Lecture 9-2: Linear Regression II

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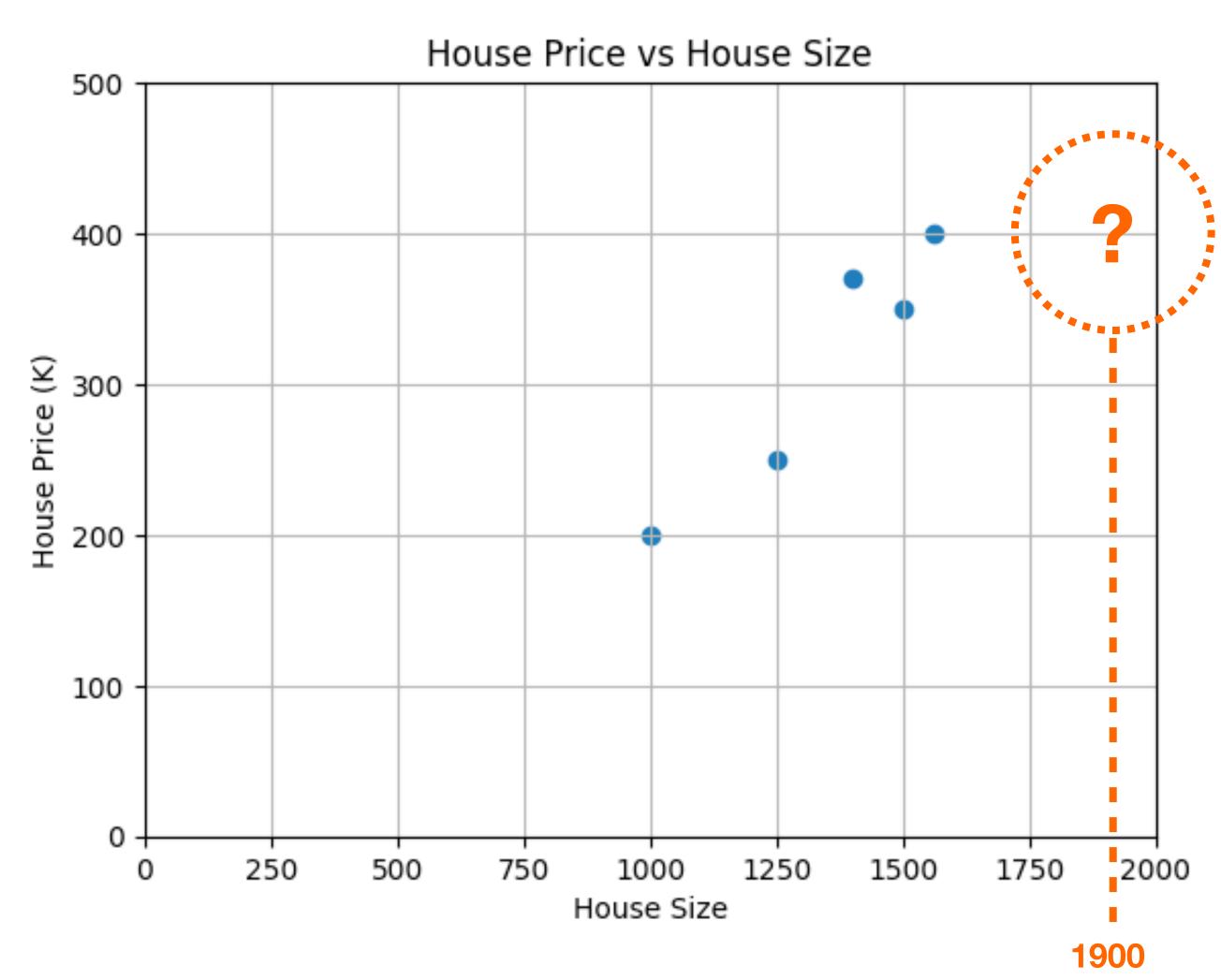
Recap - Supervised Learning

