

Chapter 1

A Taxonomy of Problems

The term “data science” has been overused in recent years, and it has become something of a buzzword as a result¹. However, I think it can best be described as:

data science: Any endeavor in which statistics, machine learning, data analysis, computer science, and information science intersect with domain knowledge.

Data science is about using the machinery of statistics and computer science to solve real-world problems. In the clinical domain, that means incorporating methods from epidemiology, biostatistics, computer science, and machine learning with insights gained from the clinical research literature and the practical experiences of physicians, nurses, hospital administrators, operational teams, and biomedical researchers.

1.1 Project Examples

Whenever I teach, I ask students to provide some examples of projects for which they think data science could be useful. The following are real examples. They provide a broad representation of most of the types of problems clinicians and health system operations/population health teams are interested in.

¹See also: “artificial intelligence”, “machine learning”, “deep learning”.

1. *Unnecessary ER trips.* “Given a number of factors (types of admissions a person has had in the past, number of admissions/re-admissions, social determinants, etc.) can we predict who is going to show up at the emergency room unnecessarily”
2. *Good/poor candidates for program.* “determine if patients are good or poor candidates for one of our specialty care model bundle programs”
3. *Predicting unplanned admissions.* “predicting unplanned inpatient admissions based on many different variables (e.g. chronic conditions, engagement with primary care, etc.) and how these inputs interact with each other”
4. *Recommending an intervention.* “...stratification/prioritization of care management or other interventions or for clinical decision support...a tool would recommend an appropriate intervention based on the profile of the patient”
5. *Recommending a diagnosis.* “Based on unstructured chat conversations and also structured questions/forms/data...map out possible care pathways. For example, if someone says they have stomach pain, gives their zip code, insurance, pain tolerance and symptoms, and is logged in so we have past history, ask a few more questions and then we could determine they are 45% likely to have ulcer vs. constipation vs. food poisoning vs. appendicitis.”
6. *Predicting the amount paid by patients.* “Patient bill estimates - learning from claims data typical amount paid by patients for appointment reasons/types (e.g. estimate of additional services/care administered, and associated cost, based on patient details such as age, gender, etc.)”
7. *Identifying patient subtypes.* “identify cohorts within a population with chronic conditions based on their differences in longitudinal care across the continuum of settings (inpatient, ambulatory, primary care, specialty care, etc.)”
8. *Which conversations are similar?* “using previous chat histories to train (a chatbot) and become more effective/efficient for different, future patient chat experiences”

9. *Predictors of COVID-19 outcomes.* "Get baseline diabetes control marker (HbA1C) and acute glycemic control (inpatient glucose values) and see if either is a stronger predictor of COVID-19 outcomes (ICU, intubation, death)."
10. *Factors influencing mortality in myelofibrosis.* "We see lots of patients who are ineligible for clinical trials based on comorbidities and underlying organ dysfunction. However it is unclear how these factors affect OS. I would like to extract comorbidity data and baseline laboratory factors in patients with myelofibrosis to see how these factors affect mortality, if controlled for such important factors such as treatment, age, sex, insurance, number of comorbidities, and clinical risk score (DIPSS)."
11. *Non-adherence and difficult-to-treat asthma.* "We want to see whether non-adherence to prescribed inhaled corticosteroids plays a major role in poorly controlled asthma. Difficult-to-treat asthma can be evaluated by the number of ED visits, hospitalizations, prescriptions of prednisone and prescriptions of biological therapies. Using EPIC [we] can obtain medicine reconciliation information, of prescriptions sent, what proportion of those prescriptions were dispensed by Pharmacy. Question is can we find associations between the percentage of prescriptions filled and difficult-to-treat asthma."
12. *Impact of diabetes and hyperglycemia on progression-free survival.* "Aim: Assess the impact of diabetes and hyperglycemia on first-line systemic therapy response (progression-free survival) in patients with advanced non-small cell lung cancer. Diabetes- defined by presence of diagnosis codes coding for diabetes. Hyperglycemia- random glucose >200 ng/dL. Covariates of interest- age, sex, other treatments (RT, surgery), malignancy characteristics (stage, histology), smoking history, ecog (performance status), comorbidities, medications (steroids, anti-hyperglycemics)"
13. *Effect of statin use on MACE.* "Retrospective cohort study in elderly patients with CAD taking statins... exposed group are patients on a high-intensity statin; control group are patients on a moderate- or low-intensity statin. Participants matched based on age, gender, LDL category, and Elixhauser index category... The primary efficacy outcome

would be the time-to-first-event of 3-point MACE².”

14. *Clustering patients with NAFLD.* “We wanted to understand non-alcoholic fatty liver disease (NAFLD) better, so we developed a cohort of NAFLD patients using EMR-based criteria and then clustered them based on comorbidities, medications, vital signs, and lab values to identify NAFLD subtypes. We then characterized the phenotypes and outcomes of the different subtypes.”

1.2 Abstracting the Problem

All of these examples describe situations where we want to use data to answer questions of clinical or operational importance. While the details differ in each scenario, the important thing to notice here is that many of the tasks themselves are structurally similar.

For example, all of the items except 7 – 8 and 14 describe situations where we want to associate information about a patient with a particular outcome or recommendation. Using information about a patient to estimate the size of a bill (#6) may appear to be a very different problem than uncovering factors influencing myelofibrosis mortality (#10), but the structure of the two problems is similar: the patient features are used as input, and the output is whatever quantity you care about (e.g. the cost to the patient in dollars or the probability of mortality by a certain timepoint).

Learning to see these types of similarities will give you a tremendous amount of power when attacking new problems in clinical data science. It will allow you to confidently deploy methods you used to solve one problem on a wide range of other problems. Each new method you learn then multiplies your capacity to solve problems, rather than adding to it.

Question 1.1

How are items 7 – 8 and 14 different from the rest?

²MACE stands for “Major Adverse Cardiac Event”. The 3-point MACE is a composite of nonfatal stroke, nonfatal myocardial infarction, and cardiovascular death.

Question 1.2

How are items 1 – 6 similar to items 9 – 13 and how are they different?

Question 1.3

How do items 1 – 3 differ from items 4 – 5 and how are they similar?

Question 1.4

How do items 1 – 3 differ from item 6? How is item 6 different from all of the other items?

Question 1.5

How do items 9 – 11 differ from items 12 – 13?

1.3 Terms and Contrasts

The basic ways in which clinical data science problems vary can be characterized using a few broad conceptual distinctions. These draw from both traditional clinical disciplines, like epidemiology, as well as machine learning/statistics.

1.3.1 Guidance vs. Understanding

Before beginning any study, it is important to carefully consider the study's goal and how the findings from the study will be used. This will help guide you in choosing appropriate methods. For example, in some studies we care mainly about using data to provide **guidance** that will enable us to perform our jobs better in the future. We may want to predict whether a patient is likely to experience an adverse outcome, or we may want to learn the type of patient who is most likely to benefit from a particular treatment. In these cases, we want the data to guide us in making better choices.

Now, contrast this with a study whose primary goal is scientific **understanding**. In this case, we care more about using data to improve our understanding of a phenomenon than in operationalizing those findings. For example, we may be interested in whether a particular genetic variant affects a phenotype, or we may want to establish a causal link between a particular treatment and an outcome.

The distinction is fuzzy and often imperfect, and the same kinds of methods can often be used in both cases. Depending on the goal, however, one may be willing to make certain compromises. For example, complex, “black box” predictive models (e.g. deep learning models) may be appropriate when the goal is guidance, but offer little in the way of understanding. Conversely, regression models have become the de facto standard for clinical trials and causal inference, but may not lead to optimal predictive ability. In situations where the primary goal is a rigorous understanding of causal relationships, that may not matter as much.

1.3.2 Observational Study vs. Experiment

In **experimental studies**, the investigator manipulates some aspect of the subjects’ experience and studies its effect on the outcome of interest. For example, here is the NIH’s definition of a **clinical trial**:

A research study in which one or more human subjects are prospectively assigned to one or more interventions (which may include placebo or other control) to evaluate the effects of those interventions on health-related biomedical or behavioral outcomes.

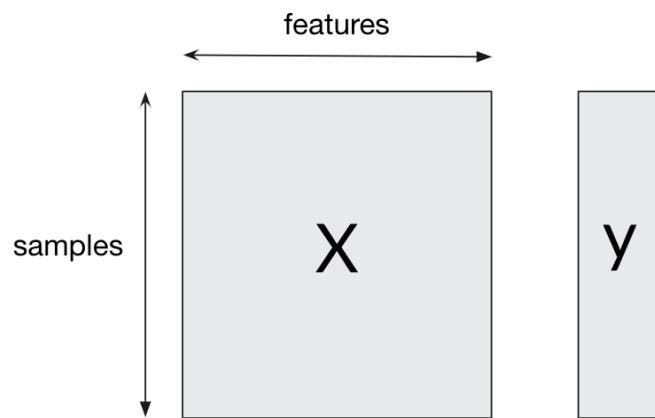
A clinical trial, therefore, is an experiment, because we control the intervention and monitor the effect of that intervention on one or more outcomes. Usually experimental studies employ some type of **randomization** to ensure that comparisons between different intervention groups are fair.

An **observational study**, in contrast, makes no attempt to interfere with its subjects. Instead, these individuals are simply observed, and inferences are made about the associations between different parameters and the outcome(s). Observational study designs and analytic plans are carefully designed to

minimize the effects of different sources of bias that can creep in due to lack of randomization. Although they're not usually referred to using this terminology, virtually all "big data" and machine learning oriented studies in healthcare are observational studies, because they use large datasets that were collected for other purposes.

1.3.3 Types of Machine Learning

This distinction, most often found in discussions of machine learning, refers to the way in which training data is applied to solve a problem. In **supervised learning**, the training data consist of pairs of input features and labels, and the algorithm learns to predict the value of the label from the input features. The general setup for supervised learning looks like this:



In **unsupervised learning**, only the input features are present (i.e. no y) and the algorithm learns to recognize patterns, clusters, or other structure in the inputs. Although they're almost never referred to using this terminology, clinical studies that examine the effect between one or more exposures and an outcome are examples of supervised learning. Studies that attempt to uncover groups, or clusters, of similar patients or samples are examples of unsupervised learning.

There are also two other types of machine learning. In **semi-supervised learning**, a small amount of labeled data is used to create a much larger,

weakly-labeled set of training data that is then fed to a supervised learning algorithm. In **reinforcement learning**, an algorithm is trained with a reward system which provides feedback on the quality of the action the system performs in a given situation instead of (as in supervised learning) simply providing the “right answer”.

Chapter 2

The Basics of Classification

Classification is a form of supervised learning in which our goal is to learn a mapping between some features, x , and an output, y . In classification, the output, y , is a category. In **binary classification** (by far the most common), there are only two categories: yes or no, usually represented as “0” (no) or “1” (yes). In **multi-class classification**, there are more than two categories.

To learn an appropriate mapping, we feed **training data** to a **learning algorithm**. Different algorithms learn different types of mappings.

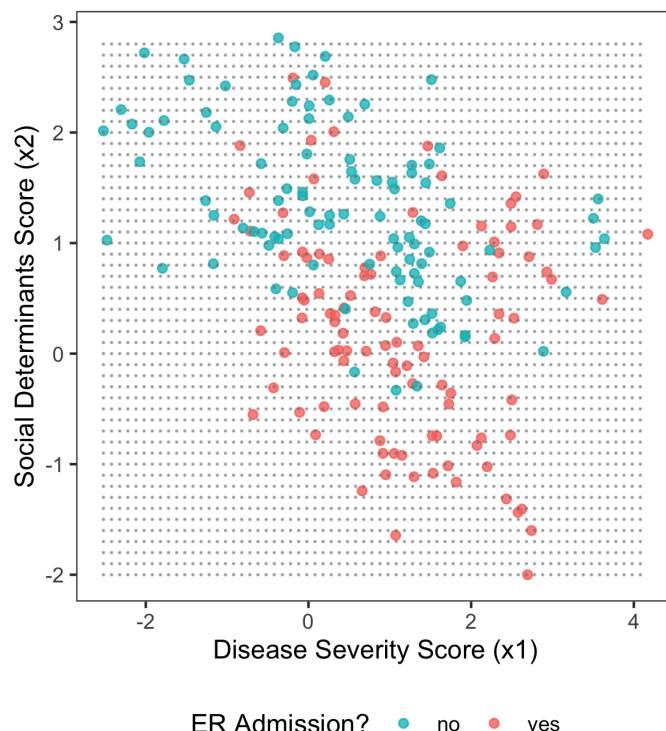
2.1 Definitions

- **Training data:** The data used, along with an appropriate learning algorithm, to create the mapping between input and output. It is composed of **training examples**, a.k.a. **samples**, each consisting of one or more input features and a single output.
- **Test data:** An independent dataset, not used in model training, on which the performance of a trained supervised learning model is evaluated.
- **Feature:** Also known as a **predictor**, or **covariate**, one of the inputs to a supervised learning algorithm.
- **Output:** Also known as the **outcome**, or **label**, the thing you are trying to predict.

- **Feature space:** Envisioning each feature as having its own axis that is orthogonal to all of the other features' axes, the multidimensional space spanned by those axes (or rather: unit vectors in the directions of those axes)
- **Extrapolation:** Making predictions outside the region of the feature space occupied by the training data. This will often lead to errors.

2.2 Visualizing the Classification Problem

Imagine we want to predict whether a patient will be readmitted to the emergency room (ER) within 30 days of hospital discharge. We gather data on two predictors: a disease severity score (x_1), which characterizes the severity of illness, and a social determinants score (x_2), which characterizes the patient's socioeconomic status. We have data on 200 patients.

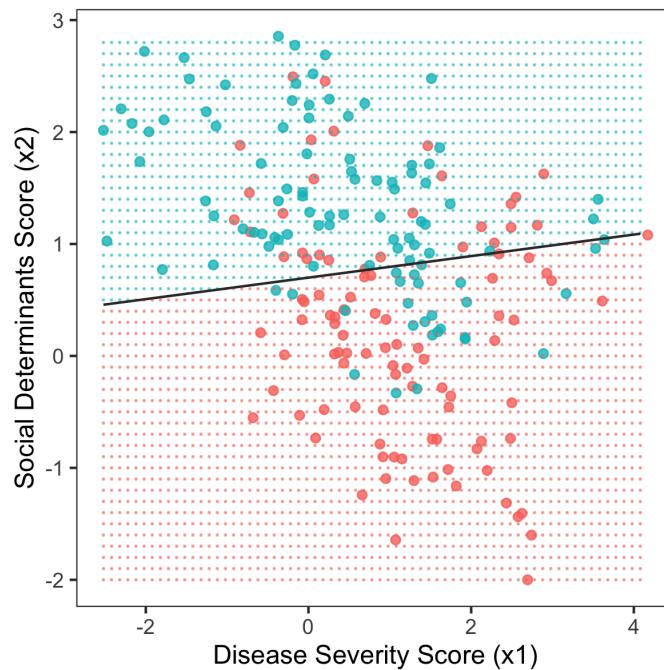


In this figure, the color refers to whether a patient was readmitted (blue = “no”, red = “yes”). The location of each point is governed by the patient’s disease severity score (x_1 , horizontal axis) and social determinants score (x_2 , vertical axis). Our goal in classification is to draw a **decision boundary** through this space, on one side of which we will predict that the patient is readmitted, and on the other side not.

2.3 Three Classification Algorithms

2.3.1 Logistic Regression

The simplest decision boundary is, arguably, a line. The logistic regression algorithm simply draws a line¹ through the feature space that divides the positive and negative training examples.



¹In a higher-dimensional feature space, the decision boundary for logistic regression is a **hyperplane**.

The output of a fitted logistic regression model from R looks like this:

```
```{r}
m3 <- glm(y ~ x1 + x2, data = df, family = "binomial")
summary(m3)
```

Call:
glm(formula = y ~ x1 + x2, family = "binomial", data = df)

Deviance Residuals:
    Min      1Q  Median      3Q     Max 
-1.88232 -0.90614 -0.05965  0.86579  2.28489 

Coefficients:
            Estimate Std. Error z value Pr(>|z|)    
(Intercept)  0.9780    0.2945   3.321 0.000897 ***
x1          0.1344    0.1372   0.980 0.327272  
x2         -1.3981    0.2316  -6.035 1.59e-09 *** 
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 277.26 on 199 degrees of freedom
Residual deviance: 209.54 on 197 degrees of freedom
AIC: 215.54

Number of Fisher Scoring iterations: 4
```

The equation of the line (or, in higher dimensions, hyperplane) that forms the decision boundary in logistic regression can be obtained by setting the linear sum of coefficients of this model equal to zero.

$$0.9780 + 0.1344x_1 - 1.3981x_2 = 0$$

$$\implies x_2 = \frac{0.9780 + 0.1344x_1}{1.3981}$$

At any point, (x_1, x_2) , in the feature space, the model's predicted probability of a positive outcome (i.e. probability of an ER readmission) is related to the coefficients by this equation

$$\log \frac{P[Y = 1]}{1 - P[Y = 1]} = 0.9780 + 0.1344x_1 - 1.3981x_2$$

The decision boundary occurs when $P[Y = 1] = 0.5$ (total uncertainty, e.g. a

coin toss). Another way to write this equation is:

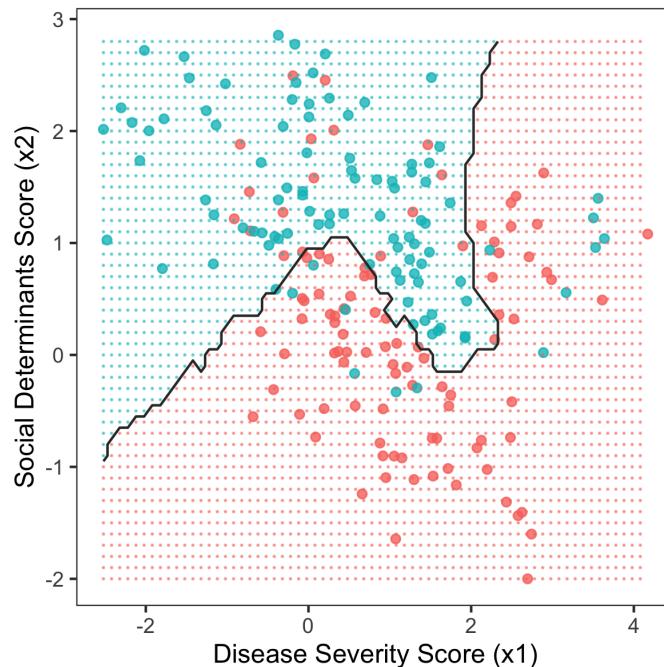
$$P[Y = 1] = \frac{1}{1 + \exp(-(0.9780 + 0.1344x_1 - 1.3981x_2))}$$

The functional form on the right, $1/(1 + \exp(-z))$, is called the **logistic function**; this is how logistic regression got its name. We will learn much more about the math behind logistic regression in subsequent chapters.

2.3.2 K Nearest Neighbors (KNN)

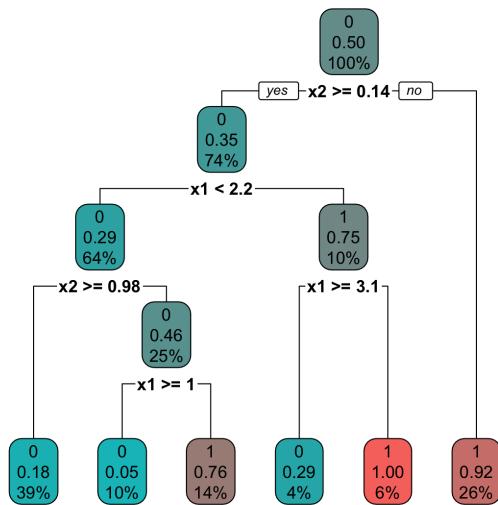
Another – completely different – approach to classification is to start with no assumptions about the shape of the decision boundary. To make a prediction about a new patient, we simply identify the K nearest neighbors to that patient from our training set and allow them to vote on whether or not the new patient will be readmitted. The parameter K must be set independently and is called a **hyperparameter**.

Here is the decision boundary for KNN with $K = 15$:

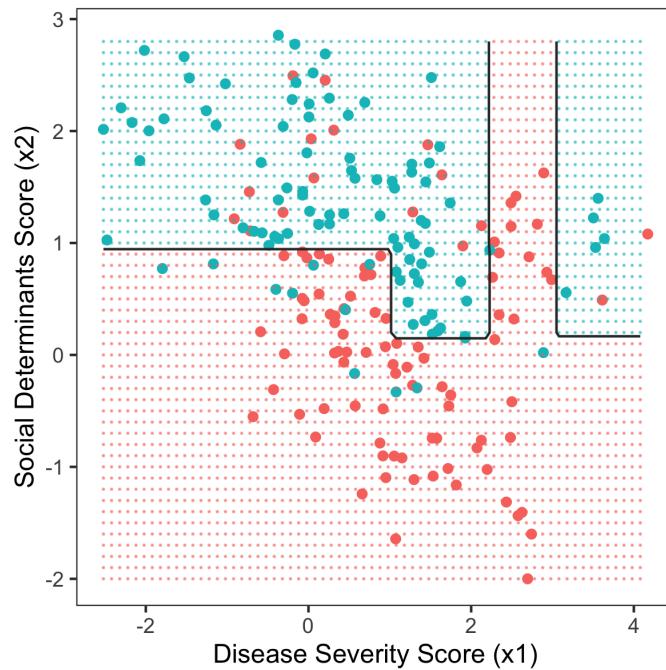


2.3.3 Decision Tree

Finally, we may choose to use our training data to build a decision tree, which will allow us to make predictions on new patients using a series of simple yes/no questions. There are different decision tree learning algorithms, but here is the tree produced by a famous one called CART:



And here is the decision boundary produced by this tree:



Question 2.1

How can you tell, just by looking at these images, which feature (x_1 or x_2) impacts the outcome the most? Which one is it?

Question 2.2

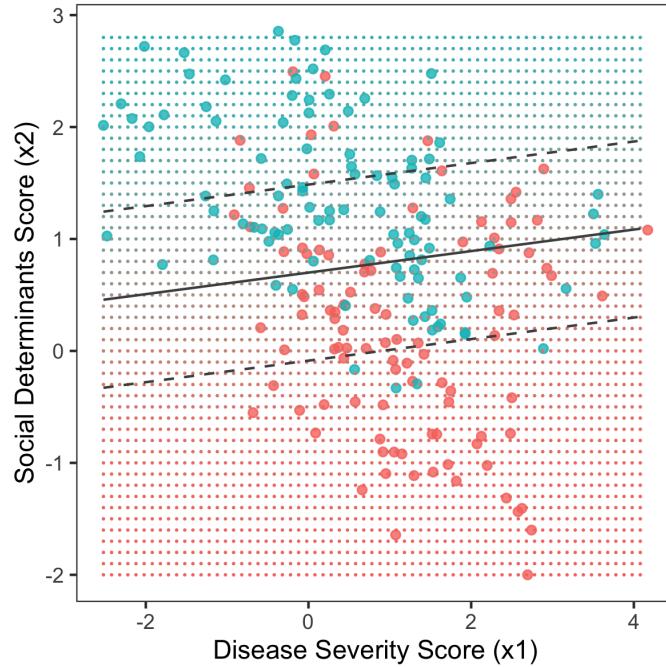
There are six rectangular regions in the picture of the decision tree decision boundary. Each corresponds to one of the six leaves of the tree. Identify all six and which leaves they correspond to on the decision tree.

2.4 Classification with Probabilities

We can think of classification as simply drawing a decision boundary, but underlying each algorithm is a quantitative assessment of each point in the feature space. Each algorithm is, in its own way, able to provide a degree of

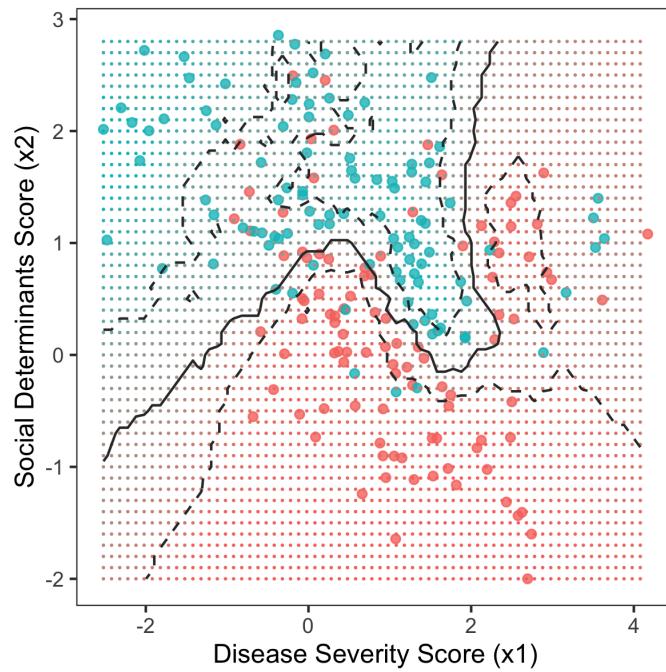
certainty, or **probability**², that a point belongs to the positive outcome class.

For example, here is the feature space of the example we just saw, colored by the probability, according to logistic regression, that a sample at each point should be classified as positive (i.e. the patient will be readmitted to the ER):

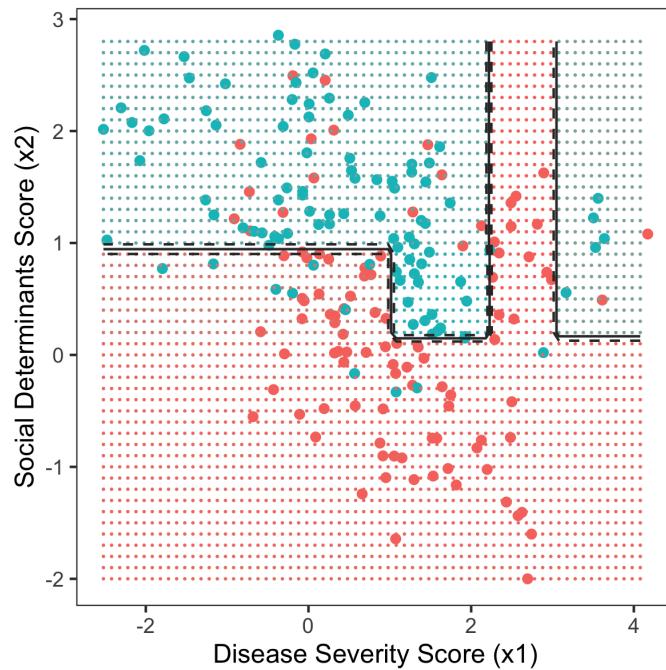


The solid line is the decision boundary, and the dashed lines indicate where the probability of a positive outcome (ER readmission) is 25% (top line) and 75% (bottom line). You can see that the color of the background gets purer red or purer blue the further you get from the decision boundary, but that near the decision boundary, the color is rather murky. That murkiness reflects the algorithm's uncertainty about the outcome. At the decision boundary, it is maximally uncertain. There the probability of a positive outcome is 50%: a coin toss. Here is a similar plot for KNN ($K = 15$):

²Pedantic footnote: this is a Bayesian definition of probability, as opposed to a frequentist definition. More on that later.



You can see that the shapes of the 25% and 75% probability lines have much more complex shapes than for logistic regression, but the story is the same: you have regions of pure blue or red, where the algorithm is certain, and you have a murky region near the decision boundary. Now, finally, here is the same plot for the decision tree:



The color of the background in the regions corresponding to the six leaves of the tree is the same throughout each region. That's because the probability in each rectangular region (corresponding to each leaf of the tree) is constant. It equals the number of red dots in that region divided by the total number of dots.

Question 2.3

What are the advantages and disadvantages of each algorithm?

1. Logistic regression?
2. KNN ($K = 15$)?
3. Decision tree?

Question 2.4

What makes a good classification algorithm? Consider issues of accuracy, generalizability, and speed (both to train the algorithm and to use it to make predictions on new samples).

