Tidy Survival Analysis: Applying R's Tidyverse to Survival Data

Module 5. Machine Learning

Lu Mao
lmao@biostat.wisc.edu
Department of Biostatistics & Medical Informatics
University of Wisconsin-Madison

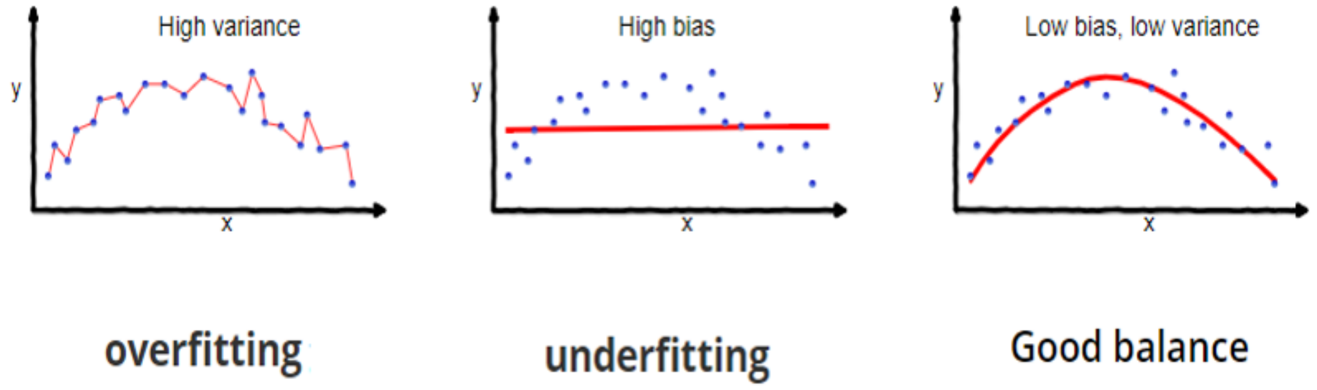
Aug 3, 2025

Table of contents

Machine Learning Survival Models

Setting

- **With many covariates**
  - **Prediction accuracy**: under- vs over-fitting



    - Too many predictors $\rightarrow$ overfitting
  - **Interpretation**: easier with fewer predictors

Regularized Cox Regression

- **Idea**
  - Penalize the magnitude of coefficients (-norm) to avoid overfitting
- **Elastic net**: minimize objective function
  - : tuning parameter that controls the strength of penalty
    - Determined by *cross-validation*
  - : controls the type of penalty
    - ridge regression: handles correlated predictors better
    - lasso regression: performs variable selection
  - **Implementation**: `glmnet` package

Survival Trees

- **Decision trees**
  - *Classification and Regression Trees* (CART; Breiman et al., 1984)
  - Root node (all sample) split into (more homogeneous) daughter nodes split recursively
- **Growing the tree**
  - Starting with root node, search partition criteria for one that minimizes “impurity” (e.g., mean squared deviance residuals) within daughter nodes
  - Recursive splitting until terminal nodes sufficiently “pure” in outcome

Complexity Control and Prediction

- **Pruning the tree**
  - Cut overgrown branches to prevent overfitting
  - Penalize number of terminal nodes
  - Tune complexity parameter (or minimum size of terminal node)
- **Prediction**
  - New terminal node KM estimates (or median survival)
- **Implementation**: `rpart` package

Random Forests

- **Limitation of a single tree**
  - High variance: small changes in data can lead to large changes in predictions
- **Random forests**
  - Bootstrap samples from training data
  - Take a random subset of covariates to split on (decorrelate the trees)
  - Tune the number of covariates to split on
- **Implementation**: `aorsf` package

