# **Data Wrangling and Visualization**

## IFT6758 Fall 2019

### **Marc-Antoine Provost**

## **Missing Values**

- 1. Selection bias. Download the IMDB and Rotten Tomatoes <u>data</u> (<a href="https://gist.githubusercontent.com/krisrs1128/9276aa2a5d9fa7ab0786bbc75f93d77a/raw/1aa5220f9e140515g">https://gist.githubusercontent.com/krisrs1128/9276aa2a5d9fa7ab0786bbc75f93d77a/raw/1aa5220f9e140515g</a>
  - a. Is there any missingness in this dataset? Which columns have the most missingness?
  - b. Make a hexbin scatterplot of rotten tomatoes vs. imdb scores against one another. Comment on the relationship between these variables.
  - c. Filter the movies to those made before 1970, and remake the scatterplot. What do you notice?
  - d. Propose explanations for what you see in part (c).

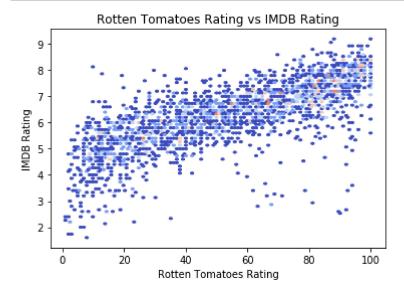
```
In [60]: import pandas as pd
         import numpy as np
         import matplotlib.pyplot as plt
         import seaborn as sns
         df = pd.read_csv("https://gist.githubusercontent.com/krisrs1128/9276aa2a5d9fa7
         ab0786bbc75f93d77a/raw/1aa5220f9e140515d04601a6c114fc43cecf1e21/movies.csv")
         df["Release_Date"] = pd.to_datetime(df.Release_Date)
         df["Release_Year"] = df["Release_Date"].dt.year
         movies = df
         #a)
         movies.isna().sum(axis=0)
Out[60]: Title
                                      1
                                      7
         US_Gross
         Worldwide_Gross
                                      7
```

US\_DVD\_Sales 2637 Production\_Budget 1 Release\_Date 0 605 MPAA Rating Running\_Time\_min 1992 Distributor 232 Source 365 Major\_Genre 275 Creative\_Type 446 Director 1331 Rotten\_Tomatoes\_Rating 880 IMDB\_Rating 213 IMDB\_Votes 213 Release\_Year 0

dtype: int64

```
In [55]: #b)

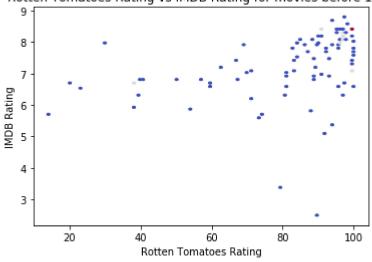
plt.hexbin(movies["Rotten_Tomatoes_Rating"], movies["IMDB_Rating"], cmap="cool
warm", mincnt=1)
plt.xlabel("Rotten Tomatoes Rating")
plt.ylabel("IMDB Rating")
plt.title("Rotten Tomatoes Rating vs IMDB Rating")
plt.show()
```



We can observe that both rating system does not have the same rating scale, i.e. Rotten Tomatoes rating scale is 0-100 and IMBB's one is from 0 to 10. Also, the ratings seem mostly linear, that is, as the IMDB ratings go up, the Rotten Tomatoes ratings follow.

```
In [56]: #c)
    movies_sub = movies.loc[movies["Release_Year"] < 1970]
    plt.hexbin(movies_sub["Rotten_Tomatoes_Rating"], movies_sub["IMDB_Rating"], cm
    ap="coolwarm", mincnt=1)
    plt.xlabel("Rotten Tomatoes Rating")
    plt.ylabel("IMDB Rating")
    plt.title("Rotten Tomatoes Rating vs IMDB Rating for movies before 1970")
    plt.show()
    movies_sub.describe()</pre>
```





#### Out[56]:

	US_Gross	Worldwide_Gross	US_DVD_Sales	Production_Budget	Running_Time_min	F
count	1.290000e+02	1.290000e+02	2.000000e+00	1.300000e+02	0.0	
mean	2.084259e+07	2.603317e+07	5.493817e+07	6.253851e+06	NaN	
std	2.618528e+07	3.756361e+07	5.034371e+07	7.648852e+06	NaN	
min	0.000000e+00	0.000000e+00	1.933979e+07	1.140000e+05	NaN	
25%	5.400000e+06	5.400000e+06	3.713898e+07	1.800000e+06	NaN	
50%	1.046250e+07	1.046250e+07	5.493817e+07	3.500000e+06	NaN	
75%	3.000000e+07	3.330000e+07	7.273736e+07	7.800000e+06	NaN	
max	1.632143e+08	2.862143e+08	9.053655e+07	5.000000e+07	NaN	

We can notice that there is a higher variance (proven by the std) for the Rotten Tomatoes ratings compared to to IMDB ratings. In fact, while IMDB's ratings are mostly around 7, which can be qualified as an average rating for a movie, the same movie can have a much lower rating according to Rotten Tomatoes. However, both IMDB and Rotten Tomatoes seem to have the same opinion for the upper ranked movies.

d) This can be explained by the people that are providing these reviews. Indeed, the ratings from IMDB are based on IMDB user's reviews, while Rotten Tomatoes' ratings are given by film critics. An average movie enthusiast often rate a movie based on a shallower analysis (i.e. how much they enjoyed the movie) than a film critic who consider many technical aspects in order to rate a movie.