X's: "input" variable / features / independent variables

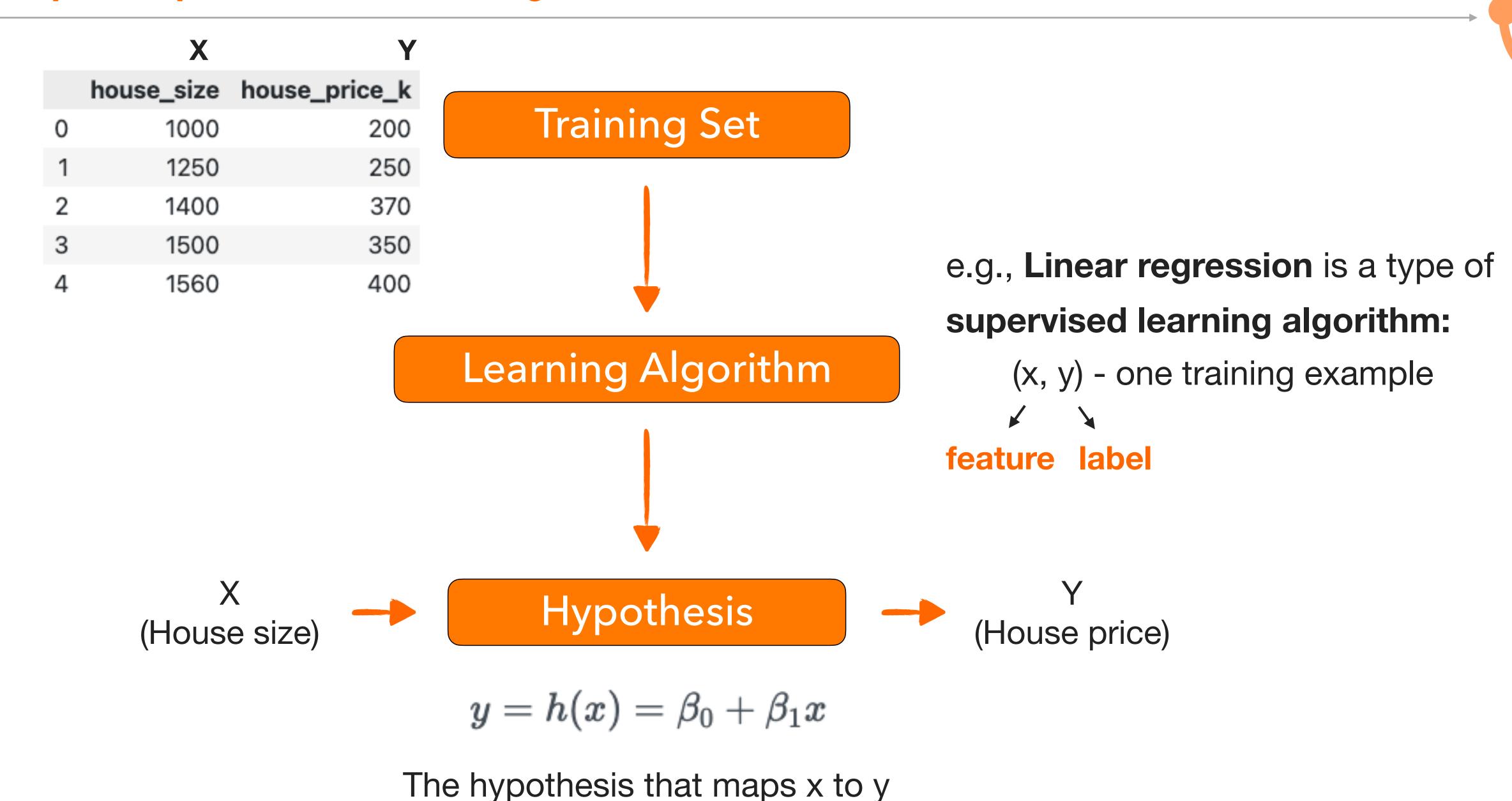
Y's: "output" variable / labels / response variables

	X	Y
	house_size	house_price_k
0	1000	200
1	1250	250
2	1400	370
3	1500	350
4	1560	400
5	1900	???

How do we predict the price?



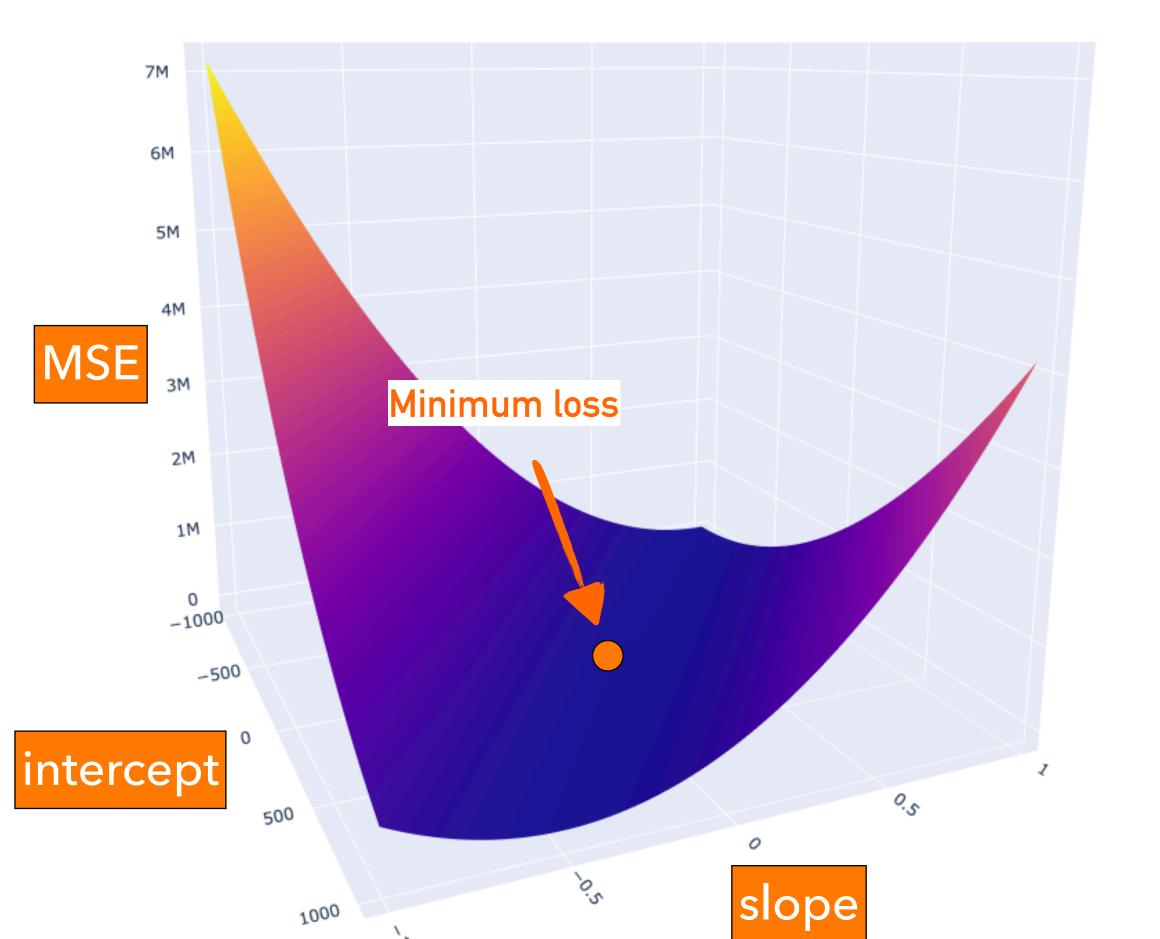
Recap - Supervised Learning



Recap - Loss Curve and Surface

How do we find a hypothesis that minimizes the loss? Differentiation!





