Applied Machine Learning - Backup Slides

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Outline

- Equivocal Zones
- Multiclass Model Statistics
- tidypredict

tidymodels

```
library(tidymodels)
## — Attaching packages
                                                                                                 tidymodels 0.0.2 -
## ✓ broom
               0.5.1
                         ✓ purrr
                                     0.2.5
## ✔ dials
                         ✔ recipes 0.1.4
               0.0.2
## ✔ dplyr
                         ✔ rsample 0.0.4
               0.7.8
## ✓ infer
               0.4.0

✓ tibble

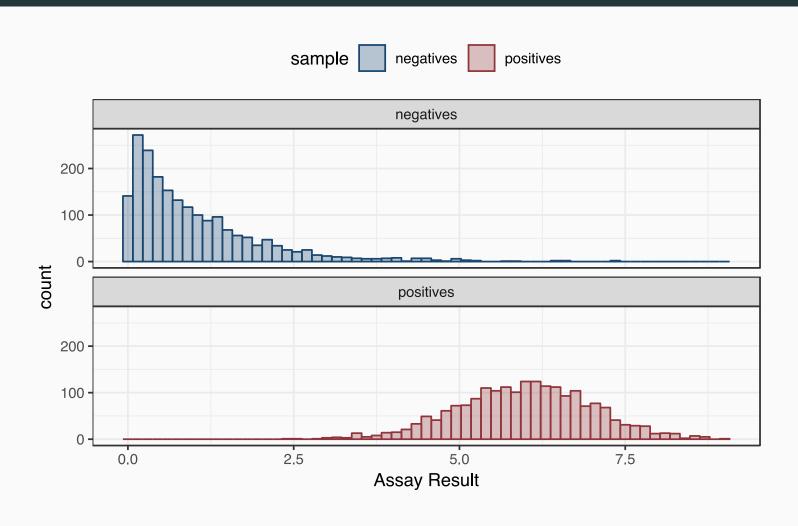
                                   2.0.0
## ✓ parsnip

✓ yardstick 0.0.2

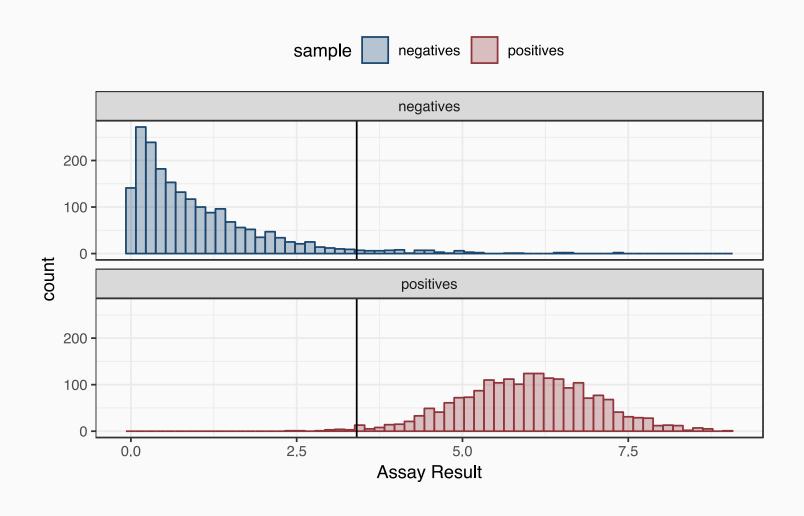
               0.0.1
## — Conflicts -
                                                                                           tidymodels_conflicts() —
## * purrr::discard()
                         masks scales::discard()
## * dplyr::filter()
                         masks stats::filter()
## * dplyr::lag()
                         masks stats::lag()
## * rsample::populate() masks Rcpp::populate()
## * recipes::step()
                         masks stats::step()
```

