# The Build Felowship

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Openavenues

# Weekly Updates

- Please provide a quick update on either:
  - Something you did/saw this week that you thought was interesting
  - What you're looking forward to about this week's workshop

(Reminder - please have your cameras on if possible)



### The Build Fellowship

# Workshop 7 Performance Evaluation

# Recap





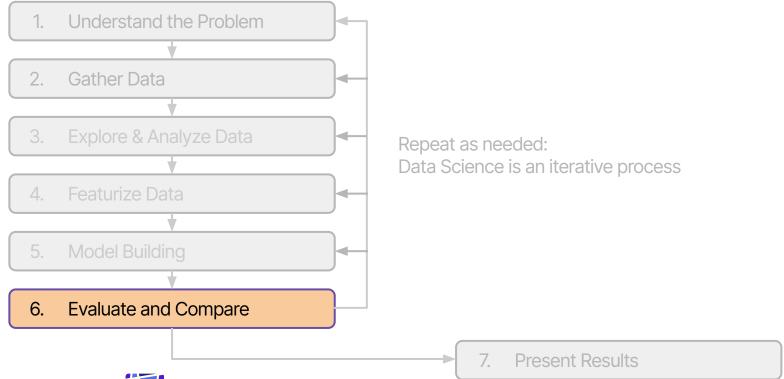
### **Sessions Overview**

- Workshop 1 Project Introduction & Setup
- Workshop 2 Genomic Data (A2 Assignment)
- Workshop 3 Data Analysis & Visualization (A3 Assignment)
- Workshop 4 Featurization & Baseline Modeling (A4 Assignment)
- Workshop 5 Model Training Approaches (Final Assignment Set)
- Workshop 6 Model Tuning
- Workshop 7 Performance Evaluation (Final Assignment Code/Testing Due)
- Workshop 8 Results Presentation & Wrap up (Final Presentation Due)





## **The Data Science Process**





# **Model Tuning & Comparison**

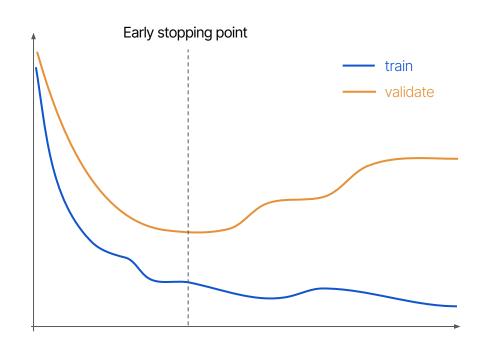
Last week we took a single Random Forest model and reviewed different methods for optimizing performance

#### Methods:

- Grid search
- Random search
- Bayesian Optimization

#### **Nested Cross Validation**

- Method for parameter selection & model comparison
- Higher complexity but fairer review across multiple held out datasets



Searching parameters

# **Evaluation Metrics**





## What is our Definition of Good?

#### Model Loss/Accuracy are the most common assessments

- Loss is a continuous measurement of model fit
- What do we care about?
- Categorial targets
- Binary S vs R

#### Why not just accuracy?

- Remember our baseline models
- Achieved ~80% accuracy with majority predictor

#### What have we used thus far?

- Balanced accuracy
- What does it actually mean and measure
- Why is it better than standard accuracy?







## Confusion - let's use it

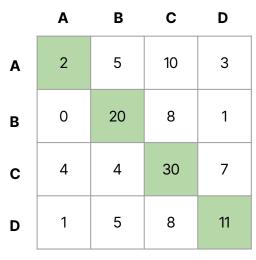
#### Categorical predictions

- Per class performance
- Confusion Matrix is an natural visual representation
- Rows = True class
- Columns = Predicted class

#### For AMR Predictions:

- **Major** errors
- Very major errors

Very major errors are a worse outcome for patients

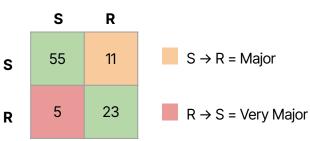


**Predicted Class** 

#### Predicted Class

True Class

True Class





# **Binary Assessments**

#### For AMR Predictions:

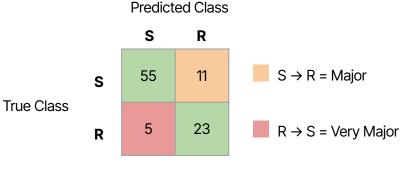
- **Major** errors
- Very major errors

In general we can think of this as Positive & Negative

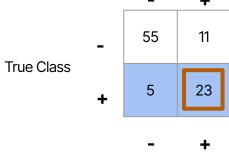
- Positive Predictions = R
- Negative Prediction = S

#### Common Metrics:

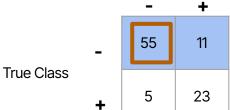
- Sensitivity
- Specificity
- **Balanced accuracy** = average of the above







# **Sensitivity**: Fraction of Positive Class predicted as Positive



**Specificity**: Fraction of Negative Class predicted as Negative





# **Binary Assessments**

#### For AMR Predictions:

- **Major** errors
- Very major errors

In general we can think of this as Positive & Negative

- Positive Predictions = R
- Negative Prediction = S

#### Common Metrics:

- Sensitivity
- Specificity
- **Balanced accuracy** = average of the above

#### **Baseline Majority Model**

**Predicted Class** 

|            |   | S  | R |
|------------|---|----|---|
| True Class | s | 80 | 0 |
|            | R | 20 | 0 |

Accuracy = ???

