Contents

This notebook investigates Breast Cancer prediction data derived from `Ming et al.` (Gail model) [1].

Mondrian Conformal Prediction is applied to the Nonconformity Measure: `InverseProbability`.

Nonconformity Measure `InverseProbability` is applied to the underlying classifier: `LogisticRegression`.

Using MCP, conditional on the category `Race`, we investigate the relationship between sample size and the equitable representation of individuals belonging to a given race that fall within the low-confidence region of predictions. The low-confidence region is defined as the Lower-Decile Region (LDR) of predictions, ranked by `confidence` and `credibility`, respectively.

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1. Ming C, Viassolo V, Probst-Hensch N, Chappuis PO, Dinov ID, Katapodi MC. Machine learning techniques for personalized breast cancer risk prediction: comparison with the BCRAT and BOADICEA models. Breast Cancer Research 2019;21(1):75 doi: 10.1186/s13058-019-1158-4[published Online First: Epub Date]].

In [4]:
```
#imports/pwd
import os

# set pwd to root of repository
repo_root = 'C:/Users/Bob/CHPC/conformal_prediction/vigilant-computing-machine/'
os.chdir(repo_root)

# 'vigilant-computing-machine/source/util.py'
import source.util as util
import matplotlib.pyplot as plt
```

---

define plot function

In [5]:
```
def plot_rep_6exp(exp_df_list):
    col = 2
    row = 3
    fig, axs = plt.subplots(row, col)
    fig.set_figheight(32)
    fig.set_figwidth(24)
    for i in range(row * col):
        row_idx = i // col
        col_idx = i % col
        util.plot_race_representation_from_experiment(exp_df_list[i], ax=axs[row_idx, col_idx])
    plt.show()
```

---

read in experiment results

In [6]:
```
experiments_rcic = \
    [
     util.read_experiment('./results/logistic_regression_1200_balanced_race-conditional_experiment.csv'),
     util.read_experiment('./results/logistic_regression_12000_balanced_race-conditional_experiment.csv'),
     util.read_experiment('./results/logistic_regression_1200_race-unique_balanced_race-conditional_experiment.csv'),
     util.read_experiment('./results/logistic_regression_12000_race-unique_balanced_race-conditional_experiment.csv'),
     util.read_experiment('./results/logistic_regression_1200_race-unique-inverted_balanced_race-conditional_experiment.csv'),
```

```
    util.read_experiment('./results/logistic_regression_12000_race-unique-inverted_balanced_race-conditional_experiment.csv')
]
```