Chapter 3

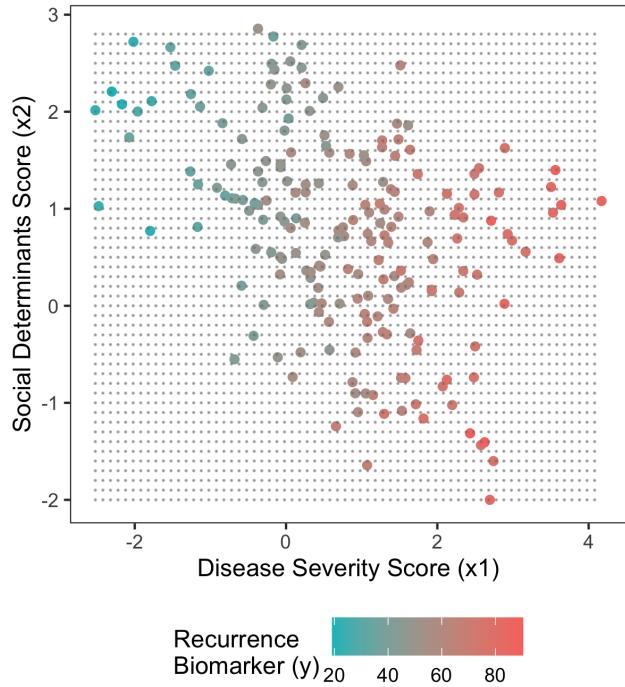
The Basics of Regression

Classification is a form of supervised learning in which the outcome is a category. **Regression** is another form of supervised learning in which the outcome is a numeric value. For example, it may be a lab value, physical characteristic (height, weight, etc.), or numeric measurement (e.g. oxygen saturation).

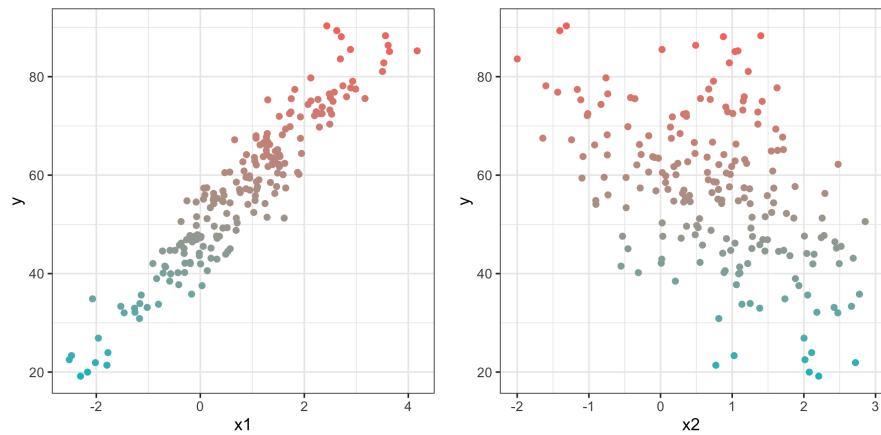
3.1 Visualizing the Regression Problem

Let's consider the same setup from Section 2.2 but this time with a quantitative outcome: a "recurrence biomarker" that indicates the likelihood of recurrence of disease.

Again, we have data on two predictors: a disease severity score (x_1), which characterizes the severity of the illness for which the patient was originally treated, and a social determinants score (x_2), which characterizes a patient's socioeconomic status. We have measurements of x_1 and x_2 on the same 200 patients as in Section 2.2.



This is a plot of the data in a single plane. The color represents the value of the recurrence biomarker – the height of the point above the plane. We want to design a model that will predict the value of the biomarker (y) based on the values of the two predictors, x_1 and x_2 . These plots show the **univariate** relationship of each predictor with the outcome.



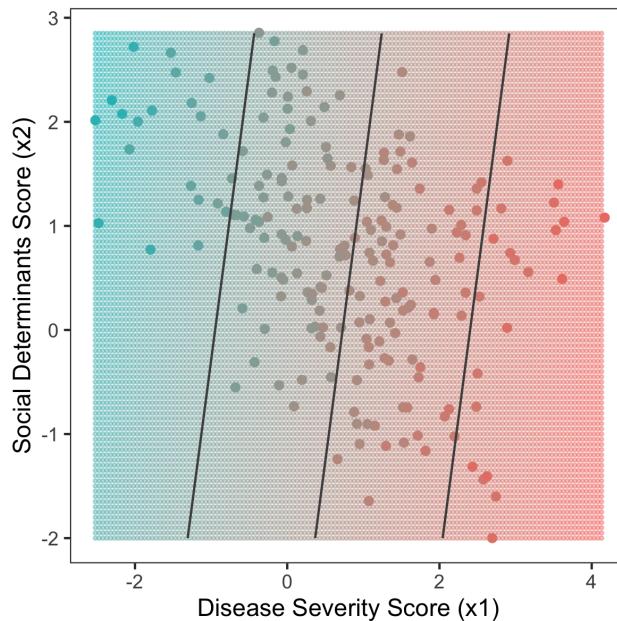
Question 3.1

Which of the two predictors, x_1 or x_2 , appears to more strongly influence the value of the recurrence biomarker? Explain your reasoning using evidence from the preceding three plots.

3.2 Three Regression Algorithms

3.2.1 Linear Regression

The regression analogue of logistic regression is **linear regression**¹. Linear regression creates a hyperplane that slices through the cloud of training data points such that it passes as close as possible, on average, to the data. This is, of course, easiest to see when the feature space is two-dimensional, as it is here:



¹The terminology here is confusing. When we learn about generalized linear models in Chapter 10, you'll see why logistic regression has the word "regression" in its name even though it's a classification algorithm.

The three lines shown here sit on the hyperplane learned by the linear regression model. They are located at heights corresponding to the 25th, 50th, and 75th percentiles of the outcome, y (the biomarker value). The plane tilts downward toward the upper left corner of the $x_1 \times x_2$ grid and upward toward the bottom right corner. It may be helpful to visualize grabbing the $x_1 \times x_2$ plane and rotating/translating it so that it passes through the middle of the training data. Here is a summary of the trained linear regression model:

```

Call:
lm(formula = y ~ x1 + x2, data = df)

Residuals:
    Min      1Q  Median      3Q     Max 
-11.9218 -3.1032  0.2891  2.8316 12.5813 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 49.8600    0.5370  92.844 < 2e-16 ***
x1          10.4372    0.2855  36.555 < 2e-16 ***
x2         -1.8824    0.3609  -5.215 4.63e-07 ***
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4.769 on 197 degrees of freedom
Multiple R-squared:  0.9026, Adjusted R-squared:  0.9016 
F-statistic: 912.4 on 2 and 197 DF,  p-value: < 2.2e-16

```

At each point (x_1, x_2) in the feature space, the model's predicted value of the recurrence biomarker, \hat{y} , is

$$\hat{y} = 49.8600 + 10.4372x_1 - 1.8824x_2$$

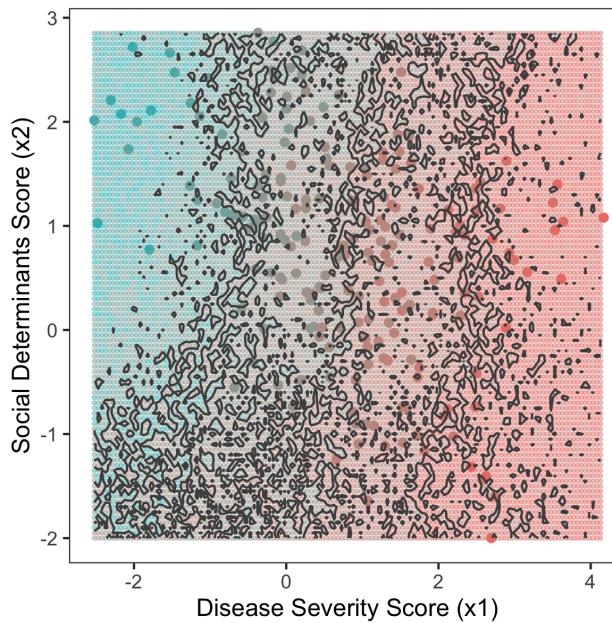
Question 3.2

Compare and contrast the output from the linear regression model with the output from the logistic regression model in Chapter 2. What looks the same? What looks different? What is being predicted in each case?

3.2.2 K Nearest Neighbors (KNN)

Regression using KNN works very similarly to KNN for classification. In classification, we allow the nearest K points to vote on the label of a new test

point. In regression, we **interpolate** between the values of the surrounding points to come up with the value of y for a test point. Typically this is done just by averaging the y values of the nearest K points, but you can also do something more sophisticated, like weight their contributions by distance to the test point. Here is a contour plot of the regression surface produced by KNN ($K = 15$) for our example:

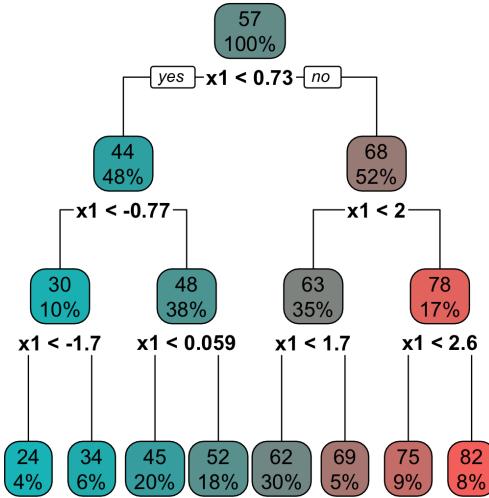


The contours are again drawn at the 25th, 50th, and 75th percentiles of the outcome, y . This looks like a bit of a mess compared to the linear regression plot, but at the same time, the KNN algorithm is able to capture arbitrarily complex relationships between x_1 , x_2 , and y that can be missed by other regression algorithms.

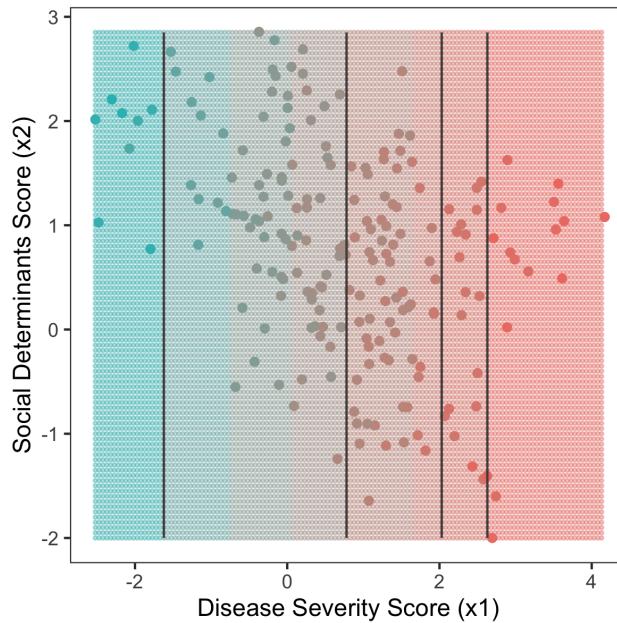
3.2.3 Decision Tree

Decision tree regression is similar to decision tree classification except that the output at each leaf is not a class label or the probability of membership in the positive training class (both of which are shown on the tree in Section 2.3.3),

but a numeric value. That value corresponds to the mean outcome value for the points in that leaf.



The predicted biomarker values for a decision tree trained on this dataset (created using the `rpart` package in R with default parameters) are shown here:



You can see that the decision tree always chooses to split on x_1 , the disease severity score, rather than x_2 . Revisit Question 3.1 to remind yourself of why this is. The regression surface produced by the decision tree looks like a set of stairs climbing higher and higher as one moves from left to right across the $x_1 \times x_2$ plane. The predicted value of y , the recurrence biomarker, is constant within each stair.

Question 3.3

Compare this decision tree with the decision tree for the classification problem in Chapter 2. What is the same? What is different?

Question 3.4

This **regression tree** has eight leaves. What region of the feature space does each leaf correspond to?

Question 3.5

What are the advantages and disadvantages of each of these three regression algorithms (linear regression, KNN, regression tree)?

Chapter 4

Probability Distributions

Many of the methods we will examine in these workshops depend on basic concepts from probability theory. For example, linear and logistic regression are members of a class of supervised learning algorithms called **generalized linear models** (see Chapter 10) which make assumptions about the type of probability distribution followed by the outcome variable. Decision trees use a concept called **entropy** (see Chapter 7), whose mathematical formulation depends on the probability distribution underlying the outcome. Many **hypothesis tests** (see Chapter 6) likewise rely on probabilistic assumptions about the data. Probability is everywhere.

The following sections review some key probability concepts – in an extremely hand-wavey and non-rigorous way – and the properties of some of the most common probability distributions you will encounter in machine learning and statistics.

4.1 Definitions

A **probability distribution** is just a mathematical function that provides the relative likelihoods of various possible outcomes of an observation. We call the quantity that is being observed a **random variable**. Probability distributions can be discrete or continuous. The random variable involved can be a number, a vector of numbers, a category/class, etc. The **sample space** is the set of all

possible outcomes. The integral (or sum) of the probability distribution over the entire sample space is 1.0. You will often hear probability distributions for continuous random variables referred to as **probability densities**.

Probability distributions are grouped into families that are characterized by their overall shapes. These families contain **parameters** that, when varied, produce different distributions. Specific probability distributions from within a single family can often look quite different.

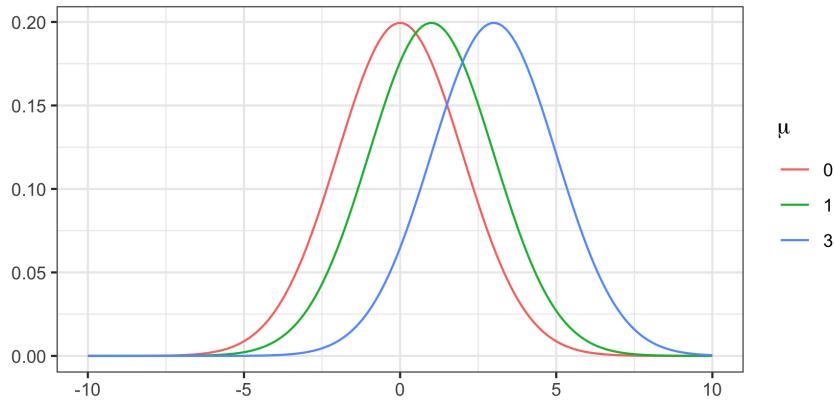
We use the notation $E[x|\theta]$ to refer to the **expected value**, or mean, of a distribution, given its parameter(s), θ . There can be more than one parameter, and it will not always be called θ ; this is just an example. We use the notation $\text{var}(x|\theta)$ to refer to the **variance**, or spread, of a distribution around its mean.

4.2 Normal Distribution

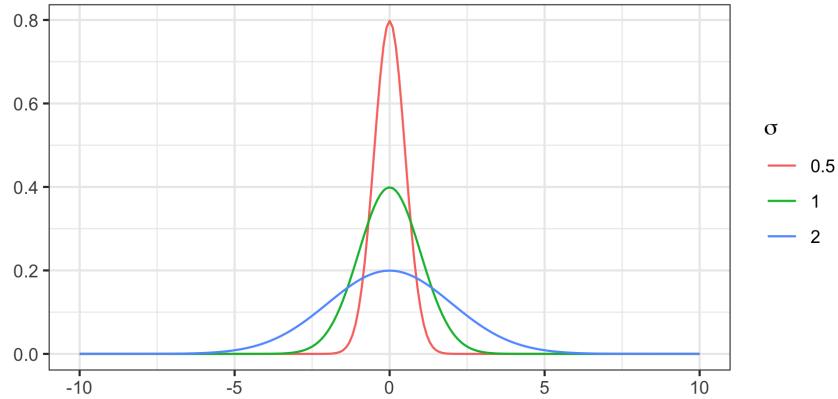
Also called the **Gaussian distribution**, the normal distribution is probably the most well-known continuous probability distribution. It has the following properties:

$$p(x|\mu, \sigma) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(x-\mu)^2}{2\sigma^2}} \quad E[x|\mu, \sigma] = \mu \quad \text{var}(x|\mu, \sigma) = \sigma^2$$

where $x \in \mathbb{R}$. We will abbreviate the normal distribution as $\mathcal{N}(\mu, \sigma)$. The value of μ changes the position of the center of the normal distribution.



The value of σ changes the width of the normal distribution.



Question 4.1

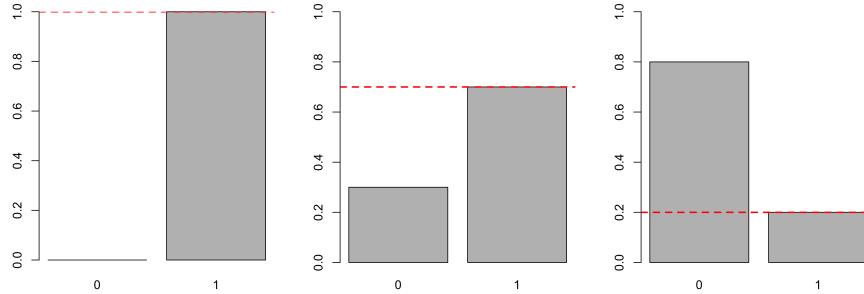
List 5 random variables from medicine or biology that should follow normal distributions.

4.3 Bernoulli Distribution

The **Bernoulli distribution** is a discrete probability distribution with the following properties:

$$p(x|\mu) = \mu^x(1-\mu)^{1-x} \quad E[x|\mu] = \mu \quad \text{var}(x|\mu) = \mu(1-\mu)$$

where $x \in \{0, 1\}$. It is used to model events where the outcome is yes/no. Think of it as a weighted coin, with μ the probability that the coin comes up “heads” on a single toss. Here are three Bernoulli distributions with (from left to right) $\mu = 1.0, 0.7, 0.2$. The number along the bottom is x , which can only be 0 or 1.



The **categorical distribution** is a generalization of the Bernoulli distribution to an outcome with more than two levels. The categorical distribution looks like this:

$$p(x|\phi_1, \dots, \phi_K) = \phi_1^{\mathbb{I}(x=1)} \phi_2^{\mathbb{I}(x=2)} \cdots \phi_K^{\mathbb{I}(x=K)}$$

where $\sum_{k=1}^K \phi_k = 1$. The term $\mathbb{I}(x=j)$ is an **indicator**. It equals 1 if $x = j$ and 0 otherwise. For example, $\mathbb{I}(x=2)$ is 1 if $x = 2$ and 0 otherwise.

Question 4.2

List 5 random variables from medicine or biology that should follow Bernoulli distributions.

4.4 Binomial Distribution

The **binomial distribution** models the number of positive outcomes, x , out of n independent¹ Bernoulli trials, each of which is positive with probability μ . This distribution has the following properties, with $x \in \{0, \dots, n\}$:

$$p(x|n, \mu) = \binom{n}{x} \mu^x (1 - \mu)^{n-x} \quad E[x|\mu] = n\mu \quad \text{var}(x|\mu) = n\mu(1 - \mu)$$

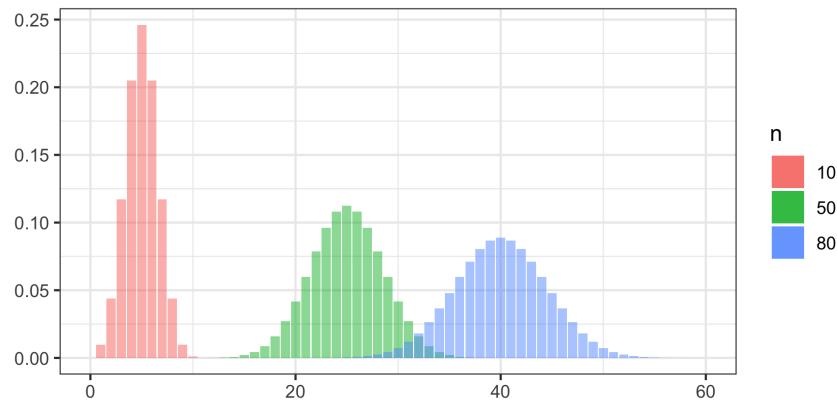
where the notation $\binom{n}{x}$ is defined as:

$$\binom{n}{x} = \frac{n!}{x!(n-x)!}.$$

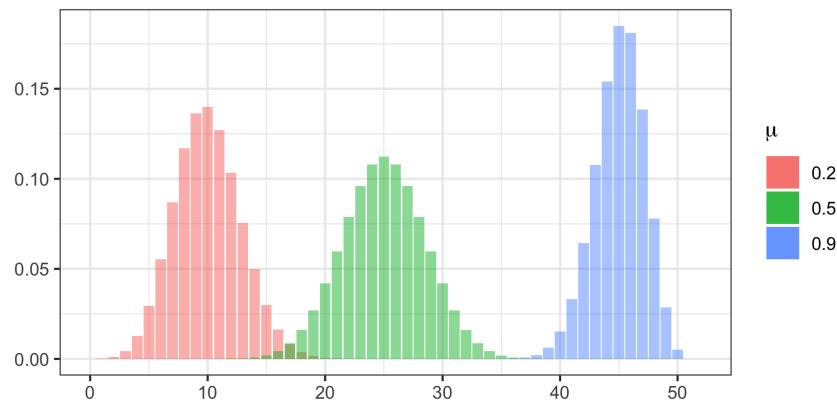
¹The word **independent** just means that the outcome of one trial does not influence the outcome of any other trial.

This notation denotes the number of ways it is possible to choose x things out of a group of n things, where the ordering doesn't matter. The exclamation point denotes the **factorial function**: $x! = x(x - 1)(x - 2) \cdots (2)(1)$.

The shape of the binomial distribution is governed by the values of n and μ . Here, we vary n but keep μ constant at 0.5:



And here we vary μ but keep n constant at 50:



Question 4.3

List 5 random variables from medicine or biology that should follow binomial distributions.

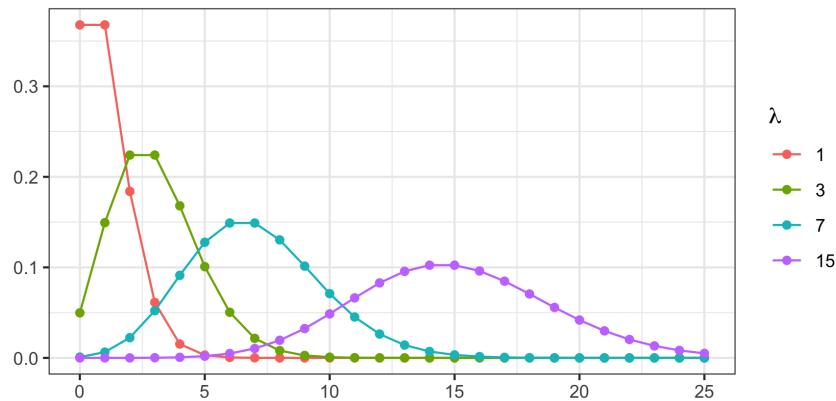
4.5 Poisson Distribution

The **Poisson distribution** is a probability distribution that is often used to model discrete quantitative data, such as counts. It has the following properties:

$$p(x|\lambda) = \frac{e^{-\lambda} \lambda^x}{x!} \quad E[x|\lambda] = \lambda \quad \text{var}(x|\lambda) = \lambda$$

where $x \in \{0, 1, 2, \dots\}$. Below are four examples of Poisson distributions. If events of a particular type occur continuously and independently at a constant rate (**Poisson process**), the number of events within a time window of fixed width will be distributed according to the Poisson distribution, with rate parameter λ proportional to the width of the window.

Situations where the population size, n , is large, the probability of an individual event, p , is small, but the expected number of events, np , is moderate (say five or more) can generally be modeled using a Poisson distribution with $\lambda = np$.



Question 4.4

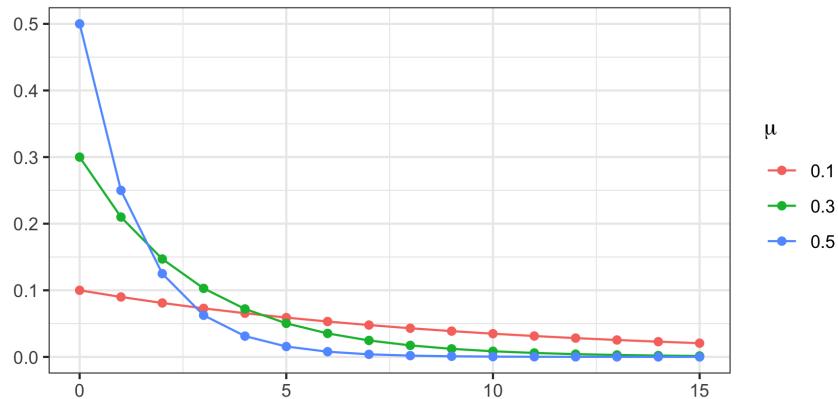
List 5 random variables from medicine or biology that should follow Poisson distributions.

4.6 Geometric

The **geometric distribution** models the number of failures in a sequence of Bernoulli trials before the first success. It has the following properties:

$$p(x|\mu) = (1 - \mu)^x \mu \quad E[x|\mu] = \frac{1 - \mu}{\mu} \quad \text{var}(x|\mu) = \frac{1 - \mu}{\mu^2}$$

for $x \in \{0, 1, 2, \dots\}$, where μ refers to the probability (in the Bernoulli trial) that the trial is a success. Some examples of geometric distributions with different μ are shown below:



Question 4.5

List 5 random variables from medicine or biology that should follow geometric distributions.

4.7 Exponential

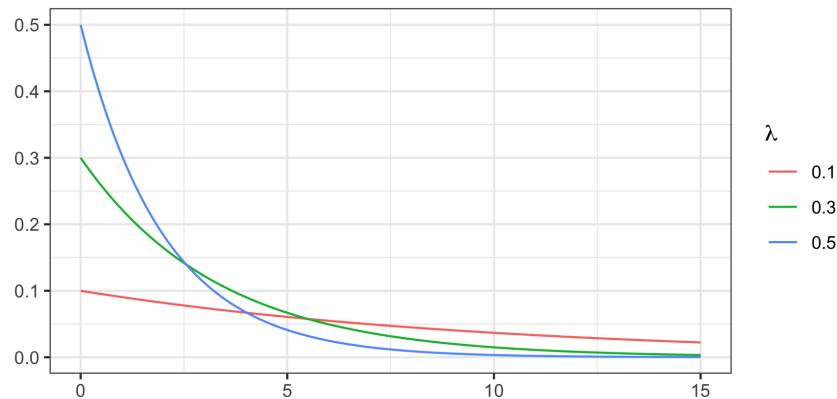
The **exponential distribution** is a continuous probability distribution that models waiting times between events that happen independently and continuously at a constant rate (Poisson process), as well as many other random

variables². It has the following properties:

$$p(x|\lambda) = \lambda e^{-\lambda x} \quad E[x|\lambda] = \frac{1}{\lambda} \quad \text{var}(x|\lambda) = \frac{1}{\lambda^2}$$

where $x \in \mathbb{R}^+$ (x is a positive real number, or zero). The exponential distribution is the continuous analogue of the geometric distribution. It is memoryless, which means that the distribution of a waiting time until an event does not depend on how much time has elapsed already.

Here are some different exponential distributions. Compare them to the geometric distribution, above.



Question 4.6

List 5 random variables from medicine or biology that should follow exponential distributions.

