Mini-batch Regression Neural Network Predicting for Median Housing Prices in the 1990 California, U.S. Census

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Background: This dataset comes from Chapter 2 of Aurélien Géron's book 'Hands-On Machine learning with Scikit-Learn and TensorFlow' (2017). The dataset itself contains various information on 1426 households from the 1990 California, U.S. census. In total, the dataset contains 20,640 observations and 9 variables as well as some missing data.

The .csv file used in this project came from the following webpage by Luís Torgo at the University of Porto: https://www.dcc.fc.up.pt/~ltorgo/Regression/cal_housing.html. His main webpage is located here: https://www.dcc.fc.up.pt/~ltorgo/.

Objective: The goal of this notebook was to predict median house values ($) in the California 1990 census dataset by performing regression with an artificial Neural Network.

Methods: Regression was done with a 3-layer neural network with He-initialized weights. The model used mini-batch gradient descent with gradient clipping and cross-validation while training. Batch normalization and dropout were also used to facilitate learning and add regularization to the model, respectively. Some missing data analysis was performed pre-modeling.

Package imports

In [2]:
```
import warnings;
warnings.filterwarnings('ignore');
```

In [3]:
```
import matplotlib.pyplot as plt
import pandas as pd
import numpy as np
import seaborn as sns

# Missing data analysis
import missingno as msno

# Enable R functions
import rpy2.robjects.numpy2ri
from rpy2.robjects.packages import importr
rpy2.robjects.numpy2ri.activate()

# Modeling
import tensorflow as tf
import sklearn.preprocessing as preprocess
from sklearn.model_selection import train_test_split
from sklearn.metrics import mean_squared_error
```

Data Exploration and Pre-processing

In [97]:
```
df = pd.read_csv('housing.csv')
df.head(4)
```

Out[97]:

	longitude	latitude	housing_median_age	total_rooms	total_bedrooms	population	households	median_income	median_house_value
0	-122.23	37.88	41.0	880.0	129.0	322.0	126.0	8.3252	452600.0
1	-122.22	37.86	21.0	7099.0	1106.0	2401.0	1138.0	8.3014	358500.0
2	-122.24	37.85	52.0	1467.0	190.0	496.0	177.0	7.2574	352100.0
3	-122.25	37.85	52.0	1274.0	235.0	558.0	219.0	5.6431	341300.0

In [462]:
```
df.shape
```

Out[462]:
```
(20640, 10)
```

In [463]:
```
df.columns
```

Out[463]:
```
Index(['longitude', 'latitude', 'housing_median_age', 'total_rooms',
       'total_bedrooms', 'population', 'households', 'median_income',
       'median_house_value', 'ocean_proximity'],
      dtype='object')
```

In [464]:
```
df.hist(figsize=(18,10), layout=(3,4), bins=25) # Some bimodal distributions.
plt.tight_layout()
plt.show()
```

Is there missing data? If so, where, and what does the surrounding data look like?

In [100]:
```
df[df.isna().any(axis=1)]
```

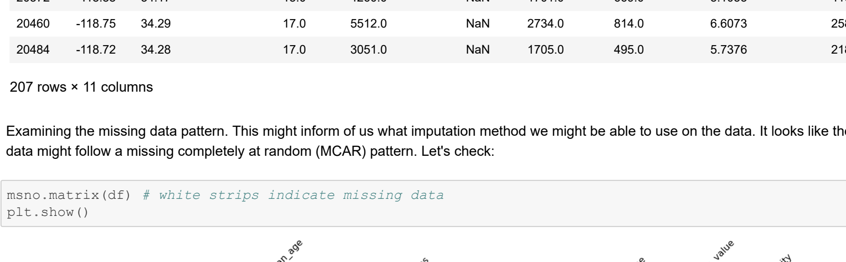
Out[100]:

	longitude	latitude	housing_median_age	total_rooms	total_bedrooms	population	households	median_income	median_house_valu
290	-122.16	37.77	47.0	1256.0	NaN	570.0	218.0	4.3750	161900
341	-122.17	37.75	38.0	992.0	NaN	732.0	259.0	1.6196	85100
538	-122.28	37.78	29.0	5154.0	NaN	3741.0	1273.0	2.5762	173400
563	-122.24	37.75	45.0	891.0	NaN	384.0	146.0	4.9489	247100
696	-122.10	37.69	41.0	746.0	NaN	387.0	161.0	3.9063	178400
...	...	...	...	...	...	...	...	...	
20267	-119.19	34.20	18.0	3620.0	NaN	3171.0	779.0	3.3409	220500
20268	-119.18	34.19	19.0	2393.0	NaN	1938.0	762.0	1.6953	167400
20372	-118.88	34.17	15.0	4260.0	NaN	1701.0	669.0	5.1033	410700
20460	-118.75	34.29	17.0	5512.0	NaN	2734.0	814.0	6.6073	258100
20484	-118.72	34.28	17.0	3051.0	NaN	1705.0	495.0	5.7376	218600