Applicability and Equivocals

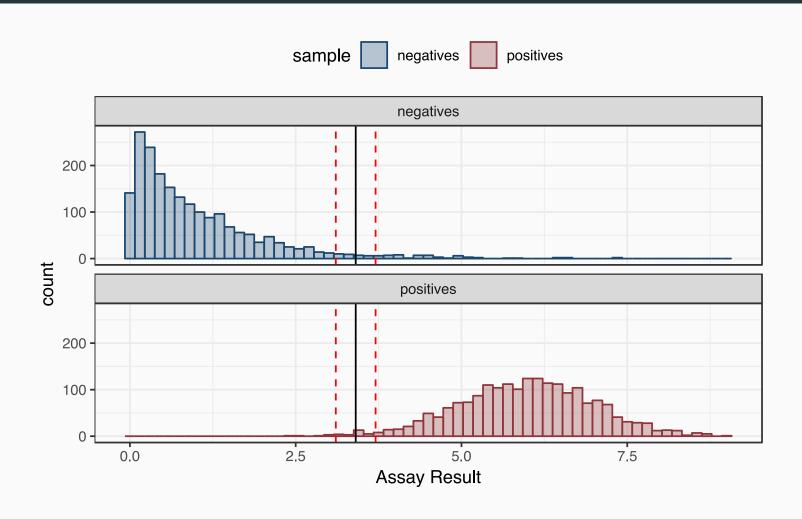
Medical diagnostic analysis of assay results



Add a cutoff via ROC curve



Mandated buffer of equivocal results



Equivocals and applicability domains

Are there times when we should *not* report a model result?

Just because we get a predicted value, it should not be assumed to be appropriate or *applicable*.

There is a modeling sub-field for determining the applicability domain of a model and deciding when to report a prediction.

As a real example, in drug discovery, computational chemistry models are built to predict various types of drug toxicity.

- Using assay results for existing compounds, predictions can be made on proposed compounds prior to their synthesis.
- Some models attempt to predict when prospective compounds are *toxic*.
- If a prediction were to be called equivocal or unapplicable (but interesting), the medicinal chemist and/or project biologist could then review the chemical structure and other properties in more detail (or send to a definitive screening assay).

OkC Data

As a simple example, let's use the OkCupid data set with a reduced set of predictors.

A Bayesian logistic regression model with diffuse Gaussian priors ($eta_j \sim N(0,10)$) was fit the data to make model predictions.

From this, we can get predictions of the probability of STEM as well as posterior distribution estimates.

A quasi standard error of fit was computed using the standard deviation of the posterior distribution.

• Recall that the standard error of the simple binomial rate p is $\sqrt{p(1-p)/n}$.

10-fold cross-validation was used to compute out-of-sample predictions of each profile.

Other models, notably random forest, can compute uncertainty measures for prediction.

Helper Functions

```
# requires rstanarm package too.
make_fit <- function(recipe, ...) {</pre>
  logistic_reg() %>%
    set_engine("stan", chains = 4, cores = 1, QR = TRUE, init = 0, iter = 5000, seed = 25622) %>%
    fit(..., data = juice(recipe))
make_preds <- function(splits, recipes, models, ...) {</pre>
  # Get the dummy variables
  holdout <- bake(recipes, new_data = assessment(splits))</pre>
  holdout %>%
    bind_cols(predict(models, holdout %>% select(-Class), type = "class")) %>%
    bind_cols(predict(models, holdout %>% select(-Class), type = "prob")) %>%
    bind_cols(predict(models, holdout %>% select(-Class), type = "conf_int", std_error = TRUE)) %>%
    dplyr::select(Class, starts_with(".")) %>%
    # Get information about the resample and the original data index
    mutate(
      resample = labels(splits) %>% pull(id),
      .row = as.integer(splits, data = "assessment")
    ) %>%
    as_tibble()
```

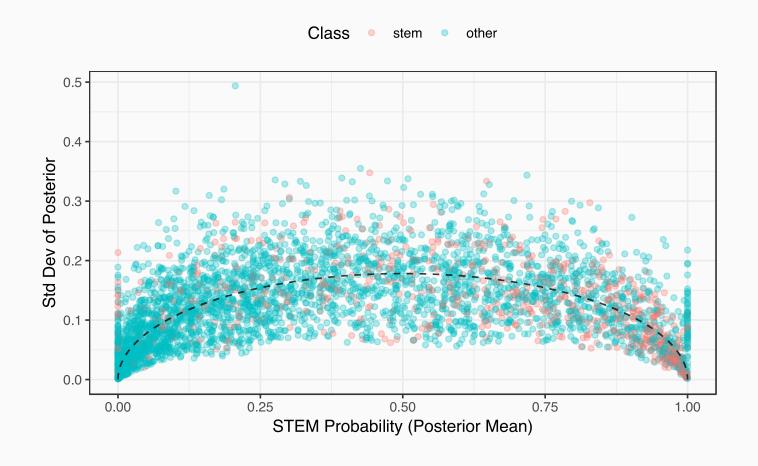
Modeling Code

```
library(furrr)

# or plan("sequential")
plan("multicore") # non-windows implementation

set.seed(9798)
okc_splits <-
    vfold_cv(okc_lr_train) %>%
    mutate(
    recipes = map(splits, prepper, dummies),
    # The next line takes a long time to execute.
    # It took 77 min using 10 cores for me.
    models = future_map(recipes, make_fit, Class ~ .)
) %>%
    mutate(
    preds = pmap(., make_preds)
)
```