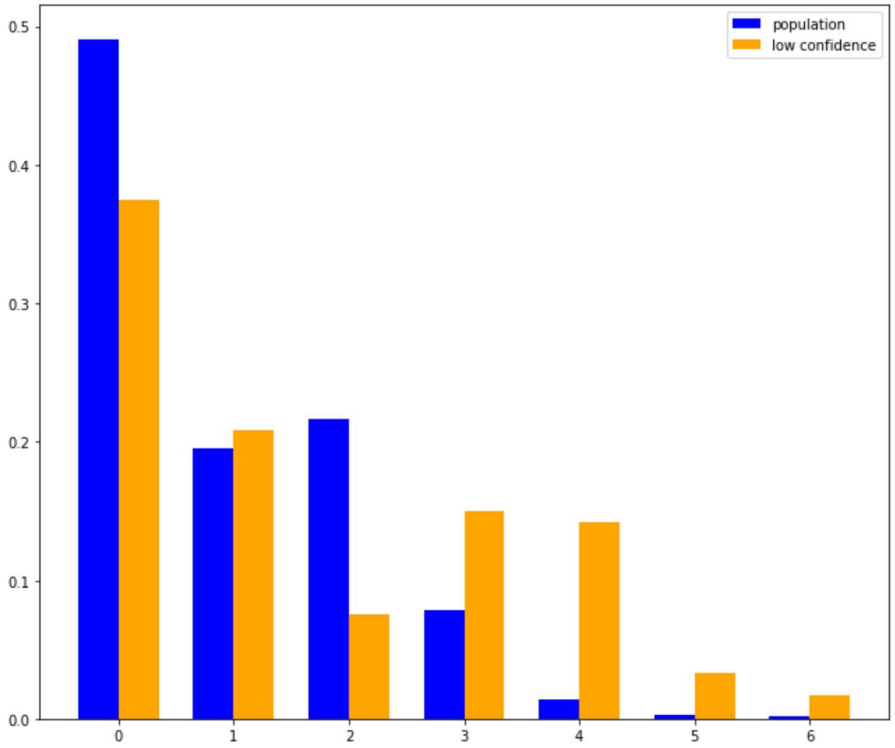
---

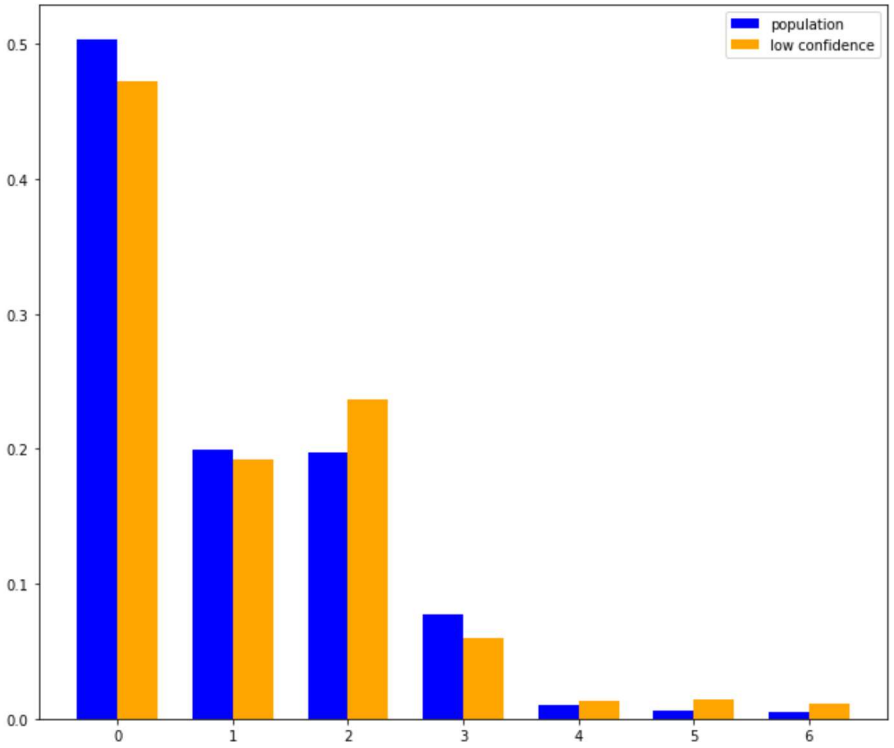
plot experiment results

- **Data**
  - **Ming et al.**
    - `n=1200`
    - `n=12000`
  - **Race-Unique Risk**
    - `n=1200`
    - `n=12000`
  - **Race-Unique Risk Inverted**
    - `n=1200`
    - `n=12000`

	`n=1200`	`n=12000`
Ming et al.	1xM	10xM
Race-Unique Risk	1xRUR	10xRUR
R-U Risk Inverted	1xRURI	10xRURI