207 rows × 11 columns

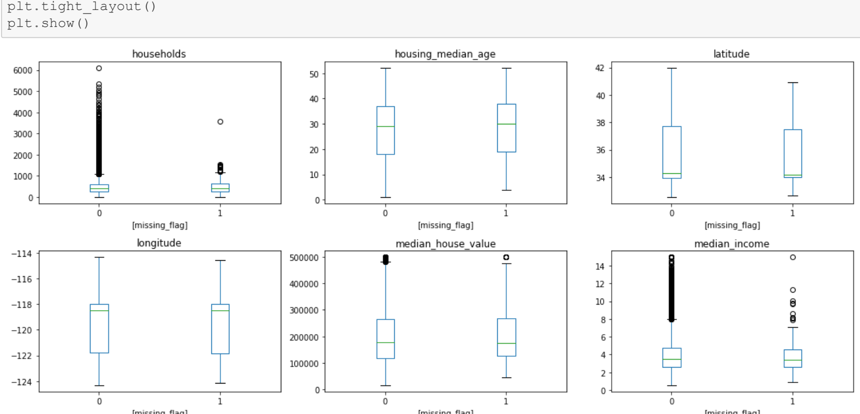
Examining the missing data pattern. This might inform of us what imputation method we might be able to use on the data. It looks like the data might follow a missing completely at random (MCAR) pattern. Let's check:

In [15]:
```
msno.matrix(df) # white strips indicate missing data
plt.show()
```



In [98]:
```
# Add a flag to indicate where the data is missing, to enable us to do some missing data analyses.
df['missing_flag'] = (df.total_bedrooms.isna()==True).astype(int)
```

In [466]:
```
fig, axs = plt.subplots(3,3, figsize=(15,10), sharey=False)

df.boxplot(by='missing_flag', ax=axs, grid=False)
plt.suptitle("")
plt.tight_layout()
plt.show()
```



In [467]:
```
(df.isnull().sum().sum()/df.isnull().count().sum())*100
```

Out[467]:
```
0.09117336152219874
```

Out of all observations, <0.10% of the data is missing. Let's examine the distribution of missing data in `total_bedrooms` along our categorical variable (`ocean_proximity`), however, before we proceed with assuming that the missing data pattern for `total_bedrooms` is truly MCAR.

Examining `ocean_proximity` (categorical) for its distribution of values

In [101]:
```
print(df.ocean_proximity.value_counts(dropna=False), "\n\nNumber of unique values: ",
      len(df.ocean_proximity.value_counts().unique()))
```

```
<1H OCEAN     9136
INLAND        6551
NEAR OCEAN    2658
NEAR BAY      2290
ISLAND           5
Name: ocean_proximity, dtype: int64

Number of unique values:  5
```

In [7]:
```
stats = importr('stats') # import R package 'stats'
```

In [8]:
```
crosstab_cat = pd.crosstab(df['ocean_proximity'], df['missing_flag'])

# Compute proportions of missing data for each ocean_proximity class and add to count table
crosstab_cat['percent_col_0'] = 100*(crosstab_cat[0]/df['missing_flag'].value_counts()[0])
crosstab_cat['percent_col_1'] = 100*(crosstab_cat[1]/df['missing_flag'].value_counts()[1])

crosstab_cat
```

Out[8]:

missing_flag	0	1	percent_col_0	percent_col_1
ocean_proximity				
<1H OCEAN	9034	102	44.212793	49.275362
INLAND	6496	55	31.791709	26.570048
ISLAND	5	0	0.024470	0.000000
NEAR BAY	2270	20	11.109480	9.661836
NEAR OCEAN	2628	30	12.861547	14.492754

In [95]:
```
print(stats.fisher_test(np.array(crosstab_cat[0]), np.array(crosstab_cat[1]))) # Significant, but massi
ve sample sizes
```

```
        Fisher's Exact Test for Count Data


data:  structure(c(9034L, 6496L, 5L, 2270L, 2628L), .Dim = 5L) and structure(c(102L, 55L, 0L, 20L, 30
L), .Dim = 5L)

p-value = 1

alternative hypothesis: two.sided
```

The Fischer's Exact test was statistically significant, but we also have massive sample sizes. Looking at the frequencies for each category of `ocean_proximity` where there is missing data versus non-missing data for `total_bedrooms`, it doesn't appear as though there is a significant association/pattern between the two. It really does appear as though the data is MCAR. Furthermore, we also have a very low percentage of missing data in the dataset. Therefore, we will proceed with a complete case analysis.