Predicted Probability versus Uncertainty

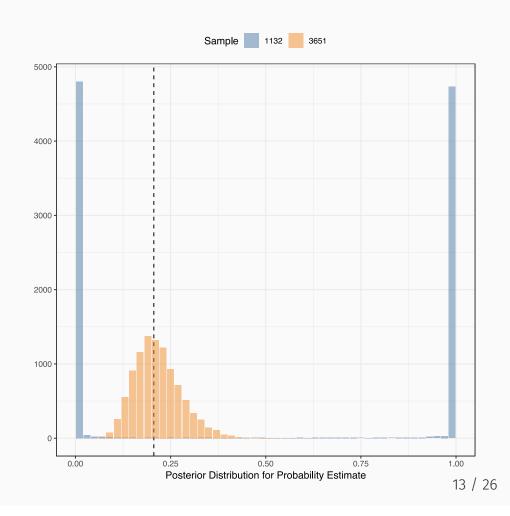


Two samples with very similar mean probabilities

| Class | STEM Prob | Std Err | Fold | Sample # |
|-------|-----------|---------|-------|----------|
| stem | 0.210 | 0.061 | 0.421 | 3651 |
| other | 0.206 | 0.494 | 3.427 | 1132 |

Why might this be? Two of many reasons are:

- It could be due to different models in crossvalidation (but it's not here).
- The sample might not be *applicable* if it is very different from the other samples in the training set (i.e. extrapolation).



Adding a *post hoc* equivocal zone

We'll label samples as equivocal using rules:

- any sample whose standard error is 10-fold above the estimated average standard error or
- any sample with a predicted probability between 0.45 and 0.55.

To estimate the average standard error, we'll use the standard deviation of the binomial parameter.

```
## # A tibble: 8 x 4
     .pred_stem .std_error exp_std_err fold_above
         <dbl>
                    <dbl>
                                  <dbl>
                                             <dbl>
      2.22e-16
                   0.0234 0.00000000531 4405600.
     1.86e- 1
                  0.102 0.139
                                             0.736
      3.77e- 1
                  0.165 0.173
                                             0.955
      6.03e- 2
                                             1.11
                  0.0942 0.0848
      2.96e- 2
                  0.0644 0.0604
                                             1.07
## 6 5.59e- 1
                                             0.549
                  0.0971 0.177
## 7 1.54e- 1
                   0.143 0.129
                                             1.11
## 8 9.67e- 1
                   0.0200 0.0638
                                             0.314
```

The probably Package

probably contains methods for post-processing class probability predictions, such as

- calibrating probability estimates (not yet implemented)
- determining appropriate thresholds for two-class data sets
- equivocal predictions

probably has a new type of object called class_pred that is like a factor but can include which samples should not be reported.

The object type builds on Hadley's new vctrs package.

class_pred Objects

```
library(probably)

okc_tr_res <-
    okc_tr_res %>%
    mutate(
    in_eq_zone =
        fold_above > 10 &
        (.pred_stem > 0.45 | .pred_stem < 0.55),
        new_pred =
        class_pred(.pred_class, which = which(in_eq_zone))
    )

okc_tr_res %>%
    dplyr::select(.pred_class, new_pred) %>%
    slice(1:5)
```

```
okc_tr_res %>% pull(new_pred) %>% class()

## [1] "class_pred" "vctrs_vctr"

okc_tr_res %>% pull(new_pred) %>% levels()

## [1] "stem" "other"

okc_tr_res %>% slice(1:6) %>% pull(new_pred) %>% as.factor()

## [1] <NA> other other other stem

## Levels: stem other
```

Performance Metrics with Equivocals

Equivocals are not included when performance is calculated (e.g. accuracy) and the *reportable rate* should also be inleuded.

When converted to a factor, equivocal values are converted to missing.

