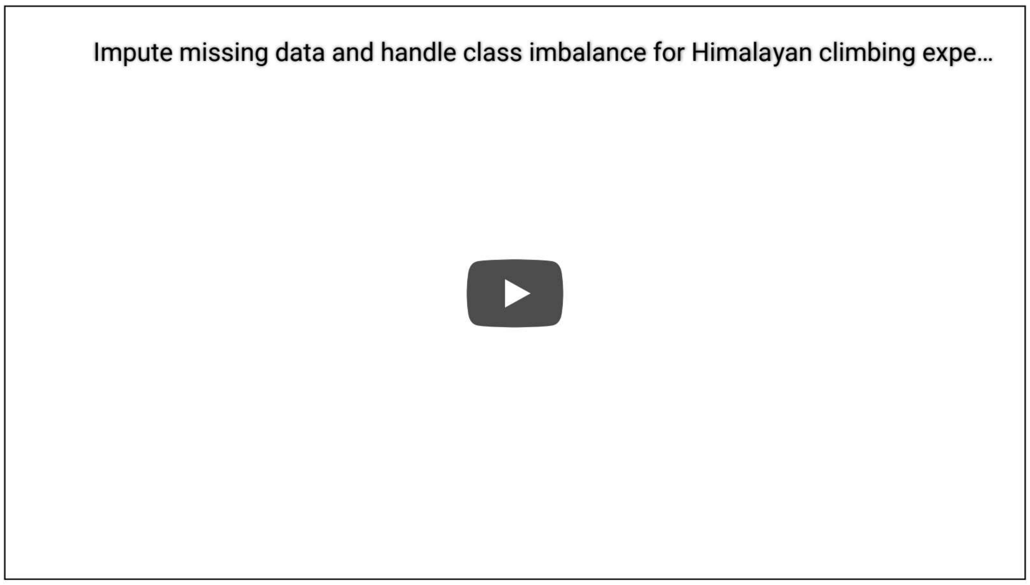
Handle class imbalance in #TidyTuesday climbing expedition data with tidymodels

Sep 23, 2020 · rstats, tidymodels

Lately I've been publishing screencasts demonstrating how to use the tidymodels framework, from starting out with first modeling steps to tuning more complex models. Today's screencast walks through a detailed model analysis from beginning to end, with important feature engineering steps and several model types, using this week's `#TidyTuesday` dataset on Himalayan climbing expeditions. ⛰


Impute missing data and handle class imbalance for Himalayan climbing expe…

Here is the code I used in the video, for those who prefer reading instead of or in addition to video.

Explore the data

Our modeling goal is to predict the probability of an Himalayan expedition member surviving or dying based on characteristics of the person and climbing expedition from this week's #TidyTuesday dataset. This dataset gives us the opportunity to talk about feature engineering steps like subsampling for class imbalance (many more people survive than die) and imputing missing data (lots of expedition members are missing age, for example).

Let's start by reading in the data.

