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Abstract:

This analysis aims to reproduce and discuss some of the results obtained by by Obermeyer et al. (2019) in their paper discussing the racial bias present in an algorithm used to refer patients for care. Through the reproduction of figures, it is shown that on average, Black patients have a lower total medical cost for a given unmber of chronic illnesses than White patients. Since the algorithm uses cost as a proxy for sickness to assign each patient a risk score, this means that Black patients are generally considered less sick than White patients for a given risk score. Contextually, this means that when making referrals to care programs based on the risk score, Black patients actually have to be more sick than White patients to get referred.

Part A: Get the Data

```
import pandas as pd
import numpy as np
import seaborn as sns
import matplotlib.pyplot as plt
from sklearn.linear_model import LinearRegression
from sklearn.model_selection import cross_val_score

url = "https://gitlab.com/labsysmed/dissecting-bias/-/raw/master/data/data_new.csv?inlin
df = pd.read_csv(url)
df.head()
```

	risk_score_t	program_enrolled_t	cost_t	cost_avoidable_t	bps_mean_t	ghba1c_mean_t	hct_mean_t	cre_mean_t	l
0	1.987430	0	1200.0	0.0	NaN	5.4	NaN	1.110000	1
1	7.677934	0	2600.0	0.0	119.0	5.5	40.4	0.860000	1
2	0.407678	0	500.0	0.0	NaN	NaN	NaN	NaN	N
3	0.798369	0	1300.0	0.0	117.0	NaN	NaN	NaN	N
4	17.513165	0	1100.0	0.0	116.0	NaN	34.1	1.303333	1

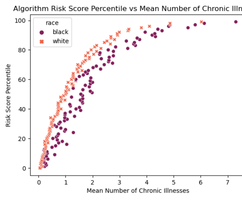
5 rows × 160 columns

Part B: Reproducing Fig. 1

```
df['risk_percentile'] = pd.qcut(df['risk_score_t'], q=100, labels=False, duplicates='dro
mean_illness_percentiles = df.groupby(['risk_percentile', 'race'])['gagne_sum_t'].mean()

percentile_plot = sns.scatterplot(data=mean_illness_percentiles, x='gagne_sum_t', y='ris
percentile_plot.set_title('Algorithm Risk Score Percentile vs Mean Number of Chronic Ill
percentile_plot.set_xlabel('Mean Number of Chronic Illnesses')
percentile_plot.set_ylabel('Risk Score Percentile')
```

```
Text(0, 0.5, 'Risk Score Percentile')
```



This figure shows that there is a disparity between Black patients and White patients risk scores as as function of their number of chronic illnesses. Specifically, Black patients on average have a lower risk score than white patients for the same number of chronic illnesses. In this context, the risk score translates to referrals to a care management program. Therefore, on average, Black patients have to be sicker than White patients to be referred into this program.

Part C: Reproducing Fig. 3

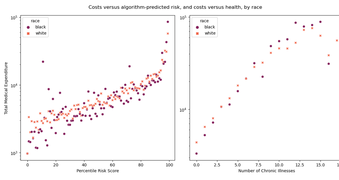
```
df['risk_percentile'] = pd.qcut(df['risk_score_t'], q=100, labels=False, duplicates='dro
cost_risk_percentiles = df.groupby(['risk_percentile', 'race'])['cost_t'].mean().reset_i
cost_illness_percentiles = df.groupby(['gagne_sum_t', 'race'])['cost_t'].mean().reset_in

fig, axs = plt.subplots(1, 2, figsize=(12, 6))

sns.scatterplot(data=cost_risk_percentiles, x='risk_percentile', y='cost_t', hue='race',
axs[0].set_ylabel('Total Medical Expenditure')
axs[0].set_xlabel('Percentile Risk Score')
axs[0].set_yscale('log')

sns.scatterplot(data=cost_illness_percentiles, x='gagne_sum_t', y='cost_t', hue='race',
axs[1].set_ylabel('')
axs[1].set_xlabel('Number of Chronic Illnesses')
axs[1].set_yscale('log')

fig.suptitle('Costs versus algorithm-predicted risk, and costs versus health, by race')
plt.tight_layout()
plt.show()
```



This first figure shows that Black patients seem to average a lower total medical expenditure per percentile risk score than White patients. I also noticed that the few outliers in the first graph are all Black patients. In the second figure, I again saw a steady pattern disparity between the cost incurred by Black patients and White patients. Specifically, Black patients tended to incur fewer costs as White patients for the same number of chronic illnesses. This pattern breaks down at high numbers of chronic illnesses, presumably because of the small amount of data avilable at that point increasing variability.

