(pets_above) / nrow(df)) * gini_above +  
    (length(pets_below) / nrow(df)) * gini_below  
  return(gini_weighted)  
}  
  
age <- seq(18, 69, 1)  
gini_age <- map_dbl(age, gini, df = okcupid3_train, v = age)  
  
p1 <- okcupid3_train %>%  
  group_by(age) %>%  
  summarise(p_dogs = mean(pets == "dogs"), n = n()) %>%  
  ggplot(aes(age, p_dogs)) +  
  geom_point(aes(size = n)) +  
  theme_bw() +  
  labs(x = "") +  
  theme(axis.text.x = element_blank())  
  
p2 <- tibble(age = age, gini = gini_age) %>%  
  ggplot(aes(age, gini)) +  
  geom_line() +
```



# CART with rpart

Let's tune  $c_p$  for our data using a 5-fold (manual) Cross Validation.  
The criterion to maximize would be AUC.

```
n_cv <- 5; cp_seq <- seq(0, 0.01, 0.0005)

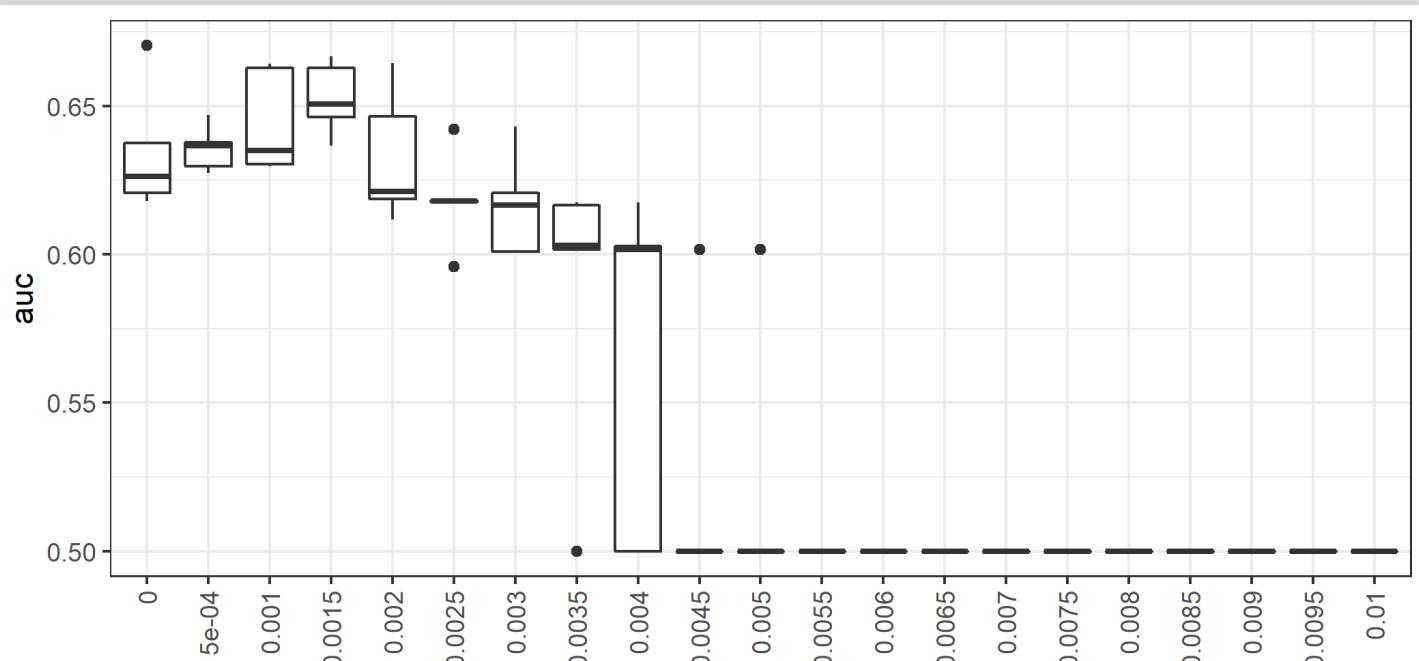
okcupid3_train_val <- okcupid3_train %>%
  mutate(val = sample(1:n_cv, n(), replace = TRUE))

get_validation_set_auc <- function(i, .cp) {
  ok_tr <- okcupid3_train_val %>% filter(val != i) %>% select(-val)
  ok_val <- okcupid3_train_val %>% filter(val == i) %>% select(-val)
  mod <- rpart(pets ~ ., data = ok_tr,
                control = rpart.control(cp = 0, xval = 1))
  mod <- prune(mod, cp = .cp)
  pred <- predict(mod, ok_val)[, 2]
  roc_obj <- roc(ok_val$pets, pred)
  as.numeric(auc(roc_obj))
}

get_cv_auc <- function(.cp) {
  tibble(cp = rep(.cp, n_cv),
        auc = map_dbl(1:n_cv, get_validation_set_auc, .cp = .cp))
}
```