Model Evaluation

- **Brier score**
  - Mean squared error between observed survival status and predicted survival probability
  - Inverse probability censoring weighting (IPCW) to account for censoring
  - Integrated Brier score: average Brier score over a time interval
- **ROC AUC**
  - Area under the receiver operating characteristic (ROC) curve for survival status
  - IPCW to handle censoring
  - Concordance index: overall AUC over time

tidymodels Workflows

Overview of `tidymodels` and `censored`

- **`tidymodels`**: a collection of packages for modeling and machine learning in R
  - Provides a *consistent interface* for model training, tuning, and evaluation
    - Key package `parsnip`
  - Supports various model types, including regression, classification, and survival analysis
- **`censored`**: a `parsnip` extension package for survival data
  - Implements parametric, semiparametric, and tree-based survival models

Data Preparation and Splitting

- **Create a `Surv` object** as response
  - `Surv(time, event)`

```r
library(tidymodels)
library(censored)
df <- df |>
  mutate(
    surv_obj = Surv(time, event), # create the Surv object as response variable
    .keep = "unused"              # discard original time and event columns
  )
```

- **Data splitting**
  - `initial_split()`: splits data into training and testing sets

```r
df_split <- initial_split(flight_data, prop = 3/4) # default ratio 3:1
df_train <- training(df_split) # obtain training set
```

Model Specification

- **Model type**
  - `survival_reg()`: parametric AFT models
  - `proportional_hazards(penalty = tune())`: (regularized) Cox PH models
  - `decision_tree(complexity = tune())`: decision trees
  - `rand_forest(mtry = tune())`: random forests
- **Set engine and mode**
  - `set_engine("survival")`: for AFT models
  - `set_engine("glmnet")`: for Cox PH models
  - `set_engine("aorsf")`: for random forests
  - `set_mode("censored regression")`: for survival models

```r
model_spec <- proportional_hazards(penalty = tune()) |>  # regularized Cox model (tune lambda)
  set_engine("glmnet") |>  # set engine to glmnet
  set_mode("censored regression") # set mode to censored regression
```

Recipe and Workflow

- **Recipe**: a series of preprocessing steps for the data
  - `recipe(response ~ ., data = df)`: specify response and predictors
  - `step_mutate()`: standardize numeric predictors
  - `step_dummy()`: convert categorical variables to dummy variables
- **Workflow**: combines model specification and recipe
  - `workflow() |> add_model(model_spec) |> add_recipe(recipe)`

```r
# Create a recipe
model_recipe <- recipe(surv_obj ~ ., data = df_train) |> # specify formula
  step_mutate(z1 = z1 / 1000) |>  # standardize z1
  step_other(z2, z3, threshold = 0.02) |> # group levels with prop < .02 into "other"
  step_dummy(all_nominal_predictors())  # convert categorical variables to dummy variables
# Create a workflow by combining model and recipe
model_wflow <- workflow() |>
  add_model(model_spec) |>   # add model specification
  add_recipe(model_recipe)   # add recipe
```

Tune Hyperparameters

- **Cross-validation**
  - `df_train_folds <- vfold_cv(df_train, v = k)`: create *k*-folds on training data (default 10)
  - `tune_grid(model_wflow, resamples = df_train_folds)`: tune hyperparameters using cross-validation

```r
# k-fold cross-validation
df_train_folds <- vfold_cv(df_train, v = 10) # 10-fold cross-validation
# Tune hyperparameters
model_res <- tune_grid(
  model_wflow,
  resamples = df_train_folds,
  grid = 10, # number of hyperparameter combinations to try
  metrics = metric_set(brier_survival, brier_survival_integrated,  # specify metrics
                       roc_auc_survival, concordance_survival),
  eval_time = seq(0, 84, by = 12) # evaluation time points
)
```