In [8]:
```
plot_rep_6exp(experiments_rcic)
```


Race Representation - Population Sample vs Low Confidence
RaceConditionalInductiveClassifier (InverseProbability (logistic regression))
Ming et al. - 1:1 - healthy:cancer
n=1200
population
low confidence
0.0
0.1
0.2
0.3
0.4
0.5
0
1
2
3
4
5
6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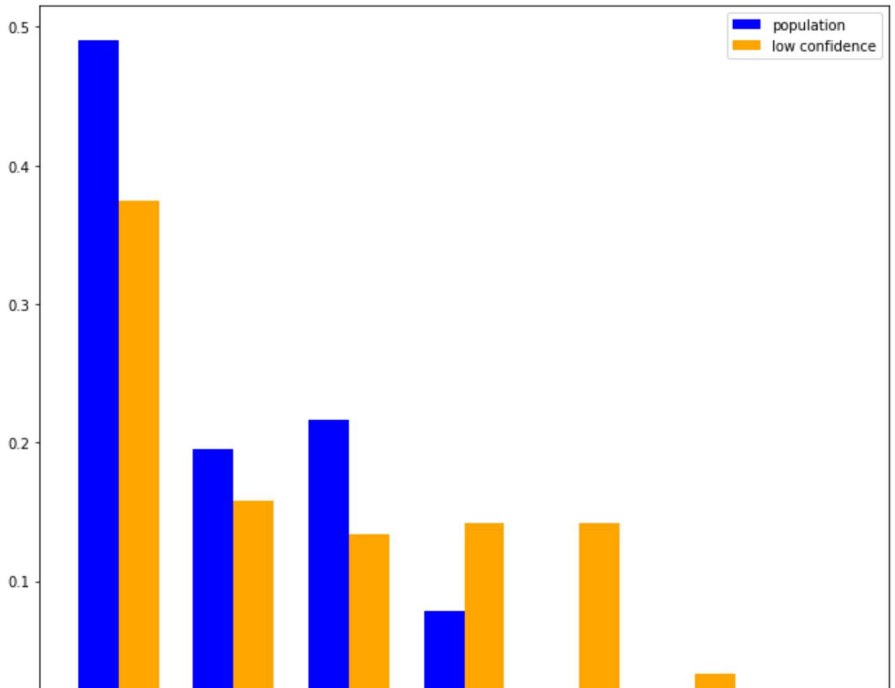
6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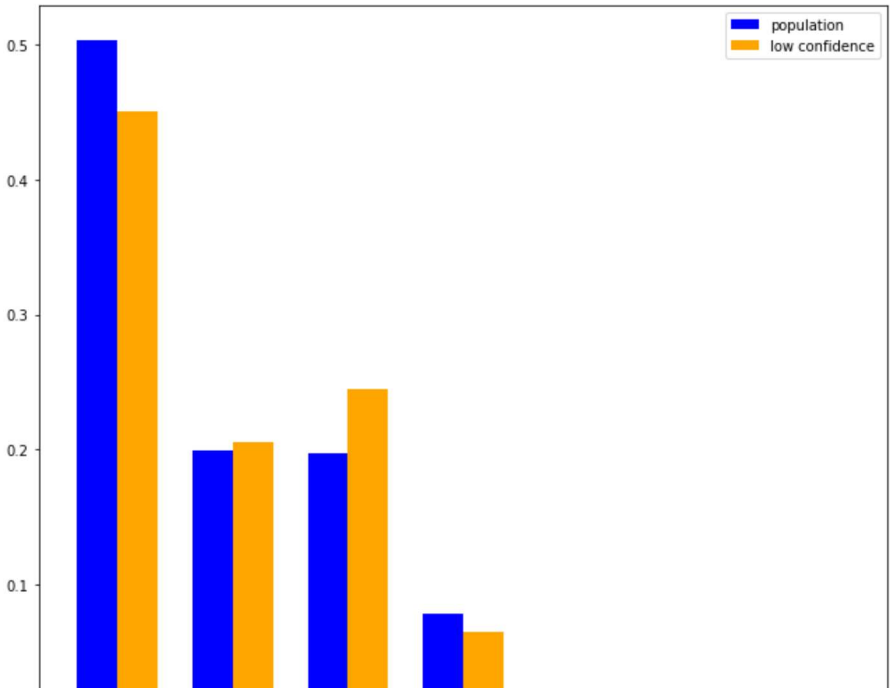
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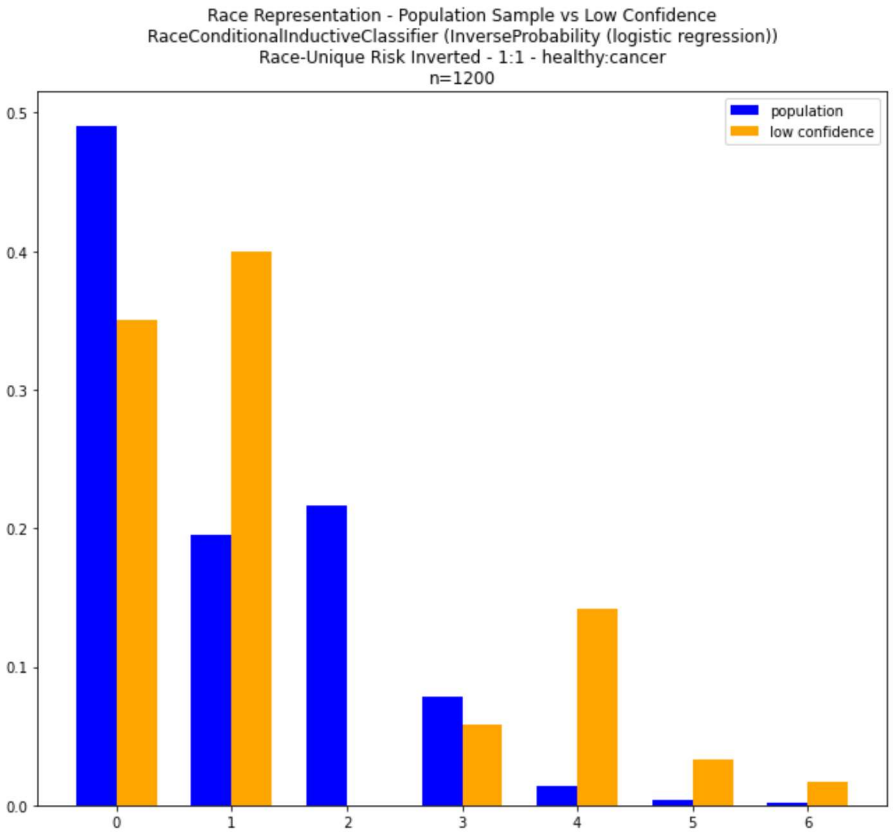