### **Tidying**

1. You have the following table in a variable called "test scores",

Student	Physics	Chemistry	English	Math
John	78	79	56	95
Alice	58	72	91	81
Rachel	22	61	88	64
Tom	78	89	56	83

(a) Explain the format of the table after running this code,

```
test_scores_clean = pd.melt(
    test_scores,
    id_vars=['Student'],
    var_name=['Subject'],
    value_name='Score'
)
```

(b) Explain what the following code does.

```
test_scores.assign(
    quant=lambda df: df["Math"] + df["Physics"],
    overall=lambda df: df.drop("Student", axis=1).sum(axis=1)
)
```

- a) The melt function of pandas basically reshapes wide data to long data, so now each student will appear 4 times with the respective subject and their respective score in the particular subject.
- b) It will create new columns quant and overall, where quant will be the sum of math and physics for each student and where overall will be the sum of scores for each student.

## **Visualization**

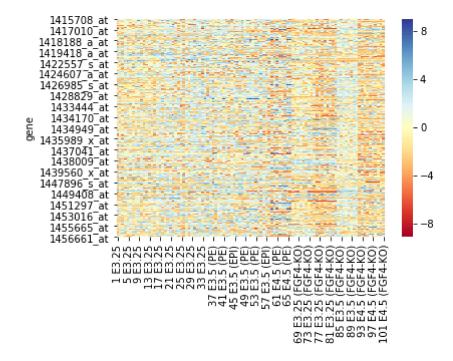
- 1. Making a heatmap. Heatmaps are a way of plotting continuous values against combinations of categorical variables. We'll use them to analyze a gene expression dataset, collected to study changes in expression after the first symmetry breaking event of the embryo. The rows of the matrix correspond to genes, and the columns are different experimental samples.
  - a. Make a heatmap of the <u>raw data</u> (<a href="https://gist.githubusercontent.com/krisrs1128/b8dc85b659186259715f8efe950ffce6/raw/77669ebdda4d6f8a02">https://gist.githubusercontent.com/krisrs1128/b8dc85b659186259715f8efe950ffce6/raw/77669ebdda4d6f8a02</a> using sns.heatmap. Make sure to use a diverging color scale, centered around zero.
  - b. The heatmap is not particularly informative. It's hard to make comparisons across either genes or samples, since there are so many of them. To remedy this, order them using a clustering method (the details are unimportant), as implemented in the clustermap function.

```
In [66]: #a)
    import pandas as pd
    import numpy as np
    import seaborn as sns
    import sys

np.set_printoptions(threshold=sys.maxsize)

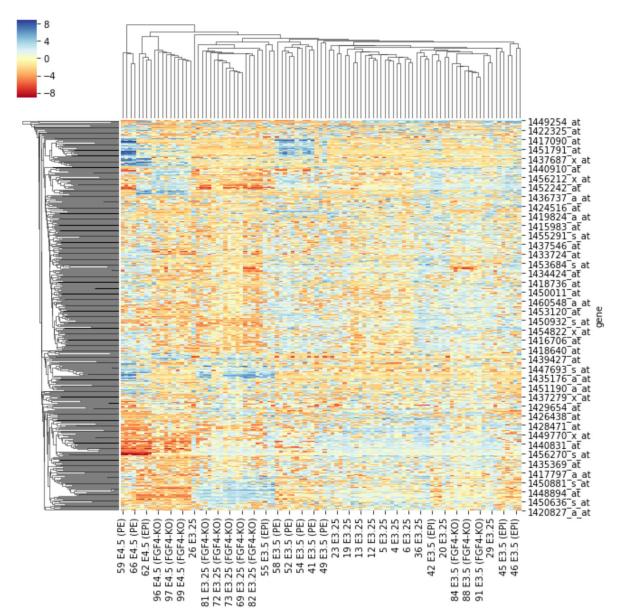
df = pd.read_csv("https://gist.githubusercontent.com/krisrs1128/b8dc85b6591862
59715f8efe950ffce6/raw/77669ebdda4d6f8a029c2fdf506f4599277b50f4/hiiragi.csv")
    df = df.set_index("gene")
    sns.heatmap(data=df, center=0, cmap='RdYlBu')
```