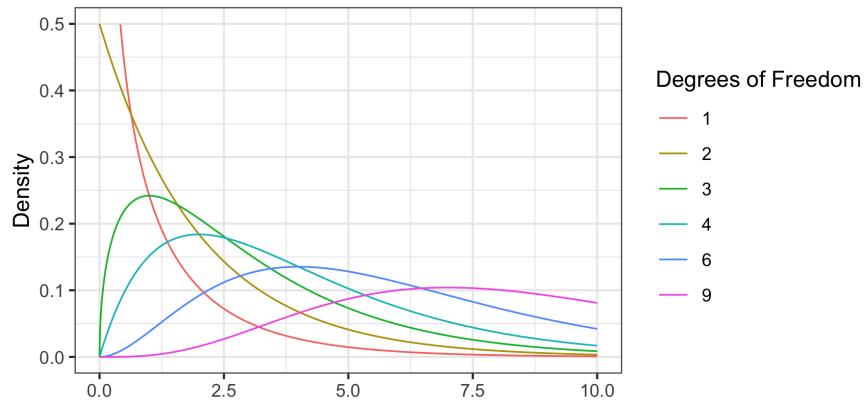
4.8 Chi-Squared Distribution

How this distribution arises:

²For example, in an epidemiologic model of an infectious process like COVID-19 community spread, exponential waiting times are often used to model transitions between the susceptible, exposed, infectious, and recovered compartments in the model.

1. If $Z \sim \mathcal{N}(0, 1)$, the distribution of $U = Z^2$ is called the chi-squared distribution with one degree of freedom.
2. If U_1, U_2, \dots, U_k are independent χ_1^2 random variables, their sum, $V = \sum_{i=1}^k U_i$ follows χ_k^2 , a chi-squared distribution with k degrees of freedom.

You'll often see the chi-squared distribution used as the sampling distribution for the sample variance in a variety of statistical hypothesis tests. It looks like this:



The parameter k , the **degrees of freedom**, controls the shape of the chi-squared distribution. The actual formula for the chi-squared distribution looks a bit intimidating, but I'm including it here so you can compare it to the other distributions we've seen:

$$p(x|k) = \frac{1}{2^{k/2}\Gamma(k/2)} x^{k/2-1} e^{-x/2}$$

$$E[x|k] = k \quad \text{var}(x|k) = 2k$$

The gamma function shown in the denominator of the probability density,

$$\Gamma(z) = \int_0^\infty x^{z-1} e^{-x} dx,$$

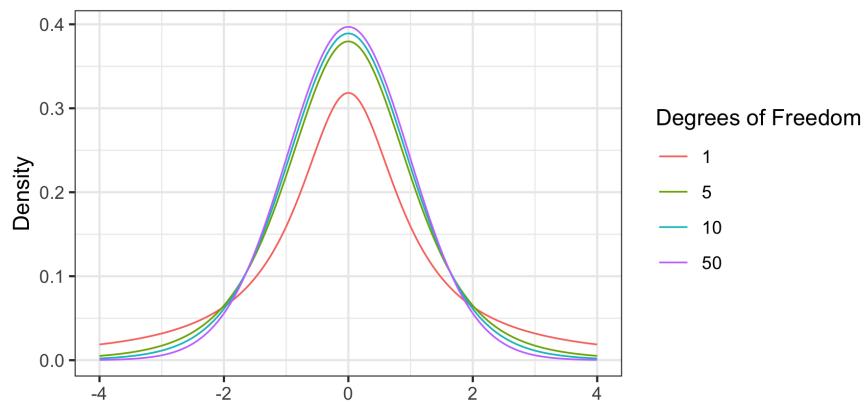
is a generalization of the factorial function to complex numbers. For any positive integer n , $\Gamma(n) = (n-1)!$.

4.9 Student's T Distribution

If $Z \sim \mathcal{N}(0, 1)$ and $U \sim \chi_k^2$ and Z and U are independent,

$$T = \frac{Z}{\sqrt{U/k}} \sim t_k$$

or in words, the statistic T follows a t -distribution with k degrees of freedom. The T distribution plays an important role in a family of statistical hypothesis tests called T-tests.



Again, the functional form of the T distribution is a bit intimidating, but I'm including it for completeness:

$$p(x|k) = \frac{\Gamma\left(\frac{k+1}{2}\right)}{\sqrt{k\pi} \Gamma\left(\frac{k}{2}\right)} \left(1 + \frac{x^2}{k}\right)^{-\frac{k+1}{2}}$$

$$E[x|k] = 0 \text{ for } k > 1; \text{ otherwise undefined}$$

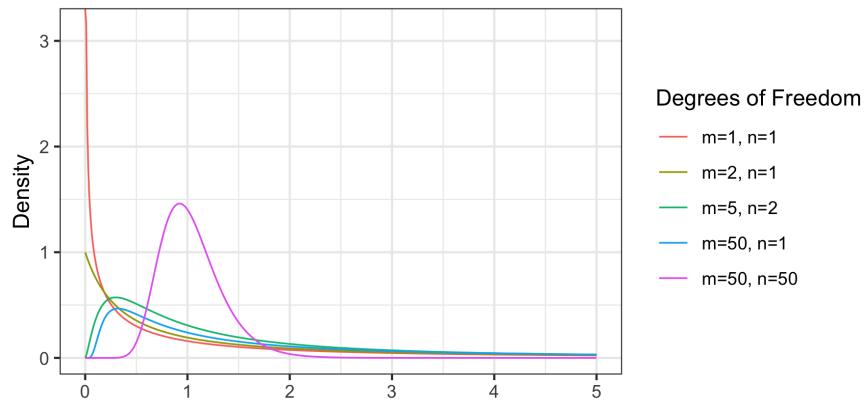
$$\text{var}(x|k) = \begin{cases} \frac{k}{k-2} & k > 2 \\ \infty & 1 < k \leq 2 \\ \text{undefined} & \text{otherwise} \end{cases}$$

4.10 F Distribution

If U and V are independent χ^2 random variables with m and n degrees of freedom,

$$W = \frac{U/m}{V/n} \sim F_{m,n}$$

or in words, the statistic W follows an F distribution with m and n degrees of freedom. I'm not writing out the functional form of the F distribution here because it's too awful-looking, but graphically it looks like this:



Note that if $T \sim t_k$, then $T^2 \sim F_{1,k}$. The F -distribution plays an important role in a class of statistical analysis techniques called **ANalysis Of VAriance**, or **ANOVA**.

Question 4.7

For each of the following experimental conditions, which distribution (from those listed above) provides the best model for how the data $x^{(1)}, \dots, x^{(n)}$ are generated?

- (a) You are observing several patients' skin in a clinical study to see how long it takes them to develop a rash. You take a picture each day. Let $x^{(i)}$ be the number of days of *no rash* before the rash occurs.

| Patient ID (i) | $x^{(i)}$ |
|--------------------|-----------|
| 1 | 4 |
| 2 | 1 |
| 3 | 0 |
| 4 | 2 |
| 5 | 2 |
| 6 | 4 |
| 7 | 3 |
| 8 | 1 |
| 9 | 0 |
| 10 | 1 |

- (b) Same situation as above except that instead of taking a picture each day, the patient texts you at the moment he/she observes a rash. The data look like this, where $x^{(i)}$ is the time (in days) at which patient i develops a rash:

| Patient ID (i) | $x^{(i)}$ |
|--------------------|-----------|
| 1 | 2.25 |
| 2 | 3.43 |
| 3 | 0.68 |
| 4 | 0.04 |
| 5 | 3.78 |
| 6 | 5.65 |
| 7 | 2.88 |
| 8 | 3.88 |
| 9 | 2.83 |
| 10 | 1.87 |

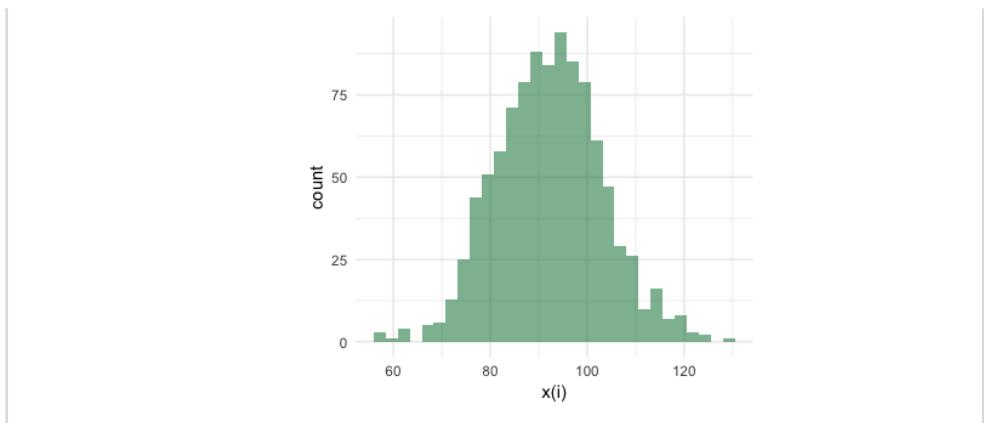
- (c) Imagine you are Ladislaus Bortkiewicz, and you are modeling the number of persons killed by mule or horse kicks in the Prussian army per year. You have data from the late 1800s over the course of 20 years. Let $x^{(i)}$ be the number of people killed in year i .

| Year (i) | $x^{(i)}$ | Year (i) | $x^{(i)}$ |
|--------------|-----------|--------------|-----------|
| 1 | 8 | 11 | 9 |
| 2 | 10 | 12 | 7 |
| 3 | 5 | 13 | 10 |
| 4 | 3 | 14 | 12 |
| 5 | 10 | 15 | 8 |
| 6 | 8 | 16 | 7 |
| 7 | 7 | 17 | 8 |
| 8 | 2 | 18 | 8 |
| 9 | 6 | 19 | 10 |
| 10 | 11 | 20 | 7 |

- (d) Every year, 10 scientists go to the same geographic area (same Lyme prevalence) and they each collect 40 ticks. They test each tick for Lyme disease and record the number of ticks that have Lyme. Let $x^{(i)}$ be the number of ticks with Lyme in the i th scientist's bunch.

| Scientist ID (i) | $x^{(i)}$ |
|----------------------|-----------|
| 1 | 8 |
| 2 | 9 |
| 3 | 14 |
| 4 | 15 |
| 5 | 12 |
| 6 | 7 |
| 7 | 6 |
| 8 | 8 |
| 9 | 8 |
| 10 | 14 |

- (e) You have waist circumference data on 1045 men aged 70 and above (see Dey's 2002 paper in the Journal of the American Geriatric Society). It looks like this:



Chapter 5

The Basics of Maximum Likelihood Estimation

Beneath our discussions of classification, regression, and probability distributions in Chapters 2, 3, and 4 lies the tricky problem of **model fitting**. We've seen what classification and regression models look like, but we still haven't addressed how to fit these models using training data.

Linear and logistic regression models are fit using a technique called **maximum likelihood (ML) estimation**, in which the model parameters are adjusted to maximize the joint probability of the observed data, or likelihood, given the model.

For example, consider the five different datasets from Question 4.7. In each case, you have some data and an assumption about which probability distribution the data are drawn from. The job of maximum likelihood estimation is to use the data to identify the correct distributional parameters, such as μ and σ (in the case of the normal distribution) or λ (in the case of the Poisson distribution). This process is a type of **statistical inference**.

5.1 The Likelihood and Log-Likelihood

Let $p(x|\theta)$ be the probability distribution that governs our data. Here, θ stands in for all of the parameters we want to fit.

If we draw independent¹ samples from $p(x|\theta)$, the **joint probability density function** for all n observations is:

$$p(x^{(1)}, x^{(2)}, \dots, x^{(n)}|\theta) = \prod_{i=1}^n p(x^{(i)}|\theta).$$

Since the data are known but the parameter(s) θ are unknown, we will view this quantity as a function of θ . This is just a change in notation:

$$\mathcal{L}(\theta) = \prod_{i=1}^n p(x^{(i)}|\theta).$$

The higher the joint probability of the data (the more “likely” the data are) given θ , the higher the value of this function. We call $\mathcal{L}(\theta)$ the **likelihood**². Frequently we will want to work with the logarithm of the likelihood, which we call the **log-likelihood**, because it has some nice properties, including allowing us to manipulate sums instead of products³:

$$\log \mathcal{L}(\theta) = \sum_{i=1}^n \log p(x^{(i)}|\theta).$$

In maximum likelihood estimation, we seek to find the θ for which the likelihood (or log-likelihood) is maximized. We do this by taking derivatives

¹Independent sampling just means that the values of different samples do not depend on each other. When the samples are drawn independently from the same distribution, their joint probability density is just the product of the individual probability densities (which are all the same).

²The distributions we have discussed so far are from a broad family of probability distributions called the **exponential family**. One of the properties of this family is that the log-likelihood is concave. Practically speaking, this means that if we maximize the log-likelihood by setting derivatives equal to zero, we are guaranteed to (a) get only one solution, and (b) find a maximum (not a minimum or an inflection point).

³Note that if the function $f(z)$ has a maximum at z' , the function $\log f(z)$ will also have a maximum at z' , because the logarithmic function is monotonically increasing. So we will get the same parameter estimate(s) either way.

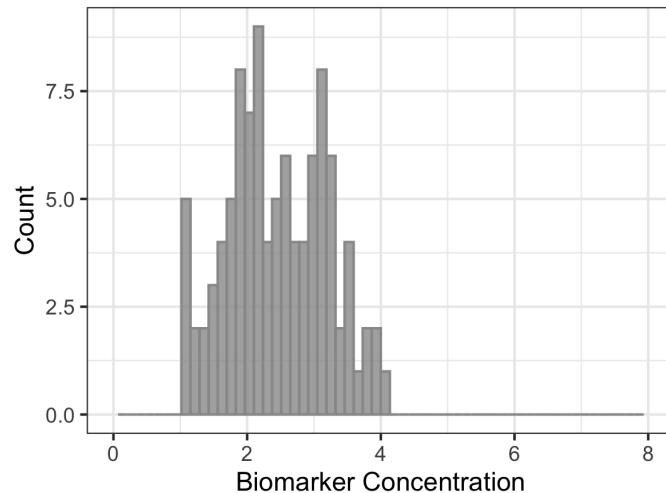
of the log-likelihood with respect to the various parameters and setting them equal to zero. The best-fit parameter estimates obtained in this way are called the **maximum likelihood estimates (MLEs)**.

Question 5.1

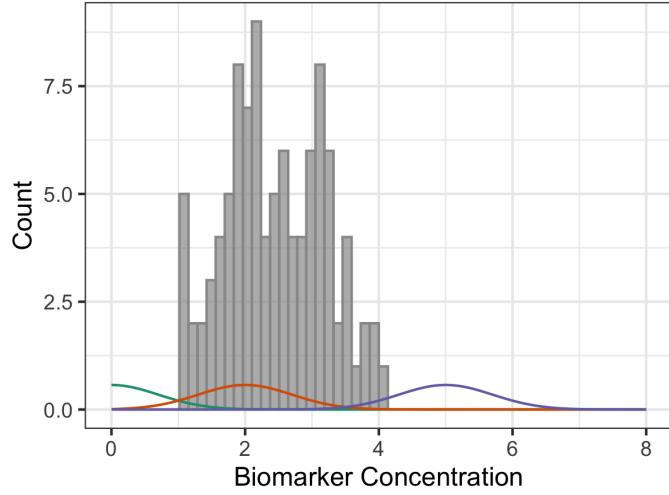
What are some reasons why we might want to fit data to a probability distribution?

5.2 Example: Fitting Data to a Normal Distribution

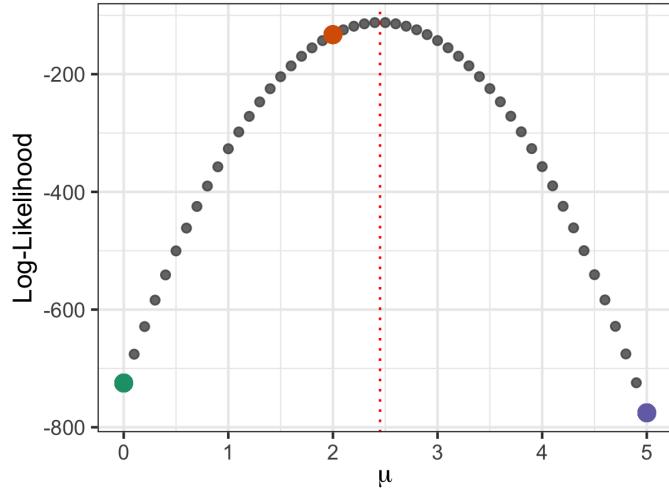
Imagine you have some data from a lab test that measures the concentration of a particular biomarker. You have data from 100 different subjects. A histogram of the raw data looks like this:



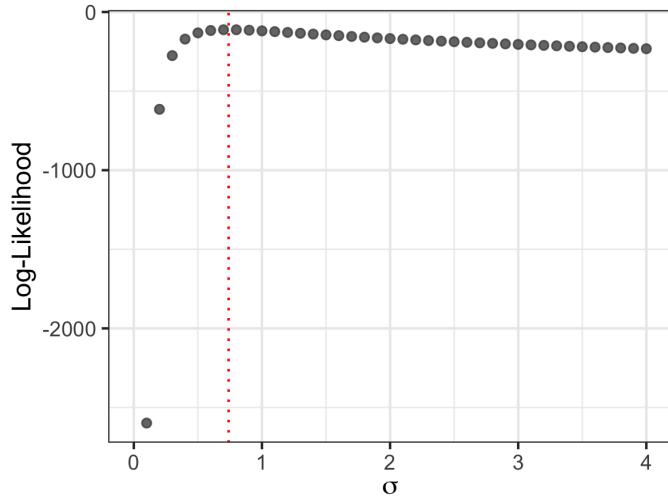
You want to find the normal distribution that best describes these data so you can create a reference distribution for this lab test. To do this, think about trying out several distributions with different values of μ and σ and choosing the one that maximizes the log-likelihood. For example, here are three different normal distributions with different values of μ and $\sigma = 0.7$:



Here is what happens to the log-likelihood as you vary μ . The log-likelihoods of the three distributions shown in the plot above are shown as dots with their corresponding colors, and the maximum likelihood estimate is shown as a vertical dotted line.



Now, here's what happens to the log-likelihood when we vary σ , keeping μ fixed at its maximum likelihood estimate from the graph above. Again, the maximum likelihood estimate is shown as a vertical dotted line.



For the record, I simulated these data from a normal distribution with $\mu = 2.5$ and $\sigma = 0.75$. The maximum likelihood estimates obtained from this dataset are $\hat{\mu} = 2.45$ and $\hat{\sigma} = 0.74$.

5.3 Analytical Calculations of MLEs

In some simple cases, the MLEs can be calculated analytically. We will now go through a bunch of examples of how to find the MLEs of the probability distributions we saw in Chapter 4.

5.3.1 Bernoulli Distribution

The Bernoulli distribution is described in Section 4.3. Our goal is to find the parameter, μ , of this distribution, given some observed data, $x^{(1)}, \dots, x^{(n)}$. The data will consist of a list of 1s and 0s, since Bernoulli random variables can only take the values 0 or 1.

To find $\hat{\mu}$, our MLE for μ , we first write down the log-likelihood:

$$\begin{aligned}\log \mathcal{L}(\mu) &= \sum_{i=1}^n \log p(x^{(i)} | \mu) \\ &= \sum_{i=1}^n \log \left(\mu^{x^{(i)}} (1-\mu)^{1-x^{(i)}} \right) \\ &= \sum_{i=1}^n \left[x^{(i)} \log(\mu) + (1-x^{(i)}) \log(1-\mu) \right]\end{aligned}$$

Then we take the derivative of the log-likelihood with respect to μ :

$$\frac{d}{d\mu} \log \mathcal{L}(\mu) = \sum_{i=1}^n \left[\frac{x^{(i)}}{\mu} - \frac{1-x^{(i)}}{1-\mu} \right]$$

The MLE of μ will occur when the likelihood is maximized, which happens when the first derivative equals zero. So to solve for $\hat{\mu}$, we set the derivative equal to zero and rearrange:

$$\begin{aligned}\sum_{i=1}^n \left[\frac{x^{(i)}}{\hat{\mu}} - \frac{1-x^{(i)}}{1-\hat{\mu}} \right] = 0 &\implies (1-\hat{\mu}) \sum_{i=1}^n x^{(i)} = \hat{\mu} \sum_{i=1}^n (1-x^{(i)}) \\ &\implies \boxed{\hat{\mu} = \frac{1}{n} \sum_{i=1}^n x^{(i)}}\end{aligned}$$

We see that the MLE, $\hat{\mu}$, is simply the sum of our data – i.e. the number of data points where the outcome is 1 – divided by the total number of observations.

This makes sense: if you want to know the probability that a coin will come up heads, a good way to estimate it is to flip the coin a bunch of times and calculate the fraction of observations in which the coin comes up heads.

5.3.2 Binomial Distribution

The binomial distribution is described in Section 4.4. We will make one notational change from that section, which is to call the number of Bernoulli trials m instead of n , since we are using n to refer to the number of data samples. To keep things simple, we will assume that m is a known quantity.

As before, we first write down the log-likelihood:

$$\begin{aligned}
\log \mathcal{L}(\mu) &= \sum_{i=1}^n \log p(x^{(i)} | m, \mu) \\
&= \sum_{i=1}^n \log \left[\binom{m}{x} \mu^x (1-\mu)^{m-x} \right] \\
&= \sum_{i=1}^n \left[\log(m!) - \log(x!) - \log((m-x)!) + x^{(i)} \log(\mu) + (m-x^{(i)}) \log(1-\mu) \right]
\end{aligned}$$

Then we take the derivative of the log-likelihood with respect to μ :

$$\frac{d}{d\mu} \log \mathcal{L}(\mu) = \sum_{i=1}^n \left[\frac{x^{(i)}}{\mu} - \frac{m-x^{(i)}}{1-\mu} \right]$$

We set this equal to zero and solve for $\hat{\mu}$ (the maximum likelihood estimate of μ):

$$\begin{aligned}
\sum_{i=1}^n \left[\frac{x^{(i)}}{\hat{\mu}} - \frac{m-x^{(i)}}{1-\hat{\mu}} \right] = 0 \implies (1-\hat{\mu}) \sum_{i=1}^n x^{(i)} = \hat{\mu} \sum_{i=1}^n (m-x^{(i)}) \\
\implies \boxed{\hat{\mu} = \frac{1}{nm} \sum_{i=1}^n x^{(i)}}
\end{aligned}$$

Question 5.2

Interpret the MLE for the parameter, μ , of a binomial distribution, assuming fixed m (number of trials). Does the MLE for μ make intuitive sense to you? Think through a few of your examples from Question 4.3.

5.3.3 Normal Distribution

The normal distribution is described in Section 4.2. We will follow the same procedure as in the previous two sections, except that now we have two parameters to solve for, μ and σ , instead of one. First, we write down the

log-likelihood:

$$\begin{aligned}
\log \mathcal{L}(\mu, \sigma) &= \sum_{i=1}^n \log p(x^{(i)} | \mu, \sigma) \\
&= \sum_{i=1}^n \log \left(\frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(x^{(i)} - \mu)^2}{2\sigma^2}} \right) \\
&= -\frac{n}{2} \log(2\pi) - \frac{n}{2} \log \sigma^2 - \frac{1}{2\sigma^2} \sum_{i=1}^n (x^{(i)} - \mu)^2
\end{aligned}$$

To find the MLE for μ , we take the derivative of the log-likelihood with respect to μ :

$$\frac{\partial}{\partial \mu} \log \mathcal{L}(\mu, \sigma) = \frac{1}{\sigma^2} \sum_{i=1}^n (x^{(i)} - \mu)$$

We set this equal to zero and solve for $\hat{\mu}$ (the maximum likelihood estimate of μ):

$$\frac{1}{\sigma^2} \sum_{i=1}^n (x^{(i)} - \mu) = 0 \implies \boxed{\hat{\mu} = \frac{1}{n} \sum_{i=1}^n x^{(i)}}$$

To find the MLE for σ , we then take the derivative of the log-likelihood with respect to σ :

$$\frac{\partial}{\partial \sigma} \log \mathcal{L}(\mu, \sigma) = -\frac{n}{\sigma} + \frac{1}{\sigma^3} \sum_{i=1}^n (x^{(i)} - \mu)^2$$

We set this equal to zero and solve for $\hat{\sigma}$ (the maximum likelihood estimate of σ)⁴. Note that the answer depends on our previously calculated MLE for μ :

$$-\frac{n}{\hat{\sigma}} + \frac{1}{\hat{\sigma}^3} \sum_{i=1}^n (x^{(i)} - \mu)^2 = 0 \implies \boxed{\hat{\sigma} = \sqrt{\frac{1}{n} \sum_{i=1}^n (x^{(i)} - \hat{\mu})^2}}$$

⁴One detail: it turns out this estimate is biased because it depends on the MLE for μ . An unbiased version has $n - 1$ in the denominator instead of n . The effect of this is minimal unless n is small.

Question 5.3

Interpret the MLEs for the parameters, μ and σ , of a normal distribution. Do these results make intuitive sense to you? Think through a few of your examples from Question 4.1.

5.3.4 Poisson Distribution

The Poisson distribution is described in Section 4.5. To find the MLE for λ , its mean, we first (as usual) write down the log-likelihood:

$$\begin{aligned}\log \mathcal{L}(\lambda) &= \sum_{i=1}^n \log p(x^{(i)} | \lambda) \\ &= \sum_{i=1}^n \log \left(\frac{e^{-\lambda} \lambda^{x^{(i)}}}{x^{(i)}!} \right) \\ &= \sum_{i=1}^n \left[-\lambda + x^{(i)} \log(\lambda) - \log(x^{(i)}!) \right]\end{aligned}$$

Now we take the derivative of the log-likelihood with respect to λ :

$$\frac{d}{d\lambda} \log \mathcal{L}(\lambda) = \sum_{i=1}^n \left[-1 + \frac{x^{(i)}}{\lambda} \right]$$

We set this equal to zero and solve for $\hat{\lambda}$ (the maximum likelihood estimate of λ):

$$\sum_{i=1}^n \left[-1 + \frac{x^{(i)}}{\hat{\lambda}} \right] = 0 \implies \boxed{\hat{\lambda} = \frac{1}{n} \sum_{i=1}^n x^{(i)}}$$

Question 5.4

Interpret the MLE for the parameter, λ , of a Poisson distribution. Does this result make intuitive sense to you? Think through a few of your examples from Question 4.4.

5.3.5 Geometric Distribution

The geometric distribution is described in Section 4.6. To find the MLE for μ , we first write down the log-likelihood:

$$\begin{aligned}\log \mathcal{L}(\mu) &= \sum_{i=1}^n \log p(x^{(i)} | \mu) \\ &= \sum_{i=1}^n \log \left((1 - \mu)^{x^{(i)}} \mu \right) \\ &= \sum_{i=1}^n \left[x^{(i)} \log(1 - \mu) + \log(\mu) \right]\end{aligned}$$

Now we take the derivative of the log-likelihood with respect to μ :

$$\frac{d}{d\mu} \log \mathcal{L}(\mu) = \sum_{i=1}^n \left[-\frac{x^{(i)}}{1 - \mu} + \frac{1}{\mu} \right]$$

We set this equal to zero and solve for $\hat{\mu}$ (the maximum likelihood estimate of μ):

$$\begin{aligned}\sum_{i=1}^n \left[-\frac{x^{(i)}}{1 - \hat{\mu}} + \frac{1}{\hat{\mu}} \right] &= 0 \implies \frac{n}{\hat{\mu}} = \frac{1}{1 - \hat{\mu}} \sum_{i=1}^n x^{(i)} \\ &\implies \boxed{\hat{\mu} = \frac{n}{\sum_{i=1}^n (x^{(i)} + 1)}}\end{aligned}$$

Question 5.5

Interpret the MLE for the parameter, μ , of a geometric distribution. Does this result make intuitive sense to you? Think through a few of your examples from Question 4.5.