Finalize Workflow

- **Examine validation results**
  - `collect_metrics(model_res)`: collect metrics from tuning results
  - `show_best(model_res, metric = "brier_survival_integrated", n = 5)`: show top 5 models based on Brier score
- **Workflow for best model**
  - `param_best <- select_best(model_res, metric = "brier_survival_integrated")`: select best hyperparameters based on Brier score
  - `final_wl <- finalize_workflow(model_wflow, param_best)`: finalize workflow with best hyperparameters

```r
# Extract the best hyperparameters based on Brier score
param_best <- select_best(model_res, metric = "brier_survival_integrated")
# Finalize the workflow with the best hyperparameters
final_wl <- model_wflow |> finalize_workflow(param_best)
```

Fit Final Model

- **Fit the finalized workflow**
  - `final_mod <- last_fit(final_wl, split = df_split)`: fit the finalized workflow on the testing set
  - `collect_metrics(final_mod)`: collect metrics of final model on test data
- **Make predictions**
  - `predict(final_mod, new_data = new_data, type = "time")`: predict survival times on new data

```r
# Fit the finalized workflow on the testing set
final_mod <- last_fit(final_wl, split = df_split)
# Collect metrics of final model on test data
collect_metrics(final_mod) %>%
  filter(.metric == "brier_survival_integrated")
# Make predictions on new data
new_data <- testing(df_split) |>  slice(1:5) # take first 5 rows of test data
predict(final_mod, new_data = new_data, type = "time")
```

A Case Study

GBC: Relapse-Free Survival

- Time to first event

```r
library(tidymodels) # load tidymodels
library(censored)
gbc <- read.table("data/gbc.txt", header = TRUE) # Load GBC dataset
df <- gbc |>  # calculate time to first event (relapse or death)
  group_by(id) |> # group by id
  arrange(time) |> # sort rows by time
  slice(1) |>      # get the first row within each id
  ungroup() |>
  mutate(
    surv_obj = Surv(time, status), # create the Surv object as response variable
    .after = id, # keep id column after surv_obj
    .keep = "unused" # discard original time and status columns
  )
```

Data Preparation

- **Analysis dataset**

```r
head(df) # show the first few rows of the dataset
```

```
# A tibble: 6 × 10
     id    surv_obj hormone   age  meno  size grade nodes  prog estrg
  <int>      <Surv>   <int> <int> <int> <int> <int> <int> <int> <int>
1     1 43.836066         1    38     1    18     3     5   141   105
2     2 46.557377         1    52     1    20     1     1    78    14
3     3 41.934426         1    47     1    30     2     1   422    89
4     4  4.852459+        1    40     1    24     1     3    25    11
5     5 61.081967+        2    64     2    19     2     1    19     9
6     6 63.377049+        2    49     2    56     1     3   356    64
```

- **Data splitting**

```r
set.seed(123) # set seed for reproducibility
gbc_split <- initial_split(df) # split data into training and testing sets
gbc_split
```

```
<Training/Testing/Total>
<514/172/686>
```

Models to be Trained

- **Regularized Cox model**
  - `proportional_hazards(penalty = tune())`
  - Default: (lasso)
  - Tune penalty parameter
  - Use `glmnet` engine for fitting
- **Random forest**
  - `rand_forest(mtry = tune(), min_n = tune())`
  - Tune number of predictors to split on and minimum size of terminal node
  - Use `aorsf` engine for fitting

```r
# Training data
gbc_train <- training(gbc_split) # obtain training set
```

Common Recipe

- **Recipe for both models**

```r
gbc_recipe <- recipe(surv_obj ~ ., data = gbc_train) |> # specify formula
  step_mutate(
    grade = factor(grade),
    age40 = as.numeric(age >= 40), # create a binary variable for age >= 40
    prog = prog / 100, # rescale prog
    estrg = estrg / 100 # rescale estrg
  ) |>
  step_dummy(grade) |>
  step_rm(id) # remove id
# gbc_recipe # print recipe information
```