Loss Surface

The minimization problem can be extended as

Recap - Ordinary Least Squares

$$egin{aligned} arg\min ext{SSE} &= arg\min_{eta} f(eta) = arg\min_{eta} (\mathbf{y} - \mathbf{X}eta)^T (\mathbf{y} - \mathbf{X}eta) \ &= arg\min_{eta} (\mathbf{y}^T - eta^T \mathbf{X}^T) (\mathbf{y} - \mathbf{X}eta) \ &= arg\min_{eta} \mathbf{y}^T \mathbf{y} - \mathbf{y}^T \mathbf{X}eta - eta^T \mathbf{X}^T \mathbf{y} + eta^T \mathbf{X}^T \mathbf{X}eta \ &= arg\min_{eta} \mathbf{y}^T \mathbf{y} - 2\mathbf{y}^T \mathbf{X}eta + eta^T \mathbf{X}^T \mathbf{X}eta \end{aligned}$$

Find the partial derivatives of $f(\beta)$ with respect to β and set it to zero:

$$rac{\partial f}{\partial eta} = eta^T \mathbf{X}^T \mathbf{X} - \mathbf{X}^T \mathbf{y} = 0$$

 $\beta = (\mathbf{X}^T \mathbf{X})^{-1} \mathbf{X}^T \mathbf{y}$ This is the learning algorithm!

Medical Insurance Dataset

In this section, we will use a real-world dataset to demonstrate the multi-variable linear regression. The dataset contains information about medical insurance costs for 1338 people. The dataset is available on Kaggle.

	data	=	<pre>pd.read_csv("insurance.csv")</pre>
	data		
~	0.0s		

	age	sex	bmi	children	smoker	region	charges
0	19	female	27.900	0	yes	southwest	16884.92400
1	18	male	33.770	1	no	southeast	1725.55230
2	28	male	33.000	3	no	southeast	4449.46200
3	33	male	22.705	0	no	northwest	21984.47061
4	32	male	28.880	0	no	northwest	3866.85520
1333	50	male	30.970	3	no	northwest	10600.54830
1334	18	female	31.920	0	no	northeast	2205.98080
1335	18	female	36.850	0	no	southeast	1629.83350
1336	21	female	25.800	0	no	southwest	2007.94500
1337	61	female	29.070	0	yes	northwest	29141.36030

1338 rows x 7 columns

Columns

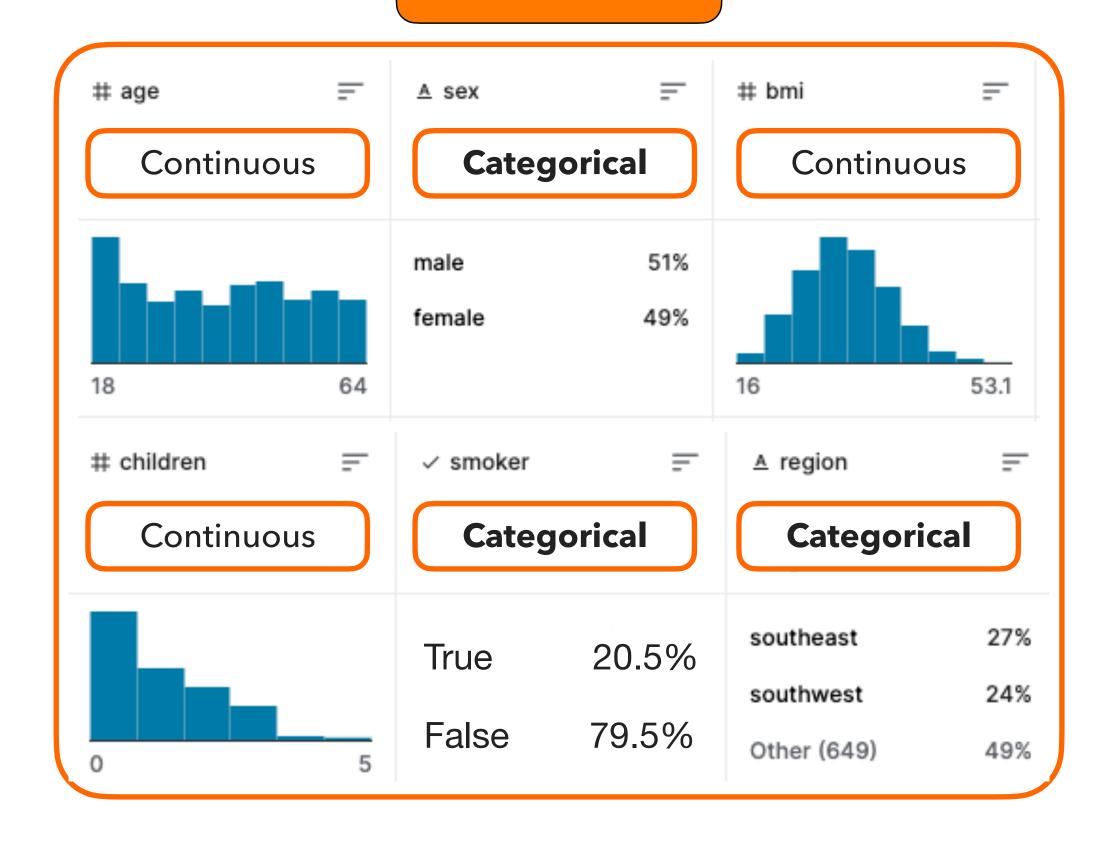
- age: age of primary beneficiary
- sex: insurance contractor gender, female, male
- bmi: Body mass index, providing an understanding of body, weights that are relatively high or low relative to height,
 - objective index of body weight (kg / m ^ 2) using the ratio of height to weight, ideally 18.5 to 24.9
- children: Number of children covered by health insurance / Number of dependents
- smoker: Smoking
- region: the beneficiary's residential area in the US, northeast, southeast, southwest, northwest.
- · charges: Individual medical costs billed by health insurance