5.3.6 Exponential Distribution

The exponential distribution is described in Section 4.7. To find the MLE for λ , we first write down the log-likelihood:

$$\begin{aligned}\log \mathcal{L}(\lambda) &= \sum_{i=1}^n \log p(x^{(i)}|\lambda) \\ &= \sum_{i=1}^n \log (\lambda e^{-\lambda x^{(i)}}) \\ &= \sum_{i=1}^n [\log(\lambda) - \lambda x^{(i)}]\end{aligned}$$

Now we take the derivative of the log-likelihood with respect to λ :

$$\frac{d}{d\lambda} \log \mathcal{L}(\lambda) = \sum_{i=1}^n \left[\frac{1}{\lambda} - x^{(i)} \right]$$

We set this equal to zero and solve for $\hat{\lambda}$ (the maximum likelihood estimate of λ):

$$\sum_{i=1}^n \left[\frac{1}{\hat{\lambda}} - x^{(i)} \right] = 0 \implies \boxed{\hat{\lambda} = \frac{n}{\sum_{i=1}^n x^{(i)}}}$$

Question 5.6

Interpret the MLE for the parameter, λ , of an exponential distribution. Does this result make intuitive sense to you? Think through a few of your examples from Question 4.6.

5.4 Summary of MLEs for Common Distributions

The table below contains a summary of the MLEs of various parameters from some common probability distributions.

| Distribution | Parameter | ML Estimate | Domain of $x^{(i)}$ |
|-----------------------|-----------|---|----------------------|
| Univariate Normal | μ | $\frac{1}{n} \sum_{i=1}^n x^{(i)}$ | \mathbb{R} |
| | σ | $\frac{1}{n} \sum_{i=1}^n (x^{(i)} - \hat{\mu})^2$ | \mathbb{R} |
| Multivariate Normal | μ | $\frac{1}{n} \sum_{i=1}^n x^{(i)}$ | \mathbb{R}^m |
| | Σ | $\frac{1}{n} \sum_{i=1}^n (x^{(i)} - \hat{\mu})(x^{(i)} - \hat{\mu})^T$ | \mathbb{R}^m |
| Bernoulli | μ | $\frac{1}{n} \sum_{i=1}^n x^{(i)}$ | $\{0, 1\}$ |
| Binomial (fixed m) | μ | $\frac{1}{nm} \sum_{i=1}^n x^{(i)}$ | $\{0, 1, \dots, m\}$ |
| Poisson | λ | $\frac{1}{n} \sum_{i=1}^n x^{(i)}$ | $\{0, 1, \dots\}$ |
| Geometric | μ | $\frac{n}{\sum_{i=1}^n (x^{(i)} + 1)}$ | $\{0, 1, \dots\}$ |
| Exponential | λ | $\frac{n}{\sum_{i=1}^n x^{(i)}}$ | \mathbb{R}^+ |

Question 5.7

In Question 4.7, we examined several examples of experimental conditions and datasets and discussed which probability distribution best modeled each one. Using the formulas above and the actual datasets from Question 4.7, calculate the MLEs for the parameter(s) of your chosen probability distributions.

Chapter 6

Introduction to Hypothesis Testing

Hypothesis testing is a central idea underpinning much of the analysis in the clinical and biomedical research literature¹. There are multiple approaches to hypothesis testing, but the most common is **null hypothesis testing**, which was developed by the statistician R.A. Fisher. In null hypothesis testing, one creates a model of how the data should look under default conditions and then quantifies the observed data's deviation from that model using a **test statistic**. If the test statistic is large enough, it means there is evidence that the default position is incorrect.

The statisticians Jerzy Neyman and Karl Pearson developed a different approach to hypothesis testing based on the idea of **model comparison**. In their approach, one sets up different models and then quantifies each model's fit to the data; the hypothesis test is used to see whether one model's fit to the data is significantly better than another's. We see the Neyman-Pearson philosophy reflected in techniques such as power calculations and likelihood ratio tests.

Most of the basic hypothesis tests we learn in introductory biostatistics courses (T-tests, chi-squared tests, etc.) follow Fisher's approach. We will

¹I should state that there is still a lot of controversy around the whole idea of hypothesis testing and whether *p*-values should be used at all, etc.

focus on null hypothesis testing in this chapter and explore other ideas in subsequent chapters.

6.1 Basic Steps of a Hypothesis Test

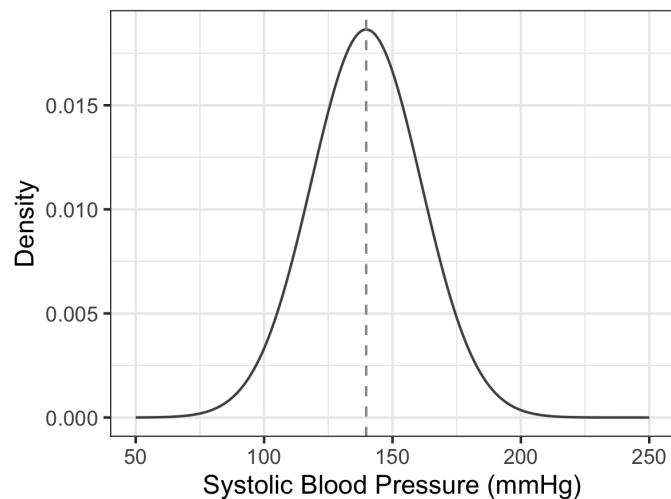
1. *State the null hypothesis.* The null hypothesis corresponds to the default, or baseline, position; for our example, the null hypothesis might be, “The events ‘has mutation’ and ‘has cancer’ are statistically independent.” The **alternative hypothesis** is the hypothesis that is contrary to the null; for our example, it might be, “The events ‘has mutation’ and ‘has cancer’ are not statistically independent.”
2. *List statistical assumptions.* All hypothesis tests make one or more assumptions about the data, and it’s important to state them clearly. For example, **parametric** hypothesis tests assume the data follow a particular probability distribution under the null, while **nonparametric** tests do not make this assumption.
3. *Decide on an appropriate test and test statistic.* The **test statistic** quantifies the degree of deviation of the observed data from what one would expect under the null hypothesis².
4. *Derive the distribution of the test statistic under the null.* This is called the **null distribution**.
5. *Select a significance level under which you’ll reject the null.* The **significance level**, usually written as α , is the probability of a type I error. A type I error is committed when one rejects the null even though it is true (false positive result).
6. *Compute the observed value of the test statistic from the data.*
7. *Decide whether or not to reject the null hypothesis.*

²Some definitions: A **statistic** is just some quantity that summarizes a set of data, or gives some information about the value of a parameter. A **sufficient statistic** is a statistic that gives the maximum amount of information about a parameter that can possibly be obtained from the sample data.

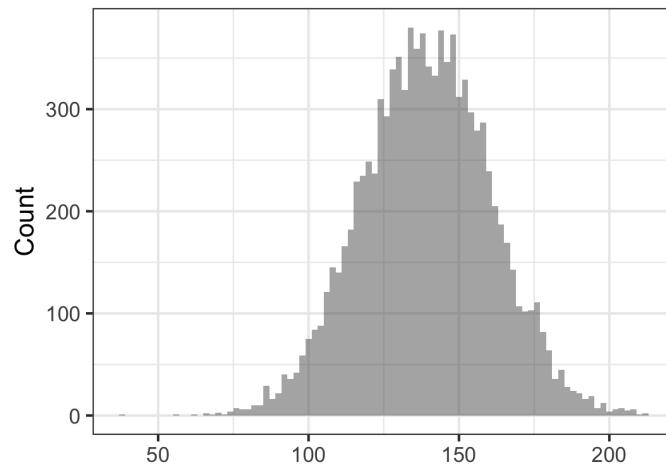
6.2 The Z-Test

A **Z-test** is a hypothesis test for which the null distribution is normal with known mean and standard deviation (i.e. known parameters μ and σ). It is most commonly used to compare the mean of a set of samples, \bar{x} , with a known population mean. It also appears in other contexts, such as significance tests of regression coefficients in generalized linear models (Chapter 10).

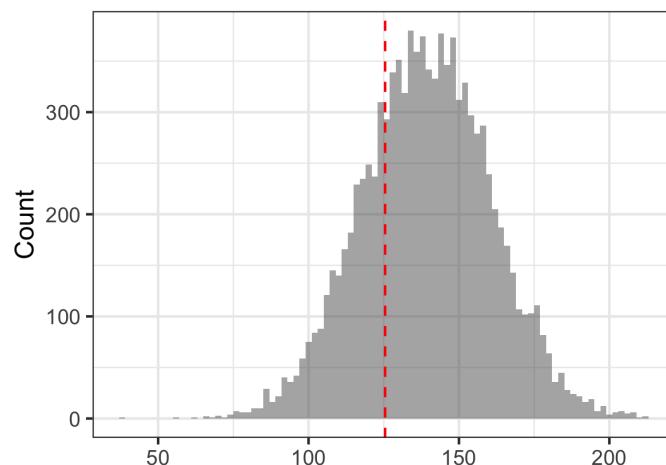
Example: SBP in an Appalachian Town The distribution of systolic blood pressure (SBP) among Caucasian males ages 55-64 in the United States is roughly normal with mean 139.75 mmHg and standard deviation 21.40 mmHg (Source: Int. J. Epidemiol. 2: 294-301, 1973). The following graph shows a normal distribution with those parameters.



Here is a histogram of 10,000 data samples drawn independently from that distribution (i.e., what we would expect if we sampled the SBPs of 10,000 men from the United States at large):



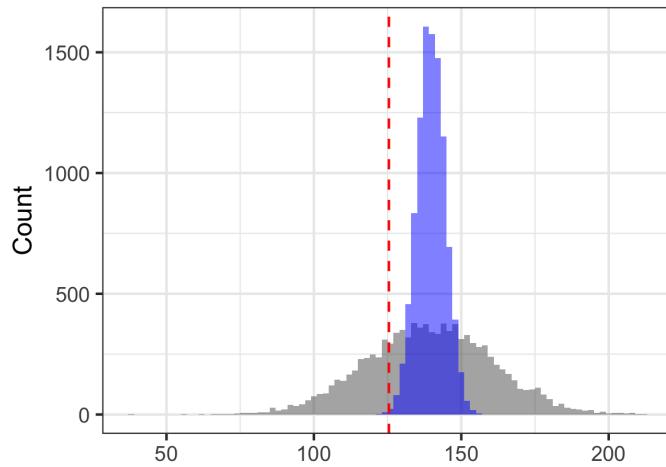
Now, assume some researchers find a small community in rural Appalachia and measure the SBP of 20 Caucasian males ages 55-64 there. Their mean SBP is 125.45 mmHg, illustrated by the red dashed line in the graph below.



At first glance, this may not appear that unusual. After all, the red line is sort of near the center of the gray distribution, right? This analysis is flawed, however, because our 125.45 mmHg value isn't for one man - it's an average

over 20 men. The distribution of the **sample mean**, \bar{x} , is different from that of each individual sample.

To see this, imagine taking 20 samples from the gray distribution, taking their mean, and recording that value. Now repeat that process 10,000 times. If you do that, you get the **distribution of the sample mean**, which is skinnier than the gray distribution:



It turns out that the distribution of the sample mean will have the same mean, μ_0 , as the population distribution, but its standard deviation will be σ / \sqrt{n} , where n is the number of samples over which the mean is taken.

Question 6.1

If $n = 1$, what is the standard deviation of the sample mean? If $n = \infty$, what is the standard deviation of the sample mean?

Question 6.2

The sample mean for our 20 sampled Appalachian men is shown as a vertical red dashed line in the figure above. Now that you know what the distribution of the sample mean looks like, do you think the observation from your Appalachian town is “weird”?

Let's conduct a hypothesis test to evaluate whether we have evidence that the mean SBP among men in this town is different from that of the general U.S. population.

1. *State the null hypothesis.* Here the null hypothesis is going to be our default position: that there is no difference. Let μ_c be the true mean SBP for men in the community and μ_0 be the mean for the general population.

$$H_0 : \mu_c = \mu_0$$

$$H_a : \mu_c \neq \mu_0$$

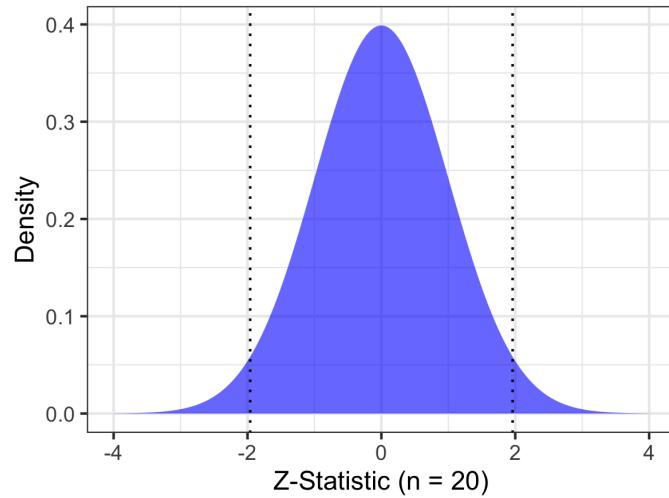
2. *List statistical assumptions.* We make two assumptions. First, we assume that the SBPs of the different men in the sample are statistically independent. Second, we assume that under the null, SBP will follow a normal distribution with mean 139.75 and standard deviation 21.40, the same as the general population of men aged 55-64.
3. *Decide on an appropriate test and test statistic.* Our test statistic in this case is going to be the **Z-statistic**, which measures the deviation of the sample mean from the population mean in units of the standard deviation of the sample mean, σ / \sqrt{n} :

$$Z = \frac{\bar{x} - \mu_0}{\sigma / \sqrt{n}} \quad \text{where} \quad \bar{x} = \frac{1}{n} \sum_{i=1}^n x^{(i)}$$

In our case, $n = 20$ because \bar{x} , our sample mean, is an average of 20 samples.

4. *Derive the distribution of the test statistic under the null.* The Z-statistic follows a **standard normal** distribution under the null, which is a normal distribution with $\mu = 0$ and $\sigma = 1$. To see this, remember that the distribution of \bar{x} under the null is $\mathcal{N}(\mu_0, \sigma / \sqrt{n})$. When you calculate the Z-statistic, you shift that distribution by a distance μ_0 so it is centered at zero, then adjust its width (standard deviation) to 1.0 by dividing by σ / \sqrt{n} .
5. *Select a significance level under which you'll reject the null.* For the purposes of this example, we will choose $\alpha = 0.05$ (5% chance of a type I error).

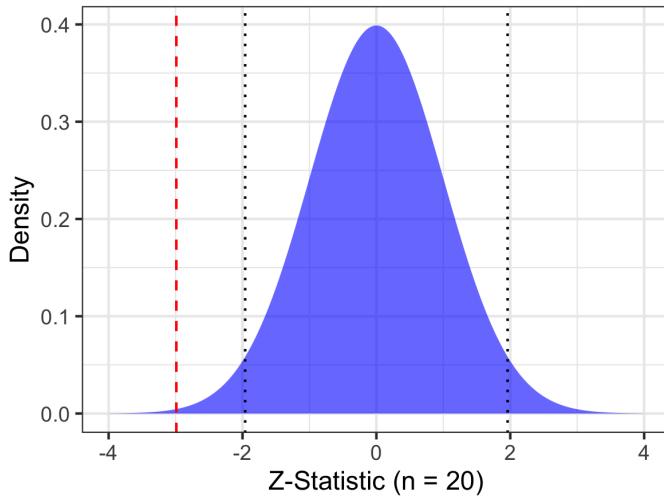
The null distribution of the Z-statistic is shown below. The vertical dotted black lines are situated at the **critical values** that produce $\alpha = 0.05$ (the area under the null distribution that is outside those lines is 0.05).



6. Compute the observed value of the test statistic from the data. The observed value of the test statistic is:

$$Z = \frac{\bar{x} - \mu_0}{\sigma / \sqrt{n}} = \frac{125.45 - 139.75}{21.40 / \sqrt{20}} = -2.99.$$

7. Decide whether or not to reject the null hypothesis. The value of our test statistic falls outside the region contained by the critical values (the **acceptance region**), so we reject the null at this value of α .



Question 6.3

As α gets smaller, are you more or less likely to reject the null for the same value of the test statistic? Hint: What does making α smaller do to the positions of the two black dotted lines in the figure, above?

6.3 Definitions

- **Type I Error:** When a hypothesis test rejects the null even though the null is true (also called a **false positive**). The type I error rate is usually denoted by α .
- **Type II Error:** When a hypothesis test fails to reject the null even though it is false (also called a **false negative**). The type II error rate is usually denoted by β .
- **P-value:** The probability of obtaining a test statistic at least as extreme as the one that was actually obtained, assuming the null is true. A *p*-value can be **one-sided** or **two-sided**. The difference lies in the definition of “extreme”. In a one-sided test, we find the probability that the test statistic is at least as extreme *in the same direction* as the one we observed. In a two-sided test, we find the probability that the test statistic is at

least as extreme *in either direction* (positive or negative deviation). In most cases, this has the practical effect of doubling the p -value.

- **Power:** The probability that a hypothesis test will reject the null when the null is false (that the test will detect a true effect if the effect is there). Usually denoted $1 - \beta$.

6.4 Pearson's Chi-Squared Test

Imagine you have data on two discrete variables for n different subjects. You want to test whether the value of one covariate is independent of the value of the other. To do this, you can arrange your data in a **contingency table** where the rows and columns correspond to the values of the two variables. **Pearson's chi-squared test** can then be used to assess the independence of row and column values.

Example: Association of Genotype and Disease Imagine you want to test whether a person's genotype at a particular locus is associated with whether or not he/she has Disease X. You find 100 people with the disease and 100 healthy controls ($n = 200$) and genotype them:

| | AA | Aa | aa | |
|---------|-----|----|----|-----|
| X | 52 | 43 | 5 | 100 |
| Control | 67 | 27 | 6 | 100 |
| | 119 | 70 | 11 | 200 |

Let's conduct a hypothesis test to examine this result.

1. *State the null hypothesis.* We consider the genotype at this locus, G , to be a random variable (see Chapter 4) with three possible outcomes: AA , Aa , and aa . We likewise consider the patient's disease status, D , to be a

random variable with two possible outcomes: disease or no disease. We state our null hypothesis mathematically as:

$$H_0 : G \perp\!\!\!\perp D$$

$$H_a : G \not\perp\!\!\!\perp D$$

where the symbol $\perp\!\!\!\perp$ refers to statistical independence of G and D . We encountered statistical independence in our discussion of maximum likelihood in Chapter 5. Mathematically, statistical independence means that the joint probability of observing a particular value for G and a particular value for D is simply equal to the product of their individual probabilities:

$$P(G = g, D = d) = P(G = g)P(D = d)$$

Under these conditions, the expected values of the cells of our table are:

Under scenario of independence (E):

| | AA | Aa | aa | |
|---------|------|------|-----|-----|
| X | 59.5 | 35.0 | 5.5 | 100 |
| Control | 59.5 | 35.0 | 5.5 | 100 |
| | 119 | 70 | 11 | 200 |

For example, consider the cell $G = AA, D = X$. Assuming the total number of patients is fixed at $n = 200$ and G and D are independent, the expected number of people in that cell is:

$$P(G = AA, D = X) \cdot n = \left(\frac{119}{200}\right) \left(\frac{100}{200}\right) \cdot 200$$

$$= 59.5$$

Our task now is to decide whether our observed table counts are different enough from what we expect under the null to cause us to reject the null.

2. *List statistical assumptions.* We assume that the data are sampled ran-

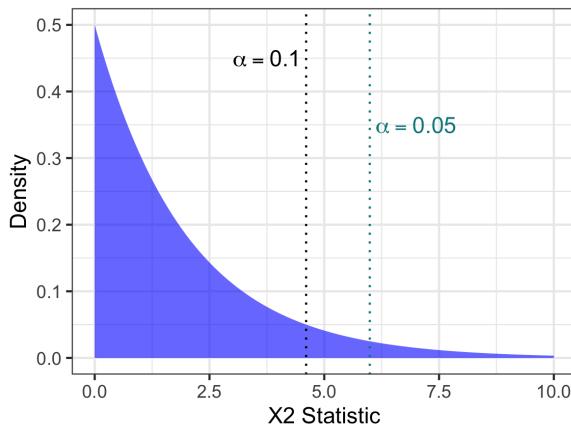
domly and independently from a fixed population where each member of the population has an equal probability of selection³.

3. *Decide on an appropriate test and test statistic.* The chi-squared test works by calculating expected counts in all $r \times c$ cells of the table (r = number of rows, c = number of columns) and then measuring the data's deviation from those expected counts. The **chi-squared test statistic** has the form

$$X^2 = \sum_{i=1}^r \sum_{j=1}^c \frac{(O_{ij} - E_{ij})^2}{E_{ij}}$$

where O refers to "observed count" and E to "expected count". The expected counts are those that assume statistical independence of rows and columns (blue table, above).

4. *Derive the distribution of the test statistic under the null.* Under the null, the X^2 test statistic follows a chi-squared distribution (Section 4.8) with $(r - 1)(c - 1)$ degrees of freedom. In the case of our genotype example, there are $r = 2$ rows and $c = 3$ columns, thus 2 degrees of freedom.
5. *Select a significance level under which you'll reject the null.* The χ^2 distribution with 2 degrees of freedom is shown below. Two vertical lines are shown at different significance levels: $\alpha = 0.05$ and $\alpha = 0.1$.

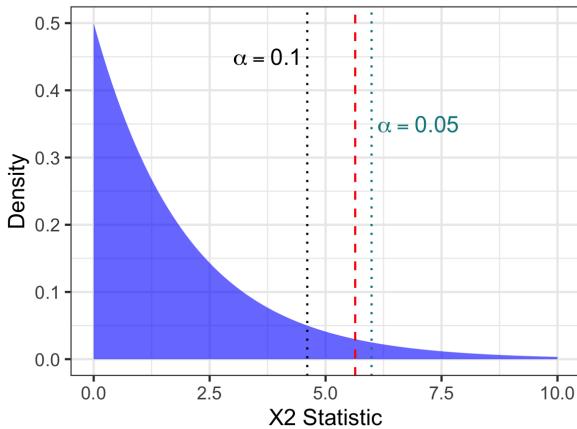


³A further assumption of the chi-squared test is that expected counts for each cell must be sufficiently high. A common rule is 5 or more in all cells of a 2×2 table, and 5 or more in 80% of cells in larger tables, but no cells with zero counts.

6. Compute the observed value of the test statistic from the data.

Question 6.4

Using the formula in step 4, above, compute the actual value of the chi-squared test statistic for this example. Hint: You should end up with a value that corresponds to the position of the red dashed line in the figure below.



7. Decide whether or not to reject the null hypothesis. Based on our calculated value of the test statistic, we will reject the null at $\alpha = 0.1$ and fail to reject the null at $\alpha = 0.05$.

Although it looks much different from the Z-test, the chi-squared test follows the same formalism: defining a null hypothesis, figuring out what the data should look like under the null, quantifying the deviation of the observed data from what's expected using a test statistic, and deciding if that test statistic presents strong enough evidence to cause us to reject the null.

6.5 Student's T-tests

The final example we will look at today is the **T-test**. Like the Z-test, the T-test (actually a family of tests) deals with situations where you have data that are assumed to be normally distributed under the null hypothesis. However, in

this scenario, the population standard deviation, σ is not known and must be estimated from the data itself.

6.5.1 One Sample T-test

Assume you have a dataset $x^{(1)}, \dots, x^{(n)}$, of real numbers that you can plausibly assume are normally distributed. You want to test whether the mean of your data is equal to a fixed value, μ_0 . Under the null hypothesis that the means are the same, the test statistic

$$T = \frac{\bar{x} - \mu_0}{s / \sqrt{n}}$$

which we call a “T statistic”, follows a T-distribution (Section 4.9) with $n - 1$ degrees of freedom⁴. Here \bar{x} refers to the sample mean, and s refers to the **sample standard deviation**:

$$s = \sqrt{\frac{1}{n-1} \sum_{i=1}^n (x^{(i)} - \bar{x})^2}$$

Question 6.5

Compare the formula for the sample standard deviation to the maximum likelihood estimate of the parameter, σ , of a normal distribution (Section 5.3.3). What is the same/different? Note in particular the use of $n - 1$ in the denominator, rather than n . This arises because the MLE for σ , $\hat{\sigma}$, is a **biased** estimate of the population standard deviation (more on this later). For large n , however, the two are nearly identical.

⁴A one-sample T-test looks a lot like a Z-test. However, because we use s to estimate the population standard deviation from data, we must account for variation in our estimate. It turns out that the sample variance, s^2 , follows a chi-squared distribution with $n - 1$ degrees of freedom, where n is the sample size. In this case, by the definition of the T-distribution (Section 4.9), the T statistic follows a Student’s T-distribution with $n - 1$ degrees of freedom. As the number of samples, n , grows, the sample standard deviation approaches the population standard deviation and the T-test becomes a Z-test. But when n is small, the T-test is quite a bit more conservative.

6.5.2 Two Independent Samples, Equal Variance

Assume you have a dataset $x^{(1)}, \dots, x^{(n)}$ and another dataset $y^{(1)}, \dots, y^{(m)}$. You assume that both are drawn from normal distributions with equal variance but potentially different means. You want to test whether the means are equal.

The same basic machinery for the one-sample T-test can be deployed in this context with a slightly different test statistic. The test statistic

$$T = \frac{\bar{x} - \bar{y}}{s_p \sqrt{\frac{1}{n} + \frac{1}{m}}}$$

where

$$\begin{aligned}s_p^2 &= \frac{(n-1)s_x^2 + (m-1)s_y^2}{m+n-2} \\ s_x^2 &= \frac{1}{n-1} \sum_{i=1}^n (x^{(i)} - \bar{x})^2 \\ s_y^2 &= \frac{1}{m-1} \sum_{i=1}^m (y^{(i)} - \bar{y})^2\end{aligned}$$

follows a t -distribution with $m+n-2$ degrees of freedom.

6.5.3 Two Independent Samples, Unequal Variance

Sometimes you have two independent samples but cannot assume the variances are equal. Again, similar machinery can be deployed. In this case, you can use **Welch's T-test**, which uses the test statistic

$$T = \frac{\bar{x} - \bar{y}}{s_{xy}}$$

where

$$s_{xy} = \sqrt{\frac{s_x^2}{n} + \frac{s_y^2}{m}}.$$

This test statistic approximately follows a t -distribution with degrees of freedom given by the Welch-Satterwaite Equation

$$\text{d.f.} = \frac{\left(\frac{s_x^2}{n} + \frac{s_y^2}{m} \right)^2}{\frac{(s_x^2/n)^2}{n-1} + \frac{(s_y^2/m)^2}{m-1}}$$

6.5.4 Matched Pairs

Assume you have a data set of matched pairs. This could be a set of measurements of the same individuals taken at two different points in time, for example, or paired measurements taken from individuals with similar characteristics. You want to test whether the second set of values have changed relative to the first set of values.

To do this, you can use a one-sample T-test on the *differences* of the individual pairs. If no change has occurred, you would expect the mean of those differences to be zero. If we define $x^{(i)}$ as the difference of the paired observations for sample i and \bar{x} as $\frac{1}{n} \sum_{i=1}^n x^{(i)}$, the sample mean of those differences, then

$$T = \frac{\bar{x}}{s/\sqrt{n}}$$

follows a T-distribution with $n - 1$ degrees of freedom.