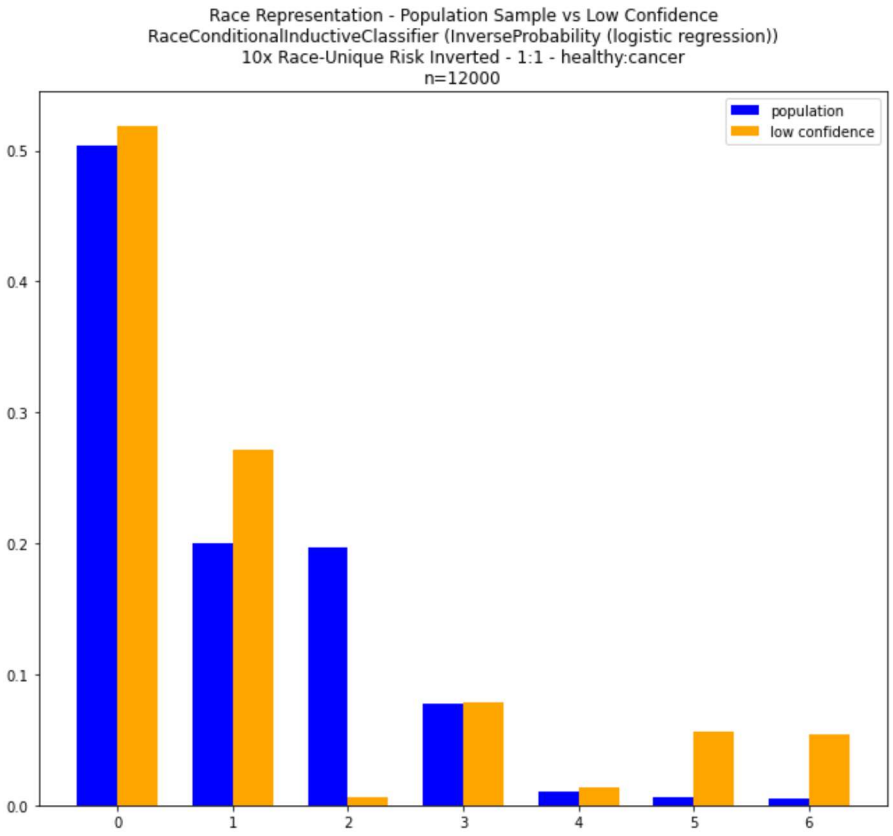

Cursory Observation:

Blind sample supplementation tends to either:

- drive equity of `Race` representation in the low-confidence region
- highlight `Race` group(s) where **reduced monetary expense** may result from **targeted** sample supplementation

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Preliminary Conclusions:

CP methods may provide a means to determine the **minimum-viable sample** size of individual groups that may otherwise be under-represented, or systematically excluded, helping **ensure equity** in the results of **clinical biomedical research** and **clinical predictive tools.**