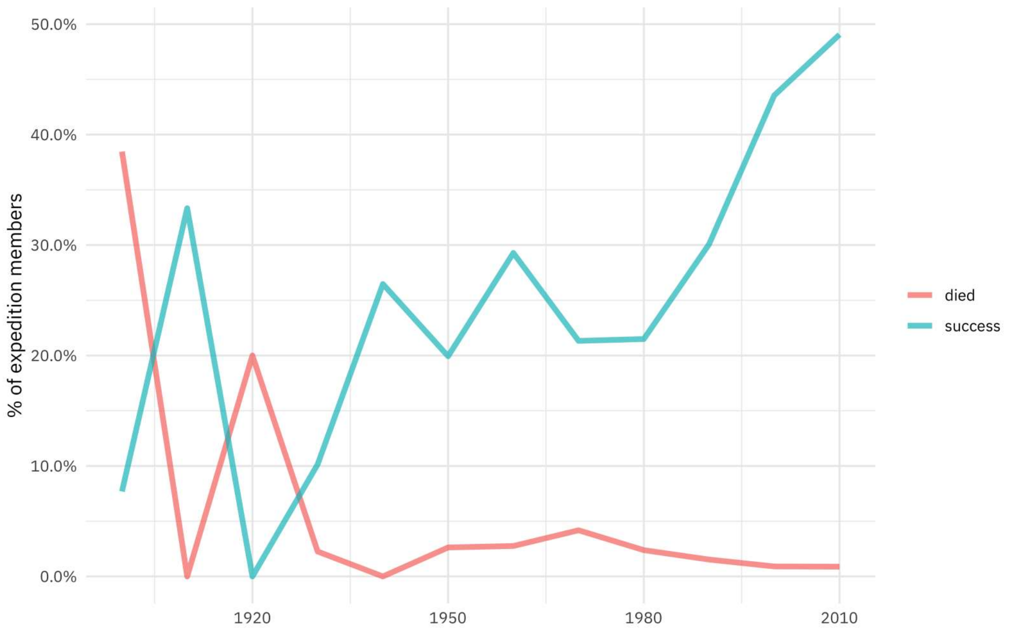
```
library(tidyverse)
members <- read_csv("https://raw.githubusercontent.com/rfordatascience/tidytuesday/master/data/2020/2020-09-22/members.csv'

members
```

```
## # A tibble: 76,519 x 21
##    expedition_id member_id peak_id peak_name  year season sex     age
##    <chr>         <chr>     <chr>   <chr>     <dbl> <chr>  <chr> <dbl>
##  1 AMAD78301     AMAD7830… AMAD    Ama Dabl…  1978 Autumn M        40
##  2 AMAD78301     AMAD7830… AMAD    Ama Dabl…  1978 Autumn M        41
##  3 AMAD78301     AMAD7830… AMAD    Ama Dabl…  1978 Autumn M        27
##  4 AMAD78301     AMAD7830… AMAD    Ama Dabl…  1978 Autumn M        40
##  5 AMAD78301     AMAD7830… AMAD    Ama Dabl…  1978 Autumn M        34
##  6 AMAD78301     AMAD7830… AMAD    Ama Dabl…  1978 Autumn M        25
##  7 AMAD78301     AMAD7830… AMAD    Ama Dabl…  1978 Autumn M        41
##  8 AMAD78301     AMAD7830… AMAD    Ama Dabl…  1978 Autumn M        29
##  9 AMAD79101     AMAD7910… AMAD    Ama Dabl…  1979 Spring M        35
## 10 AMAD79101     AMAD7910… AMAD    Ama Dabl…  1979 Spring M        37
## # … with 76,509 more rows, and 13 more variables: citizenship <chr>,
## #   expedition_role <chr>, hired <lgl>, highpoint_metres <dbl>, success <lgl>,
## #   solo <lgl>, oxygen_used <lgl>, died <lgl>, death_cause <chr>,
## #   death_height_metres <dbl>, injured <lgl>, injury_type <chr>,
## #   injury_height_metres <dbl>
```

On the video, I walk through the results of `skimr::skim()`, and notice which variables have missing data, how many unique values there are for variables like citizenship or mountain peak, and so forth.

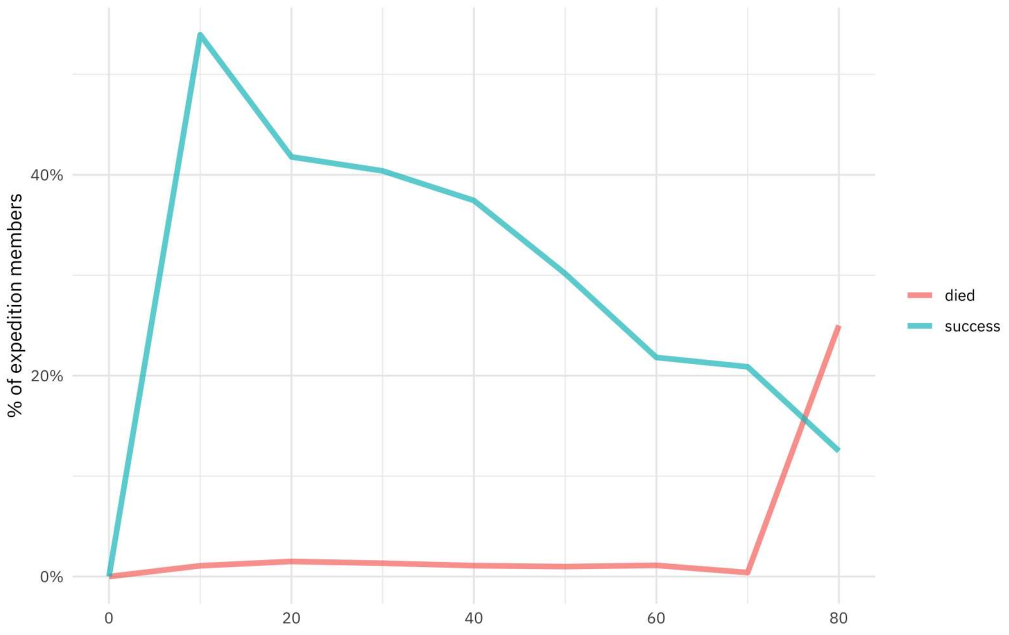
How has the rate of expedition success and member death changed over time?

```
members %>%
  group_by(year = 10 * (year %/% 10)) %>%
  summarise(
    died = mean(died),
    success = mean(success)
  ) %>%
  pivot_longer(died:success, names_to = "outcome", values_to = "percent") %>%
  ggplot(aes(year, percent, color = outcome)) +
  geom_line(alpha = 0.7, size = 1.5) +
  scale_y_continuous(labels = scales::percent_format()) +
  labs(x = NULL, y = "% of expedition members", color = NULL)
```



