

Chapter 1

Overview of Clinical Data Science DRAFT

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.

So why is data science considered its own thing, and why am I creating a separate course about it instead of pointing you to Khan Academy, Coursera, etc., all of which have excellent courses on these various technical domains? Because (a) if you tried to learn data science that way, you’d never get anywhere; there are simply too many different subjects you’d have to master,

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

and (b) clinical data has issues that are domain-specific, and that rarely come up in general courses on machine learning and related topics. Many times I will think I know what method to use to solve a particular problem, but then when it comes time to gather the data, unusual and unforeseen problems arise. This happens all the time to all of the biomedical and clinical data science researchers I know, and it is particularly problematic for people who are encountering data analysis and statistical/machine learning methods for the first time. Many assume the problem is them and give up, when in reality they are encountering a genuine difficulty with the data they're working with that the folks doing ad recommendations at Google never have to face.

However, my main reason for doing this is that I believe clinical and operational teams will increasingly come to rely on data, and that the people on those teams who can confidently interact with data will be our future leaders. And I'd like those people to be you.

1.1 Project Examples

Whenever I teach, I ask students to provide some examples of projects for which they think data and machine learning/statistics could be useful. The following are real examples. There are many and some of them are long, but I encourage you to read through all of them to see the diversity of problems that physicians and folks working in population health, health system operations, etc. come up with.

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."

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

1.2 A Taxonomy of Problems

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

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

Question 2

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

Question 3

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

Question 4

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

Question 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

TODO

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.

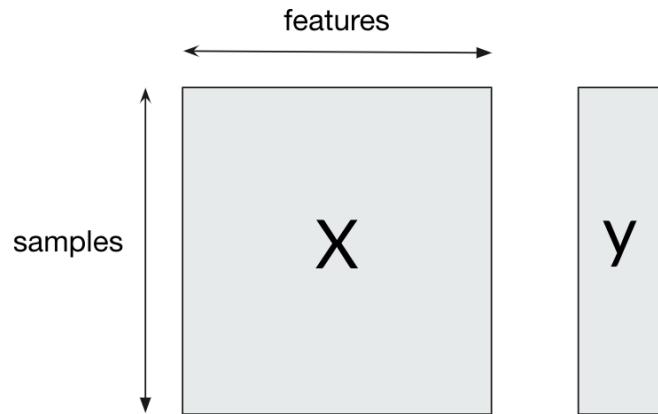
We can think of a clinical trial, therefore, as an experiment in which we control the intervention.

1.3.3 Prospective vs. Retrospective

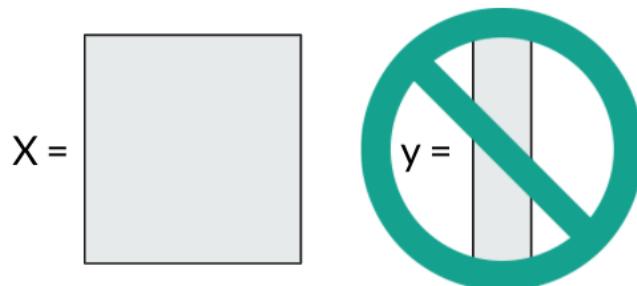
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1.3.4 Supervised vs. Unsupervised Learning

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 and the algorithm learns to recognize patterns or structure in the inputs. The general setup for unsupervised learning looks like this:



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

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.

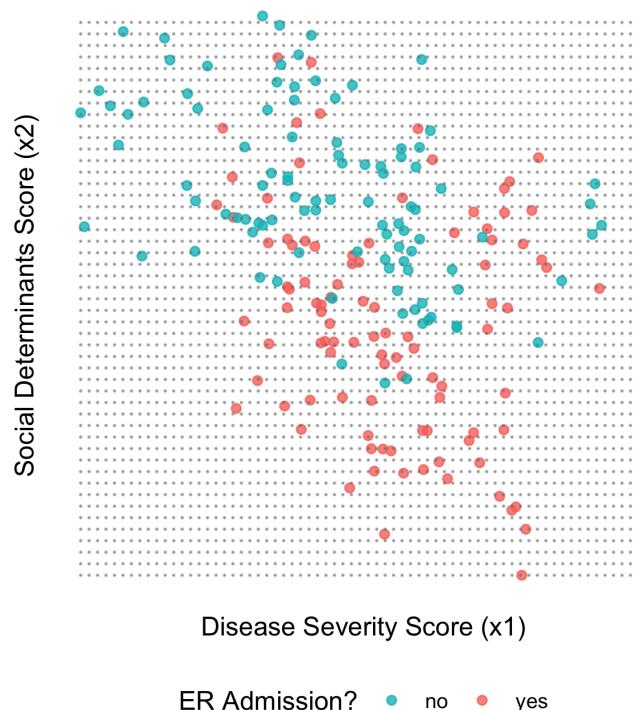
2.1 Definitions

- **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.