Question 6.6

Here are some sample data. They come from a study that looked at the effect of ozone, a component of smog, on the weight gain of rats. (Original source: Biometrika 63: 421-434, 1976, reproduced in Rice's *Mathematical Statistics and Data Analysis*, p. 465.) A group of 22 seventy-day-old rats were kept in an environment containing ozone for 7 days, and their weight gains were recorded. Another group of 23 rats of a similar age were kept in an ozone-free environment for a similar time and their weight gains were also recorded. Here are the data for the control group:

| | group | original_weight | weight_gain |
|----|---------|-----------------|-------------|
| 1 | control | 340.8 | 41.0 |
| 2 | control | 389.1 | 25.9 |
| 3 | control | 355.2 | 13.1 |
| 4 | control | 421.8 | -16.9 |
| 5 | control | 377.1 | 15.4 |
| 6 | control | 404.3 | 22.4 |
| 7 | control | 321.2 | 29.4 |
| 8 | control | 447.5 | 26.0 |
| 9 | control | 305.9 | 38.4 |
| 10 | control | 335.9 | 21.9 |
| 11 | control | 386.3 | 27.3 |
| 12 | control | 377.0 | 17.4 |
| 13 | control | 357.2 | 27.4 |
| 14 | control | 441.7 | 17.7 |
| 15 | control | 383.7 | 21.4 |
| 16 | control | 373.7 | 26.6 |
| 17 | control | 336.0 | 24.9 |
| 18 | control | 419.4 | 18.3 |
| 19 | control | 287.1 | 28.5 |
| 20 | control | 602.8 | 21.8 |
| 21 | control | 325.4 | 19.2 |
| 22 | control | 452.4 | 26.0 |
| 23 | control | 398.9 | 22.7 |
| | Mean | control | 384.4 |
| | St.Dev. | control | 65.5 |
| | | | 10.8 |

And here are the data for the ozone group:

| | group | original_weight | weight_gain |
|---------|-------|-----------------|-------------|
| 1 | ozone | 437.4 | 10.1 |
| 2 | ozone | 275.9 | 7.3 |
| 3 | ozone | 296.3 | -9.9 |
| 4 | ozone | 295.9 | 17.9 |
| 5 | ozone | 379.7 | 6.6 |
| 6 | ozone | 274.1 | 39.9 |
| 7 | ozone | 360.0 | -14.7 |
| 8 | ozone | 331.9 | -9.0 |
| 9 | ozone | 531.8 | 6.1 |
| 10 | ozone | 350.5 | 14.3 |
| 11 | ozone | 345.7 | 6.8 |
| 12 | ozone | 268.1 | -12.9 |
| 13 | ozone | 339.9 | 12.1 |
| 14 | ozone | 352.4 | -15.9 |
| 15 | ozone | 435.8 | 44.1 |
| 16 | ozone | 476.9 | 20.4 |
| 17 | ozone | 462.5 | 15.5 |
| 18 | ozone | 368.0 | 28.2 |
| 19 | ozone | 504.3 | 14.0 |
| 20 | ozone | 188.0 | 15.7 |
| 21 | ozone | 466.9 | 54.6 |
| 22 | ozone | 288.8 | -9.0 |
| Mean | ozone | 365.0 | 11.0 |
| St.Dev. | ozone | 88.6 | 19.0 |

- (a) Imagine that the population weight distribution of rats is known to be normal with $\mu = 350$ (grams) and unknown σ . How would you test the hypothesis that the mean of the control group is equal to the population mean? How would you test the hypothesis that the mean of the ozone group is equal to the population mean?
- (b) How would you test the hypothesis that the mean original weights of the ozone and control groups are equal? Do not assume equal variance.
- (c) How would you test the hypothesis that the mean weight gain in the ozone group is equal to the mean weight gain in the control group? Do not assume equal variance.
- (d) How would your approach in part (c) change if you assumed the weight gains in the two groups had equal variance?

Plug in the relevant numbers from the tables above to perform each hypothesis test with $\alpha = 0.05$. The following table of critical values for the T -distribution^a may help you:

Critical Values for Student's t -Distribution.

| df | Upper Tail Probability: $\Pr(T > t)$ | | | | | | | | | |
|----|--------------------------------------|-------|-------|-------|--------|--------|--------|--------|--------|---------|
| | 0.2 | 0.1 | 0.05 | 0.04 | 0.03 | 0.025 | 0.02 | 0.01 | 0.005 | 0.0005 |
| 1 | 1.376 | 3.078 | 6.314 | 7.916 | 10.579 | 12.706 | 15.895 | 31.821 | 63.657 | 636.619 |
| 2 | 1.061 | 1.886 | 2.920 | 3.320 | 3.896 | 4.303 | 4.849 | 6.965 | 9.925 | 31.599 |
| 3 | 0.978 | 1.638 | 2.353 | 2.605 | 2.951 | 3.182 | 3.482 | 4.541 | 5.841 | 12.924 |
| 4 | 0.941 | 1.533 | 2.132 | 2.333 | 2.601 | 2.776 | 2.999 | 3.747 | 4.604 | 8.610 |
| 5 | 0.920 | 1.476 | 2.015 | 2.191 | 2.422 | 2.571 | 2.757 | 3.365 | 4.032 | 6.869 |
| 6 | 0.906 | 1.440 | 1.943 | 2.104 | 2.313 | 2.447 | 2.612 | 3.143 | 3.707 | 5.959 |
| 7 | 0.896 | 1.415 | 1.895 | 2.046 | 2.241 | 2.365 | 2.517 | 2.998 | 3.499 | 5.408 |
| 8 | 0.889 | 1.397 | 1.860 | 2.004 | 2.189 | 2.306 | 2.449 | 2.896 | 3.355 | 5.041 |
| 9 | 0.883 | 1.383 | 1.833 | 1.973 | 2.150 | 2.262 | 2.398 | 2.821 | 3.250 | 4.781 |
| 10 | 0.879 | 1.372 | 1.812 | 1.948 | 2.120 | 2.228 | 2.359 | 2.764 | 3.169 | 4.587 |
| 11 | 0.876 | 1.363 | 1.796 | 1.928 | 2.096 | 2.201 | 2.328 | 2.718 | 3.106 | 4.437 |
| 12 | 0.873 | 1.356 | 1.782 | 1.912 | 2.076 | 2.179 | 2.303 | 2.681 | 3.055 | 4.318 |
| 13 | 0.870 | 1.350 | 1.771 | 1.899 | 2.060 | 2.160 | 2.282 | 2.650 | 3.012 | 4.221 |
| 14 | 0.868 | 1.345 | 1.761 | 1.887 | 2.046 | 2.145 | 2.264 | 2.624 | 2.977 | 4.140 |
| 15 | 0.866 | 1.341 | 1.753 | 1.878 | 2.034 | 2.131 | 2.249 | 2.602 | 2.947 | 4.073 |
| 16 | 0.865 | 1.337 | 1.746 | 1.869 | 2.024 | 2.120 | 2.235 | 2.583 | 2.921 | 4.015 |
| 17 | 0.863 | 1.333 | 1.740 | 1.862 | 2.015 | 2.110 | 2.224 | 2.567 | 2.898 | 3.965 |
| 18 | 0.862 | 1.330 | 1.734 | 1.855 | 2.007 | 2.101 | 2.214 | 2.552 | 2.878 | 3.922 |
| 19 | 0.861 | 1.328 | 1.729 | 1.850 | 2.000 | 2.093 | 2.205 | 2.539 | 2.861 | 3.883 |
| 20 | 0.860 | 1.325 | 1.725 | 1.844 | 1.994 | 2.086 | 2.197 | 2.528 | 2.845 | 3.850 |
| 21 | 0.859 | 1.323 | 1.721 | 1.840 | 1.988 | 2.080 | 2.189 | 2.518 | 2.831 | 3.819 |
| 22 | 0.858 | 1.321 | 1.717 | 1.835 | 1.983 | 2.074 | 2.183 | 2.508 | 2.819 | 3.792 |
| 23 | 0.858 | 1.319 | 1.714 | 1.832 | 1.978 | 2.069 | 2.177 | 2.500 | 2.807 | 3.768 |

Answers: (a) One-sample T -test of control group original weights vs. null of $\mu_0 = 350$; T -statistic is 2.5165, 22 d.f., two-sided p -value is 0.01964, reject null at $\alpha = 0.05$. One-sample T -test of ozone group original weights vs. null of $\mu_0 = 350$; T -statistic is 0.7961, 21 d.f., two-sided p -value is 0.4349, fail to reject null at $\alpha = 0.05$. (b) Welch's two-sample T -test of control vs. ozone group original weights; T -statistic is 0.8293, d.f. is estimated using the Welch-Satterwaite equation at 38.619, two-sided p -value is 0.4120, fail to reject null at $\alpha = 0.05$. (c) Welch's two-sample T -test of control vs. ozone group weight gains; T -statistic is 2.4629, d.f. is estimated using the Welch-Satterwaite equation at 32.918, two-sided p -value is 0.01918, reject null at $\alpha = 0.05$. (d) You would use Pearson's two-sample T -test, which assumes equal variances; T -statistic is 2.4919, d.f. is 43, two-sided p -value is 0.01664, reject null at $\alpha = 0.05$.

^aBorrowed with gratitude from <https://www.stat.purdue.edu/~lfindsen/stat503/t-Dist.pdf>

Chapter 7

Building a Decision Tree

Decision trees were developed as an alternative to neural networks in the 1970s. We already saw them in Chapters 2 and 3 as examples of supervised learning algorithms. Now we're going to get into a bit more detail about how these trees are learned from data.

Decision trees can be adapted to solve supervised learning problems with different types of outcomes. We will focus on **classification trees** in this chapter, but the same tree building principles can be applied to solve regression problems (see Chapter 3). Similar modifications can also allow us to construct **survival trees**, which model survival outcomes (represented as Kaplan-Meier curves; see Chapter 11). Decision trees can also handle count outcomes, modeling them using Poisson distributions (see Chapter 4).

7.1 Example: The Wisconsin Breast Cancer Dataset

The Wisconsin breast cancer dataset¹ contains information about imaging features of a fine needle aspirate (FNA) of a breast mass from 569 different subjects. Ten real-valued features are computed for each cell nucleus in the image:

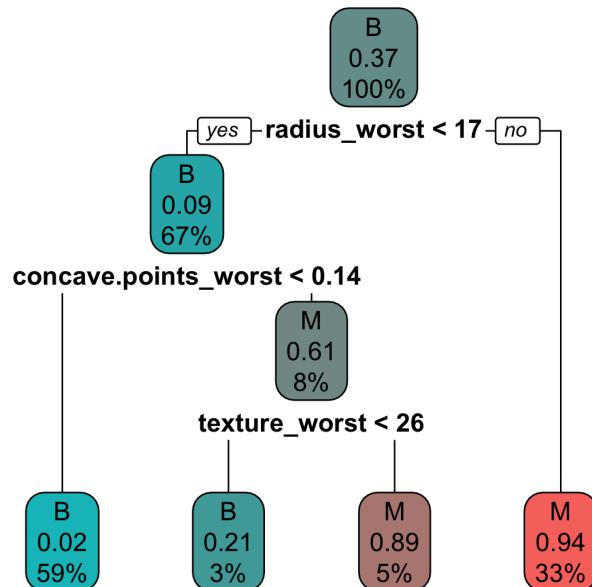
- (a) radius (mean of distances from center to points on the perimeter)

¹You can download the dataset from the UCI Machine Learning Repository here:
[https://archive.ics.uci.edu/ml/datasets/Breast+Cancer+Wisconsin+\(Diagnostic\)](https://archive.ics.uci.edu/ml/datasets/Breast+Cancer+Wisconsin+(Diagnostic)).

- (b) texture (standard deviation of gray-scale values)
- (c) perimeter
- (d) area
- (e) smoothness (local variation in radius lengths)
- (f) compactness ($\text{perimeter}^2 / \text{area} - 1.0$)
- (g) concavity (severity of concave portions of the contour)
- (h) concave points (number of concave portions of the contour)
- (i) symmetry
- (j) fractal dimension, a statistical index of complexity quantifying how detail in a pattern changes with the scale on which it is measured

The mean, standard deviation, and worst value of each feature are then computed, creating a total of 30 features. Each image is also labeled by its true diagnosis: *B* (for benign) or *M* (for malignant).

Here is a decision tree for this dataset, built using the `rpart` package in R with default parameters:



Question 7.1

What is the most important feature, as identified by the decision tree learning algorithm, for determining whether a breast mass is benign or malignant? What two other features are considered important by the tree? Which features are ignored completely?

Question 7.2

Looking at the decision tree for the Wisconsin Breast Cancer dataset, what do you think the advantages of a decision tree are for this problem over other classification methods, such as logistic regression and KNN?

Although there are several tree building algorithms, all of them are conceptually similar. They all try to reduce “impurity”, or “uncertainty”, in the outcome variable by intelligently splitting on the predictors. Trees are built recursively from root to leaves. Each internal node of the tree “contains” a subset of the overall dataset (this is why tree building is often called **recursive partitioning**, and why the R package is named `rpart`). At each stage, the algorithm will consider each of the existing leaf nodes and choose the split variable that maximally reduces uncertainty in the outcome. To understand how trees are built computationally, all we need to do is look at the math behind this idea.

7.2 The ID3 Algorithm

One of the earliest approaches to building decision trees was the **ID3 algorithm**². The ID3 Algorithm uses the concepts of entropy and information gain to build trees.

7.2.1 Entropy

Entropy, usually abbreviated H , is a measure of the uncertainty in the value of a random variable. It is the number of bits (on average) required to describe

²Quinlan, J.R. "Induction of decision trees", Machine Learning, num. 1, pp. 81- 106, 1986.

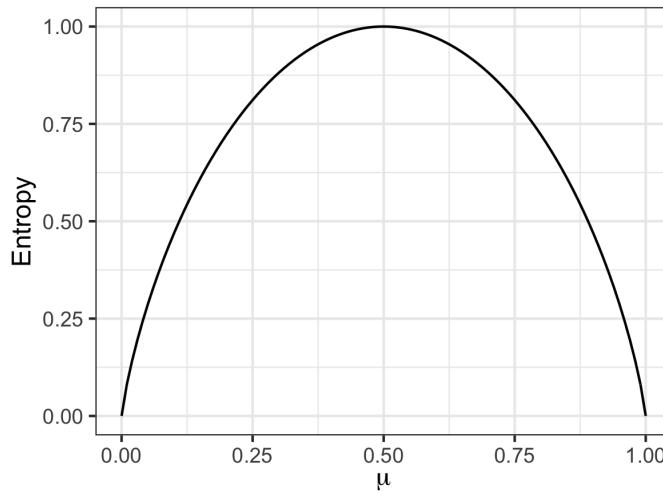
the outcome of the random variable. Here is the formula for the entropy of the discrete probability distribution governing the outcome of a random variable, X:

$$H(X) = - \sum_x P(X = x) \log_2 (P(X = x))$$

For a Bernoulli random variable (see Chapter 4, Section 4.3), there are only two possible outcomes: 0 and 1. The entropy of this random variable is given by:

$$H_{\text{Bernoulli}} = -\mu \log_2(\mu) - (1 - \mu) \log_2(1 - \mu)$$

where μ is the sole parameter of the Bernoulli distribution: the probability of a positive outcome. Here is what the entropy of a Bernoulli distribution looks like as a function of μ :



Question 7.3

At which value(s) of μ are we maximally uncertain about the outcome? At which value(s) of μ are we completely certain about the outcome? This should make intuitive sense if you consider the meaning of μ .

7.2.2 Information Gain

The goal of a decision tree is to reduce uncertainty about the outcome with every split. Let Y be the outcome variable of a training set. Let X be one of

the predictors. **Information gain** is defined as:

$$\begin{aligned}\text{Gain}(Y, X) &= H(Y) - \sum_{x \in \text{Values}(X)} \frac{|Y(X = x)|}{|Y|} H(Y(X = x)) \\ &= H(Y) - H(Y|X)\end{aligned}$$

Since entropy is a measure of uncertainty, or impurity, in the outcome, information gain is the reduction in that uncertainty achieved by conditioning on the predictor, X . The tree will choose split variables for which the information gain is maximized.

Question 7.4

Say you have a dataset where the outcome is $Y = [0, 1, 0, 1, 0, 1]$ and there are two predictors: $X = [0, 0, 1, 1, 2, 2]$, and $Z = [1, 2, 1, 2, 1, 2]$. Intuitively, which predictor would make the better splitting variable and why? Calculate $\text{Gain}(Y, X)$ and $\text{Gain}(Y, Z)$. Which value is higher?

7.2.3 Using Entropy to Build a Decision Tree

By understanding the concepts of entropy and information gain, we arrive naturally at the ID3 Algorithm:

1. Start with a single node: the root of the tree.
2. At each current leaf node:
 - (a) Compute the information gain for each feature.
 - (b) Split on the one with the highest gain.
3. Return to Step 2. Stop when either the class distributions at all leaf nodes are entirely pure or there are no more variables left to split on.

7.3 Example: Happiness Dataset

Let's build a decision tree for a simple example, using the ID3 algorithm. Assume we surveyed 10 people and asked them whether they were happy or

unhappy. We also asked whether they had friends (yes/no), money (poor/enough/rich), and free time (none/some). The data look like this:

| Datapoint ID | friends (X_1) | money (X_2) | free time (X_3) | happy (Y) |
|--------------|-------------------|-----------------|---------------------|---------------|
| 1 | 1 | 1 | 0 | 0 |
| 2 | 1 | 1 | 1 | 0 |
| 3 | 0 | 1 | 1 | 0 |
| 4 | 0 | 0 | 0 | 0 |
| 5 | 1 | 0 | 0 | 0 |
| 6 | 0 | 0 | 0 | 0 |
| 7 | 1 | 2 | 1 | 1 |
| 8 | 1 | 0 | 1 | 1 |
| 9 | 0 | 0 | 1 | 1 |
| 10 | 1 | 0 | 0 | 1 |

$$x_1 = \begin{cases} 0 & \text{no friends} \\ 1 & \text{friends} \end{cases} \quad x_2 = \begin{cases} 0 & \text{poor} \\ 1 & \text{enough money} \\ 2 & \text{rich} \end{cases} \quad x_3 = \begin{cases} 0 & \text{no free time} \\ 1 & \text{some free time} \end{cases}$$

Question 7.5

Build a decision tree for this dataset using the ID3 algorithm. To get started, you need to know the entropy of the overall outcome distribution. It is:

$$H(Y) = -\frac{4}{10} \log_2 \frac{4}{10} - \frac{6}{10} \log_2 \frac{6}{10} = 0.971$$

We will go through the calculations below. As we go, you can start to draw the tree on another page.

- (a) Perform the initial split at the tree root to determine which variable to split on first. Update the tree with this information.

$$\frac{|Y(X_1 = 0)|}{|Y|} H[Y(X_1 = 0)] =$$

$$\frac{|Y(X_1 = 1)|}{|Y|} H[Y(X_1 = 1)] =$$

$$\text{Gain}(Y, X_1) =$$

$$\frac{|Y(X_2 = 0)|}{|Y|} H[Y(X_2 = 0)] =$$

$$\frac{|Y(X_2 = 1)|}{|Y|} H[Y(X_2 = 1)] =$$

$$\frac{|Y(X_2 = 2)|}{|Y|} H[Y(X_2 = 2)] =$$

$$\text{Gain}(Y, X_2) =$$

$$\frac{|Y(X_3 = 0)|}{|Y|} H[Y(X_3 = 0)] =$$

$$\frac{|Y(X_3 = 1)|}{|Y|} H[Y(X_3 = 1)] =$$

$$\text{Gain}(Y, X_3) =$$

- (b) We see that two of the leaves of our tree are “pure”, meaning that all of the training examples that arrive there are of one outcome class. For those two leaves, we’re done. However, for the third ($X_2 = 0$, or poor), we need to perform another split. Perform the split at the $X_2 = 0$ node to find which variable to split on next and update the tree with this information.

$$\begin{aligned}
H[Y(X_2 = 0)] &= \\
\frac{|Y(X_2 = 0, X_1 = 0)|}{|Y(X_2 = 0)|} H[Y(X_2 = 0, X_1 = 0)] &= \\
\frac{|Y(X_2 = 0, X_1 = 1)|}{|Y(X_2 = 0)|} H[Y(X_2 = 0, X_1 = 1)] &= \\
\text{Gain}(Y(X_2 = 0), X_1) &= \\
\frac{|Y(X_2 = 0, X_3 = 0)|}{|Y(X_2 = 0)|} H[Y(X_2 = 0, X_3 = 0)] &= \\
\frac{|Y(X_2 = 0, X_3 = 1)|}{|Y(X_2 = 0)|} H[Y(X_2 = 0, X_3 = 1)] &= \\
\text{Gain}(Y(X_2 = 0), X_3) &=
\end{aligned}$$

- (c) We need to do one more split on the $X_2 = 0, X_3 = 0$ node. The only variable left to split on is X_1 (friends). Perform this split and add this information to the tree.

7.4 Alternative Splitting Criteria

Information gain is not the only criterion that is used in decision tree algorithms. In fact, the tree built for the Wisconsin Breast Cancer dataset in Section 7.1 used a different criterion, Gini impurity, because it is the default in R's `rpart` package.

The **Gini impurity** measures how often a randomly chosen element from a set would be incorrectly labeled if it were randomly labeled using the distribution of labels in the subset. It sums up the probability of an item with label i being chosen (p_i) multiplied by the probability $\sum_{j \neq i} p_j = 1 - p_i$ that a mistake is made in classifying it. The formula is:

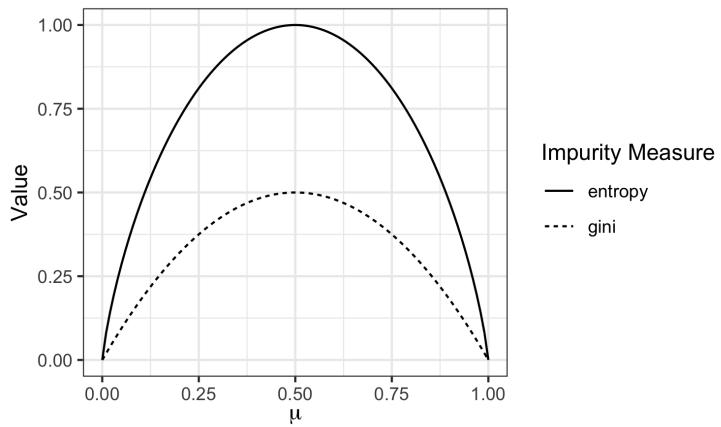
$$G(p) = \sum_i p_i(1 - p_i) = 1 - \sum_i p_i^2$$

which for a Bernoulli distribution is

$$G_{\text{Bernoulli}} = 1 - \mu^2 - (1 - \mu)^2.$$

Question 7.6

Plots of the Gini impurity vs. entropy for a Bernoulli distribution are shown below. What do you notice about the value(s) of μ for which each is maximized or minimized?



Although the two metrics are similar and usually yield similar trees, depending on the dataset, the trees can look quite different. The Gini impurity is computationally faster because it does not make use of logarithms as the entropy does. This can make a difference as the number of features grows.

7.5 Decision Tree Regression

So far we've assumed that our outcome is discrete. But what happens if it's numeric? (That is, what if we want to perform regression instead of classification?)

In that case, we use **standard deviation reduction** instead of information gain to decide which variables to split on. The sample standard deviation of

an outcome, y , is defined as:

$$S(Y) = \sqrt{\frac{\sum_i (y^{(i)} - \bar{y})^2}{n - 1}}$$

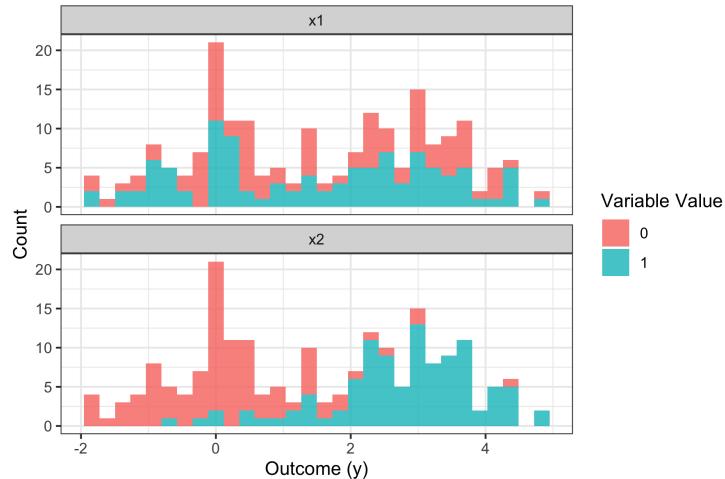
The procedure is identical to the ID3 algorithm except that it uses conditional standard deviation instead of information gain to decide on features. We define

$$S(Y, X) = \sum_x P(X = x) S(Y|X = x)$$

and at each current leaf node, we split on the variable where the reduction in standard deviation, $S(Y) - S(Y, X)$, is the highest.

Question 7.7

Imagine you have a dataset with two predictors, x_1 and x_2 , each of which is binary (can only be 0 or 1). Here are the distributions of outcome values associated with x_1 and x_2 :



Based on the idea of standard deviation reduction, which of these two variables, x_1 or x_2 , would make the most sense for a decision tree to split on? What would such a split look like and what would the output value of the tree (the predicted value of y) be for each side of the split?

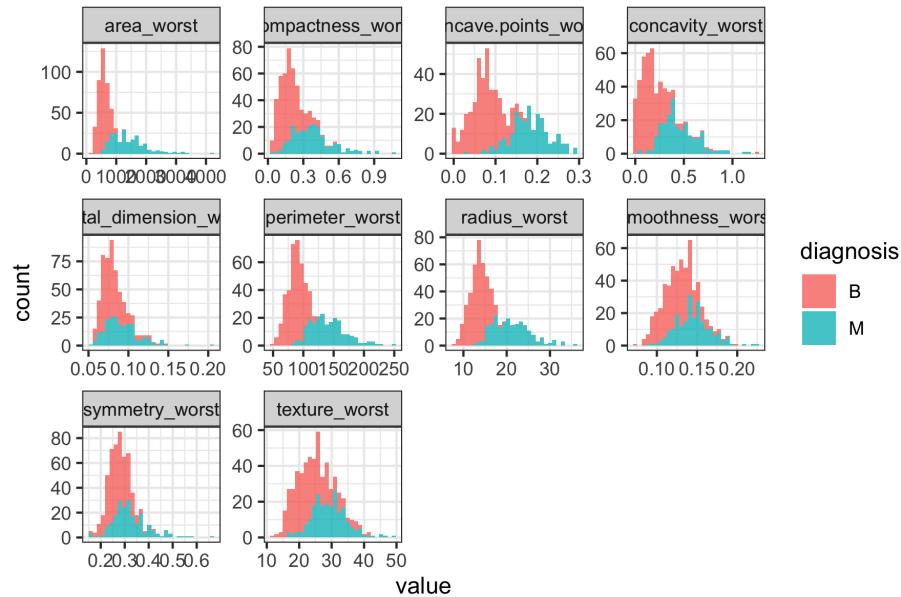
7.6 Numeric Predictors

Although the Happiness Dataset contained only discrete predictors, decision trees can also handle numeric predictors. We've seen this already with the Wisconsin Breast Cancer dataset.

There are different strategies for deciding on an optimal split for a predictor. The most common approach is to consider all possible splits. So for example, if a predictor has values 10, 11, 16, 18, 20, and 35, the tree building algorithm would consider all $N - 1 = 5$ possible split points. If a dataset has a large number of numeric features or features with lots of different possible values, therefore, it can really slow down the construction of the tree.

Question 7.8

Here are histograms of 10 of the predictors in the Wisconsin Breast Cancer dataset. Only the “worst” variable version of each predictor is shown for clarity. Which variable, and which threshold, appears to show the clearest division of samples into *B* and *M* groups? Compare your choice to the first split of the tree in Section 7.1.



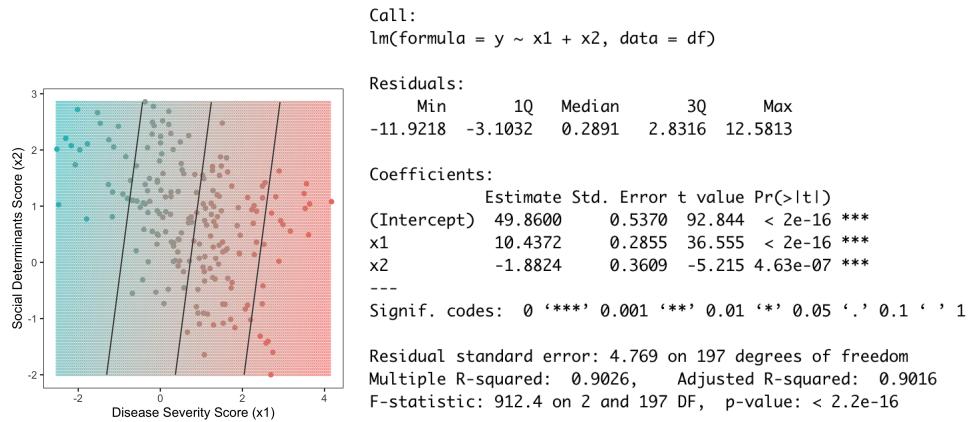
Chapter 8

Interpreting a Linear Regression Model

This chapter is devoted to understanding the structure of linear regression models. We first encountered them in Chapter 3 as “just one example” of a regression model. However, linear regression’s overwhelming popularity in the clinical domain means that one cannot do clinical data science without fully understanding these models’ structure and how to interpret the software output.