Is there a relationship between the expedition member's age and success of the expedition or death? We can use the same code but just switch out `year` for `age`.

```
members %>%
  group_by(age = 10 * (age %/% 10)) %>%
  summarise(
    died = mean(died),
    success = mean(success)
  ) %>%
  pivot_longer(died:success, names_to = "outcome", values_to = "percent") %>%
  ggplot(aes(age, percent, color = outcome)) +
  geom_line(alpha = 0.7, size = 1.5) +
  scale_y_continuous(labels = scales::percent_format()) +
  labs(x = NULL, y = "% of expedition members", color = NULL)
```



Are people more likely to die on unsuccessful expeditions?

```
members %>%
  count(success, died) %>%
  group_by(success) %>%
  mutate(percent = scales::percent(n / sum(n))) %>%
  kable(
    col.names = c("Expedition success", "Died", "Number of people", "% of people"),
    align = "llrr"
  )
```

Expedition success	Died	Number of people	% of people
FALSE	FALSE	46452	98%
FALSE	TRUE	868	2%
TRUE	FALSE	28961	99%
TRUE	TRUE	238	1%

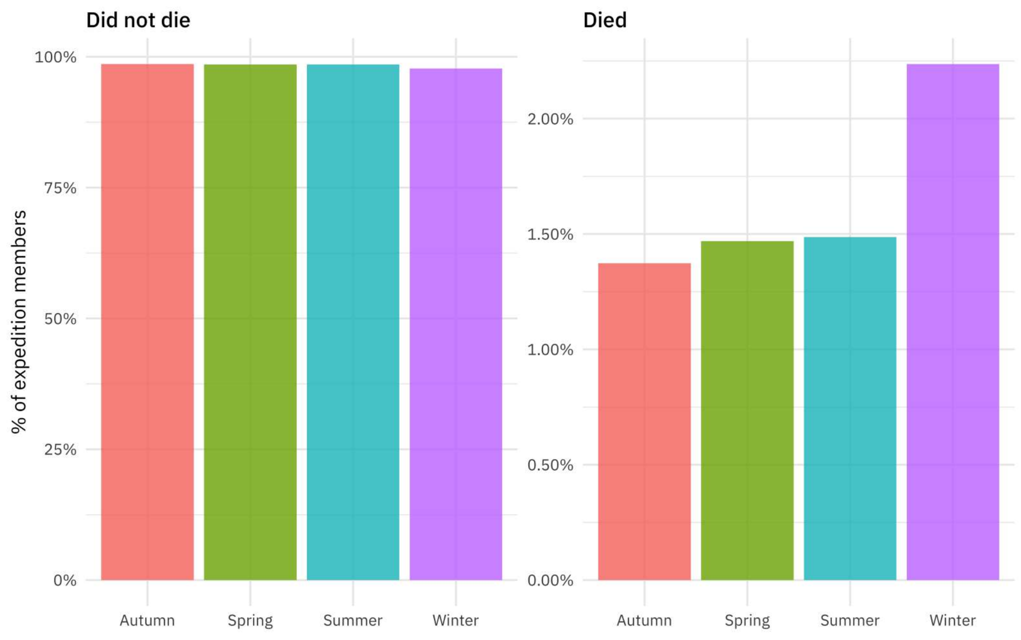
We can use a similar approach to see how different the rates of death are on different peaks in the Himalayas.

```
members %>%
  filter(!is.na(peak_name)) %>%
  mutate(peak_name = fct_lump(peak_name, prop = 0.05)) %>%
  count(peak_name, died) %>%
  group_by(peak_name) %>%
  mutate(percent = scales::percent(n / sum(n))) %>%
  kable(
    col.names = c("Peak", "Died", "Number of people", "% of people"),
    align = "llrr"
  )
```