Regularized Cox Model

- **Cox model specification and workflow**

```r
# Regularized Cox model specification
cox_spec <- proportional_hazards(penalty = tune()) |>  # tune lambda
  set_engine("glmnet") |>  # set engine to glmnet
  set_mode("censored regression") # set mode to censored regression
cox_spec # print model specification
```

```
Proportional Hazards Model Specification (censored regression)

Main Arguments:
  penalty = tune()

Computational engine: glmnet
```

```r
# Create a workflow by combining model and recipe
cox_wflow <- workflow() |>
  add_model(cox_spec) |>   # add model specification
  add_recipe(gbc_recipe)   # add recipe
```

Model Tuning

- **Cross-validation set-up**
  - For both models

```r
set.seed(123) # set seed for reproducibility
gbc_folds <- vfold_cv(gbc_train, v = 10) # 10-fold cross-validation
# Set evaluation metrics
gbc_metrics <- metric_set(brier_survival, brier_survival_integrated,
                          roc_auc_survival, concordance_survival)
gbc_metrics # evaluation metrics info
```

```
A metric set, consisting of:
- `brier_survival()`, a dynamic survival metric               | direction:
minimize
- `brier_survival_integrated()`, a integrated survival metric | direction:
minimize
- `roc_auc_survival()`, a dynamic survival metric             | direction:
maximize
- `concordance_survival()`, a static survival metric          | direction:
maximize
```

```r
# Set evaluation time points
time_points <- seq(0, 84, by = 12) # evaluation time points
```

Cox Model Tuning

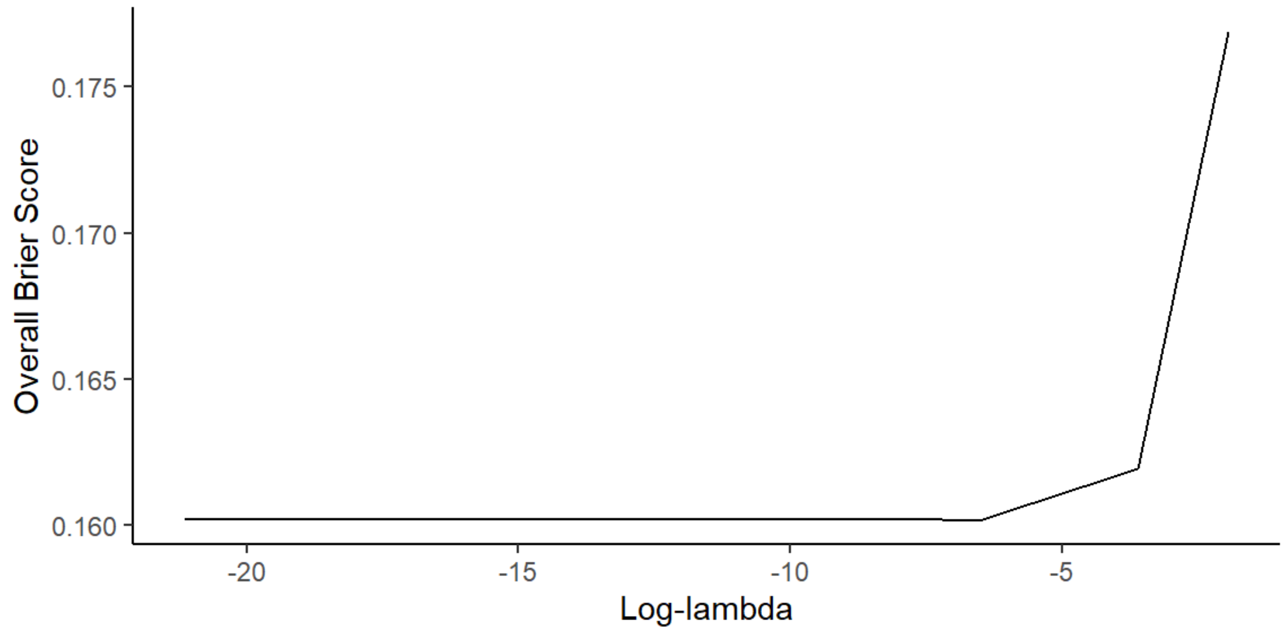
- **Tune the regularized Cox model**
  - Use `tune_grid()` to perform hyperparameter tuning
  - Evaluate performance using Brier score and ROC AUC

```r
set.seed(123) # set seed for reproducibility
# Tune the regularized Cox model (this will take some time)
cox_res <- tune_grid(
  cox_wflow,
  resamples = gbc_folds,
  grid = 10, # number of hyperparameter combinations to try
  metrics = gbc_metrics, # evaluation metrics
  eval_time = time_points, # evaluation time points
  control = control_grid(save_workflow = TRUE) # save workflow
)
```