In [9]:
```
df = df[df.total_bedrooms.isna()==False] # Drop the rows with missing data.
df = df.reset_index(drop=True)

df.tail() # Showing the end of the dataframe.
```

Out[9]:

	longitude	latitude	housing_median_age	total_rooms	total_bedrooms	population	households	median_income	median_house_valu
20428	-121.09	39.48	25.0	1665.0	374.0	845.0	330.0	1.5603	78100
20429	-121.21	39.49	18.0	697.0	150.0	356.0	114.0	2.5568	77100
20430	-121.22	39.43	17.0	2254.0	485.0	1007.0	433.0	1.7000	92300
20431	-121.32	39.43	18.0	1860.0	409.0	741.0	349.0	1.8672	84700
20432	-121.24	39.37	16.0	2785.0	616.0	1387.0	530.0	2.3886	89400

OneHotEncoding and train-test splits

In [10]:
```
x, y = df.loc[: , df.columns!='median_house_value'], df['median_house_value']
```

In [11]:
```
# OneHotEncode 'ocean_proximity'.
enc = preprocess.OneHotEncoder()
trans = enc.fit_transform(x[['ocean_proximity']]).toarray()
trans_df = pd.DataFrame(trans, columns = enc.get_feature_names(['ocean_proximity']))

x = pd.concat([x, trans_df], axis=1)
x = x.drop(['ocean_proximity', 'missing_flag'], axis = 1)
x.head(3)
```

Out[11]:

	longitude	latitude	housing_median_age	total_rooms	total_bedrooms	population	households	median_income	ocean_proximity_<1H OCEAN
0	-122.23	37.88	41.0	880.0	129.0	322.0	126.0	8.3252	0.0
1	-122.22	37.86	21.0	7099.0	1106.0	2401.0	1138.0	8.3014	0.0
2	-122.24	37.85	52.0	1467.0	190.0	496.0	177.0	7.2574	0.0

In [23]:
```
seed = 100
test_size = 0.20

x_train, x_test, y_train, y_test = train_test_split(x, y, test_size=test_size, random_state=seed) # tra
in-test split
```

Feature Standardization

In [24]:
```
sc = preprocess.MinMaxScaler(feature_range = (0,1)) # NN like normalized data

# only perform feature scaling on the non-dummy variables.
x_train = sc.fit_transform(x_train.loc[:,:'median_income'])
x_test = sc.transform(x_test.loc[:,:'median_income'])
```

In [25]:
```
y_train = sc.fit_transform(np.array(y_train).reshape(-1,1))
y_test = sc.transform(np.array(y_test).reshape(-1,1))
```

Creating the neural network

Here is where we add the layers to our neural network for regression while incorporating batch normalization, He-initialized weights, mini-batch gradient descent, and gradient clipping.

Note that I played around with several of the model's parameters and hyperparameters before settling on these ones!

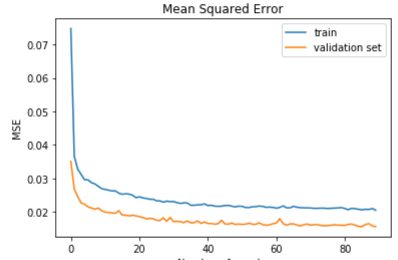
In [15]:
```
def make_model():
    model = tf.keras.models.Sequential()
    model.add(tf.keras.layers.Dense(units= 40, activation='relu', kernel_initializer='he_normal'))
    model.add(tf.keras.layers.BatchNormalization())
    model.add(tf.keras.layers.Dropout(0.2))

    model.add(tf.keras.layers.Dense(units= 40, activation='relu', kernel_initializer='he_normal'))
    model.add(tf.keras.layers.BatchNormalization())
    model.add(tf.keras.layers.Dropout(0.2))

    model.add(tf.keras.layers.Dense(units= 40, activation='relu', kernel_initializer='he_normal'))
    model.add(tf.keras.layers.BatchNormalization())
    model.add(tf.keras.layers.Dropout(0.2))

    model.add(tf.keras.layers.Dense(1, activation='linear'))
    model.add(tf.keras.layers.BatchNormalization())
    # Compile model
    sgd = tf.keras.optimizers.SGD(learning_rate=0.005, momentum=0.9, clipvalue=5.0)
    #model.compile(loss='mean_squared_error', optimizer='adam', metrics=['mean_squared_error'])
    model.compile(loss='mean_squared_error', optimizer=sgd, metrics=['mean_squared_error'])
    return model
```

In [16]:
```
model = make_model()
```

Running the model with cross-validation. How did the loss of the model (mean squared error [MSE]) change over time in the training and validation sets?