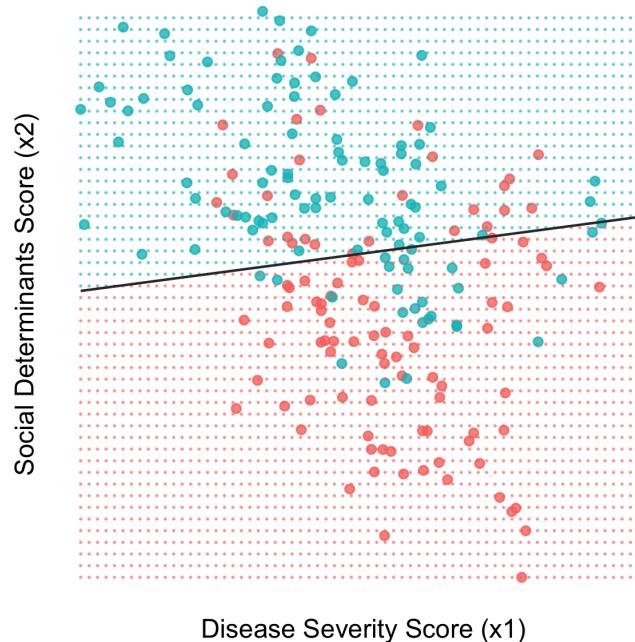


In this figure, the color refers to whether a patient was readmitted (blue = “no”, red = “yes”). The location of each point is governed by the patient’s disease severity score (x_1 , horizontal axis) and social determinants score (x_2 , vertical axis). Our goal in classification is to draw a **decision 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.

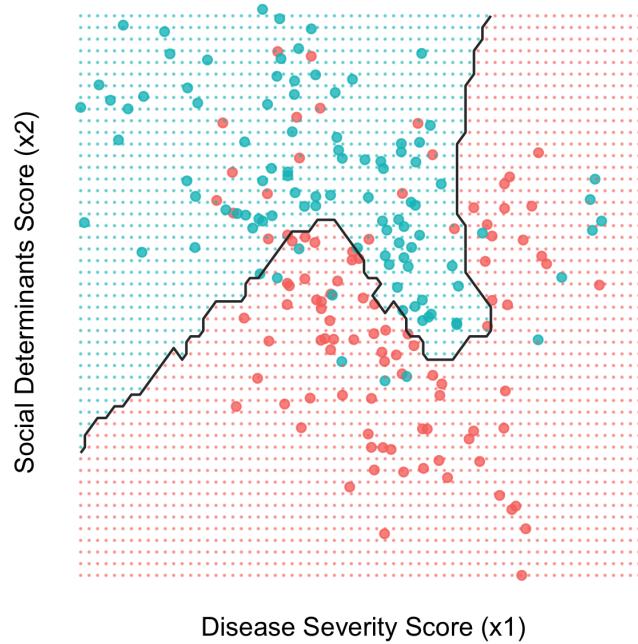


¹In a higher-dimensional feature space, the decision boundary for logistic regression is a **hyperplane**.

2.3.2 K Nearest Neighbors (KNN)

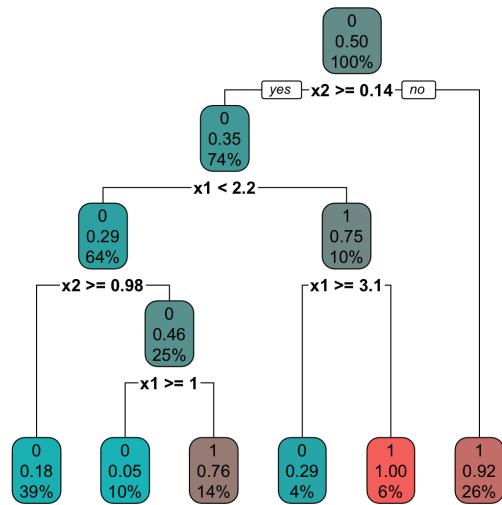
Another approach is to make no assumptions about the shape of the decision boundary. To make a prediction about a new patient, we simply allow the K nearest neighbors to vote. The parameter K must be set independently and is called a **hyperparameter**.