Cox Model Tuning Results

- Plot Brier score as function of

```r
collect_metrics(cox_res) |>  # collect metrics from tuning results
  filter(.metric == "brier_survival_integrated") |>  # filter for Brier score
  ggplot(aes(log(penalty), mean)) + # plot log-lambda vs Brier score
  geom_line() +  # plot line
  labs(x = "Log-lambda", y = "Overall Brier Score") + # labels
  theme_classic() # classic theme
```



Best Cox Models

- **Show best models**
  - Based on Brier score

```
show_best(cox_res, metric = "brier_survival_integrated", n = 5) # top 5 models
```

```
# A tibble: 5 × 8
       penalty .metric          .estimator .eval_time  mean     n std_err .config
         <dbl> <chr>            <chr>           <dbl> <dbl> <int>   <dbl> <chr>
1 0.00147      brier_survival… standard           NA 0.160    10 0.00775 Prepro…
2 0.0000127    brier_survival… standard           NA 0.160    10 0.00775 Prepro…
3 0.0000000105 brier_survival… standard           NA 0.160    10 0.00775 Prepro…
4 0.000754     brier_survival… standard           NA 0.160    10 0.00775 Prepro…
5 0.00000409   brier_survival… standard           NA 0.160    10 0.00775 Prepro…
```

Random Forest Model

- **Random forest specification and workflow**

```r
# Random forest model specification
rf_spec <- rand_forest(mtry = tune(), min_n = tune()) |>  # tune mtry and min_n
  set_engine("aorsf") |>  # set engine to aorsf
  set_mode("censored regression") # set mode to censored regression
rf_spec # print model specification
```

```
Random Forest Model Specification (censored regression)

Main Arguments:
  mtry = tune()
  min_n = tune()

Computational engine: aorsf
```

```r
# Create a workflow by combining model and recipe
rf_wflow <- workflow() |>
  add_model(rf_spec) |>   # add model specification
  add_recipe(gbc_recipe)   # add recipe
```

Random Forest Tuning

- **Tune the random forest model**
  - Similar to Cox model tuning

```r
set.seed(123) # set seed for reproducibility
# Tune the random forest model (this will take some time)
rf_res <- tune_grid(
  rf_wflow,
  resamples = gbc_folds,
  grid = 10, # number of hyperparameter combinations to try
  metrics = gbc_metrics, # evaluation metrics
  eval_time = time_points # evaluation time points
)
```

Random Forest Tuning Results

- **View validation results**

```
collect_metrics(rf_res) |> head()   # collect metrics from tuning results
```

```
# A tibble: 6 × 9
   mtry min_n .metric         .estimator .eval_time   mean     n std_err .config
  <int> <int> <chr>           <chr>           <dbl>  <dbl> <int>   <dbl> <chr>  
1     3    30 brier_survival  standard            0 0         10 0       Prepro…
2     3    30 roc_auc_surviv… standard            0 0.5       10 0       Prepro…
3     3    30 brier_survival  standard           12 0.0635    10 0.00706 Prepro…
4     3    30 roc_auc_surviv… standard           12 0.827     10 0.0314  Prepro…
5     3    30 brier_survival  standard           24 0.163     10 0.0114  Prepro…
6     3    30 roc_auc_surviv… standard           24 0.747     10 0.0475  Prepro…
```