Peak	Died	Number of people	% of people
Ama Dablam	FALSE	8374	100%
Ama Dablam	TRUE	32	0%
Cho Oyu	FALSE	8838	99%
Cho Oyu	TRUE	52	1%
Everest	FALSE	21507	99%
Everest	TRUE	306	1%
Manaslu	FALSE	4508	98%
Manaslu	TRUE	85	2%
Other	FALSE	32171	98%
Other	TRUE	631	2%

Let's make one last exploratory plot and look at seasons. How much difference is there in survival across the four seasons?

```
members %>%
  filter(season != "Unknown") %>%
  count(season, died) %>%
  group_by(season) %>%
  mutate(
    percent = n / sum(n),
    died = case_when(
      died ~ "Died",
      TRUE ~ "Did not die"
    )
  ) %>%
  ggplot(aes(season, percent, fill = season)) +
  geom_col(alpha = 0.8, position = "dodge", show.legend = FALSE) +
  scale_y_continuous(labels = scales::percent_format()) +
  facet_wrap(~died, scales = "free") +
  labs(x = NULL, y = "% of expedition members")
```



There are lots more great examples of #TidyTuesday EDA out there to explore on Twitter! Let's now create the dataset that we'll use for modeling by filtering on some of the variables and transforming some variables to a be factors. There are still lots of `NA` values for age but we are going to *impute* those.

```
members_df <- members %>%
  filter(season != "Unknown", !is.na(sex), !is.na(citizenship)) %>%
  select(peak_id, year, season, sex, age, citizenship, hired, success, died) %>%
  mutate(died = case_when(
    died ~ "died",
    TRUE ~ "survived"
  )) %>%
  mutate_if(is.character, factor) %>%
  mutate_if(is.logical, as.integer)

members_df
```

```
## # A tibble: 76,507 x 9
##    peak_id  year season sex     age citizenship hired success died
##    <fct>   <dbl> <fct>  <fct> <dbl> <fct>       <int>   <int> <fct>
##  1 AMAD     1978 Autumn M        40 France          0       0 survived
##  2 AMAD     1978 Autumn M        41 France          0       0 survived
##  3 AMAD     1978 Autumn M        27 France          0       0 survived
##  4 AMAD     1978 Autumn M        40 France          0       0 survived
##  5 AMAD     1978 Autumn M        34 France          0       0 survived
##  6 AMAD     1978 Autumn M        25 France          0       0 survived
##  7 AMAD     1978 Autumn M        41 France          0       0 survived
##  8 AMAD     1978 Autumn M        29 France          0       0 survived
##  9 AMAD     1979 Spring M        35 USA             0       0 survived
## 10 AMAD     1979 Spring M        37 W Germany       0       1 survived
## # … with 76,497 more rows
```

Build a model

We can start by loading the tidymodels metapackage, and splitting our data into training and testing sets.

```
library(tidymodels)

set.seed(123)
members_split <- initial_split(members_df, strata = died)
members_train <- training(members_split)
members_test <- testing(members_split)
```

We are going to use resampling to evaluate model performance, so let's get those resampled sets ready.

```
set.seed(123)
members_folds <- vfold_cv(members_train, strata = died)
members_folds
```

```
## #  10-fold cross-validation using stratification
## # A tibble: 10 x 2
##    splits               id
##    <list>               <chr>
##  1 <split [51.6K/5.7K]> Fold01
##  2 <split [51.6K/5.7K]> Fold02
##  3 <split [51.6K/5.7K]> Fold03
##  4 <split [51.6K/5.7K]> Fold04
##  5 <split [51.6K/5.7K]> Fold05
##  6 <split [51.6K/5.7K]> Fold06
##  7 <split [51.6K/5.7K]> Fold07
##  8 <split [51.6K/5.7K]> Fold08
##  9 <split [51.6K/5.7K]> Fold09
## 10 <split [51.6K/5.7K]> Fold10
```

Next we build a recipe for data preprocessing.