Check the features and labels

	age	sex	bmi	children	smoker	region	charges
0	19	female	27.900	0	yes	southwest	16884.92400
1	18	male	33.770	1	no	southeast	1725.55230
2	28	male	33.000	3	no	southeast	4449.46200
3	33	male	22.705	0	no	northwest	21984.47061
4	32	male	28.880	0	no	northwest	3866.85520
1333	50	male	30.970	3	no	northwest	10600.54830
1334	18	female	31.920	0	no	northeast	2205.98080
1335	18	female	36.850	0	no	southeast	1629.83350
1336	21	female	25.800	0	no	southwest	2007.94500
1337	61	female	29.070	0	yes	northwest	29141.36030

1338 rows × 7 columns

Features



Labels





Log-transformation

We want to avoid a **skew** label distribution as the model would tend to focus on that data-rich region and be **less sensitive** to **rare** cases (but important).

Original

```
# plot histogram of charges
   plt.hist(data['charges'], bins=20)
   plt.xlabel('Charges')
   plt.ylabel('Frequency')
   plt.title('Distribution of Charges')
√ 0.2s
Text(0.5, 1.0, 'Distribution of Charges')
                      Distribution of Charges
  250
  200
Frequency
120
  100
   50
                                   40000
             10000
                    20000
                           30000
                                          50000
                                                 60000
                             Charges
```

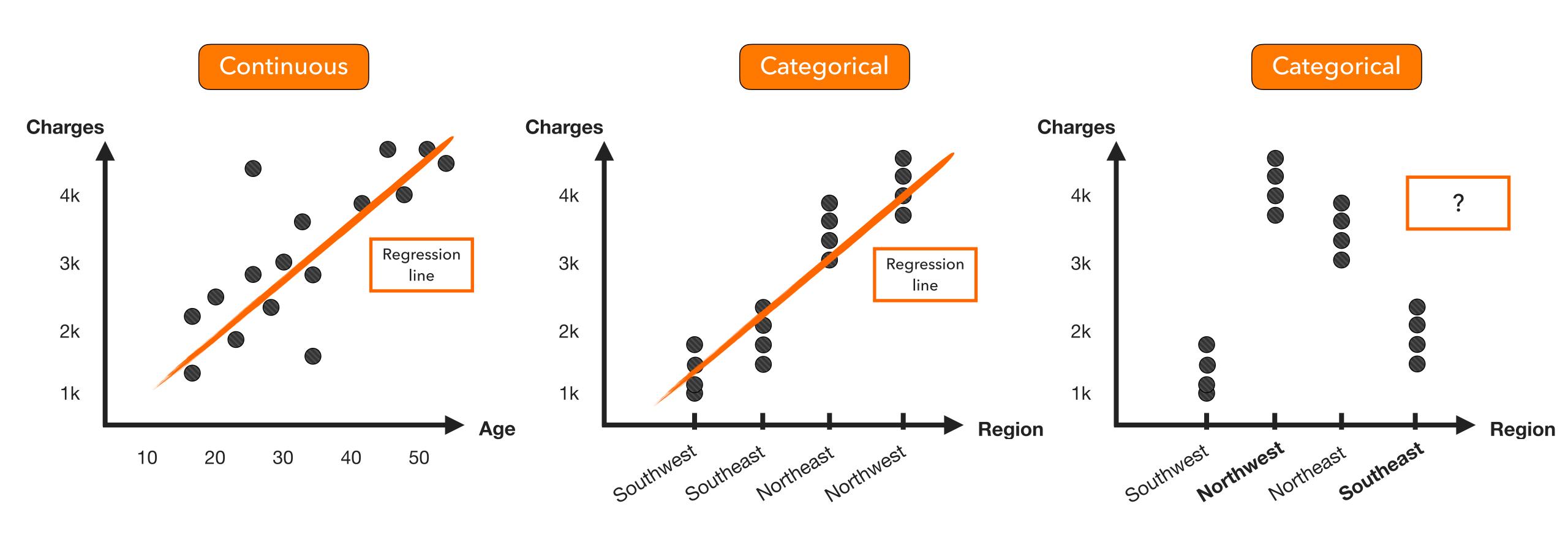
Transformed

```
# plot histogram of charges
   plt.hist(np.log(data['charges']), bins=20)
   plt.xlabel('Charges')
   plt.ylabel('Frequency')
   plt.title('Distribution of Charges')

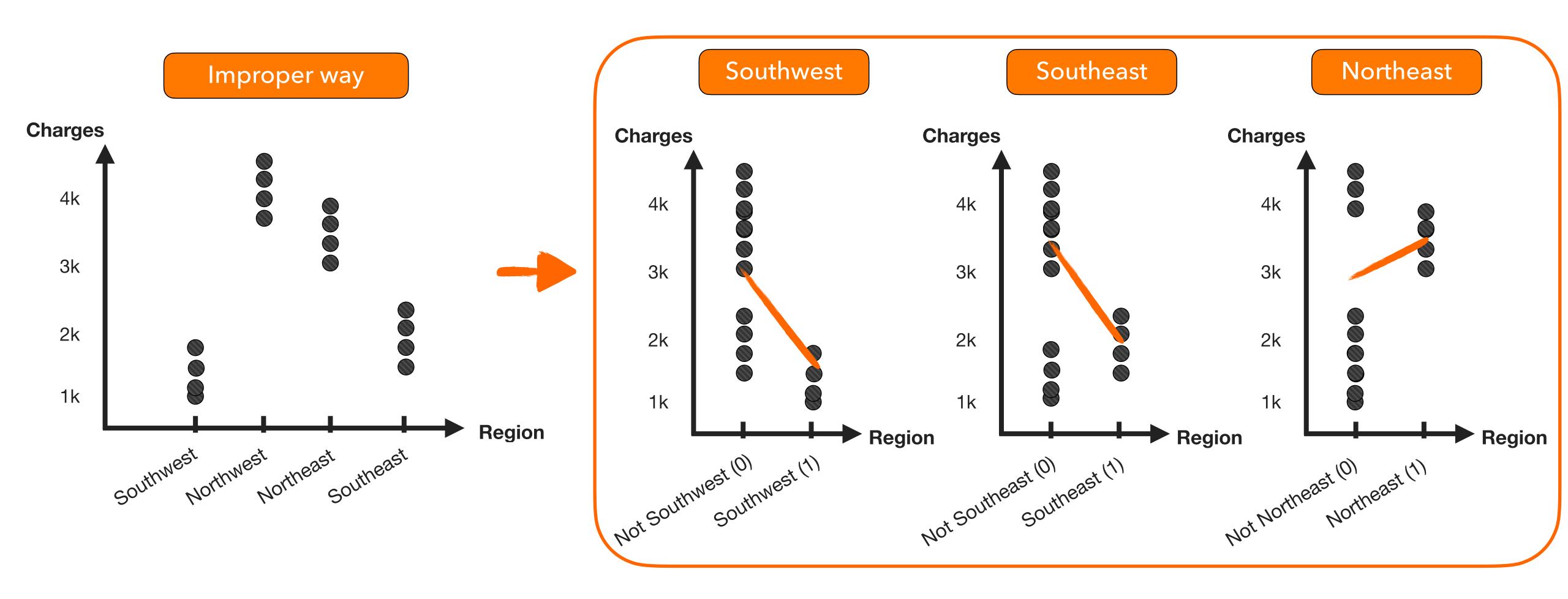
√ 0.2s

Text(0.5, 1.0, 'Distribution of Charges')
                      Distribution of Charges
  160
  140
  120
  100
Frequency
   60
   40
   20
                                    9.5
             7.5
                  8.0
                        8.5
                              9.0
                                         10.0
                                               10.5 11.0
       7.0
                             Charges
```