```
cv_table <- map_dfr(cp_seq, get_cv_auc)

cv_table %>%
  mutate(cp = factor(cp)) %>%
  ggplot(aes(cp, auc)) +
  geom_boxplot() +
  theme_bw() +
  labs(x = "") +
  theme(axis.text.x = element_text(angle = 90, hjust = 1, vjust =
```

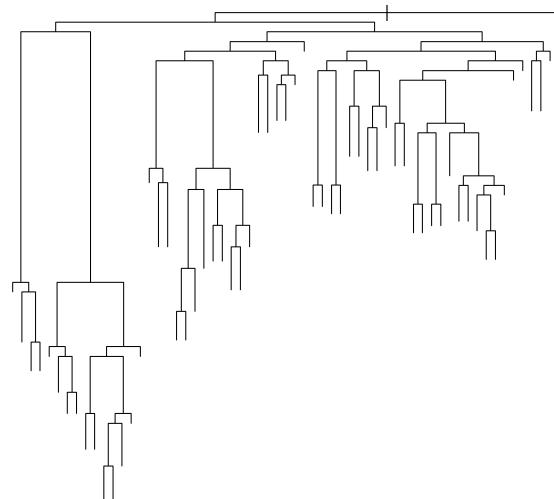


## Training on the entire training set:

```
mod_tree_na_class <- rpart(pets ~ ., data = okupid3_train,  
                           control = rpart.control(cp = 0, xval =  
mod_tree_na_class <- prune(mod_tree_na_class, cp = 0.0015)
```

There's no way to plot this tree nicely...

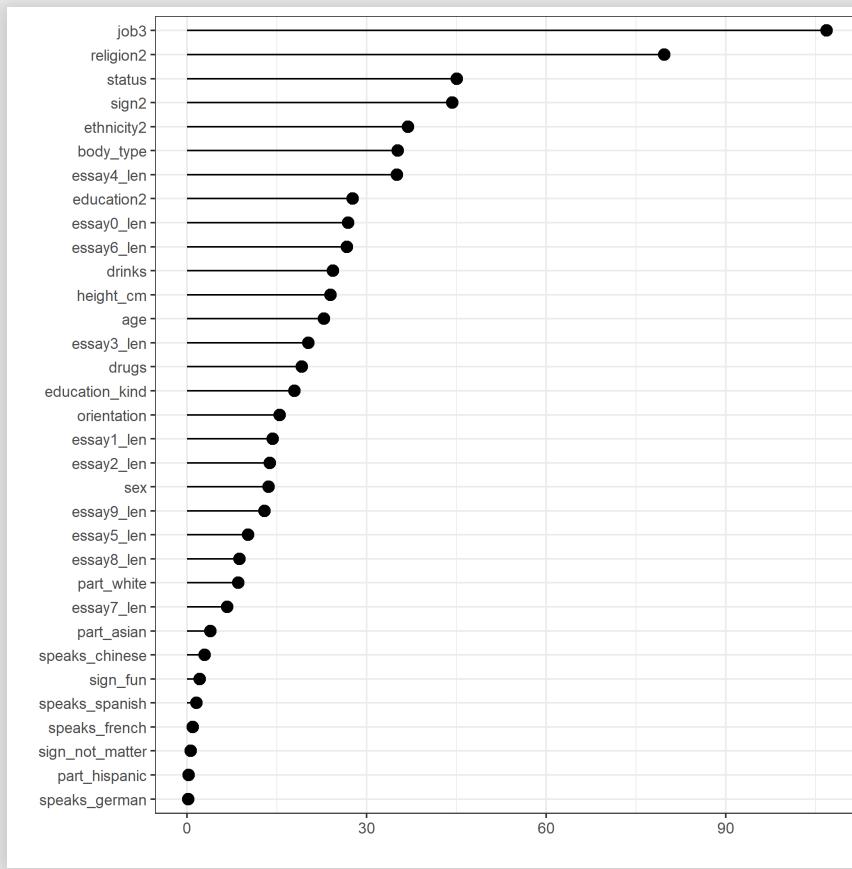
```
plot(mod_tree_na_class)
```



Printing the tree it seems like after splitting observations by religion, those who are Christian, Jewish or Hindu have a 88% of being dogs people, and the rest are then split by Status, Body Type, the length of their 9th Essay, etc...