Best Random Forest Models

- **Show best models**
  - Based on Brier score

```r
show_best(rf_res, metric = "brier_survival_integrated", n = 5) # top 5 models
```

```
# A tibble: 5 × 9
   mtry min_n .metric            .estimator .eval_time  mean     n std_err .config
  <int> <int> <chr>              <chr>           <dbl> <dbl> <int>   <dbl> <chr>
1     6    24 brier_survival_… standard           NA 0.155    10 0.00765 Prepro…
2     5    27 brier_survival_… standard           NA 0.155    10 0.00782 Prepro…
3     4    20 brier_survival_… standard           NA 0.156    10 0.00777 Prepro…
4     9    36 brier_survival_… standard           NA 0.156    10 0.00743 Prepro…
5     2     7 brier_survival_… standard           NA 0.156    10 0.00829 Prepro…
```

- **Conclusion**
  - Best RF model has lower Brier score than best Cox model

Finalize and Fit Best Model

- **Fit final RF model**

```r
# Select best RF hyperparameters (mtry, min_n) based on Brier score
param_best <- select_best(rf_res, metric = "brier_survival_integrated")
param_best # view results
```

```
# A tibble: 1 × 3
   mtry min_n .config
  <int> <int> <chr>
1     6    24 Preprocessor1_Model07
```

```r
# Finalize the workflow with the best hyperparameters
rf_final_wflow <- finalize_workflow(rf_wflow, param_best) # finalize workflow
# Fit the finalized workflow on the testing set
set.seed(123) # set seed for reproducibility
final_rf_fit <- last_fit(
  rf_final_wflow,
  split = gbc_split, # use the original split
  metrics = gbc_metrics, # evaluation metrics
  eval_time = time_points # evaluation time points
)
```

Test Performance (I)

- **Collect metrics on test data**

```r
collect_metrics(final_rf_fit) |> # collect overall performance metrics
  filter(.metric %in% c("concordance_survival", "brier_survival_integrated"))
```