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

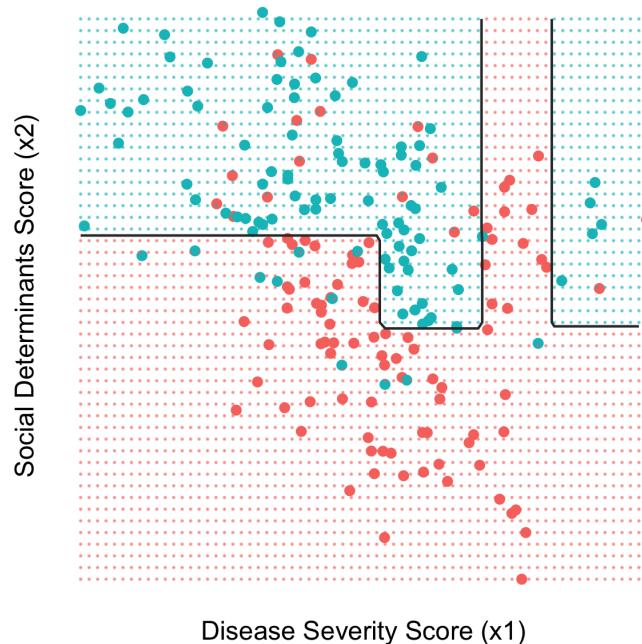


2.3.3 Decision Tree

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 1

There are six rectangular regions in this picture corresponding to the six leaves of the tree. Identify all six and which leaves they correspond to on the decision tree, above.

Question 2

What are the advantages and disadvantages of the decision boundaries produced by:

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

Question 3

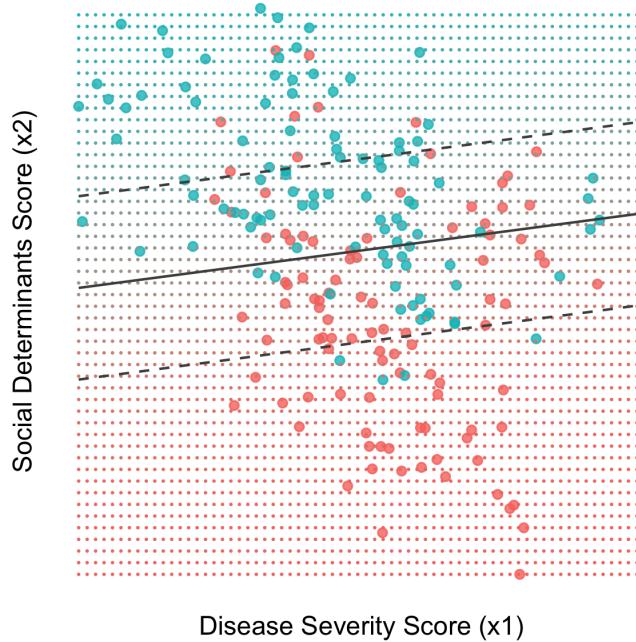
What makes a good classification algorithm? Consider issues of accuracy, generalizability, and speed (both to train the algorithm and to use it to make predictions on new samples).