Part D: Modeling Cost Disparity

To model the cost disparity, I first focused on patients in the data with 5 or fewer chronic illnesses. This represents 96% of the data, which justifies focusing on these patients. Then, I calculated the log cost of each patient to use as the target variable. Log cost works better in this context because the cost varies by orders of magnitude. To avoid the undefined $log(0)$, I subsetted the data to be only patients with costs greater than 0. I then one-hot encoded the race column to be 0 for 'White' and 1 for 'Black'. Finally, I separated the data into predictor and target sets, X and y respectively. Based on the graph in the previous part, the relationship between the number of chronic conditions and the cost might be nonlinear. For that reason, I fit a linear regression model with polynomial features in the number of active chronic conditions. To find the best degree, I looped through different degrees and evaluated each with cross-validation to find the best preforming model. To investigate the cost incurred by a Black patient in comparison to an equally sick white patient, I wanted to calculate e^{w_5}, as that would provide an estimate of the percentage of that cost. To find w_5, I extracted the model's coefficients with `LR.coef_` and saw that the coefficient corresponding to the race column was -0.267. Finally, using this coefficient, I calculated $e^{w_5} = 0.766$. Therefore, the estimate of the percentage of cost incurred by a Black patient in comparison to an equally sick white patient was about 76.6%.

```
(df['gagne_sum_t'] <= 5 ).sum() / len(df) * 100 # percent of patients with 5 or fewer ch
```

```
95.53952115447689
```

```
model_df = df.copy()
model_df = model_df[model_df['cost_t'] > 0]

model_df['log_cost'] = np.log(model_df['cost_t'])
model_df['dummy_race'] = model_df['race'].apply(lambda x: 1 if x == 'black' else 0)

X = model_df[['gagne_sum_t', 'dummy_race']]
y = model_df['log_cost']]
```

```
def add_polynomial_features(X, degree):
  X_ = X.copy()
  for j in range(1, degree):
    X_[f"poly_{j}"] = X_["gagne_sum_t"]**j
  return X_

scores = []
degrees = range(1, 20, 1)
for degree in degrees:
  X_ = add_polynomial_features(X, degree)
  LR = LinearRegression()
  LR.fit(X_, y)
  cv_score = cross_val_score(LR, X_, y, cv=5)
  scores.append((degree, cv_score.mean()))

print(max(scores, key=lambda x: x[1]))
```

```
(10, 0.14830062441981076)
```

```
X_poly = add_polynomial_features(X, 10)
LR = LinearRegression()
LR.fit(X_poly, y)

print(X_poly)
print(LR.coef_) # race coefficient is the 9th one
```

```
       gagne_sum_t  dummy_race  poly_1  poly_2  poly_3  poly_4  poly_5  \
0                0           0       0       0       0       0       0
1                3           0       3       9      27      81     243
2                0           0       0       0       0       0       0
3                0           0       0       0       0       0       0
4                1           0       1       1       1       1       1
...            ...         ...     ...     ...     ...     ...     ...
48779            0           0       0       0       0       0       0
48780            1           0       1       1       1       1       1
48781            0           0       0       0       0       0       0
48782            3           0       3       9      27      81     243
48783            0           0       0       0       0       0       0

       poly_6  poly_7  poly_8  poly_9
0           0       0       0       0
1         729    2187    6561   19683
2           0       0       0       0
3           0       0       0       0
4           1       1       1       1
...       ...     ...     ...     ...
48779       0       0       0       0
48780       1       1       1       1
48781       0       0       0       0
48782     729    2187    6561   19683
48783       0       0       0       0

[46887 rows x 11 columns]
[[ 5.08816357e-01 -2.67114886e-01  5.08816361e-01 -1.03056773e+00
   5.88024780e-01 -1.77621997e-01  3.11556829e-02 -3.27057852e-03
   2.01927004e-04 -6.74580399e-06  9.39007115e-08]]
```

```
wb = LR.coef_[0][1]
```

```
np.exp(wb)
```

```
0.7655851117427583
```

Discussion:

From this analysis, I learned that the presence of bias in an algorithm can be heavily dependent on the target variable, and it is therefore important to choose a target variable that accurately reflects what the model is trying to predict. For example, the target variable of cost was chosen to be a proxy for sickness, with the idea being that if a patient incurred more costs, they were sicker. Therefore, predicting the costs incurred by a patient could predict how sick they would be, allowing the algorithm to refer them to more care earlier. The problem with this, however, is that access to healthcare is not the same for all, so some patients incur fewer costs simply because they cannot access health care, which has nothing to do with how sick they actually are. This was the bias found by by Obermeyer et al. (2019), who showed that "At a given level of health (again measured by number of chronic illnesses), Blacks generate lower costs than Whites—on average, $1801 less per year, holding constant the number of chronic illnesses."

The bias as described by Obermeyer et al. (2019) is generally not best supported by the sufficiency discrimination criteria. The sufficiency criteria for discrimination is that the sensitive characteristic, in this case race, and the target variable, in this case the cost incurred, are conditionally independent given the score. They mention this in their paper, saying "conditional on risk score, predictions do not favor Whites or Blacks anywhere in the risk distribution." Therefore, the predictions are sufficient. Instead, the statistical independence definition of discrimination more accurately describes the bias present in this models predictions. For the predictor to be unbiased from a statistical independence perspective, the probabilty of a positive prediction does not depend on group membership. However, with this model we see that for a given number of chronic illnesses, Black patients will generally have a lower risk score, and therefore have a lower probability of being referred for care.