Out[66]: <matplotlib.axes.\_subplots.AxesSubplot at 0x103929d0>



```
In [69]: #b)
sns.clustermap(data=df, center=0, cmap='RdYlBu')
```

Out[69]: <seaborn.matrix.ClusterGrid at 0xb01c9f0>



# **Function Fitting**

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### **Marc-Antoine Provost**

## **Linear Regression**

1. [ISLR 3.7.5] Consider the fitted values that result from performing linear regression without an intercept. In this setting, the  $i^{th}$  fitted value takes the form,  $\hat{y}_i = x_i \hat{\beta}$  where

$$\hat{eta} = rac{\sum_{i=1}^{n} x_i y_i}{\sum_{i=1}^{n} x_i^2}$$

Show that we can write

$$\hat{y}_i = \sum_{i'} a_{i'} y_{i'}.$$

What is  $a_{i'}$ ? Note: We interpret this result by saying that the fitted values from linear regression are **linear** combinations of the response values.

#### **Answer**

$$egin{aligned} {\hat y}_i &= x_i imes rac{\sum_{i'=1}^n \left( x_{i'} y_{i'} 
ight)}{\sum_{j=1}^n x_j^2} \ {\hat y}_i &= \sum_{i'=1}^n rac{\left( x_{i'} y_{i'} 
ight) imes x_i}{\sum_{j=1}^n x_j^2} \ {\hat y}_i &= \sum_{i'=1}^n \left( rac{x_i x_{i'}}{\sum_{j=1}^n x_j^2} imes y_{i'} 
ight) \ a_{i'} &= rac{x_i x_{i'}}{\sum_{j=1}^n x_j^2} \end{aligned}$$

1. [ISLR 7.9.3] Suppose we fit a curve with basis functions  $b_1(x)=x, b_2(x)=(x-1)^21\{x\geq 1\}$ . (Note that  $1\{x\geq 1\}$  equals 1 for  $x\geq 1$  and 0 otherwise.) We fit the linear regression model,

$$y=eta_{0}+eta_{1}b_{1}\left( x
ight) +eta_{2}b_{2}\left( x
ight) +\epsilon$$

and obtain coefficient estimates

$${\hat eta}_0 = 1, {\hat eta}_1 = 1 {\hat eta}_2 = -2.$$

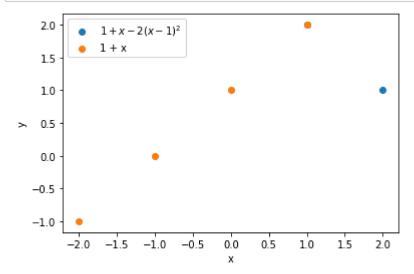
Sketch the estimated curve between x=-2 and x=2. Note the intercepts, slopes, and other relevant information.

```
x < 1: Y = 1 + x \ x \geq 1: Y = 1 + x - 2(x-1)^2
```

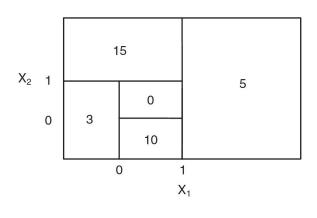
```
In [56]: import matplotlib.pyplot as plt
import numpy as np
x = np.linspace(-2,1, 4)
y = 1 + x

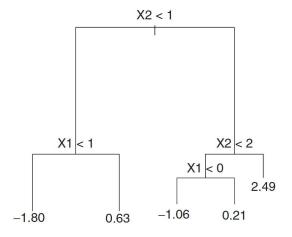
x_two = np.linspace(1,2,2)
y_two = 1 + x_two -2*(x_two-1)**2
plt.scatter(x_two, y_two, label = '$1 + x -2(x-1)^2$')

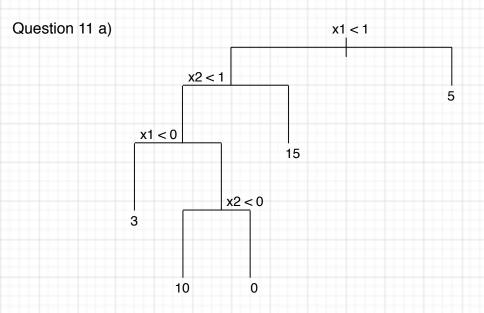
plt.scatter(x,y, label = "1 + x")
plt.legend()
plt.xlabel("x")
plt.ylabel("y")
plt.ylabel("y")
plt.show()
```



- 1. [ISLR 8.4.4] Consider the figure below.
  - a. Sketch the tree corresponding to the partition of the predictor space illustrated in the left-hand panel. The numbers inside the boxes indicate the mean of Y within each region.
  - b. Create a diagram similar to the left-hand panel, using the tree illustrated in the right-hand panel. You should divide up the predictor space into the correct regions, and indicate the mean for each region.







## Question 11 b)

