Week1 Mushroom

Sedo

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Import Data

Also, setnames of columns

```r
library(data.table)

mushroom_DB = read.csv("https://archive.ics.uci.edu/ml/machine-learning-databases/mushroom/agaricus-lep
mushroom_DB = data.table(mushroom_DB)
names(mushroom_DB) <-
  c(
  "Poison_Edible",
  "cap_shape",
  "cap_surface",
  "cap_color",
  "bruises",
  "odor",
  "gill_attachment",
  "gill_spacing",
  "gill_size",
  "gill_color",
  "stalk_shape",
  "stalk_root",
  "stalk_surface_above_ring",
  "stalk_surface_below_ring",
  "stalk_color_above_ring",
  "stalk_color_below_ring",
  "veil_type",
  "veil_color",
  "ring_number",
  "ring_type",
  "spore_print_color",
  "population",
  "habitat"
  )
```

Subset and Transformation

```r
mushroom_DB_sub <- mushroom_DB[,c(1,2:4,6)]

library(car)
mushroom_DB_sub$Poison_Edible <- recode(mushroom_DB_sub$Poison_Edible, "'e'='edible'; 'p'='poisonous'")
mushroom_DB_sub$cap_shape <- recode(mushroom_DB_sub$cap_shape, "'b'='bell';'c'='conical';'x'='convex';'
mushroom_DB_sub$cap_surface <- recode(mushroom_DB_sub$cap_surface, "'f'='fibrous';'g'='grooves';'y'='sca
mushroom_DB_sub$cap_color <- recode(mushroom_DB_sub$cap_color, "'n'='brown';'b'='buff';'c'='cinnamon';'
mushroom_DB_sub$odor <- recode(mushroom_DB_sub$odor, "'a'='almond';'l'='anise';'c'='creosote';'y'='fish
```

```
summary(mushroom_DB_sub)
```

```
##    Poison_Edible     cap_shape      cap_surface       cap_color
##  edible   :4208    bell   : 452   fibrous:2320    brown  :2284
##  poisonous:3916    conical:   4   grooves:   4    gray   :1840
##                    convex :3656   scaly  :3244    red    :1500
##                    flat   :3152   smooth :2556    yellow :1072
##                    knobbed: 828                   white  :1040
##                    sunken :  32                   buff   : 168
##                                                   (Other): 220
##       odor
##  none   :3528
##  foul   :2160
##  fishy  : 576
##  spicy  : 576
##  almond : 400
##  anise  : 400
##  (Other): 484
```