## STATS 369 test

There are 6 questions.

Answer all the questions

There are 64 marks in total

You have 75 minutes

Upload your answers to Canvas as a pdf, ensuring that it is clear what question you are answering.

## **Integrity Statement**

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- 1. Answer the questions below in the context of this course (9 marks total, 3 marks each)
- (a) Explain when cross-validation is preferable to using a test-train spilt and when a test-train split is preferable to cross-validation.
- (b) What is mean-squared prediction error and why is it hard to estimate?
- (c) Define apparent error (defining any terms used) and discuss whether it is a useful estimate for MSPE.

2. Consider the sales data frame, for which the header is given, and the code fragment below. Assume sales has at least one entry for every month from 2015 until now.

```
## # A tibble: 9004 x 6
## date item_name item_cost item_code discount notes
## <chr> <chr> <dbl> <dbl> <dbl>. <chr>
## # ... with 9004 more rows
```

```
sales %>%
separate(date, into=c("year","month","day","other"), sep = "-") %>%
filter(year == "2019")
group_by(month) %>%
summarise(inc = sum(item_cost), trans = n(), disc = mean(discount))
```

What columns will the output of this code have, what data will be in each column, and how many rows will it have? (7 marks)

3. In a regression framework, for **each** scenario below, name **two** methods covered in the course so far that are suitable for addressing the scenario. Briefly discuss their pros, cons, and how they compare with each other.

You can name six different methods, or repeat if appropriate. (15 marks total, 5 marks each)

- a) p >> n: The number of predictors p is much larger than the number of observations n
- b) Non-linearity: The relationship between predictors and response is non-linear. (5 marks)
- c) **Heteroscedasticity**: The variance of the error term,  $\sigma^2 = \text{Var}(\epsilon)$  is not constant. (5 marks)

4. You are interested in predicting presence or absence of a type of cancer (Y) using protein measurements (X) from blood samples on 200 people. There are about 2000 X variables measured, but the biochemists only give you a subset of 100 of them. You do cross-validated model selection to end up with a predictive model and an estimated error rate from cross-validation.

Would you expect the estimated error to be biased (and why or why not) if:

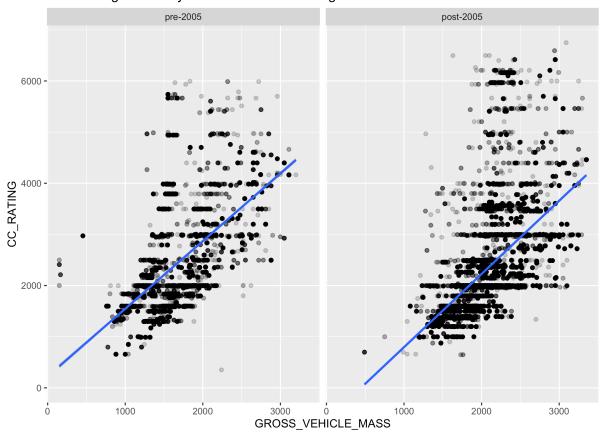
- (a) The 100 variables were chosen because they were correlated with cancer status in the same 200-person data set (3 marks)
- (b) The 100 variables were chosen because they had predicted cancer in previous research (3 marks)
- (c) The 100 variables were pre-selected based on a prior cross-validation process on the same 200-person data set (3 marks)

5. The following plot is made from the New Zealand vehicles data that we have seen several times in lectures.

Name the ggplot commands that could have been used to make this plot, including any geoms or aesthetic mappings, and explain what each does.

(10 marks)

Vehicle engine size by vehicle mass in cars registered before and after 2005



6. Download the files q6.Rmd and strains.csv. Answer the questions in the Rmd file and knit the result to html.
Upload both the html and Rmd
(14 marks total)