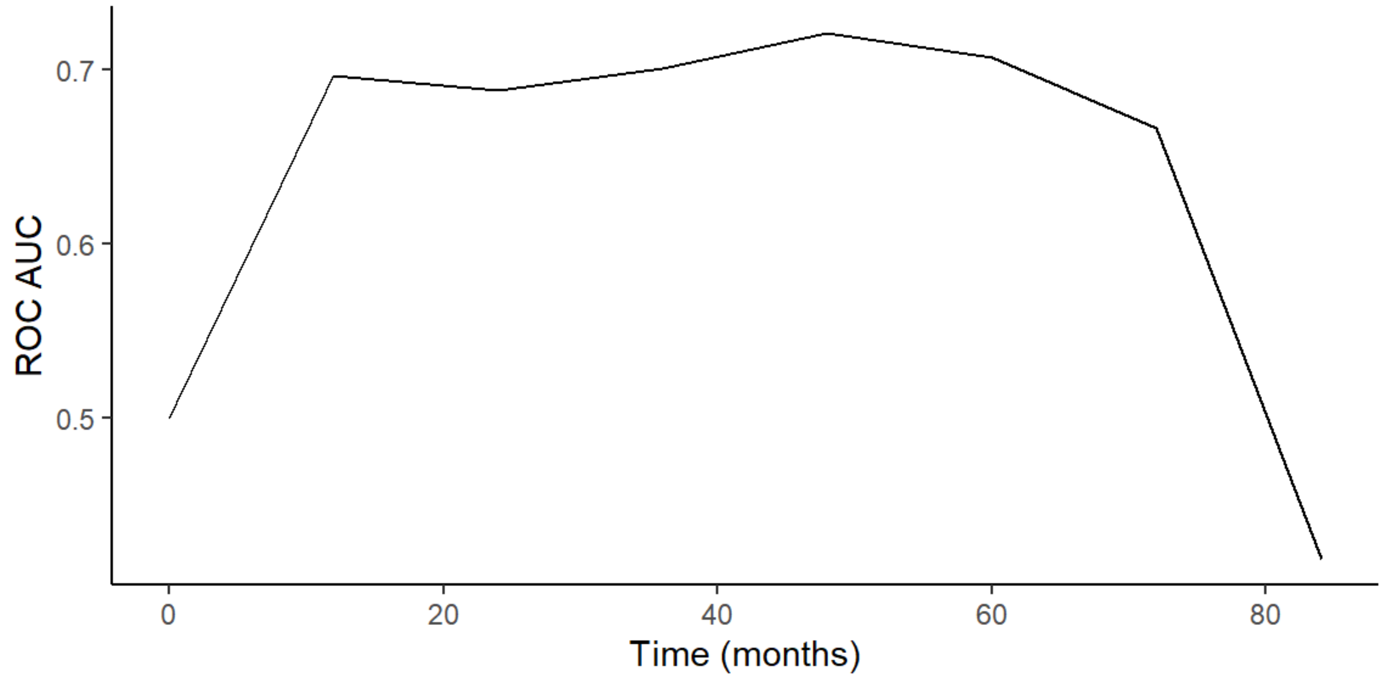
```
# A tibble: 2 × 5
  .metric                   .estimator .eval_time .estimate .config             
  <chr>                     <chr>           <dbl>     <dbl> <chr>               
1 brier_survival_integrated standard           NA     0.237 Preprocessor1_Model1
2 concordance_survival      standard           NA     0.655 Preprocessor1_Model1
```

```r
# Extract test ROC AUC over time
roc_test <- collect_metrics(final_rf_fit) |>
  filter(.metric == "roc_auc_survival") |>  # filter for ROC AUC
  rename(mean = .estimate) # rename mean column
```

Test Performance (II)

- **Plot test ROC AUC over time**

```r
roc_test |>  # pass the test ROC AUC data
  ggplot(aes(.eval_time, mean)) +  # plot evaluation time vs mean ROC AUC
  geom_line() + # plot line
  labs(x = "Time (months)", y = "ROC AUC") + # labels
  theme_classic()
```



Prediction by Final RF Model

- **Extract the fitted workflow**
  - Use `extract_workflow()` to get the final model

```r
gbc_rf <- extract_workflow(final_rf_fit) # extract the fitted workflow
# Predict on new data
gbc_5 <- testing(gbc_split) |>  slice(1:5) # take first 5 rows of test data
predict(gbc_rf, new_data = gbc_5, type = "time") # predict survival times
```

```
# A tibble: 5 × 1
  .pred_time
       <dbl>
1       47.6
2       67.1
3       67.2
4       36.1
5       49.7
```

Cox Model Exercise (I)

- **Task**: extract the best Cox model from `cox_res` and fit it to test data

▶ Solution

Cox Model Exercise (II)

- Solution - continued

Cox Model Exercise (III)

- **Task**: find the parameter estimates of final Cox model
  - Hint: use `tidy()` function from `broom` package

▶ Solution

Survival Tree Exercise

- **Task**: fit a survival tree model to the GBC data
  - Use `decision_tree()` with `set_engine("rpart")`
  - Tune complexity parameter `cp` using `tune()`
  - Use the same recipe as for Cox and RF models
  - Evaluate performance using Brier score and ROC AUC

Summary

Key Takeaways

- **Machine learning**: powerful tools for survival analysis with many covariates
  - Regularized Cox regression, survival trees, and random forests
- **`tidymodels`**: a consistent interface for modeling and machine learning
  - `parsnip` for model specification and tuning
  - `censored` packages for survival data
  - **Model evaluation**: Brier score and ROC AUC for survival models