8.1 Biomarker Example from Chapter 3

In Chapter 3, we saw an example where information about two predictors – a disease severity score (x_1) and a social determinants score (x_2) – was used to predict the numeric level of a disease recurrence biomarker. One of the three supervised learning algorithms we tried was a **linear regression** model (Section 3.2.1). The output from that model is repeated below.



8.2 Example: Small Cities Pollution Dataset

The following data come from an early study that examined the possible link between air pollution and mortality. The authors examined 60 cities throughout the United States and recorded the following data:

| | |
|----------|---|
| MORT | Total age-adjusted mortality from all causes,
in deaths per 100,000 population |
| PRECIP | Mean annual precipitation (in inches) |
| EDUC | Median number of school years completed
for persons of age 25 years or older |
| NONWHITE | Percentage of the 1960 population that is nonwhite |
| NOX | Relative pollution potential of oxides of nitrogen |
| SO2 | Relative pollution potential of sulfur dioxide |

Note: “Relative pollution potential” refers to the product of the tons emitted per day per square kilometer and a factor correcting the SMSA dimensions and exposure.

We want to predict the value of MORT (y) using the predictors PRECIP, EDUC, NONWHITE, NOX, and SO2 (x_1, x_2, x_3, x_4 and x_5). Here is the GLM output for this model in R:

Call:

```

glm(formula = MORT ~ PRECIP + EDUC + NONWHITE + NOX + SO2,
    family = "gaussian", data = d)

Deviance Residuals:
    Min      1Q  Median      3Q     Max 
-91.38 -18.97 -3.56   16.00   91.83 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 995.63646   91.64099 10.865 3.35e-15 ***
PRECIP       1.40734    0.68914   2.042 0.046032 *  
EDUC        -14.80139   7.02747  -2.106 0.039849 *  
NONWHITE      3.19909    0.62231   5.141 3.89e-06 ***
NOX          -0.10797   0.13502  -0.800 0.427426    
SO2          0.35518    0.09096   3.905 0.000264 *** 
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 1375.723)

Null deviance: 228275  on 59  degrees of freedom
Residual deviance: 74289  on 54  degrees of freedom
AIC: 611.56

```

Number of Fisher Scoring iterations: 2

Side note: Most models can be fit multiple ways. Linear regression models are normally fit using **ordinary least squares** and the `lm` package, as opposed to **maximum likelihood** and the `glm` package. The coefficients and most of the output are exactly the same:

```

Call:
lm(formula = MORT ~ PRECIP + EDUC + NONWHITE + NOX + SO2,
    data = d)

Residuals:
    Min      1Q  Median      3Q     Max 
-91.38 -18.97 -3.56   16.00   91.83 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 995.63646   91.64099 10.865 3.35e-15 ***
PRECIP       1.40734    0.68914   2.042 0.046032 *  
EDUC        -14.80139   7.02747  -2.106 0.039849 *  
NONWHITE      3.19909    0.62231   5.141 3.89e-06 ***
NOX          -0.10797   0.13502  -0.800 0.427426    
SO2          0.35518    0.09096   3.905 0.000264 *** 

```

```

(Intercept) 995.63646   91.64099   10.865 3.35e-15 ***
PRECIP      1.40734    0.68914    2.042 0.046032 *
EDUC       -14.80139   7.02747   -2.106 0.039849 *
NONWHITE     3.19909   0.62231    5.141 3.89e-06 ***
NOX        -0.10797   0.13502   -0.800 0.427426
SO2         0.35518    0.09096    3.905 0.000264 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 37.09 on 54 degrees of freedom
Multiple R-squared:  0.6746, Adjusted R-squared:  0.6444
F-statistic: 22.39 on 5 and 54 DF,  p-value: 4.407e-12

```

Question 8.1

Interpret the values of each of these coefficients. Based on the coefficient values and their standard errors, which predictor(s) do you think have the greatest impact on mortality?

Question 8.2

In this model, is the effect of one predictor (say, PRECIP) impacted by the value(s) of any of the other predictor(s)? How does this differ from the other regression algorithms we've seen (KNN and decision trees)? What are the advantages and disadvantages of this choice?

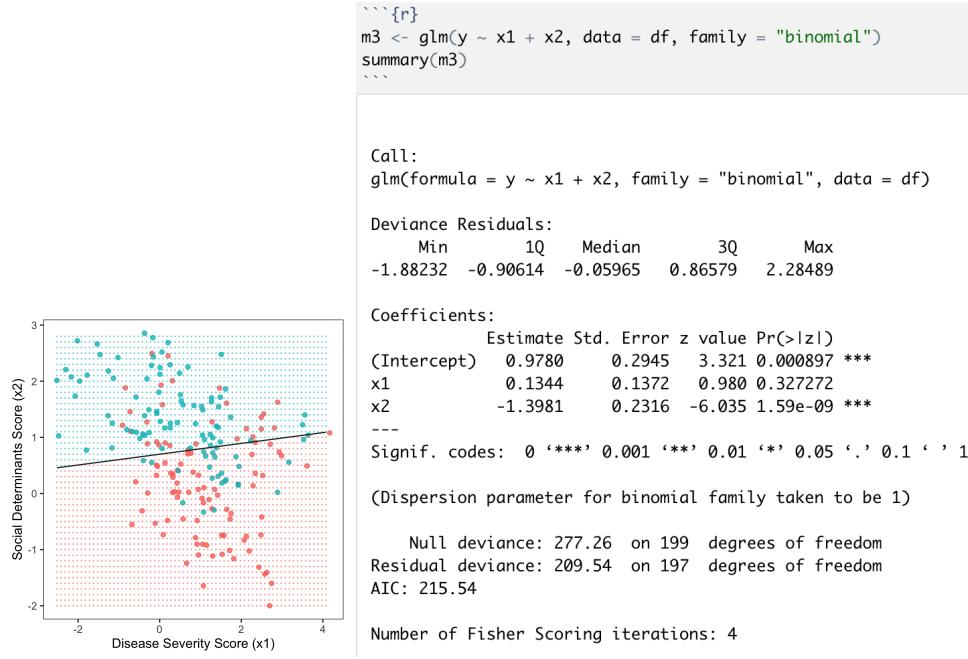
Chapter 9

Interpreting a Logistic Regression Model

This chapter is similar to Chapter 8 but focuses on logistic regression models. We first encountered these models as examples of classification algorithms in Chapter 2. Because of their popularity in the clinical domain, it's important to understand how these models are fit and how to interpret the summary output produced by software.

9.1 ER Readmissions Example from Chapter 2

In Chapter 2, we saw an example where information about two predictors – a disease severity score (x_1) and a social determinants score (x_2) – was used to predict a binary outcome: whether a patient would be readmitted to the ER within 30 days of discharge. We tried three different supervised learning algorithms, one of which was a **logistic regression** model (Section 2.3.1). The output from that model is repeated below.



9.2 Example: Low Birthweight Dataset

The goal of this study was to identify risk factors associated with giving birth to a low birth weight baby (a baby weighing less than 2500 grams). Infant mortality rates and birth defect rates are very high for low birth weight babies. A woman's behavior during pregnancy (including diet, smoking habits, and receiving prenatal care) can greatly alter the chances of carrying the baby to term and, consequently, of delivering a baby of normal birth weight.

Data were collected on 189 women, 59 of which had low birth weight babies and 130 of which had normal birth weight babies.

| | |
|-------|---|
| LOW | Low birth weight (0 = birth weight \geq 2500 g;
1 = birth weight < 2500 g) |
| AGE | Age of mother in years |
| LWT | Mother's weight in pounds at last menstrual period |
| RACE | Race (1 = white, 2 = black, 3 = other) |
| SMOKE | Smoking status during pregnancy (1 = yes, 0 = no) |
| PTL | History of premature labor (0 = none, 1 = one, etc.) |
| HT | History of hypertension (0 = no, 1 = yes) |
| UI | Presence of uterine irritability (0 = no, 1 = yes) |
| FTV | Number of physician visits during the first trimester |
| BWT | Birth weight in grams |

SOURCE: Hosmer and Lemeshow (2000) *Applied Logistic Regression: Second Edition*. Data were collected at Baystate Medical Center, Springfield, Massachusetts during 1986.

We would like to predict LOW based on all of the other covariates except BWT. (Why not use BWT?) The GLM output of this model is:

Call:

```
glm(formula = LOW ~ AGE + LWT + RACE + SMOKE + PTL + HT + UI +
    FTV, family = "binomial", data = d)
```

Deviance Residuals:

| Min | 1Q | Median | 3Q | Max |
|---------|---------|---------|--------|--------|
| -1.8946 | -0.8212 | -0.5316 | 0.9818 | 2.2125 |

Coefficients:

| | Estimate | Std. Error | z value | Pr(> z) |
|----------------|-----------|------------|----------|------------|
| (Intercept) | 0.480623 | 1.196888 | 0.402 | 0.68801 |
| AGE | -0.029549 | 0.037031 | -0.798 | 0.42489 |
| LWT | -0.015424 | 0.006919 | -2.229 | 0.02580 * |
| RACE2 | 1.272260 | 0.527357 | 2.413 | 0.01584 * |
| RACE3 | 0.880496 | 0.440778 | 1.998 | 0.04576 * |
| SMOKE | 0.938846 | 0.402147 | 2.335 | 0.01957 * |
| PTL | 0.543337 | 0.345403 | 1.573 | 0.11571 |
| HT | 1.863303 | 0.697533 | 2.671 | 0.00756 ** |
| UI | 0.767648 | 0.459318 | 1.671 | 0.09467 . |
| FTV | 0.065302 | 0.172394 | 0.379 | 0.70484 |
| <hr/> | | | | |
| Signif. codes: | 0 '***' | 0.001 '**' | 0.01 '*' | 0.05 '.' |
| | 0.1 '' | 1 | | |

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 234.67 on 188 degrees of freedom
Residual deviance: 201.28 on 179 degrees of freedom
AIC: 221.28

Number of Fisher Scoring iterations: 4

Question 9.1

In this model, is the effect of one predictor (say, AGE) impacted by the value(s) of any of the other predictor(s)? How does this differ from the other classification algorithms we've seen (KNN and decision trees)? What are the advantages and disadvantages of this choice?

Question 9.2

Comment on how the variable RACE enters into the model here. Does this make sense in light of what that variable means and how it potentially interacts with the other study variables?

Question 9.3

Interpret the values of each of these coefficients. Based on the coefficient values and their standard errors, which predictor(s) do you think have the greatest impact on whether or not a woman has a low birthweight baby?

Chapter 10

Generalized Linear Models

Generalized linear models (GLMs) are a class of supervised learning models that form a convenient bridge between machine learning and traditional statistics. The basic idea behind a GLM is that your outcome variable (a.k.a. response variable, see Chapter 2), y , follows a probability distribution. The expected value, or mean, of that distribution is related to the values of the predictors (a.k.a. covariates; see Chapters 2 and 3), x_1, \dots, x_p in a model-specific way.

Linear and logistic regression, which we have already seen in Chapters 2, 3, 8, and 9, are both GLMs. Linear regression models data in which the outcome, y , is numeric ($y \in \mathbb{R}$) and follows a normal distribution. Logistic regression models data in which the outcome is binary ($y \in \{0, 1\}$) and follows a Bernoulli distribution¹. There are many more GLMs corresponding to outcomes that follow other types of probability distributions. For example, **loglinear (Poisson) regression** models data in which the outcome is a positive integer, or count ($y \in \{0, 1, 2, \dots\}$).

¹In grouped logistic regression, the outcome follows a binomial distribution. More on that later.

10.1 Model Assumptions

In GLMs, the predictors can be anything – interval, ordinal, or nominal – regardless of the specific model one chooses. However, there are several other assumptions that are important to consider before fitting one of these models:

- We assume that the outcome follows a certain type of distribution (e.g. Bernoulli distribution for a logistic regression model, normal for linear, etc.) conditional on the predictors. This assumption is baked into the model structure. It is, therefore, important to consider whether the outcome distribution you chose actually makes sense for your particular problem. It is generally not advisable to use a linear regression model, for example, when your outcome is a count.
- We assume that the predictors are fixed and known, and thus have no error associated with their measurements².
- We assume that the predictors enter the model as a linear combination. This is why GLMs are referred to as “linear models”.
- We assume that the n samples in our dataset are collected independently, so that the errors of the n sample outcomes are uncorrelated³.

10.2 Modeling the Predictors

All of the GLMs we will see today incorporate a **linear combination** of predictors. A linear combination is an expression constructed from a set of terms by multiplying each term by a constant and adding the results. We denote the number of predictors in the model by p and the vector of predictors by x ,

²Bayesian versions of these models relax this assumption, but we will not encounter these until much later

³Think back to our formulation of the likelihood in Chapter 5 and how it depended on the samples’ being independent and identically distributed, or iid.

where

$$x = \begin{bmatrix} 1 \\ x_1 \\ x_2 \\ \vdots \\ x_p \end{bmatrix}$$

and we have included a “1” as the first element to allow for an **intercept**. We write $x^{(i)}$ to denote the vector of predictors associated with the i th training example. The coefficients of the linear combination (i.e. the model parameters we are hoping to learn) are denoted by:

$$\beta = \begin{bmatrix} \beta_0 \\ \beta_1 \\ \beta_2 \\ \vdots \\ \beta_p \end{bmatrix}$$

and we often express the linear combination as an inner product, written as

$$\beta^T x = \beta_0 + \sum_{j=1}^p \beta_j x_j.$$

Generalized linear models model the **expected value** of the outcome, $E[y]$, as a function of this linear combination of predictors. The function that relates the two is called the **link function**. Different types of GLM use different link functions.

10.3 Linear Regression

The linear regression model has a long history of development before the advent of GLMs, so it’s typically taught in its own course with all of the associated model diagnostics, goodness of fit tests, etc. long before a student ever sees other GLMs. I think a comparative approach is more effective, which

is why we're doing it this way⁴.

10.3.1 Modeling the Outcome

In linear regression, we assume that the outcome, y , follows a normal distribution (see Section 4.2), conditional on the values of the predictors. Recall that the normal distribution is a continuous probability distribution with the following properties:

$$p(y|\mu, \sigma) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{(y-\mu)^2}{2\sigma^2}} \quad E[y|\mu, \sigma] = \mu \quad \text{var}(y|\mu, \sigma) = \sigma^2$$

where $y \in \mathbb{R}$.

10.3.2 Linking the Predictors to the Outcome

In linear regression, the mean of the outcome distribution, which is normal, can be any real number. We therefore use the **identity link**, setting $E[y]$ directly equal to the linear combination of predictors. Since the outcome is normal, we know that $E[y] = \mu$, the mean of the normal distribution. We therefore write:

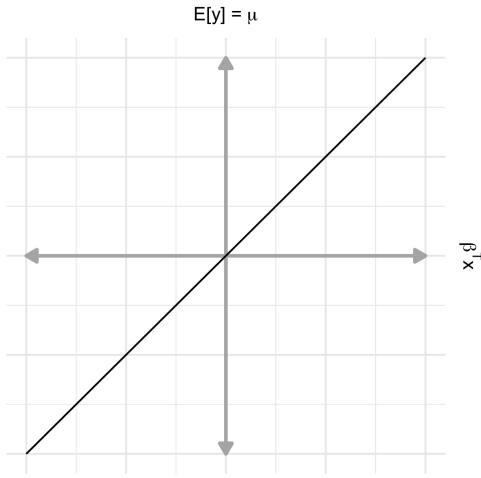
$$E[y] = \mu = \beta^T x \tag{10.1}$$

which is usually rearranged and rewritten as:

$$y = \beta^T x + \varepsilon$$

where $\varepsilon \sim N(0, \sigma^2)$. The relationship between $E[y]$ and $\beta^T x$ is shown below.

⁴The other thing about linear regression models is that they are usually fit using least squares methods instead of maximum likelihood. The parameter estimates are the same in both cases, as we will see much later.



10.4 Logistic Regression

Logistic regression models data where the outcome is binary; i.e. where y is “yes” or “no”. Variants of logistic regression, called **multinomial logistic regression** and the **proportional odds model**, can also be used to model data where the outcome contains multiple categories that either have an ordering (ordinal) or do not (nominal). We will see how this works in a second.

10.4.1 Modeling the Outcome

In logistic regression the outcome, y , is either 0 or 1. We model it using the Bernoulli distribution (see Section 4.3), which is a discrete probability distribution with the following properties:

$$p(y|\mu) = \mu^y(1-\mu)^{1-y} \quad E[y|\mu] = \mu \quad \text{var}(y|\mu) = \mu(1-\mu)$$

where $y \in \{0,1\}$.

10.4.2 Linking the Predictors to the Outcome

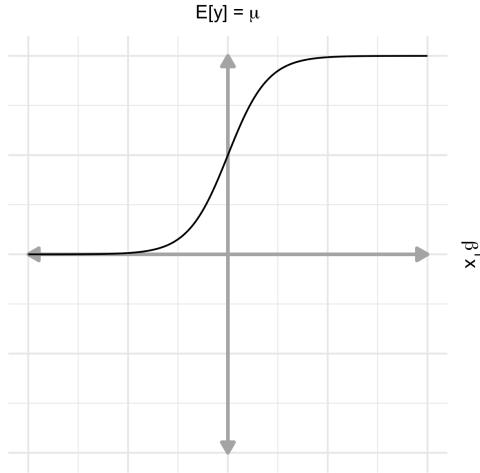
In logistic regression, the mean of the outcome distribution, which is Bernoulli, is a probability. It must therefore be a real number between 0 and 1. No matter how large or small $\beta^T x$ gets, the value of $E[y] = \mu$ cannot be outside this range. We therefore apply the **logistic function**, $f(x) = 1/(1 + \exp(-x))$, which has the range $(0, 1)$, to $\beta^T x$ to squash it:

$$E[y] = \mu = \frac{1}{1 + \exp(-\beta^T x)} \quad (10.2)$$

The relationship between $E[y]$ and $\beta^T x$ is shown below. We typically invert the model to write

$$\log \frac{\mu}{1 - \mu} = \beta^T x$$

which is the standard form of the logistic regression model. The function $\log(\mu/(1 - \mu))$ is called the logit, and in logistic regression we say we use the **logit link**.



10.5 Poisson Regression

In Poisson regression, the outcome is a count. This type of regression is less common than linear and logistic regression, but we include it here mainly

so you can see how the ideas from GLM extend to many different classes of outcome distributions within the exponential family.

10.5.1 Modeling the Outcome

In Poisson regression, we model the outcome using the Poisson distribution, which is a discrete probability distribution with the following properties:

$$p(y|\lambda) = \frac{e^{-\lambda} \lambda^y}{y!} \quad E[y|\lambda] = \lambda \quad \text{var}(y|\lambda) = \lambda$$

where $y \in 0, 1, 2, \dots$

10.5.2 Linking the Predictors to the Outcome

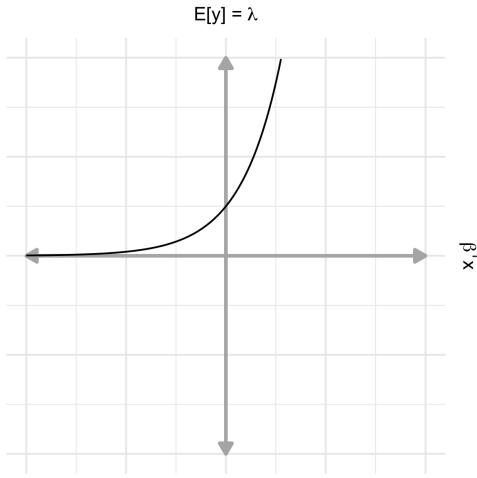
In Poisson regression, the mean of the outcome distribution, which is Poisson, is the expected value of a count. It must therefore be a real number greater than or equal to zero. In particular, no matter how small $\beta^T x$ gets, the value of $E[y] = \lambda$ cannot be negative. We therefore exponentiate $\beta^T x$ to ensure that the result is greater than zero:

$$E[y] = \lambda = \exp(\beta^T x) \tag{10.3}$$

The relationship between $E[y]$ and $\beta^T x$ is shown below. We typically invert the model to write

$$\log(\lambda) = \beta^T x$$

which is the standard form of the Poisson regression model. We say we use the **log link**.



10.6 Maximum Likelihood for GLMs

GLMs are typically fit using maximum likelihood estimation (see Chapter 5). A full treatment of MLE for GLMs is outside the scope of these notes, but I've put the start of the calculations for each type of model below.

10.6.1 Linear Regression

The likelihood for the linear regression model is:

$$\mathcal{L}(\mu^{(1)}, \dots, \mu^{(n)}, \sigma) = \prod_{i=1}^n \frac{1}{\sqrt{2\pi\sigma^2}} \exp \left[-\frac{(y^{(i)} - \mu^{(i)})^2}{2\sigma^2} \right]$$

where we use $\mu^{(i)}$ to represent the model's estimate of the mean of the outcome at the position of training example i . We can use Equation 10.1 to rewrite this as a function of the predictors:

$$\mathcal{L}(\beta, \sigma) = \prod_{i=1}^n \frac{1}{\sqrt{2\pi\sigma^2}} \exp \left[-\frac{(y^{(i)} - \beta^T x^{(i)})^2}{2\sigma^2} \right]$$

Taking the log, we obtain the log-likelihood:

$$\log \mathcal{L}(\beta, \sigma) = -\frac{n}{2} \log(2\pi) - \frac{n}{2} \log(\sigma^2) - \frac{1}{2\sigma^2} \sum_{i=1}^n (y^{(i)} - \beta^T x^{(i)})^2$$

Taking derivatives of the log-likelihood with respect to the β s, we find that we can maximize the likelihood by minimizing the sum-squares: $\sum_{i=1}^n (y^{(i)} - \beta^T x^{(i)})^2$.

10.6.2 Logistic Regression

The likelihood for the logistic regression model is:

$$\mathcal{L}(\mu^{(1)}, \dots, \mu^{(n)}) = \prod_{i=1}^n \mu^{(i)^{y^{(i)}}} (1 - \mu^{(i)})^{1-y^{(i)}}$$

Rewriting this as a function of the predictors, we get:

$$\mathcal{L}(\beta) = \prod_{i=1}^n \left(\frac{1}{1 + \exp(-\beta^T x^{(i)})} \right)^{y^{(i)}} \left(\frac{\exp(-\beta^T x^{(i)})}{1 + \exp(-\beta^T x^{(i)})} \right)^{1-y^{(i)}}$$

Taking the log, we obtain the log-likelihood:

$$\log \mathcal{L}(\beta) = \sum_{i=1}^n \left[-y^{(i)} \log [1 + \exp(-\beta^T x^{(i)})] + (1 - y^{(i)}) \log [1 + \exp(-\beta^T x^{(i)})] \right]$$

Again, we will take derivatives of the log-likelihood with respect to the β s to maximize it. However, we cannot solve for the optimal β s analytically; numerical optimization methods are used to perform the optimization.

10.6.3 Loglinear (Poisson) Regression

The likelihood for the Poisson regression model is:

$$\mathcal{L}(\lambda^{(1)}, \dots, \lambda^{(n)}) = \prod_{i=1}^n \frac{\lambda^{(i)^{y^{(i)}}} e^{-\lambda^{(i)}}}{y^{(i)}!}$$

Rewriting this as a function of the predictors, we get:

$$\mathcal{L}(\beta) = \prod_{i=1}^n \frac{\exp(y^{(i)}\beta^T x^{(i)})e^{-\exp(\beta^T x^{(i)})}}{y^{(i)}!}$$

Taking the log, we obtain the log-likelihood:

$$\log \mathcal{L}(\beta) = \sum_{i=1}^n \left[y^{(i)}\beta^T x^{(i)} - \exp(\beta^T x^{(i)}) - \log(y^{(i)}!) \right]$$

As with logistic regression, we cannot solve for the optimal β s analytically; numerical optimization methods are used.

10.7 Standard Errors and Hypothesis Tests

The magnitudes of the coefficients in these models matter only in relation to:

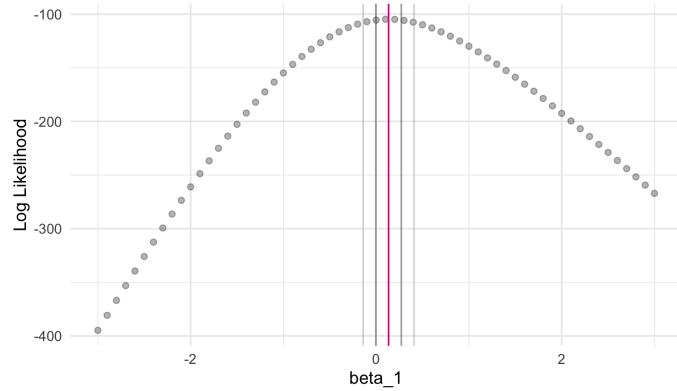
1. The scale on which the predictors are measured.
2. The amount of uncertainty the model has about their values.

For example, if a predictor varies only across a tiny range of values, its model coefficient may be large, since it quantifies the change in the link-function-transformed outcome when the predictor changes by 1.0. However, that doesn't mean that the predictor itself is important to the outcome⁵.

Similarly, the model may be highly uncertain about a coefficient's value, owing to factors like a small dataset (small n) or collinearity among the predictors. Mathematically, high uncertainty means that the value of the likelihood doesn't change very rapidly as you move away from the maximum likelihood estimate of a coefficient. For example, here is how the log-likelihood for the logistic regression example above changes when we vary β_1 (the

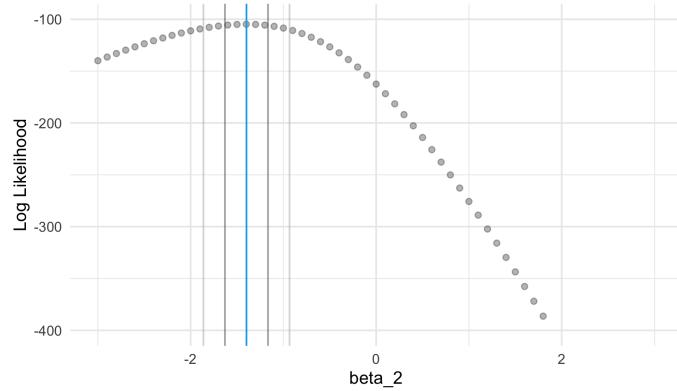
⁵This is one reason many advocate **scaling** and **centering** predictors before fitting a model. Centering means subtracting the mean value of a predictor from all of its individual measurements so that the mean of each centered predictor is zero. Scaling means dividing the values of each predictor by their standard deviation, so that the standard deviation of each predictor is 1.0. This enables the relative magnitudes of the model coefficients to be compared directly.

coefficient of x_1), keeping β_0 (the intercept) and β_2 (the coefficient of x_2) fixed at their MLEs:



The gray vertical lines are related to the **standard error** of the model coefficient, which is in turn related to the “flatness” of the likelihood surface around the MLE. The gray lines are situated at 1 and 2 standard errors away from the MLE in either direction. You can see that in the case of β_1 , the gray lines overlap zero. The value zero (no effect) is a plausible estimate of the impact of x_1 on the outcome.

Contrast this with how the log-likelihood varies around the MLE for β_2 :



Here the standard error is larger, but the magnitude of the coefficient is also larger, so the range of the gray lines does not overlap zero. These findings are reflected in the relative values of the **Z-statistic** (z value) and **P-value**

($\Pr(|z|)$) in the model output for the two coefficients. Whether a coefficient's value is likely to be nonzero is typically evaluated using a formalism called a **hypothesis test**. We will discuss hypothesis tests in much greater detail in Chapter 6.