- First, we must tell the `recipe()` what our model is going to be (using a formula here) and what our training data is.
- Next, we impute the missing values for `age` using the median age in the training data set. There are more complex steps available for imputation, but we'll stick with a straightforward option here.
- Next, we use `step_other()` to collapse categorical levels for peak and citizenship. Before this step, there were hundreds of values in each variable.
- After this, we can create indicator variables for the non-numeric, categorical values, except for the outcome `died` which we need to keep as a factor.
- Finally, there are many more people who survived their expedition than who died (thankfully) so we will use `step_smote()` to balance the classes.

The object `members_rec` is a recipe that has **not** been trained on data yet (for example, which categorical levels should be collapsed has not been calculated).

```
library(themis)

members_rec <- recipe(died ~ ., data = members_train) %>%
  step_medianimpute(age) %>%
  step_other(peak_id, citizenship) %>%
  step_dummy(all_nominal(), -died) %>%
  step_smote(died)

members_rec
```

```
## Data Recipe
##
## Inputs:
##
##       role #variables
##    outcome          1
##  predictor          8
##
## Operations:
##
## Median Imputation for age
## Collapsing factor levels for peak_id, citizenship
## Dummy variables from all_nominal(), -died
## SMOTE based on died
```

We're going to use this recipe in a `workflow()` so we don't need to stress a lot about whether to `prep()` or not. If you want to explore the what the recipe is doing to your data, you can first `prep()` the recipe to estimate the parameters needed for each step and then `bake(new_data = NULL)` to pull out the training data with those steps applied.

Let's compare *two* different models, a logistic regression model and a random forest model; these are the same two models I used in the post on the Palmer penguins. We start by creating the model specifications.

```
glm_spec <- logistic_reg() %>%
  set_engine("glm")

glm_spec
```

```
## Logistic Regression Model Specification (classification)
##
## Computational engine: glm
```

```
rf_spec <- rand_forest(trees = 1000) %>%
  set_mode("classification") %>%
  set_engine("ranger")

rf_spec
```

```
## Random Forest Model Specification (classification)
##
## Main Arguments:
##   trees = 1000
##
## Computational engine: ranger
```

Next let's start putting together a tidymodels `workflow()`, a helper object to help manage modeling pipelines with pieces that fit together like Lego blocks. Notice that there is no model yet: `Model: None`.

```
members_wf <- workflow() %>%
  add_recipe(members_rec)

members_wf
```

```
## ══ Workflow ════════════════════════════════════════════════════════════════════════════════════
## Preprocessor: Recipe
## Model: None
##
## ── Preprocessor ────────────────────────────────────────────────────────────────────────────────
## 4 Recipe Steps
##
## • step_medianimpute()
## • step_other()
## • step_dummy()
## • step_smote()
```

Now we can add a model, and the fit to each of the resamples. First, we can fit the logistic regression model. Let's set a non-default metric set so we can add sensitivity and specificity.

```
members_metrics <- metric_set(roc_auc, accuracy, sensitivity, specificity)

doParallel::registerDoParallel()
glm_rs <- members_wf %>%
  add_model(glm_spec) %>%
  fit_resamples(
    resamples = members_folds,
    metrics = members_metrics,
    control = control_resamples(save_pred = TRUE)
  )

glm_rs
```

```
## # Resampling results
## # 10-fold cross-validation using stratification
## # A tibble: 10 x 5
##    splits              id     .metrics        .notes          .predictions
##    <list>              <chr>  <list>          <list>          <list>
##  1 <split [51.6K/5.7K… Fold01 <tibble [4 × 3… <tibble [0 × … <tibble [5,739 × 5…
##  2 <split [51.6K/5.7K… Fold02 <tibble [4 × 3… <tibble [0 × … <tibble [5,738 × 5…
##  3 <split [51.6K/5.7K… Fold03 <tibble [4 × 3… <tibble [0 × … <tibble [5,738 × 5…
##  4 <split [51.6K/5.7K… Fold04 <tibble [4 × 3… <tibble [0 × … <tibble [5,738 × 5…
##  5 <split [51.6K/5.7K… Fold05 <tibble [4 × 3… <tibble [0 × … <tibble [5,738 × 5…
##  6 <split [51.6K/5.7K… Fold06 <tibble [4 × 3… <tibble [0 × … <tibble [5,738 × 5…
##  7 <split [51.6K/5.7K… Fold07 <tibble [4 × 3… <tibble [0 × … <tibble [5,738 × 5…
##  8 <split [51.6K/5.7K… Fold08 <tibble [4 × 3… <tibble [0 × … <tibble [5,738 × 5…
##  9 <split [51.6K/5.7K… Fold09 <tibble [4 × 3… <tibble [0 × … <tibble [5,738 × 5…
## 10 <split [51.6K/5.7K… Fold10 <tibble [4 × 3… <tibble [0 × … <tibble [5,738 × 5…
```