How does a linear model handle (understand) categorical variables?



What if we change the order?
Will the hypothesis (e.g., slope) remain the same?



We use the fourth category, "Northwest," as a <u>reference category</u> (intercept) in our regression model. This means that we only need to create three dummy variables to represent the other three categories. The <u>reference category</u> is represented by the intercept term in the regression model.

The Regression Model

The regression problem

Say, we want to know how the listed factors, which include age, sex, bmi, children, smoker, region, affect the charges of medical insurance. We can define the hypothesis h as follows:

$$h(x) = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \beta_3 x_3 + \beta_4 x_4 + \beta_5 x_5 + \beta_6 x_6 + \beta_7 x_7 + \beta_8 x_8$$

where

- x_1 = age
- x₂ = sex; 0 for male, 1 for female
- 2 1 = 1 variables

- $x_3 = bmi$
- x_4 = children
- $x_5 = \text{smoker}$; 0 for non-smoker (no), 1 for smoker (yes) 2 1 = 1 variables
- $x_6 = \text{region is southwest (1) or not (0)}$
- $x_7 = \text{region is southeast (1) or not (0)}$
- x_8 = region is northwest (1) or not (0)

4 - 1 = 3 variables

Matrix form

$$y = X\beta$$

$$\downarrow \qquad \qquad \downarrow$$

$$N \times 1 \quad N \times 9 \quad 9 \times$$

$$\begin{bmatrix} y_1 \\ y_2 \\ y_3 \\ \vdots \\ y_n \end{bmatrix} = \begin{bmatrix} 1 & X_{11} & X_{12} & X_{13} & X_{14} & X_{15} & X_{16} & X_{17} & X_{18} \\ 1 & X_{21} & X_{22} & X_{23} & X_{24} & X_{25} & X_{26} & X_{27} & X_{28} \\ 1 & X_{31} & X_{32} & X_{33} & X_{34} & X_{35} & X_{36} & X_{37} & X_{38} \\ \vdots & \vdots \\ 1 & X_{n1} & X_{n2} & X_{n3} & X_{n4} & X_{n5} & X_{n6} & X_{n7} & X_{n8} \end{bmatrix} \begin{bmatrix} \beta_1 \\ \beta_2 \\ \beta_3 \\ \beta_4 \\ \beta_5 \\ \beta_6 \\ \beta_7 \\ \beta_8 \end{bmatrix}$$

Dummy variables

$$X\beta = y$$

	age	sex	bmi	children	smoker	region	charges
0	19	female	27.900	0	yes	southwest	16884.92400
1	18	male	33.770	1	no	southeast	1725.55230
2	28	male	33.000	3	no	southeast	4449.46200
3	33	male	22.705	0	no	northwest	21984.47061
4	32	male	28.880	0	no	northwest	3866.85520
1333	50	male	30.970	3	no	northwest	10600.54830
1334	18	female	31.920	0	no	northeast	2205.98080
1335	18	female	36.850	0	no	southeast	1629.83350
1336	21	female	25.800	0	no	southwest	2007.94500
1337	61	female	29.070	0	yes	northwest	29141.36030