In [17]:
```
results = model.fit(x_train, y_train, epochs=90, batch_size=32, validation_split=0.2, verbose=0)
```

In [18]:
```
plt.plot(results.history['loss'], label='train')
plt.plot(results.history['val_loss'], label='validation set')
plt.title('Mean Squared Error'), plt.legend(), plt.xlabel('Number of epochs'), plt.ylabel('MSE')
plt.show()
```



In [107]:
```
train_mse = results.history['loss'][-1]
val_mse = results.history['val_loss'][-1]
```

In [111]:
```
print(f'Final train MSE: {round(train_mse,4)}, final validation MSE: {round(val_mse,4)}')
```

```
Final train MSE: 0.0206, final validation MSE: 0.0157
```

What's our MSE if we use our final model to predict house prices back in the training set? What about when we try it on the test set?

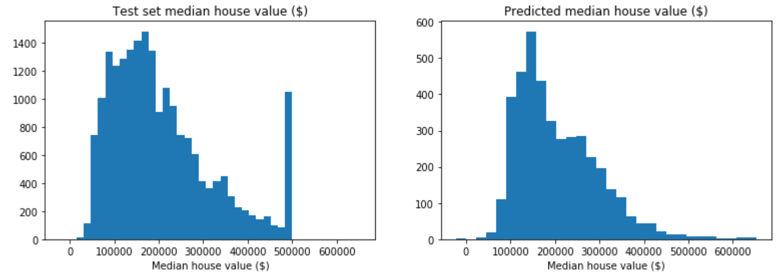
In [110]:
```
y_pred = model.predict(x_test)
print(f'Train MSE: {mean_squared_error(y_train, model.predict(x_train)).round(4)}, test MSE: {mean_squa
red_error(y_test, y_pred).round(4)}')
```

```
Train MSE: 0.0158, test MSE: 0.0164
```

How does the distribution of our predicted median house values compare to that of the test set's?

In [29]:
```
y_pred = sc.inverse_transform(y_pred) # Remember, trained (and predicted) on standardized housing price
s
```

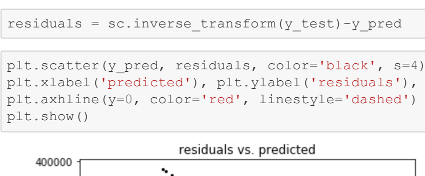
In [30]:
```
fig, axs = plt.subplots(1,2, figsize=(13,4), sharex=True)
axs[0].hist(df.median_house_value, bins=30)
axs[0].set_title('Test set median house value ($)'), axs[0].set_xlabel('Median house value ($)')
axs[1].hist(y_pred, bins=30)
axs[1].set_title('Predicted median house value ($)'), axs[1].set_xlabel('Median house value ($)')
plt.show()
```



The MSE here looks highly comparable to the validation error (MSE) we got at the end of our training. This is good. Now we can plot the residuals from our model as well as compute the root mean squared error (RMSE) for more information.

In [55]:
```
residuals = sc.inverse_transform(y_test)-y_pred
```

In [56]:
```
plt.scatter(y_pred, residuals, color='black', s=4)
plt.xlabel('predicted'), plt.ylabel('residuals'), plt.title('residuals vs. predicted')
plt.axhline(y=0, color='red', linestyle='dashed')
plt.show()
```

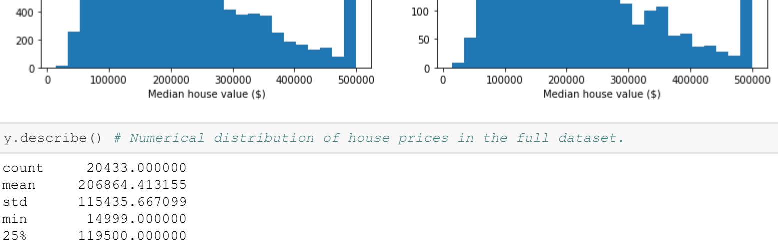


In [60]:
```
rmse = np.sqrt(mean_squared_error(sc.inverse_transform(y_test), y_pred))
print(f"Average error in predicting house prices: +-{round(rmse, 3)} off from the true median house pri
ce.")
```

```
Average error in predicting house prices: +-62153.487 off from the true median house price.
```

Checking the distributions of our target variable (median house value) in both our training and test sets.

In [62]:
```
fig, axs = plt.subplots(1,2, figsize=(13,4), sharex=True)
axs[0].hist(sc.inverse_transform(y_train), bins=25)
axs[0].set_title('Training set median house value ($)'), axs[0].set_xlabel('Median house value ($)')
axs[1].hist(sc.inverse_transform(y_test), bins=25)
axs[1].set_title('Test set median house value ($)'), axs[1].set_xlabel('Median house value ($)')
plt.show()
```



In [64]:
```
y.describe() # Numerical distribution of house prices in the full dataset.
```

Out[64]:
```
count     20433.000000
mean     206864.413155
std      115435.667099
min       14999.000000
25%      119500.000000
50%      179700.000000
75%      264700.000000
max      500001.000000
Name: median_house_value, dtype: float64
```