Sensitivity = ???

Specificity = ???

Balanced accuracy = ???





# **Binary Assessments**

#### For AMR Predictions:

- **Major** errors
- Very major errors

In general we can think of this as Positive & Negative

- Positive Predictions = R
- Negative Prediction = S

#### Common Metrics:

- Sensitivity
- Specificity
- **Balanced accuracy** = average of the above

#### **Baseline Majority Model**

**Predicted Class** 

|            |   | S  | R |
|------------|---|----|---|
| True Class | s | 80 | 0 |
|            | R | 20 | 0 |

Accuracy = 80 %

Sensitivity = 0 %

Specificity = 100 %

Balanced accuracy = 50 %





# Uncertainty





# QUIZTIME!?

# Why do we need to use statistical uncertainty?

- To add a touch of mystery and suspense to our data analysis.
- To make more accurate predictions on future data points.
- To ensure that our model perfectly fits the data.
- To provide a range of outcomes for better decision making.



# **Uncertainty, why?**

In almost all of Data Science be it inference or predictions:

We are never certain.

We're using some sample of data to try to generalize to a population

- We took ~1,000 E coli samples from BV-BRC
- How representative are they?

In our predictive modeling problem we have three main pieces of uncertainty:

- 1. Sample size uncertainty how much data?
- 2. Model variability what if I trained the model again?
- 3. Generalizability will this work on new data?







## Sample Size - Statistical Power

Our first layer of uncertainty. Simply put is there a difference between:

- 1. 9 / 10 predictions = 90% accuracy
- 2. 900 / 1000 predictions = 90% accuracy

Both cases have identical accuracy but we have different levels of evidence

More data points = more certainty in our assessment

Can calculate confidence intervals using common statistical tests (in this case a binomial proportion CI)

```
import pandas as pd
import numpy as np

from statsmodels.stats.proportion import proportion_confint

ci_l, ci_h = proportion_confint(9, 10)
print(f"95% CI for 9/10 Prop: {np.round(ci_l, 2)} - {np.round(ci_h, 2)}")

95% CI for 9/10 Prop: 0.71 - 1.0

ci_l, ci_h = proportion_confint(900, 1000)
print(f"95% CI for 900/1000 Prop: {np.round(ci_l, 2)} - {np.round(ci_h, 2)}")

95% CI for 900/1000 Prop: 0.88 - 0.92
```





## Sample Size - Statistical Power

```
import pandas as pd
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ci_l, ci_h = proportion_confint(9, 10)
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95% CI for 900/1000 Prop: 0.88 - 0.92
```





# **Model variability**

#### As we saw last week:

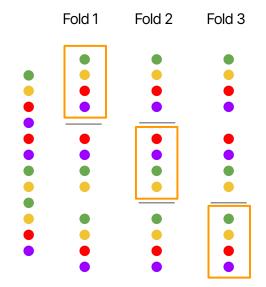
- Train a model multiple times
- Get difference assessments each time

#### Can we capture the variability across models?

- One common use for nested CV
- Inner folds to optimize model
- Outer fold to assess uncertainty

#### After completion of model assessment on CV:

Use the final test dataset to get a single unbiased estimate



From last week's workshop, three Random Forest models:

```
Fold 1 Balanced accuracy: 80.4% Fold 2 Balanced accuracy: 81.4% Fold 3 Balanced accuracy: 80.6%
```

Each model was optimized on the inner fold splits





# Generalizability

More of an expert knowledge question

- How representative is our data?
- Will it work on new data?

Need to review and assess your dataset carefully, in our case:

- Where did we get the E coli data from?
- Was it geographically diverse or from one state?
- Can we measure bacterial diversity? (Phylogeny)

Important to comment on your data collection!



If we train here



Can we predict here?





## **Summary**

Not always necessary to calculate everything out

#### BUT:

- Vital to acknowledge and communicate uncertainty
- If not in numbers then in words

For interviews/take-home exercises I'm always looking out for candidates that are aware of and acknowledge uncertainty:

- Did they highlight places where they were unsure?
- Did they list assumptions/questions?
- Did they report any confidence levels?







# Workshop 7 Performance Evaluation