1338 rows × 7 columns

X	=	data.iloc[:, :-1]
у	=	data["charges"]

X shape: (1338, 6)

	age	sex	bmi	children	smoker	region
0	19	female	27.900	0	yes	southwest
1	18	male	33.770	1	no	southeast
2	28	male	33.000	3	no	southeast
3	33	male	22.705	0	no	northwest
4	32	male	28.880	0	no	northwest
1333	50	male	30.970	3	no	northwest
1334	18	female	31.920	0	no	northeast
1335	18	female	36.850	0	no	southeast
1336	21	female	25.800	0	no	southwest
1337	61	female	29.070	0	yes	northwest

1338 rows × 6 columns

y shape	: (1338,)
0	16884.92400
1	1725.55230
2	4449.46200
3	21984.47061
4	3866.85520
	•••
1333	10600.54830
1334	2205.98080
1335	1629.83350
1336	2007.94500
1337	29141.36030

Name: charges, Length: 1338

	age	sex	bmi	children	smoker	region
0	19	female	27.900	0	yes	southwest
1	18	male	33.770	1	no	southeast
2	28	male	33.000	3	no	southeast
3	33	male	22.705	0	no	northwest
4	32	male	28.880	0	no	northwest
1333	50	male	30.970	3	no	northwest
1334	18	female	31.920	0	no	northeast
1335	18	female	36.850	0	no	southeast
1336	21	female	25.800	0	no	southwest
1337	61	female	29.070	0	yes	northwest

1338 rows x 6 columns

One-hot encoding

We need to encode the categorical variables, such as sex, smoker, and region, to numerical values in the regression problem. The idea is to turn a categorical variable into a set of binary variables. For example, the variable region has four categories: southwest, southeast, northwest, and northeast. We can turn it into three (not four) binary variables:

- region is southwest (1) or not (0)
- region is southeast (1) or not (0)
- region is northwest (1) or not (0)

We don't need to encode the variable northeast because it can be inferred from the other three variables. That is, if all three variables are 0, then the region must be northeast.

There is a handy function in pandas to do this encoding. It's called get_dummies().

```
# turn categorical variable into dummy variables
# only keep k-1 dummy variables, k is the number of categories
X = pd.get_dummies(X, drop_first=True)
display(X)
```

	age	bmi	children	sex_male	smoker_yes	region_northwest	region_southeast	region_southwest
0	19	27.900	0	0	1	0	0	1
1	18	33.770	1	1	0	0	1	0
2	28	33.000	3	1	0	0	1	0
3	33	22.705	0	1	0	1	0	0
4	32	28.880	0	1	0	1	0	0
1333	50	30.970	3	1	0	1	0	0
1334	18	31.920	0	0	0	0	0	0
1335	18	36.850	0	0	0	0	1	0
1336	21	25.800	0	0	0	0	0	1
1337	61	29.070	0	0	1	1	0	0

1338 rows × 8 columns

√ 0.0s

Dataframe

	age	bmi	children	sex_male	smoker_yes	region_northwest	region_southeast	region_southwest
0	19	27.900	0	0	1	0	0	1
1	18	33.770	1	1	0	0	1	0
2	28	33.000	3	1	0	0	1	0
3	33	22.705	0	1	0	1	0	0
4	32	28.880	0	1	0	1	0	0
1333	50	30.970	3	1	0	1	0	0
1334	18	31.920	0	0	0	0	0	0
1335	18	36.850	0	0	0	0	1	0
1336	21	25.800	0	0	0	0	0	1
1337	61	29.070	0	0	1	1	0	0

1338 rows x 8 columns

Numpy Array

```
# add intercept
X = np.array(X)
X = np.hstack([np.ones((len(X), 1)), X]) Add an intercept vector
y = np.array(y)

v 0.0s
```

Check the dimensions of X and y.

```
print("X shape: ", X.shape)
display(X)
print("y shape: ", y.shape)
display(y)
```

Manual Solution

```
solve_OLS(X, y)

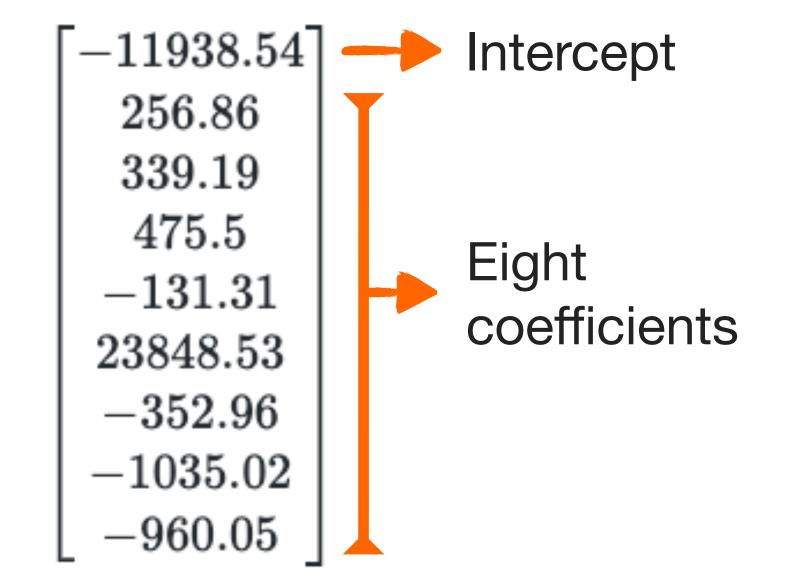
✓ 0.0s

array([-11938.53857617, 256.85635254, 339.19345361, 475.50054515,

-131.3143594 , 23848.53454191, -352.96389942, -1035.02204939,

-960.0509913 ])
```