```
Fitted party:
[1] root
| [2] religion2 in atheist, buddhist, muslim
| | [3] status in available, married, seeing someone
| | | [4] body_type in a little extra, curvy, full figured, skinny, thin
| | | | [5] job3 in administrative, craftsmanship, hardware, health, management, musical, other, tech
| | | | | [6] essay3_len >= 4.45447: cats (n = 35, err = 11.4%)
| | | | | [7] essay3_len < 4.45447
| | | | | | [8] sign2 in aquarius, cancer, capricorn, virgo: cats (n = 9, err = 11.1%)
| | | | | | [9] sign2 in aries, gemini, leo, pisces, sagittarius, scorpio: dogs (n = 15, err = 26.7%)
| | | | | [10] job3 in academia, financial, government, legal services, marketing, media, rather not say, student, transportation, travel: dogs
| | | | [11] body_type in athletic, average, fit, jacked, overweight, rather not say, used up
| | | | | [12] diet2 in kosher, vegan, vegetarian
| | | | | | [13] essay0_len < 6.77815: cats (n = 30, err = 23.3%)
| | | | | | [14] essay0_len >= 6.77815: dogs (n = 16, err = 31.2%)
| | | | | [15] diet2 in anything, halal, other
| | | | | | [16] essay8_len >= 5.30087
| | | | | | | [17] essay2_len < 5.59658: cats (n = 17, err = 17.6%)
| | | | | | | [18] essay2_len >= 5.59658: dogs (n = 27, err = 37.0%)
| | | | | | [19] essay8_len < 5.30087
| | | | | | | [20] essay4_len >= 7.88766: cats (n = 9, err = 22.2%)
| | | | | | | [21] essay4_len < 7.88766: dogs (n = 150, err = 24.7%)
[22] status in single
| [23] body_type in a little extra, average, curvy, fit, full figured, jacked, overweight, skinny, thin, used up
| | [24] ethnicity2 in native american, other, white
| | | [25] drinks in desperately, not at all, rarely, very often
| | | | [26] job3 in academia, administrative, hardware, legal services, management, media, other, rather not say, tech, transportation
| | | | | [27] education2 in degree3, other, student0, student1
| | | | | | [28] body_type in a little extra, average, full figured, jacked, overweight, skinny, thin
| | | | | | | [29] job3 in academia, administrative, hardware, media, rather not say, tech: cats (n = 39, err = 12.8%)
| | | | | | | [30] job3 in legal services, other: dogs (n = 7, err = 28.6%)
| | | | | | [31] body_type in curvy, fit, used up: dogs (n = 27, err = 33.3%)
| | | | | [32] education2 in college, degree1, degree2, high_school, student1, student2
| | | | | | [33] body_type in a little extra, curvy, full figured: cats (n = 16, err = 25.0%)
| | | | | | [34] body_type in average, fit, jacked, overweight, skinny, thin, used up
| | | | | | | [35] education2 in degree1, degree2, student2
| | | | | | | | [36] sign2 in capricorn, gemini, libra, pisces, taurus
| | | | | | | | | [37] essay5_len < 5.02025
| | | | | | | | | | [38] job3 in hardware, legal services, management, media: cats (n = 16, err = 18.8%)
| | | | | | | | | | [39] job3 in academia, other, tech: dogs (n = 13, err = 38.5%)
| | | | | | | | | | [40] essay5_len >= 5.02025: dogs (n = 8, err = 25.0%)
| | | | | | | | | [41] sign2 in aquarius, aries, cancer, leo, sagittarius, scorpio, virgo
```

# Variables Importance



# Prediction

```
pred_tree_na_class <- predict(mod_tree_na_class, okcupid3_valid)
report_accuracy_and_auc(okcupid3_valid$pets, pred_tree_na_class[,  

  ## AUC: 0.598
  ## ACC: 0.751
  ## Dogs: Recall: 0.842
  ##           Precision: 0.855
  ## Cats: Recall: 0.317
  ##           Precision: 0.296
```

As expected, far from impressive.

## Let's try using the imputed NA data:

```
mod_tree_imp_class <- rpart(pets ~ ., data = okcupid3_imp_mice_train,
                             control = rpart.control(cp = 0, xval = 10))
mod_tree_imp_class <- prune(mod_tree_imp_class, cp = 0.0015)

pred_tree_imp_class <- predict(mod_tree_imp_class, okcupid3_imp_mice_train)

report_accuracy_and_auc(okcupid3_valid$pets, pred_tree_imp_class[, 1])

## AUC: 0.635
## ACC: 0.75
## Dogs: Recall: 0.828
##           Precision: 0.864
## Cats: Recall: 0.381
##           Precision: 0.317
```

# Are you impressed?

Me neither. To be continued.