10.8 Example: Nesting Horseshoe Crabs Dataset

These data come from a study of nesting horseshoe crabs. Each of the 173 observed female horseshoe crabs had a male crab resident in her nest. The study investigated factors affecting whether the female crab had any other males, called *satellites*, residing nearby. (Source: Agresti, *Categorical Data Analysis*, Table 4.3. Data courtesy of Jane Brockmann, Zoology Department, University of Florida; study described in *Ethology* 102: 1-21, 1996.)

| | |
|--------|--|
| SATELL | Number of satellites |
| COLOR | Color of the female crab
(1 = light medium, 2 = medium, 3 = dark medium,
4 = dark) |
| SPINE | Spine condition
(1 = both good, 2 = one weak or broken,
3 = both worn or broken) |
| WIDTH | Carapace width of the female crab (cm) |
| WEIGHT | Weight of the female crab (g) |

The GLM output of this model is:

```

Call:
glm(formula = satell ~ color + spine + width + weight, family = "poisson",
     data = d)

Deviance Residuals:
    Min      1Q  Median      3Q      Max
-3.0126 -1.8846 -0.5406  0.9448   4.9602

Coefficients:
              Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.3435447  0.9684204 -0.355  0.72278

```

```

color      -0.1849325  0.0665236  -2.780  0.00544  **
spine      0.0399764  0.0568062   0.704  0.48160
width      0.0275251  0.0479425   0.574  0.56588
weight     0.0004725  0.0001649   2.865  0.00417  **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for poisson family taken to be 1)

Null deviance: 632.79  on 172  degrees of freedom
Residual deviance: 551.85  on 168  degrees of freedom
AIC: 917.15

Number of Fisher Scoring iterations: 6

```

Question 10.1

Comment on how the variables `color` and `spine` are coded here. Does this make sense in light of what those variables mean?

Question 10.2

Interpret the values of each of these coefficients. Based on the coefficient values and their standard errors, which predictor(s) do you think have the greatest impact on the number of male satellites around a nesting female horseshoe crab?

Chapter 11

Survival Data and the Kaplan-Meier Curve

We have already investigated supervised learning models and hypothesis tests in cases where the outcome of interest is a category or number. But what if the outcome is a *time duration*? For example, what if we're comparing the effects of two treatments and our outcome is the time between treatment administration and disease progression?

Data where the outcome is a time duration are very common in clinical data science and are called **time-to-event** data or **survival data**. The field of **survival analysis** develops methods to analyze and interpret such data. We will examine one such method today and many more in subsequent chapters.

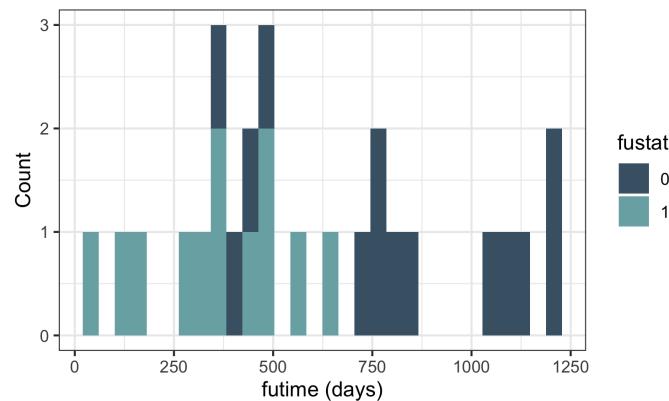
11.1 Example: Ovarian Cancer Survival Dataset

Today we'll examine some data from a study of ovarian cancer¹. The dataset contains information on 26 women. The variables are:

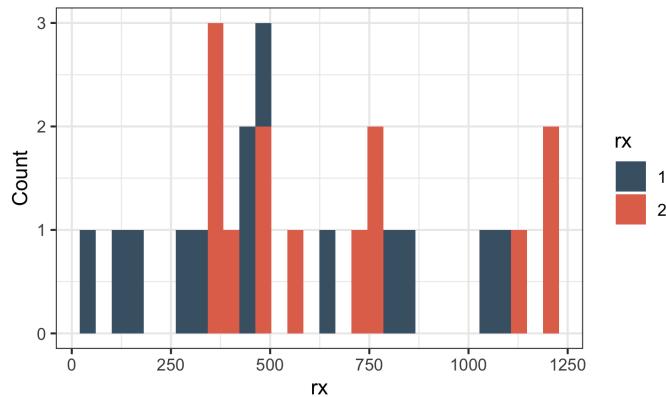
¹The dataset comes from the `survival` package in R and is labeled `ovarian`. The original study is Edmonson JH *et al*, "Different chemotherapeutic sensitivities and host factors affecting prognosis in advanced ovarian carcinoma versus minimal residual disease", *Cancer Treatment Reports*, 63(2): 241-247; 1979.

- `futime`: The number of days from enrollment in the study until death or censoring, whichever came first
- `fustat`: An indicator of death (1) or censoring (0)
- `age`: The patient's age in years at the time of treatment administration
- `resid.ds`: Residual disease present at the time of treatment administration (1 = no, 2 = yes)
- `rx`: Treatment group (1 = cyclophosphamide, 2 = cyclophosphamide + adriamycin)
- `ecog.ps`: A measure of performance score or functional status at the time of treatment administration, using the Eastern Cooperative Oncology Group's (ECOG) scale. It ranges from 0 (fully functional) to 4 (completely disabled). Level 4 subjects are usually considered too ill to enter a randomized trial such as this. The patients in this dataset are all at Levels 1 and 2.

Here is a histogram of the follow-up times (`futime`) in days, colored according to whether the patient died or was censored (`fustat`):



And here is the same graph colored by treatment group (`rx`):



Now, imagine that we want to study the effect of the treatment group (`rx`) on the outcome of death or no death (1 = death, 0 = no death). We could think of this as a classification problem with only a single feature: treatment group. Unfortunately, this method of analyzing time-dependent data is fraught with problems:

1. How do you choose the time horizon at which to evaluate mortality?
2. How do you handle people who dropped out of the study before that time?

11.2 Definitions

Censoring occurs when the event of interest in a time-to-event analysis is not observed. It is a form of missing data problem (see Chapter ??) and can be caused by a variety of factors, including inconsistencies in follow-up, the study's ending before all subjects have experienced the event, or a lack of knowledge about when, exactly, the event occurred. The type of censoring represented in the `ovarian` dataset is called **right-censoring**. We will focus on right-censoring today and investigate other types later.

Right censoring: A situation that arises when the event of interest has not occurred by the end of the follow-up period. This may be because (a) the study itself ends, (b) a patient is lost to follow-up

during the study period, or (c) a patient experiences a different event that makes further follow-up impossible².

Survival data are generally described using two probabilities, called the survival and hazard.

Survival: Also called the **survival function** or **survival probability** and abbreviated $S(t)$, this is the probability that an individual survives to time t (i.e., does not experience the event by time t).

Hazard: Usually denoted by $h(t)$ or $\lambda(t)$, this is the probability that an individual who has not yet experienced the event at time t experiences it at that exact time. In other words, it is the instantaneous event rate for an individual who has already survived to time t .

We will focus on the survival function now and learn more about the hazard later.

11.3 The Kaplan-Meier Estimator

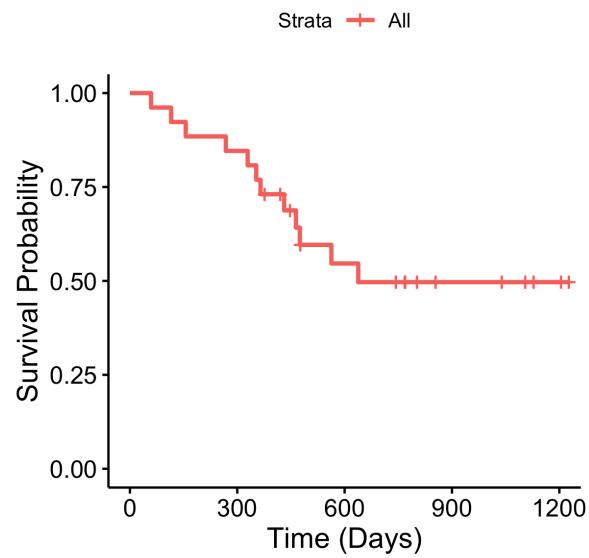
The **Kaplan-Meier estimator** is a nonparametric estimate of the survival function, usually represented graphically by a **Kaplan-Meier curve**³. The Kaplan-Meier estimator looks like this:

$$\hat{S}(t) = \prod_{j|t_j \leq t} \frac{n_j - d_j}{n_j}$$

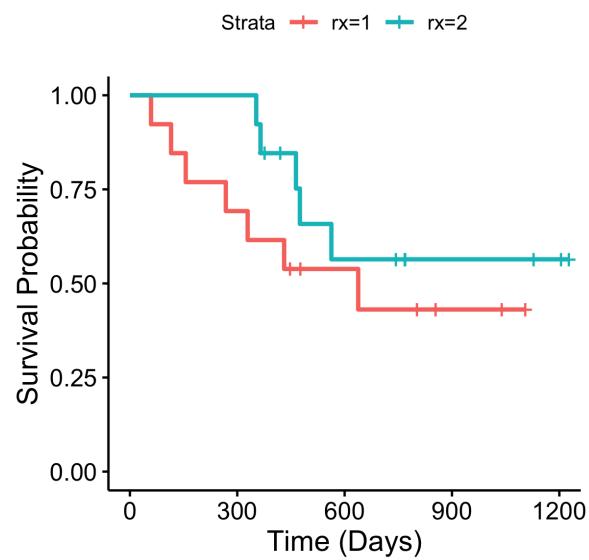
where d_j is the number of subjects who fail at time t_j and n_j is the number of subjects at risk just prior to t_j . Here is a Kaplan-Meier curve for the ovarian dataset. The little “+” signs correspond to censoring events.

²For more information, please see Clark TG *et al*, “Survival Analysis Part I: Basic Concepts and First Analyses”, *British Journal of Cancer*, 89, 232–238; 2003.

³It can be shown mathematically that the Kaplan-Meier estimator is the maximum likelihood estimator (see Chapter 5) of the survival function in the case of censoring.



And here are Kaplan-Meier curves for the two treatment groups separately:



Question 11.1

Here are the raw data from treatment group 1 of the ovarian dataset. Using these data, fill in the remaining cells of the table below.

| | rx | futime | fustat |
|----|----|--------|--------|
| 1 | 1 | 59 | 1 |
| 2 | 1 | 115 | 1 |
| 3 | 1 | 156 | 1 |
| 4 | 1 | 268 | 1 |
| 5 | 1 | 329 | 1 |
| 6 | 1 | 431 | 1 |
| 7 | 1 | 448 | 0 |
| 8 | 1 | 477 | 0 |
| 9 | 1 | 638 | 1 |
| 10 | 1 | 803 | 0 |
| 11 | 1 | 855 | 0 |
| 12 | 1 | 1040 | 0 |
| 13 | 1 | 1106 | 0 |

| j | t_j | n_j | d_j | $\hat{S}(t_j)$ | Calculation |
|----|-------|-------|-------|----------------|---|
| 0 | 0 | 13 | 0 | 1.000 | $\frac{13-0}{13}$ |
| 1 | 59 | 13 | 1 | 0.923 | $\hat{S}(t_0) \left(\frac{13-1}{13} \right)$ |
| 2 | 115 | 12 | 1 | 0.846 | $\hat{S}(t_1) \left(\frac{12-1}{12} \right)$ |
| 3 | 156 | | | | |
| 4 | 268 | | | | |
| 5 | 329 | 9 | 1 | 0.615 | $\hat{S}(t_4) \left(\frac{9-1}{9} \right)$ |
| 6 | 431 | 8 | 1 | 0.538 | $\hat{S}(t_5) \left(\frac{8-1}{8} \right)$ |
| 7 | 448 | 7 | 0 | 0.538 | $\hat{S}(t_6) \left(\frac{7-0}{7} \right)$ |
| 8 | 477 | 6 | 0 | 0.538 | $\hat{S}(t_7) \left(\frac{6-0}{6} \right)$ |
| 9 | 638 | 5 | 1 | 0.431 | $\hat{S}(t_8) \left(\frac{5-1}{5} \right)$ |
| 10 | 803 | 4 | 0 | | |
| 11 | 855 | 3 | 0 | | |
| 12 | 1040 | 2 | 0 | | |
| 13 | 1106 | 1 | 0 | | |

Question 11.2

Based solely on the Kaplan-Meier curves for the two treatment groups, which treatment appears to prolong survival more effectively?

11.4 Assumptions of the Kaplan-Meier Estimator

The Kaplan-Meier estimator makes three important assumptions:

1. The probability of censoring is unrelated to the outcome of interest.
2. The survival probabilities are the same for participants recruited at different times during the study (e.g., circumstances that could alter the survival, such as treatments, do not change over calendar time).
3. The events occurred at exactly the times specified.

Question 11.3

What is one way each of these assumptions could be violated?

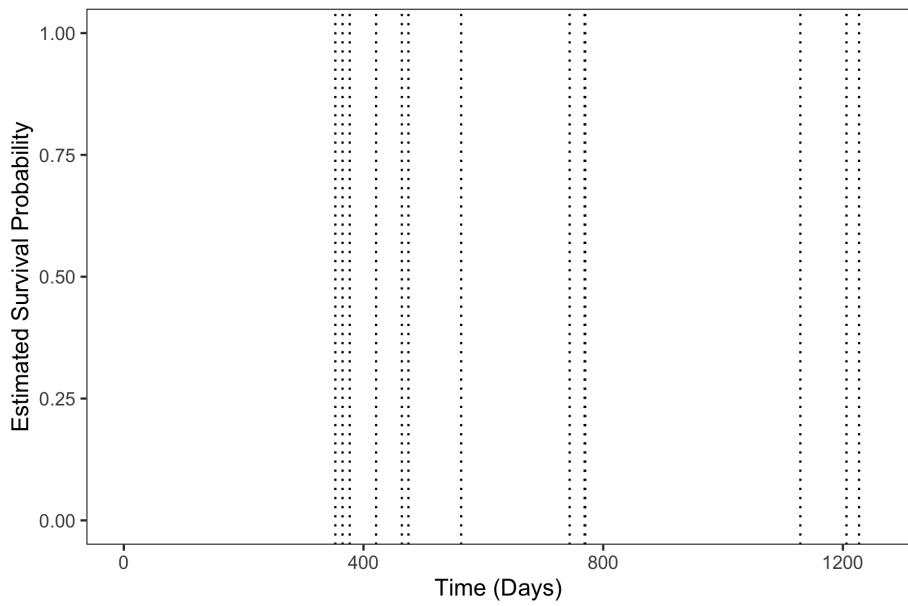
11.5 Comparing Kaplan-Meier Curves

Of course, now the question arises: How do we formally compare two Kaplan-Meier curves? There is a nonparametric hypothesis test for comparing Kaplan-Meier curves called the log-rank test; we will see it in Chapter ???. There is also an entire family of linear models, called Cox proportional hazards models, that use the Kaplan-Meier curve as their backbone and model the effects of different covariates on this curve. We will see them in Chapter ??.

Question 11.4

Here are the data for treatment group 2 of the ovarian dataset. Perform the calculations of $\hat{S}(t_j)$ for $j = 0, \dots, 13$, starting with $t_0 = 0$. Draw the Kaplan-Meier curve, adding symbols for the censoring events.

| | rx | futime | fustat |
|----|----|--------|--------|
| 1 | 2 | 353 | 1 |
| 2 | 2 | 365 | 1 |
| 3 | 2 | 377 | 0 |
| 4 | 2 | 421 | 0 |
| 5 | 2 | 464 | 1 |
| 6 | 2 | 475 | 1 |
| 7 | 2 | 563 | 1 |
| 8 | 2 | 744 | 0 |
| 9 | 2 | 769 | 0 |
| 10 | 2 | 770 | 0 |
| 11 | 2 | 1129 | 0 |
| 12 | 2 | 1206 | 0 |
| 13 | 2 | 1227 | 0 |



Chapter 12

Feature Selection

The methods we've studied in Chapters 2 and 3, as well as all other supervised (and unsupervised) machine learning algorithms, all depend on the concept of a **feature**. A feature is some aspect of each training example that the model designer believes will influence its relationship to the outcome, or that captures some aspect of the data in a way that is relevant to the problem he/she is trying to solve.

Before any algorithm can be applied, therefore, it is necessary to decide how to represent the data: which features to include and how to extract them from the raw data. This task is called **feature engineering**. In most cases, the model designer will also want to incorporate some form of **feature selection**: a process that automatically or semi-automatically decides which features are most relevant to the model and discards the others.

Question 12.1

Choose 2-3 examples from the list of problems in Section 1.1. Describe the setup of each problem and what types of features one would need to collect to build an accurate/useful model.

12.1 Sample Dataset

The so-called “Pima Indians diabetes dataset” was collected in the 1980s. It includes information on 768 women from the Pima people, who live near Phoenix, Arizona. The Pima were, as of the late 1980s, under continuous study by the National Institute of Diabetes and Digestive and Kidney Diseases because of their high incidence of diabetes¹. There are eight predictors in the dataset and one outcome. The predictors are:

| Predictor | Description |
|--------------------------|---|
| Pregnancies | Number of times pregnant |
| Glucose | Plasma glucose concentration in a two-hour oral glucose tolerance test |
| BloodPressure | Diastolic blood pressure (mm Hg) |
| SkinThickness | Triceps skin fold thickness (mm) |
| Insulin | Two-hour serum insulin (μ U/mL) |
| BMI | Body mass index (weight in kg/(height in m) ²) |
| DiabetesPedigreeFunction | Diabetes pedigree function (developed by research team; described in paper) |
| Age | Age in years |

The outcome is whether or not the woman went on to develop type II diabetes within 5 years from the time of the survey.

Question 12.2

Why is coding this outcome as 0/1, or yes/no, potentially problematic?

Question 12.3

What type of problem is this? What methods should we consider when solving this problem? Name at least three learning algorithms that might be appropriate.

¹The causative factors behind this high diabetes rate are not clear. Some scholars believe that it was driven by a sudden shift in diet during the last century from traditional agricultural crops to processed foods, together with a decline in physical activity **schulz2006effects**.

12.2 Feature Engineering

Feature engineering mostly depends on domain expertise. There are three major analytical considerations when performing feature engineering: how the raw data is represented/summarized into features, how those features enter the model (e.g., do they need to be transformed or combined), and how different features are related to each other.

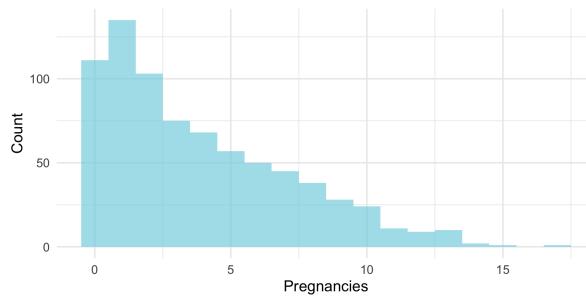
12.2.1 Representation

Rarely will raw data, especially observational data, feed directly into a model. More often, one must decide how to design features that capture aspects of the data that are likely to be important to the model.

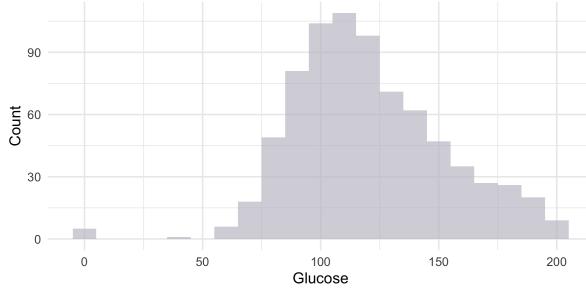
Question 12.4

These histograms show the distributions of the individual predictors in the Pima dataset. In each case, what is one alternative way that the same information could be represented as a feature? For predictors 2–6, what do you think the zero values mean and how should they be dealt with?

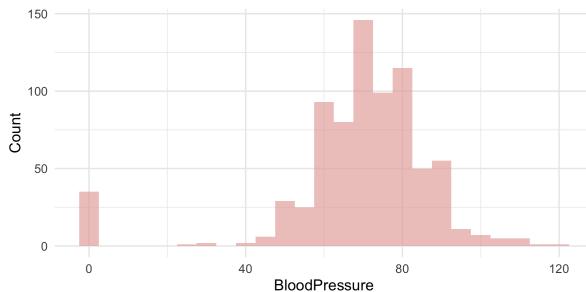
1. Pregnancies



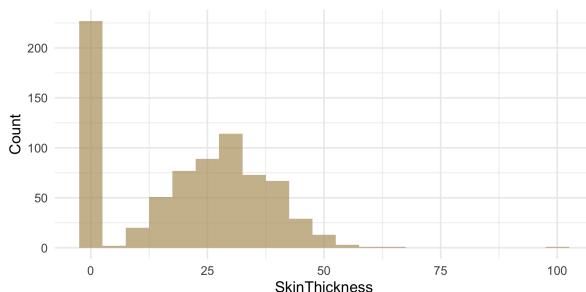
2. Glucose



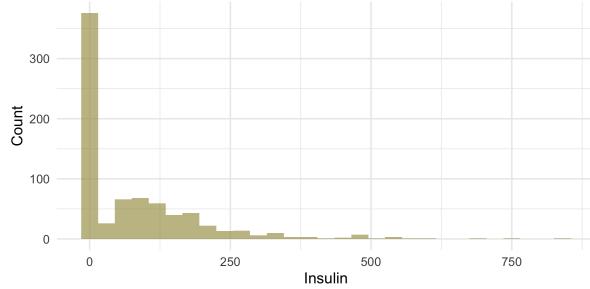
3. BloodPressure



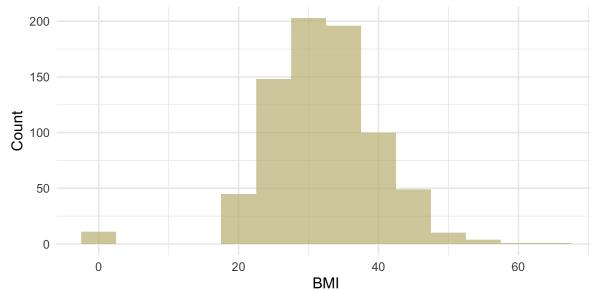
4. SkinThickness



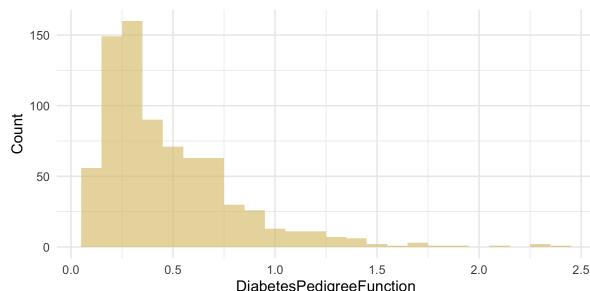
5. Insulin



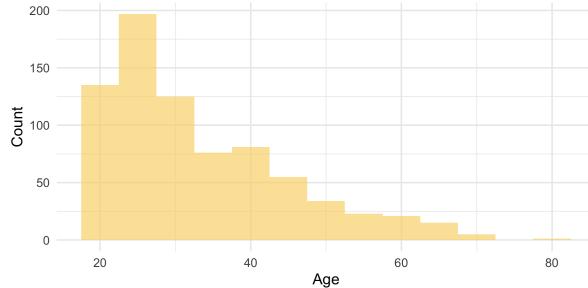
6. BMI



7. DiabetesPedigreeFunction



8. Age



Question 12.5

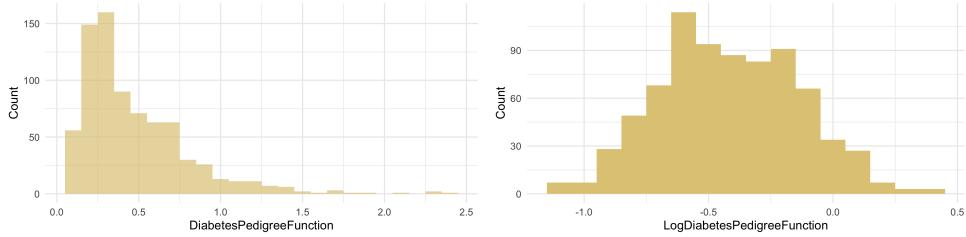
The type of study design here is called a **prospective cohort study**. How would you collect information on these eight predictors if this were a **retrospective cohort study** (e.g., if you collected information about these women and their subsequent development of diabetes from the EHR)? How might this change affect how you extract and code the predictors?

12.2.2 Transformations

Depending on the learning algorithm you’re using and the goal of your project, you may or may not decide to employ transformations. A **transformation** is simply the application of a deterministic mathematical function to your data. In a supervised learning problem, you can transform one or more of the predictors and/or the outcome. Transformations are used to improve the interpretability of the model and/or to ensure that the model fulfills the assumptions of the statistical inference method(s) being used (e.g., a hypothesis test).

For example, here is what happens to the “diabetes pedigree function” predictor in the Pima dataset when we employ a common transformation called a **log transformation**²:

²Here we are using log base 10, but you could also perform a similar transformation with the natural log, \log_2 , etc.



Question 12.6

In the log transformation shown here, we simply replace each value, x , by $\log_{10}(x)$. Every unit increase on a \log_{10} scale corresponds to a 10-fold multiplication on the usual scale of the predictor. If you put the log-transformed predictor into a regression model in place of the original (linear is the easiest to understand, but you could also consider logistic, Poisson, etc.), how would that change your interpretation of the model?

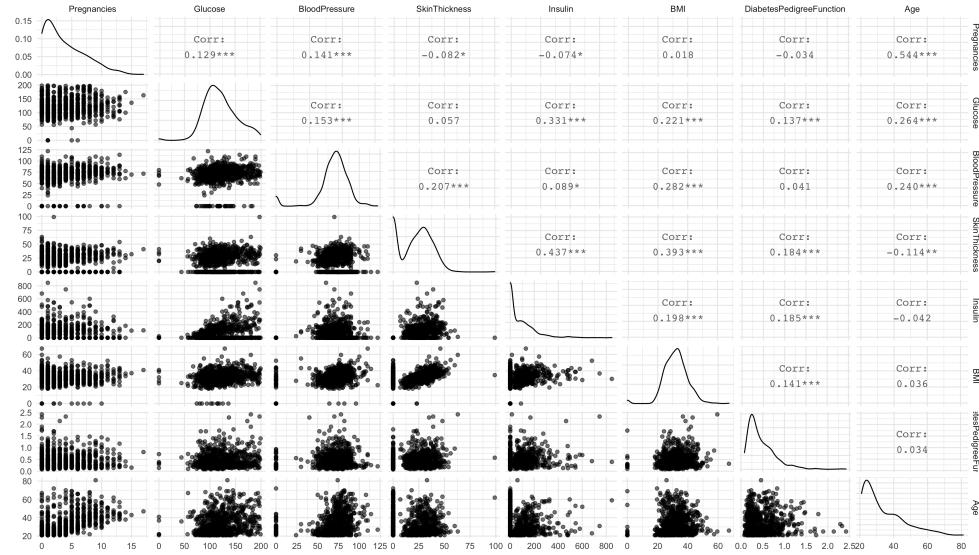
Political science, economics, sociology, and related disciplines, which are heavily dependent on the use of linear regression models and hypothesis tests, rely extensively on transformations. In my experience, machine learning folks spend almost no time on them because their primary concern is predictive accuracy, not model interpretation. Machine learning practitioners, however, very frequently **scale and center** their predictors (see footnote in Section 10.7), which is another type of transformation. We will get into more detail on transformations as we continue to learn about regression models.

12.2.3 Correlations and Redundancy

Including dozens or hundreds of predictors in a model does not guarantee that each contributes independent information. A good rule of thumb for any model is that it should be **parsimonious**: it should accomplish its goal with as little complexity and as few parameters as possible.

Finding a parsimonious model often means identifying sources of redundancy in a dataset. Often, two or more variables will be **correlated**, meaning that the value of one provides at least some information about the value of the other(s). A good way to alert yourself to the presence of highly correlated predictors is to create some sort of **correlogram**, or scatterplot matrix, which

looks at associations between all pairs of variables. A correlogram for the Pima dataset is below.