 The next version of yardstick will automatically convert class_pred to factor before computing metrics.

```
okc_tr_res %>%
  mutate(new_pred = as.factor(new_pred)) %>%
  kap(Class, new_pred)
```

Multiclass Metrics

Multiclass Metrics With yardstick



Multiclass? This just means your outcome has >2 possibilities (Religion: Catholic, Atheist, Buddhist, etc).

Consider binary precision():

$$Pr = rac{TP}{TP + FP}$$

```
## # A tibble: 5 x 2
## truth estimate
## 2
## 3
## 4
## 5
```

$$TP=2$$
 $FP=1$ $Pr=rac{2}{2+1}=rac{2}{3}$

precision(prec_example, truth, estimate)

Macro Averaging



What does this look like in multiclass world?

```
## # A tibble: 5 x 2
## truth estimate
## <fct> <fct>
## 1
## 2
## 3
## 4
## 5
```

One technique for dealing with this is *macro* averaging. This reduces the problem to multiple one-vs-all comparisons.

Macro Averaging



What does this look like in multiclass world?

```
## # A tibble: 5 x 2
## truth estimate
## 2
## 3
## 4
## 5
```

One technique for dealing with this is *macro* averaging. This reduces the problem to multiple one-vs-all comparisons.

- Convert truth / estimate to binary with levels:
 and other.
- 2) Compute precision() to get Pr_1.
- 3) Repeat 1) and 2) for each level to get Pr_1, Pr_2, Pr_3.
- 4) Average the results:

$$Pr_{macro} = rac{Pr_1 + Pr_2 + Pr_3}{3}$$

Macro Averaging



prec_multi

```
## # A tibble: 5 x 2
## truth estimate
## <fct> <fct>
## 1
## 2
## 3
## 4
## 5
```

$$Pr_1 = rac{2}{2+0} = 1$$
 $Pr_2 = rac{1}{1+1} = 0.5$ $Pr_3 = rac{0}{0+1} = 0$

$$Pr_{macro} = rac{1 + 0.5 + 0}{3} = 0.5$$

precision(prec_multi, truth, estimate)

Caveats



Macro averaging gives each class *equal weight* to the total precision value (1/3 here). This may not be realistic when a class imbalance is present.

In that case, you can use a weighted macro average which weights by the frequency of that class in the truth column.

Caveats



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In that case, you can use a weighted macro average which weights by the frequency of that class in the truth column.

There is additionally a *micro average* that gives each *observation* equal weight rather than each *class*. This gives classes with more observations more influence.

Find more information at the yardstick vignette.

tidypredict

Converting Prediction Equations to SQL

tidypredict can convert some R model objects into SQL code that can be used for deployment.

The current set of models are: lm(), glm(), randomForest(), and ranger().

There is work underway for earth(), cubist(), and tree-based models via as.party().

There are currently some restrictions: no-line functions, non-treatment contrasts, and a few others.

Linear model prediction intervals can be computed though!

An Example

```
library(tidymodels)
library(AmesHousing)
library(tidypredict)

ames <- make_ames() %>%
    dplyr::select(-matches("Qu")) %>%
    # Manually log the variables :-(
    mutate(
        Sale_Price = log10(Sale_Price),
        Lot_Area = log10(Lot_Area),
        Gr_Liv_Area = log10(Gr_Liv_Area)
)

set.seed(4595)
data_split <-
    initial_split(ames, strata = "Sale_Price")

ames_train <- training(data_split)
ames_test <- testing(data_split)</pre>
```

```
## tidypredict test results
## Difference threshold: 1e-12
##
## All results are within the difference threshold
```

Scoring

A taste of the model equation as an R expression:

```
## 18.5002644076146 + (ifelse(Bldg_Type == "TwoFmCon", 1, 0)) *
## (-0.0164418404830365) + (ifelse(Bldg_Type == "Duplex", 1,
## 0)) * (-0.0790188658258443) + (ifelse(Bldg_Type == "Twnhs",
## 1, 0)) * (-0.0476581323558805) + (ifelse(Bldg_Type == "TwnhsE",
## 1, 0)) * (-0.00400678175266399) + (ifelse(Neighborhood ==
```

or SQL:

```
tidypredict_sql(ames_mod, dbplyr::simulate_mssql()) %>% substr(1, 85)

## [1] "18.5002644076146 + (CASE WHEN ((`Bldg_Type` = 'TwoFmCon') = 'TRUE') THEN (1.0) WHEN ..."
```

One cool thing about this is that these expressions do not require all of the predictors when the model includes feature selection (a la MARS or CART).