Second, we can fit the random forest model.

```
rf_rs <- members_wf %>%
  add_model(rf_spec) %>%
  fit_resamples(
    resamples = members_folds,
    metrics = members_metrics,
    control = control_resamples(save_pred = TRUE)
  )

rf_rs
```

```
## # Resampling results
## # 10-fold cross-validation using stratification
## # A tibble: 10 x 5
##    splits              id     .metrics        .notes          .predictions
##    <list>              <chr>  <list>          <list>          <list>
##  1 <split [51.6K/5.7K… Fold01 <tibble [4 × 3… <tibble [0 × … <tibble [5,739 × 5…
##  2 <split [51.6K/5.7K… Fold02 <tibble [4 × 3… <tibble [0 × … <tibble [5,738 × 5…
##  3 <split [51.6K/5.7K… Fold03 <tibble [4 × 3… <tibble [0 × … <tibble [5,738 × 5…
##  4 <split [51.6K/5.7K… Fold04 <tibble [4 × 3… <tibble [0 × … <tibble [5,738 × 5…
##  5 <split [51.6K/5.7K… Fold05 <tibble [4 × 3… <tibble [0 × … <tibble [5,738 × 5…
##  6 <split [51.6K/5.7K… Fold06 <tibble [4 × 3… <tibble [0 × … <tibble [5,738 × 5…
##  7 <split [51.6K/5.7K… Fold07 <tibble [4 × 3… <tibble [0 × … <tibble [5,738 × 5…
##  8 <split [51.6K/5.7K… Fold08 <tibble [4 × 3… <tibble [0 × … <tibble [5,738 × 5…
##  9 <split [51.6K/5.7K… Fold09 <tibble [4 × 3… <tibble [0 × … <tibble [5,738 × 5…
## 10 <split [51.6K/5.7K… Fold10 <tibble [4 × 3… <tibble [0 × … <tibble [5,738 × 5…
```

We have fit each of our candidate models to our resampled training set!

Evaluate model

Now let's check out how we did.

```
collect_metrics(glm_rs)
```

```
## # A tibble: 4 x 5
##   .metric  .estimator  mean     n std_err
##   <chr>    <chr>      <dbl> <int>   <dbl>
## 1 accuracy binary     0.619    10 0.00230
## 2 roc_auc  binary     0.705    10 0.00721
## 3 sens     binary     0.678    10 0.0139
## 4 spec     binary     0.619    10 0.00243
```

Well, this is middling but at least mostly consistent for the positive and negative classes. The function `collect_metrics()` extracts and formats the `.metrics` column from resampling results like the ones we have here.

```
collect_metrics(rf_rs)
```

```
## # A tibble: 4 x 5
##   .metric  .estimator  mean     n  std_err
##   <chr>    <chr>      <dbl> <int>    <dbl>
## 1 accuracy binary     0.972    10 0.000514
## 2 roc_auc  binary     0.746    10 0.00936
## 3 sens     binary     0.164    10 0.0125
## 4 spec     binary     0.984    10 0.000499
```

The accuracy is great but that sensitivity… YIKES! The random forest model has not done a great job of learning how to recognize *both* classes, even with our oversampling strategy. Let's dig deeper into how these models are doing to see this more. For example, how are they predicting the two classes?

```
glm_rs %>%
  conf_mat_resampled()
```

```
## # A tibble: 4 x 3
##   Prediction Truth      Freq
##   <fct>      <fct>     <dbl>
## 1 died       died       55.5
## 2 died       survived 2157.
## 3 survived   died       26.5
## 4 survived   survived 3499.
```