Beta vector



Sklearn

We can solve the same problem using the sklearn library

```
X = data.iloc[:, :-1]
   X = pd.get_dummies(X, drop_first=True)
   y = data["charges"]
   model = LinearRegression()
   model.fit(X, y)

√ 0.0s

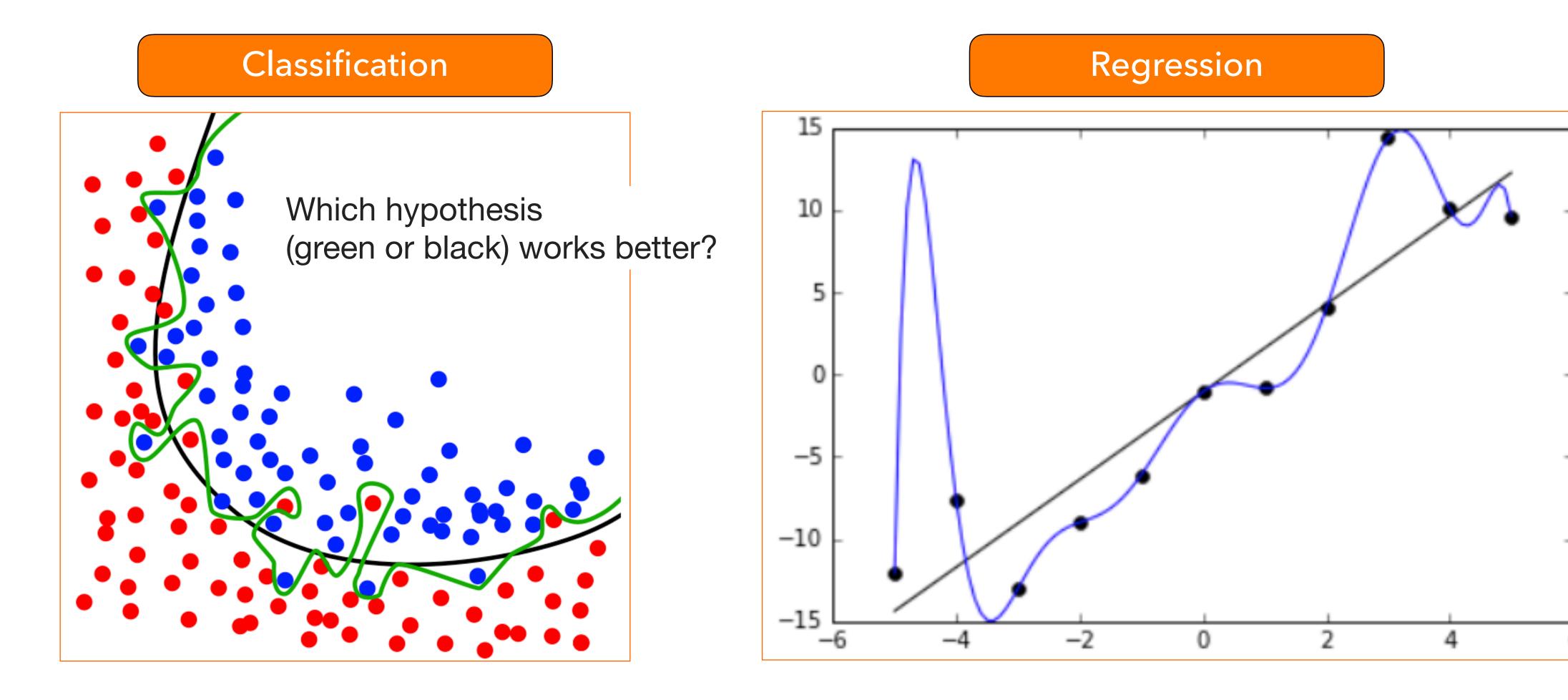
LinearRegression
LinearRegression()
   print("coef.: ", model.coef_)
   print("intercept: ", model.intercept_)

√ 0.0s

          256.85635254
coef.: [
                         339.19345361 475.50054515 -131.3143594
23848.53454191 -352.96389942 -1035.02204939 -960.0509913 ]
intercept: -11938.53857616715
```

Overfitting

Intuitively, as we increase the number of variables in the model, the model will be more accurate. However, this is not always the case. There is a chance that a model with more variables may lose its predictability on new data. This problem is called overfitting.

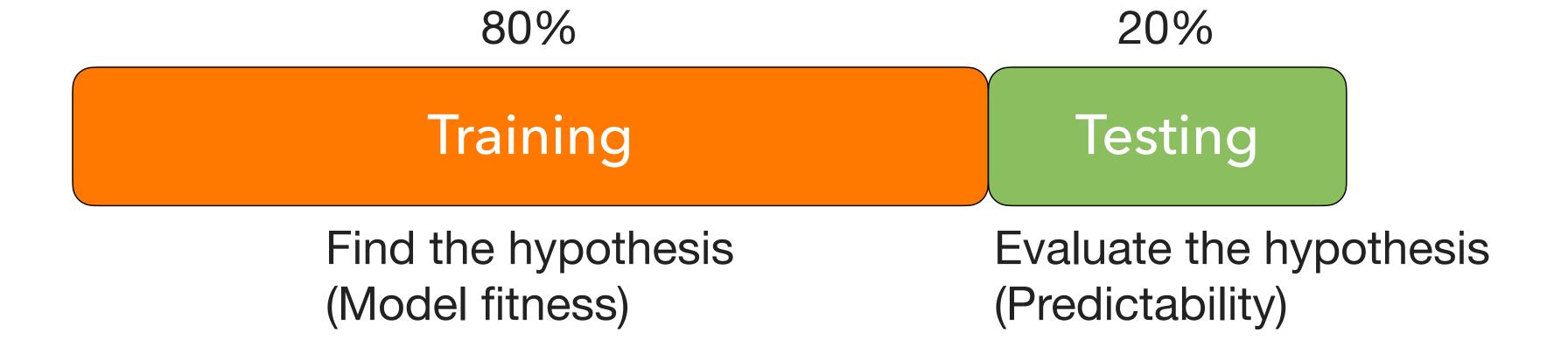


Five-fold validation: 80% training, 20% testing

To demonstrate this problem, we will need to split the data into two parts: training data and testing data. The training data is used to estimate the model coefficients β , and the testing data is treated as new data to evaluate the model. In a common practice, we use 80% of the data for training and 20% for testing.

```
# split the data
from sklearn.model_selection import train_test_split

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2)
```



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Do we need all the available variables?

