

Class Activity 22

Your name here

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Group Activity 1

Load the `mlbench` package to get `PimaIndiansDiabetes2` dataset.

```
# Load the data - diabetes
data(PimaIndiansDiabetes2)
db <- PimaIndiansDiabetes2
db <- db %>% drop_na() %>% mutate(diabetes = fct_rev(factor(diabetes)))
db_raw <- db %>% select(glucose, insulin, diabetes)
```

a. Split the data 75-25 into training and test set using the following code.

```
set.seed(123)

db_split <- initial_split(db, prop = 0.75)

# Create training data
db_train <- db_split %>% training()

# Create testing data
db_test <- db_split %>% testing()
```

b. Follow the steps to train a 7-NN classifier using the `tidymodels` toolkit

```
# define recipe and preprocess the data
db_recipe <- recipe(diabetes ~ ., data = db_raw) %>%
  step_scale(all_predictors()) %>%
  step_center(all_predictors()) %>%
  prep()

# specify the model
db_knn_spec7 <- nearest_neighbor(mode = "classification",
  engine = "knn",
  weight_func = "rectangular",
  neighbors = 7)

# define the workflow
db_workflow <- workflow() %>%
```

```
add_recipe(db_recipe) %>%
add_model(db_knn_spec7)

# fit the model
db_fit <- fit(db_workflow, data = db_train)
```

c. Classify the penguins in the test data frame.

```
test_features <- db_test %>% select(glucose, insulin)
db_pred <- predict(db_fit, test_features, type = "raw")

db_results <- db_test %>%
  select(glucose, insulin, diabetes) %>%
  bind_cols(predicted = db_pred)

head(db_results, 6)
```

	glucose	insulin	diabetes	predicted
4	89	94	neg	neg
7	78	88	pos	neg
15	166	175	pos	pos
19	103	83	neg	neg
32	158	245	pos	pos
36	103	192	neg	neg

Group Activity 2

Calculate the accuracy, sensitivity, specificity, and positive predictive value by hand using the following confusion matrix.

```
conf_mat(db_results, truth = diabetes, estimate = predicted)
```

	Truth	
Prediction	pos	neg
pos	17	8
neg	12	61

```
accuracy(db_results, truth = diabetes,
  estimate = predicted)
# A tibble: 1 x 3
  .metric .estimator .estimate
  <chr>   <chr>       <dbl>
1 accuracy binary      0.796
```

```
sens(db_results, truth = diabetes,
  estimate = predicted)
# A tibble: 1 x 3
  .metric .estimator .estimate
  <chr>   <chr>       <dbl>
1 sens    binary      0.586
```

```
spec(db_results, truth = diabetes,
  estimate = predicted)
# A tibble: 1 x 3
  .metric .estimator .estimate
  <chr>   <chr>       <dbl>
```

```
1 spec      binary      0.884

ppv(db_results, truth = diabetes,
    estimate = predicted)
# A tibble: 1 x 3
  .metric .estimator .estimate
  <chr>   <chr>      <dbl>
1 ppv     binary      0.68
```

Extra: Code to recreate the plot in the slides for the diabetes dataset.

```
metrics_for_k <- function(k, db_train, db_test){
  db_knn_spec <- nearest_neighbor(mode = "classification",
    engine = "kkn",
    weight_func = "rectangular",
    neighbors = k)

  db_knn_wkflow <- workflow() %>%
    add_recipe(db_recipe) %>%
    add_model(db_knn_spec)

  db_knn_fit <- fit(db_knn_wkflow, data = db_train)
  test_features <- db_test %>% select(glucose, insulin)
  nn1_pred <- predict(db_knn_fit, test_features, type = "raw")

  db_results <- db_test %>%
    select(diabetes) %>%
    bind_cols(predicted = nn1_pred)
  custom_metrics <- metric_set(accuracy, sens, spec, ppv)

  metrics <- custom_metrics(db_results,
    truth = diabetes,
    estimate = predicted)
  metrics <- metrics %>% select(-.estimator) %>% mutate(k = rep(k,4))

  return(list = metrics)
}

k <- seq(1,40, by=1)
optim.results <- purrr::map_df(k, ~metrics_for_k(.x, db_train, db_test))

optim.results %>%
  ggplot(aes(x = k, y = .estimate, color = forcats::fct_reorder2(.metric, k, .estimate))) +
  geom_line(size = 1) +
  geom_point(size = 2) +
  theme_minimal() +
  ggthemes::scale_color_wsj() +
  scale_x_continuous(breaks = k) +
  theme(panel.grid.minor.x = element_blank(),
    axis.text=element_text(size=6, angle = 20))+
  labs(color='Metric', y = "Estimate", x = "K")
```