Question 12.7

This correlogram quantifies correlation using a metric called the **Pearson correlation coefficient**. Which pairs of predictors are the most tightly correlated? Are they positively or negatively correlated? How might you modify your dataset to eliminate redundancies in the information contributed by the different predictors?

Including correlated predictors is not always a bad thing, especially if your goal is prediction rather than model interpretation (see [guyon2003introduction](#), Figures 1, 2, and 3). The presence of correlations will also affect different types of models in different ways, and some suffer more than others.

For example, here are eight univariate logistic regression models that capture the effect of each predictor in the Pima dataset on the outcome of diabetes vs. no diabetes:

```

Call:
glm(formula = Outcome ~ Pregnancies, family = "binomial", data = d)
Deviance Residuals:
    Min      1Q   Median     3Q     Max
-1.4433 -0.8741 -0.7782  1.2707  1.7003
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -1.17675   0.12312 -9.558 <2e-16 ***
Pregnancies  0.13716   0.02291  5.986 2.15e-09 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 993.48 on 767 degrees of freedom
Residual deviance: 956.21 on 766 degrees of freedom
AIC: 960.21

Number of Fisher Scoring iterations: 4

Call:
glm(formula = Outcome ~ Glucose, family = "binomial", data = d)
Deviance Residuals:
    Min      1Q   Median     3Q     Max
-2.1096 -0.7837 -0.5365  0.8566  3.2726
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -5.350080  0.420827 -12.71 <2e-16 ***
Glucose      0.037873  0.003252  11.65 <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 993.48 on 767 degrees of freedom
Residual deviance: 808.72 on 766 degrees of freedom
AIC: 812.72

Number of Fisher Scoring iterations: 4

Call:
glm(formula = Outcome ~ BloodPressure, family = "binomial", data = d)
Deviance Residuals:
    Min      1Q   Median     3Q     Max
-1.0797 -0.9389 -0.9000  1.4097  1.6838
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -1.140092  0.299822 -3.893 0.000143 ***
BloodPressure 0.007425  0.004141  1.793 0.072994 .
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 993.48 on 767 degrees of freedom
Residual deviance: 990.13 on 766 degrees of freedom
AIC: 994.13

Number of Fisher Scoring iterations: 4

Call:
glm(formula = Outcome ~ SkinThickness, family = "binomial", data = d)
Deviance Residuals:
    Min      1Q   Median     3Q     Max
-1.0781 -0.9455 -0.8508  1.3900  1.5439
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -0.829853  0.126816 -6.544 6e-11 ***
SkinThickness 0.009862  0.004773  2.066 0.0388 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 993.48 on 767 degrees of freedom
Residual deviance: 989.19 on 766 degrees of freedom
AIC: 993.19

Number of Fisher Scoring iterations: 4

Call:
glm(formula = Outcome ~ BMI, family = "binomial", data = d)
Deviance Residuals:
    Min      1Q   Median     3Q     Max
-1.9209 -0.9178 -0.6838  1.2351  2.7244
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -3.68641   0.40896 -9.014 <2e-16 ***
BMI         0.09353   0.01205  7.761 8.45e-15 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 993.48 on 767 degrees of freedom
Residual deviance: 920.71 on 766 degrees of freedom
AIC: 924.71

Number of Fisher Scoring iterations: 4

Call:
glm(formula = Outcome ~ Age, family = "binomial", data = d)
Deviance Residuals:
    Min      1Q   Median     3Q     Max
-1.7809 -0.8512 -0.7505  1.2811  1.6950
Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept) -2.047511  0.238847 -8.572 <2e-16 ***
Age        0.042026  0.006587  6.380 1.77e-10 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 993.48 on 767 degrees of freedom
Residual deviance: 950.72 on 766 degrees of freedom
AIC: 954.72

Number of Fisher Scoring iterations: 4

```

The coefficients on each predictor here are called the **unadjusted coefficients**, and the p-values on the predictor-specific hypothesis tests are called **unadjusted p-values**. If you exponentiate a coefficient in a univariate logistic regression model, you get an **unadjusted odds ratio**³. Here is a summary table:

| Predictor | Unadjusted
Coefficient | Unadjusted
Odds Ratio | Unadjusted
P-value |
|--------------------------|---------------------------|--------------------------|-----------------------|
| Pregnancies | 0.137 | 1.147 | <0.001 |
| Glucose | 0.038 | 1.039 | <0.001 |
| BloodPressure | 0.007 | 1.007 | 0.073 |
| SkinThickness | 0.010 | 1.010 | 0.039 |
| Insulin | 0.002 | 1.002 | <0.001 |
| BMI | 0.094 | 1.100 | <0.001 |
| DiabetesPedigreeFunction | 1.083 | 2.953 | <0.001 |
| Age | 0.042 | 1.043 | <0.001 |

Now let's create one big logistic regression model that includes all eight predictors. This is called a **multivariate** model. The coefficients, exponentiated coefficients, and p-values are often called **adjusted** in this case, or one might say that the odds ratio measures the effect of one predictor, **controlling for** the effects of the other predictors. Here are the adjusted estimates:

| Predictor | Adjusted
Coefficient | Adjusted
Odds Ratio | Adjusted
P-value |
|--------------------------|-------------------------|------------------------|---------------------|
| Pregnancies | 0.123 | 1.131 | <0.001 |
| Glucose | 0.035 | 1.036 | <0.001 |
| BloodPressure | -0.013 | 0.987 | 0.011 |
| SkinThickness | 0.001 | 1.001 | 0.929 |
| Insulin | -0.001 | 0.999 | 0.186 |
| BMI | 0.090 | 1.094 | <0.001 |
| DiabetesPedigreeFunction | 0.945 | 2.573 | 0.002 |
| Age | 0.015 | 1.015 | 0.111 |

³See Chapter 10 if you don't understand why you're exponentiating or where the term "odds ratio" comes from. The odds ratio compares the odds of having a positive outcome among two groups separated by a one unit difference of the predictor in question, all else being the same.

Question 12.8

How can the odds ratio for Insulin be so close to 1.0 yet its p-value so low? (Hint: See Section 10.7.)

Question 12.9

Why might the coefficient and p-value for SkinThickness change so much in the shift from unadjusted to adjusted?

12.3 Feature Selection

The process of feature selection is largely about eliminating redundancies and useless predictors in an effort to come up with the most parsimonious model possible. In many cases, it is also about increasing the accuracy of model interpretation. There are three basic approaches to feature selection: filters, wrappers, and embedded methods.

12.3.1 Filters

Filter methods select subsets of variables as a preprocessing step, *independently of the chosen model*. These methods use **proxy measures** to rank variables; the proxy measure is often chosen to be computationally fast so that large numbers of features can be sifted through quickly.

A predetermined threshold of the proxy measure is usually used to determine which features pass to the multivariate modeling stage. Alternatively, the modeler may decide on a fixed number of features to include. Some examples of filter methods include:

- Any kind of univariate model (e.g. univariate logistic or linear regression)
- Any kind of hypothesis test (e.g. t-test, chi-squared test; see Chapter 6)
- Any kind of correlation coefficient (e.g. Pearson, Spearman)

- Mutual information⁴

$$MI(X_i, Y) = \sum_x \sum_y P(X_i = x, Y = y) \log \frac{P(X_i = x, Y = y)}{P(X_i = x)P(Y = y)}$$

- Variance thresholding (simply remove features with low variance)

Question 12.10

If you wanted to use the univariate logistic regression models above in Section 12.2.3 as a filter for a downstream model (potentially not even multivariate logistic regression - it could be a decision tree, etc.), how would you rank them and how would you decide on an appropriate cutoff?

Question 12.11

How would you apply a filter-based selection method in a case where you had dozens of different predictors of different types (e.g. some categorical, some binary, some numeric)?

Question 12.12

How might you choose the appropriate threshold for a filter-based method in a data-driven way?

Question 12.13

What is problematic about testing each potential feature, one at a time?

12.3.2 Wrappers

Wrapper methods use a search algorithm to traverse the space of possible features, evaluating each subset by running the chosen model using that subset. They are generally computationally intensive (e.g., imagine trying to

⁴The mutual information, in another format, is the most common splitting criterion used for decision trees; see Chapter 7. In the case of continuous variables, the sums are replaced by integrals.

find the optimal subset of 10,000 features, or even 50) so **heuristics** generally have to be used to pare down the search space. Some examples of wrapper methods include:

- **Exhaustive search.** Try all possible subsets of features. If there are m features, this means trying 2^m possible subsets.
- **Forward selection.** Start with a baseline (e.g., intercept only) model. Add in each of m possible predictors individually and take the best one based on some performance criterion. Repeat, adding one predictor at each step, until the performance criterion stops getting better or you run out of predictors.
- **Backward elimination.** Start with a complete model (all predictors included). Try removing each predictor and take the one whose removal causes the performance criterion to increase the most. Repeat, removing one predictor at each step, until the performance criterion stops getting better or you are left with no predictors (null model).
- **Forward-backward selection.** A combination of forward selection and backward elimination.
- **Simulated annealing.** Add or remove predictors with some probability depending on how well the model is doing. At each stage, if the new model is better, accept it; it becomes the new baseline. If the new model is worse, accept it with some probability, p , that decreases over time according to a “cooling schedule”. This helps prevent the variable selection process from getting stuck in local optima.

Question 12.14

Why is exhaustive search problematic for almost any reasonably sized m ?

Question 12.15

Here is the output of forward selection for the Pima example, using R’s MASS package and the **Akaike Information Criterion (AIC)** as the model performance metric.

Start: AIC=995.48

Outcome ~ 1

| | Df | Deviance | AIC |
|----------------------------|----|----------|--------|
| + Glucose | 1 | 808.72 | 812.72 |
| + BMI | 1 | 920.71 | 924.71 |
| + Age | 1 | 950.72 | 954.72 |
| + Pregnancies | 1 | 956.21 | 960.21 |
| + DiabetesPedigreeFunction | 1 | 970.86 | 974.86 |
| + Insulin | 1 | 980.81 | 984.81 |
| + SkinThickness | 1 | 989.19 | 993.19 |
| + BloodPressure | 1 | 990.13 | 994.13 |
| <none> | | 993.48 | 995.48 |

Step: AIC=812.72

Outcome ~ Glucose

| | Df | Deviance | AIC |
|----------------------------|----|----------|--------|
| + BMI | 1 | 771.40 | 777.40 |
| + Pregnancies | 1 | 784.95 | 790.95 |
| + DiabetesPedigreeFunction | 1 | 796.99 | 802.99 |
| + Age | 1 | 797.36 | 803.36 |
| <none> | | 808.72 | 812.72 |
| + SkinThickness | 1 | 807.07 | 813.07 |
| + Insulin | 1 | 807.77 | 813.77 |
| + BloodPressure | 1 | 808.59 | 814.59 |

Step: AIC=777.4

Outcome ~ Glucose + BMI

| | Df | Deviance | AIC |
|----------------------------|----|----------|--------|
| + Pregnancies | 1 | 744.12 | 752.12 |
| + Age | 1 | 755.68 | 763.68 |
| + DiabetesPedigreeFunction | 1 | 762.87 | 770.87 |
| + Insulin | 1 | 767.79 | 775.79 |
| + BloodPressure | 1 | 769.07 | 777.07 |
| <none> | | 771.40 | 777.40 |
| + SkinThickness | 1 | 770.20 | 778.20 |

Step: AIC=752.12

Outcome ~ Glucose + BMI + Pregnancies

| | Df | Deviance | AIC |
|----------------------------|----|----------|--------|
| + DiabetesPedigreeFunction | 1 | 734.31 | 744.31 |
| + BloodPressure | 1 | 738.43 | 748.43 |
| + Age | 1 | 742.10 | 752.10 |

```

<none>                      744.12 752.12
+ Insulin                     1    742.43 752.43
+ SkinThickness                1    743.60 753.60

Step: AIC=744.31
Outcome ~ Glucose + BMI + Pregnancies +
          DiabetesPedigreeFunction

              Df Deviance     AIC
+ BloodPressure   1    728.56 740.56
+ Insulin         1    731.51 743.51
<none>                  734.31 744.31
+ Age             1    732.51 744.51
+ SkinThickness   1    733.06 745.06

Step: AIC=740.56
Outcome ~ Glucose + BMI + Pregnancies +
          DiabetesPedigreeFunction +
          BloodPressure

              Df Deviance     AIC
+ Age             1    725.46 739.46
+ Insulin         1    725.97 739.97
<none>                  728.56 740.56
+ SkinThickness   1    728.00 742.00

Step: AIC=739.46
Outcome ~ Glucose + BMI + Pregnancies +
          DiabetesPedigreeFunction +
          BloodPressure + Age

              Df Deviance     AIC
+ Insulin         1    723.45 739.45
<none>                  725.46 739.46
+ SkinThickness   1    725.19 741.19

Step: AIC=739.45
Outcome ~ Glucose + BMI + Pregnancies +
          DiabetesPedigreeFunction +
          BloodPressure + Age + Insulin

              Df Deviance     AIC
<none>                  723.45 739.45
+ SkinThickness   1    723.45 741.45

```

What does the final model look like? Which predictor is missing from the final model? Note: AIC is an estimate of out-of-sample prediction error and depends on the likelihood; thus it does not work for models that do not calculate some form of likelihood.

Question 12.16

Here is the output of backward selection for the Pima example, again using R's MASS package and AIC as the model performance metric.

```

Start:  AIC=741.45
Outcome ~ Pregnancies + Glucose + BloodPressure + SkinThickness +
          Insulin + BMI + DiabetesPedigreeFunction + Age

                    Df Deviance    AIC
- SkinThickness      1   723.45 739.45
- Insulin            1   725.19 741.19
<none>                  723.45 741.45
- Age                1   725.97 741.97
- BloodPressure       1   729.99 745.99
- DiabetesPedigreeFunction 1   733.78 749.78
- Pregnancies         1   738.68 754.68
- BMI                1   764.22 780.22
- Glucose             1   838.37 854.37

Step:  AIC=739.45
Outcome ~ Pregnancies + Glucose + BloodPressure + Insulin + BMI +
          DiabetesPedigreeFunction + Age

                    Df Deviance    AIC
<none>                  723.45 739.45
- Insulin            1   725.46 739.46
- Age                1   725.97 739.97
- BloodPressure       1   730.13 744.13
- DiabetesPedigreeFunction 1   733.92 747.92
- Pregnancies         1   738.69 752.69
- BMI                1   768.77 782.77
- Glucose             1   840.87 854.87

```

What does the final model look like? How does it compare to the model obtained through forward selection?

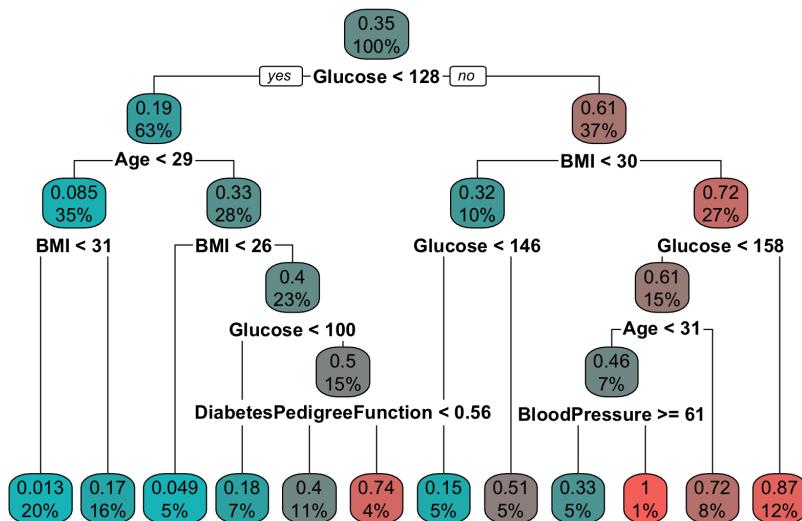
12.3.3 Embedded Methods

Embedded methods perform feature selection during the process of model training. They are usually specific to a particular type of model.

One example of an embedded method is a decision tree (see Chapter 7), which implicitly performs feature selection by placing the most informative predictors at the top of the tree and ignoring those that are unassociated with the outcome.

Question 12.17

Here is the decision tree produced by CART, using information gain/mutual information as the splitting criterion as usual:



Which features were selected for this tree and which were ignored? How were the features transformed from their original forms in the dataset?

Another example of an embedded method is **regularization**. The easiest way to understand regularization is through our discussion of maximum likelihood estimation for GLMs in Chapter 10. The goal of maximum likelihood

estimation is to find the set of model coefficients, β s, that maximize the joint probability (likelihood) of our observed data given the model. The trouble with this is that more complex models, with more parameters, will generally fit the data better: i.e. produce a higher likelihood.

Regularization addresses this by introducing a penalty term on the likelihood that is proportional to the size of the parameters. In L_1 regularization, a.k.a. **Lasso**, the penalty term is proportional to the absolute values of the coefficients. It looks like this:

$$\lambda \sum_{j=1}^p |\beta_j|$$

where p is the number of predictors. This creates a tradeoff in the model between the likelihood and the number of parameters. During optimization, the model will set the coefficients on predictors to zero if including those predictors does not sufficiently improve the likelihood. The relative importance of the penalty term and likelihood is adjusted using the parameter λ . We will see regularized regression methods in much greater detail in Chapter ??.

Question 12.18

Here is the raw model output from the multivariate logistic regression model that includes all eight predictors:

```

Call:
glm(formula = Outcome ~ . - LogDiabetesPedigreeFunction, family = "binomial",
     data = d)

Deviance Residuals:
    Min      1Q      Median      3Q      Max 
-2.5566 -0.7274 -0.4159  0.7267  2.9297 

Coefficients:
              Estimate Std. Error z value Pr(>|z|)    
(Intercept) -8.4046964  0.7166359 -11.728 < 2e-16 ***
Pregnancies   0.1231823  0.0320776   3.840 0.000123 ***
Glucose       0.0351637  0.0037087   9.481 < 2e-16 ***
BloodPressure -0.0132955  0.0052336  -2.540 0.011072 *  
SkinThickness  0.0006190  0.0068994   0.090 0.928515  
Insulin        -0.0011917  0.0009012  -1.322 0.186065  
BMI            0.0897010  0.0150876   5.945 2.76e-09 ***
DiabetesPedigreeFunction 0.9451797  0.2991475   3.160 0.001580 ** 
Age             0.0148690  0.0093348   1.593 0.111192  
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1

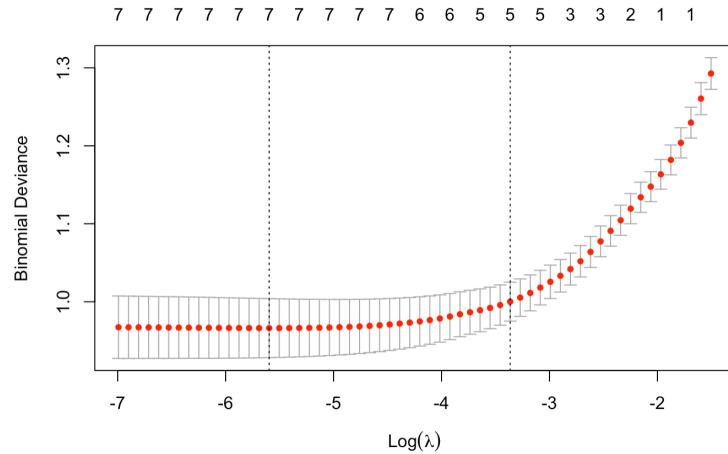
(Dispersion parameter for binomial family taken to be 1)

Null deviance: 993.48 on 767 degrees of freedom
Residual deviance: 723.45 on 759 degrees of freedom
AIC: 741.45

Number of Fisher Scoring iterations: 5

```

Now let's consider what happens when we use a L_1 regularized logistic regression model, produced using the R package *glmnet*. Here is what happens to the model's error (assessed using 10-fold cross validation; measured using a metric called **binomial deviance**) when we vary λ :



Measure: Binomial Deviance

| | Lambda | Measure | SE | Nonzero |
|-----|----------|---------|---------|---------|
| min | 0.004468 | 0.9686 | 0.02647 | 7 |
| 1se | 0.028723 | 0.9922 | 0.02118 | 5 |

We choose λ to be equal to the value that produces the minimum deviance. Here are the coefficients of the final model:

```
9 x 1 sparse Matrix of class "dgCMatrix"
   1
(Intercept) -8.048785391
Pregnancies  0.115632123
Glucose      0.033559189
BloodPressure -0.010901115
SkinThickness .
Insulin      -0.000837989
BMI          0.083305233
DiabetesPedigreeFunction 0.847558021
Age          0.013503422
```

Compare this output to the results of models obtained through forward and backward selection methods, as well as to the full (unregularized) logistic regression model. What are the advantages and disadvantages of the regularization approach vs. wrappers and filters?

Chapter 13

Model Complexity and the Bias-Variance Tradeoff

In classification, **model complexity** (i.e. the effective number of parameters the model must fit) is typically related to the intricacy and complexity of the decision boundary; the more parameters in the model, the more complex the boundary.

13.1 Goodness of Fit vs. Generalizability

Training vs. test error

13.2 Bias vs. Variance

This figure shows the training and test error for KNN as a function of K for a classification example similar to the one discussed in Chapter 2, as well as the training and test error for a linear model (which doesn't vary with K). You can see that the curves have characteristic shapes that vary with K . It turns out these shapes reflect a general principle for all supervised learning called the **bias-variance tradeoff**.

The bias-variance tradeoff: KNN example. The Bayes error rate, or ir-

reducible error, is the probability an instance is misclassified by a classifier that knows the true class probabilities given the predictors. From *Elements of Statistical Learning*, Figure 2.4.

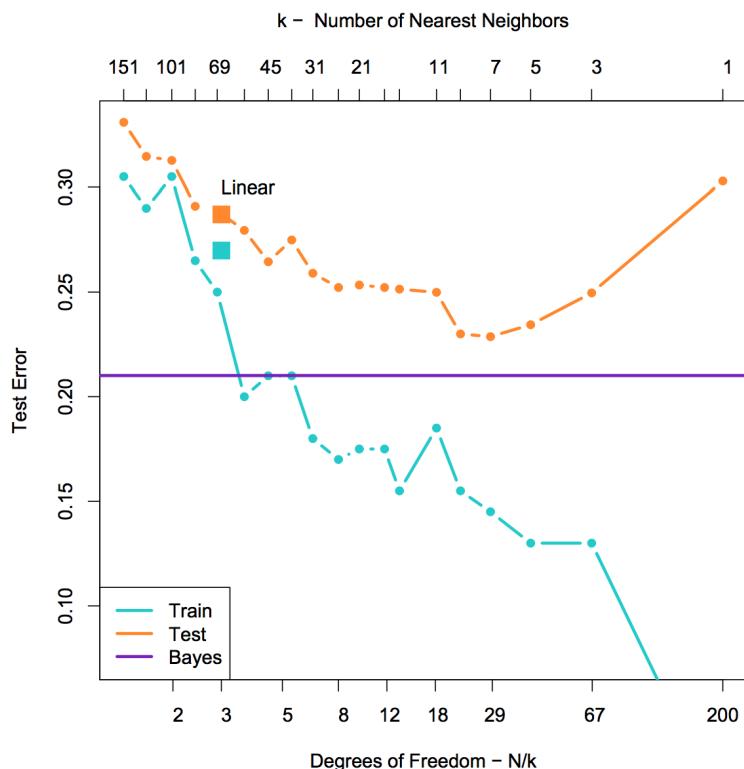
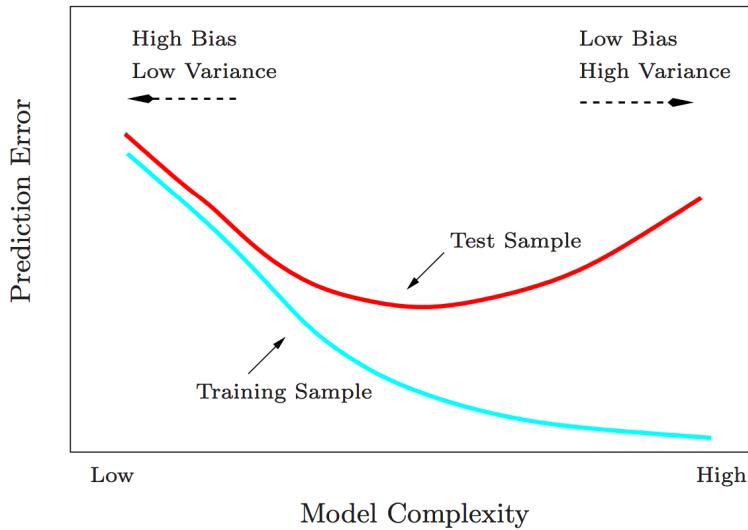
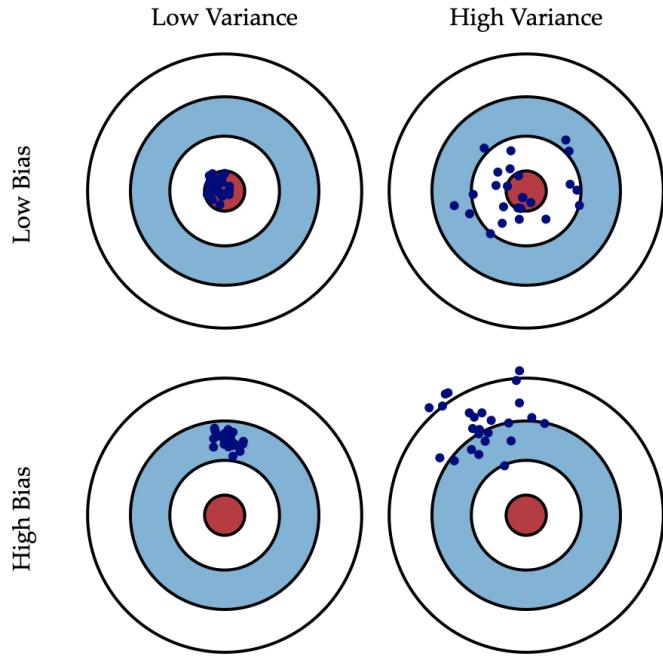


Illustration of training vs. test error as a function of model complexity, as well as the bias-variance tradeoff. From *Elements of Statistical Learning*, Figure 2.11.



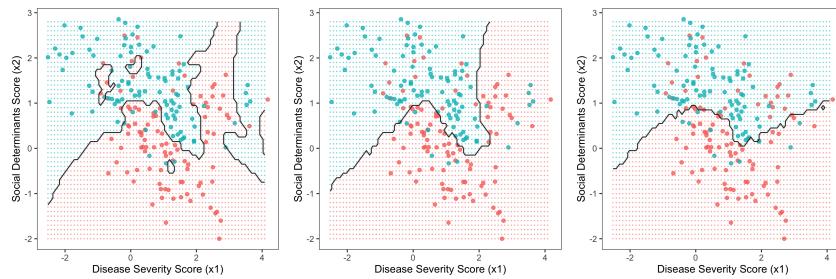
A graphical illustration of the difference between bias and variance. Think of each dot as representing a single test example evaluated under the same model trained on slightly different datasets. The center of the target is the prediction the model should make for that test example. In the case of high bias and low variance, all of the models are off, but they are “wrong in the same way”. If you average their predictions, the answer is still way off the mark. In the case of high variance, the models all make very different predictions on the same training example. However, their predictions are off in random directions from the center, so if you average their outputs, you’ll get closer to the right answer.



13.3 Overfitting vs. Underfitting

Question 13.1

What are the advantages and disadvantages of KNN with low K (e.g. $K = 3$) vs. high K (e.g. $K = 50$)? The decision boundaries for the previous example with (left to right) $K = 3, 15$, and 50 are shown below.



Question 13.2

We have discussed bias and variance in the context of classification (a yes/no outcome). How would training and test error, overfitting vs. underfitting, etc. be quantified if the outcome was a number, as in a regression problem (Chapter 3)?