We can design several models with different combinations of variables:

- Model A, full model: all eight variables
- Model B, reduced model: age, bmi, children, smoker_yes, region_southeast, region_southwest
- Model C, reduced model: age, bmi, smoker_yes, region_southeast
- Model D, reduced model: age, smoker_yes

age	bmi	children	sex_male	smoker_yes	region_northwest	region_southeast	region_southwest
19	27.900	0	0	1	0	0	1
18	33.770	1	1	0	0	1	0
28	33.000	3	1	0	0	1	0
33	22.705	0	1	0	1	0	0
32	28.880	0	1	0	1	0	0
						•••	
50	30.970	3	1	0	1	0	0
18	31.920	0	0	0	0	0	0
18	36.850	0	0	0	0	1	0
21	25.800	0	0	0	0	0	1
61	29.070	0	0	1	1	0	0

Python implementation

Fit the model (training)

Predict on the new data (testing)

```
# evaluate using MSE
from sklearn.metrics import mean_squared_error

y_pred_A = model_A.predict(X_test_A)
mse_A = mean_squared_error(y_test, y_pred_A)
print("MSE for model A: ", mse_A)

MSE for model A: 34776935.79071038
```

Iterate the validation for 100 times

The evaluation results can be biased due to the data splitting. To reduce the bias, we can repeat the splitting and evaluation for multiple times. In this example, we will repeat the splitting and evaluation for 100 times.

We need to define several functions to reduce the code repetition:

- subset_X(): subset the X matrix based on the variable names
- split_data(): split the data into training and testing
- fit_eval_model(): fit and evaluate the model, return MSE as the evaluation metric

```
def subset_X(data, var):
    X = data.loc[:, var]
    return X
```

```
def split_data(X, y):
    X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2)
    return X_train, X_test, y_train, y_test
```

```
def fit_eval_model(X_train, X_test, y_train, y_test):
    model = LinearRegression()
    model.fit(X_train, y_train)
    y_pred = model.predict(X_test)
    mse = mean_squared_error(y_test, y_pred)
    return mse
```

```
DICT_MODEL

A VAR_A
MSE

B VAR_B
MSE

C VAR_C
MSE
```

```
# load data
X = data.iloc[:, :-1]
X = pd.get_dummies(X, drop_first=True)
y = data["charges"]
# run experiment
for model in DICT_MODEL:
    # retrieve variables
    var = DICT_MODEL[model]["var"]
    # subset data
   X_{sub} = subset_X(X, var)
    for i in range(N_ITER):
        # split data
        X_train, X_test, y_train, y_test = split_data(X_sub, y)
        # fit and evaluate model
        mse = fit_eval_model(X_train, X_test, y_train, y_test)
        # store mse
        DICT_MODEL[model]["mse"].append(mse)
```

- Model A, full model: all eight variables
- Model B, reduced model: age, bmi, children, smoker_yes, region_southeast, region_southwest
- Model C, reduced model: age, bmi, smoker_yes, region_southeast



There are two common model selection criteria: Akalke's Information Criterio (AIC) and Bayesian Information Criterion (BIC). The idea of AIC and BIC is to balance the goodness of fit and the complexity of the model. The lower the AIC and BIC, the better the model. The AIC and BIC are defined as:

$$AIC = -2\log(L) + 2k$$
 $BIC = -2\log(L) + k\log(n)$

where L is the likelihood of the model, k is the number of parameters, and n is the number of observations. The difference between AIC and BIC is that BIC penalizes the model complexity more than AIC. Empirically, we can replace L with the residual sum of squares (RSS):

$$AIC = n \log(RSS) + 2k$$

 $BIC = n \log(RSS) + k \log(n)$

```
def get_AIC(MSE, n, k):
    RSS = MSE * n
    AIC = n * np.log(RSS) + 2 * k
    return AIC

def get_BIC(MSE, n, k):
    RSS = MSE * n
    BIC = n * np.log(RSS) + k * np.log(n)
    return BIC
```

```
# sample size of each fold
n = round(X.shape[0] / 5)

# inspect AIC and BIC for each model
for model in DICT_MODEL:
    mse = np.median(DICT_MODEL[model]["mse"] * n)
    k = len(DICT_MODEL[model]["var"])
    aic = get_AIC(mse, n, k)
    bic = get_BIC(mse, n, k)
    print("Model: ", model, DICT_MODEL[model]["var"])
    print("AIC: ", aic)
    print("BIC: ", bic)
```

```
Model: A ['age', 'bmi', 'children', 'sex_male', 'smoker_yes', 'region_northwest', 'region_AIC: 6183.680080968096
BIC: 6212.407976812183
Model: B ['age', 'bmi', 'smoker_yes', 'region_southeast']
AIC: 6178.738314582675
BIC: 6193.102262504719
Model: C ['age', 'bmi', 'smoker_yes']
AIC: 6171.194635640093
BIC: 6181.967596581626
Model: D ['age', 'smoker_yes']
AIC: 6199.231197573322
BIC: 6206.413171534344
```