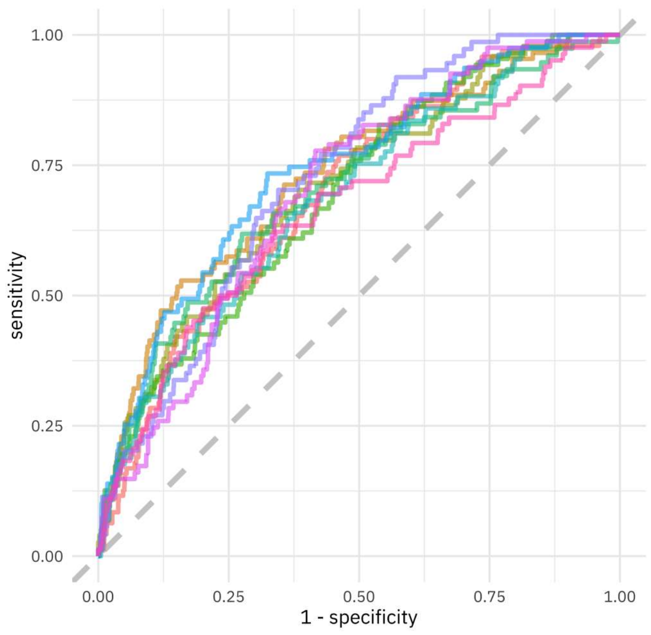
```
rf_rs %>%
  conf_mat_resampled()
```

```
## # A tibble: 4 x 3
##   Prediction Truth      Freq
##   <fct>      <fct>     <dbl>
## 1 died       died       13.5
## 2 died       survived   89.9
## 3 survived   died       68.5
## 4 survived   survived 5566.
```

The random forest model is quite bad at identifying which expedition members died, while the logistic regression model does about the same for both classes.

We can also make an ROC curve.

```
glm_rs %>%
  collect_predictions() %>%
  group_by(id) %>%
  roc_curve(died, .pred_died) %>%
  ggplot(aes(1 - specificity, sensitivity, color = id)) +
  geom_abline(lty = 2, color = "gray80", size = 1.5) +
  geom_path(show.legend = FALSE, alpha = 0.6, size = 1.2) +
  coord_equal()
```



It is finally time for us to return to the testing set. Notice that we have not used the testing set yet during this whole analysis; to compare and assess models we used resamples of the training set. Let's *fit* one more time to the training data and *evaluate* on the testing data using the function `last_fit()`.

```
members_final <- members_wf %>%
  add_model(glm_spec) %>%
  last_fit(members_split)

members_final
```

```
## # Resampling results
## # Manual resampling
## # A tibble: 1 x 6
##   splits         id          .metrics     .notes      .predictions     .workflow
##   <list>         <chr>       <list>       <list>      <list>           <list>
## 1 <split [57.4K… train/test… <tibble [2 … <tibble [0… <tibble [19,126… <workflo…
```

The metrics and predictions here are on the *testing* data.

```
collect_metrics(members_final)
```

```
## # A tibble: 2 x 3
##   .metric  .estimator .estimate
##   <chr>    <chr>          <dbl>
## 1 accuracy binary         0.619
## 2 roc_auc  binary         0.689
```

```
collect_predictions(members_final) %>%
  conf_mat(died, .pred_class)
```

```
##           Truth
## Prediction  died survived
##   died       196     7204
##   survived    90    11636
```

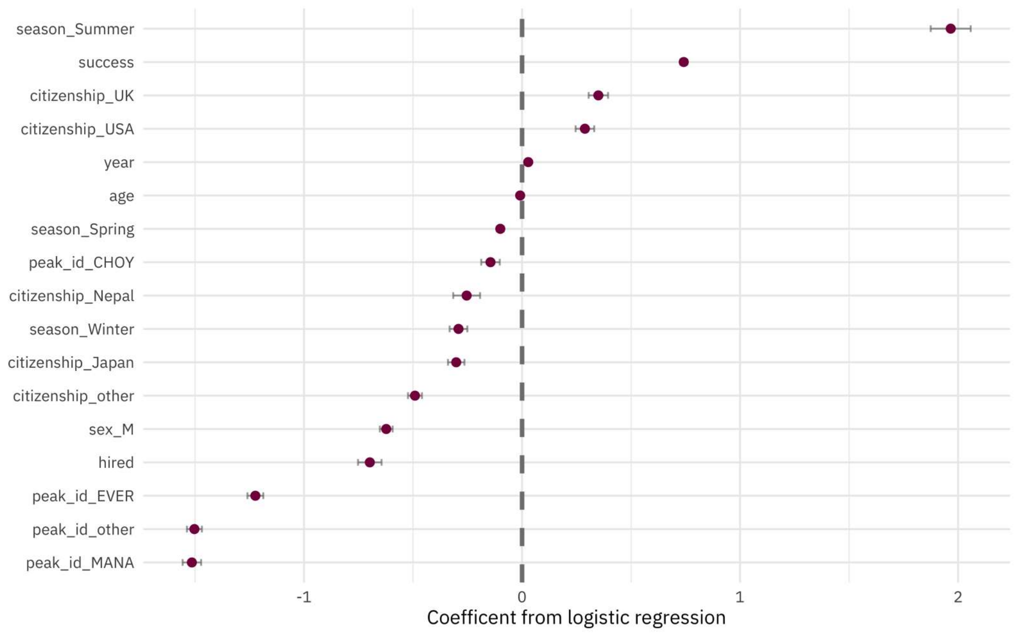
The coefficients (which we can get out using `tidy()`) have been estimated using the *training* data. If we use `exponentiate = TRUE`, we have odds ratios.

```
members_final %>%
  pull(.workflow) %>%
  pluck(1) %>%
  tidy(exponentiate = TRUE) %>%
  arrange(estimate) %>%
  kable(digits = 3)
```

term	estimate	std.error	statistic	p.value
(Intercept)	0.000	0.944	-57.309	0.000
peak_id_MANA	0.220	0.042	-35.769	0.000
peak_id_other	0.223	0.034	-43.635	0.000
peak_id_EVER	0.294	0.036	-33.641	0.000
hired	0.497	0.054	-12.928	0.000
sex_M	0.536	0.029	-21.230	0.000
citizenship_other	0.612	0.032	-15.299	0.000
citizenship_Japan	0.739	0.038	-7.995	0.000
season_Winter	0.747	0.041	-7.180	0.000
citizenship_Nepal	0.776	0.062	-4.128	0.000
peak_id_CHOY	0.865	0.043	-3.404	0.001
season_Spring	0.905	0.016	-6.335	0.000
age	0.991	0.001	-12.129	0.000
year	1.029	0.000	59.745	0.000
citizenship_USA	1.334	0.043	6.759	0.000
citizenship_UK	1.419	0.045	7.858	0.000
success	2.099	0.016	46.404	0.000
season_Summer	7.142	0.092	21.433	0.000

We can also visualize these results.

```r
members_final %>%
  pull(.workflow) %>%
  pluck(1) %>%
  tidy() %>%
  filter(term != "(Intercept)") %>%
  ggplot(aes(estimate, fct_reorder(term, estimate))) +
  geom_vline(xintercept = 0, color = "gray50", lty = 2, size = 1.2) +
  geom_errorbar(aes(
    xmin = estimate - std.error,
    xmax = estimate + std.error
  ),
  width = .2, color = "gray50", alpha = 0.7
  ) +
  geom_point(size = 2, color = "#85144B") +
  labs(y = NULL, x = "Coefficent from logistic regression")
```



- The features with coefficients on the positive side (like climbing in summer, being on a successful expedition, or being from the UK or US) are associated with surviving.
- The features with coefficients on the negative side (like climbing specific peaks including Everest, being one of the hired members of a expedition, or being a man) are associated with dying.

Remember that we have to interpret model coefficients like this in light of the predictive accuracy of our model, which was somewhat middling; there are more factors at play in who survives these expeditions than what we have accounted for in the model directly. Also note that we see evidence in this model for how dangerous it is to be a native Sherpa climber in Nepal, hired as an expedition member, as pointed out in this week's #TidyTuesday `README`.

rstats   tidymodels

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I'm an author, international keynote speaker, and real-world practitioner focusing on data analysis and machine learning practice. I love making beautiful charts and communicating about technical topics with diverse audiences.

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