2.4 Classification with Probabilities

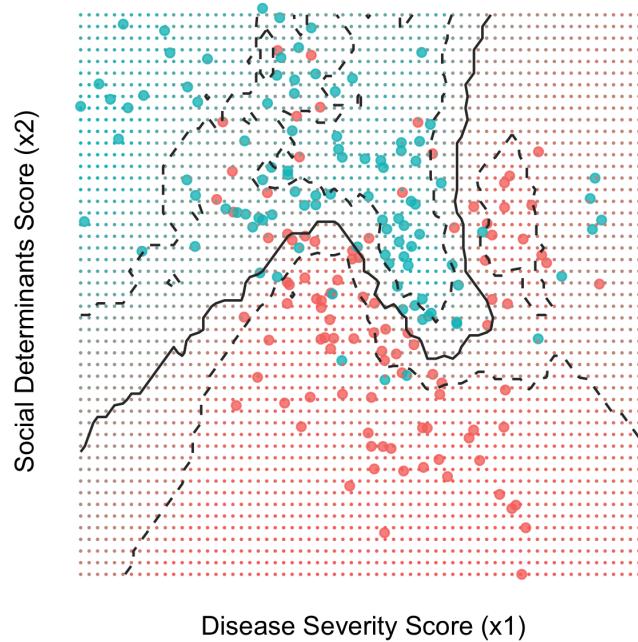
We can think of classification as simply drawing a decision boundary, but underlying each algorithm is a quantitative assessment of each point in the feature space. Each algorithm is, in its own way, able to provide a degree of certainty, or **probability**², that a point belongs to the positive outcome 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):

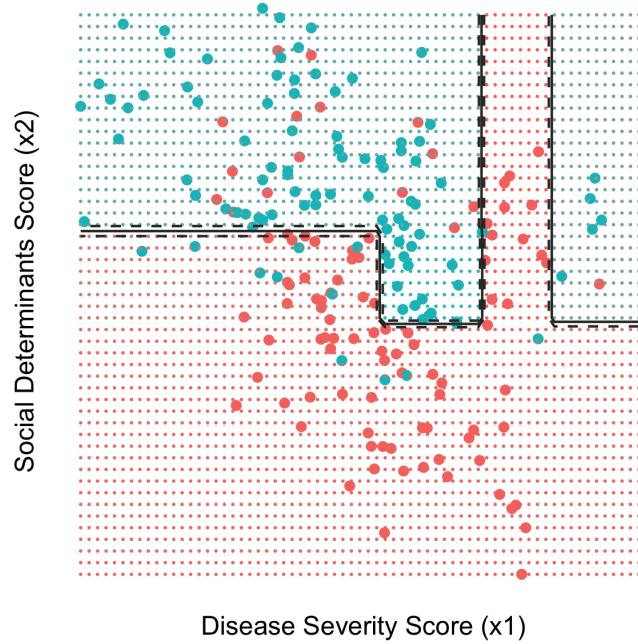
²Pedantic footnote: this is a Bayesian definition of probability, as opposed to a frequentist definition. More on that later.



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 ($K = 15$):



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:



In this case, the color of the background in the different regions is relatively flat. 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. (Convince yourself of this.)

Chapter 3

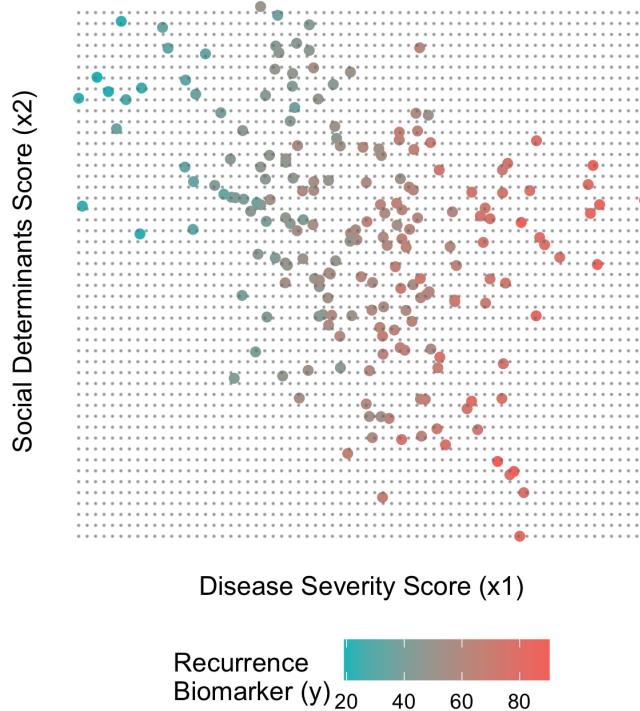
Regression

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. The goal of regression is to predict the value of the biomarker (y) based on the values of the two predictors, x_1 and x_2 .

Question 1

Just looking at the two predictors, which one appears to more highly influence the value of the recurrence biomarker? Why?

Question 2

Think about the three algorithms we discussed in Chapter 2. Now think about our new task, which is to predict the *numeric value* of the recurrence biomarker as a function of the two predictors, x_1 and x_2 .

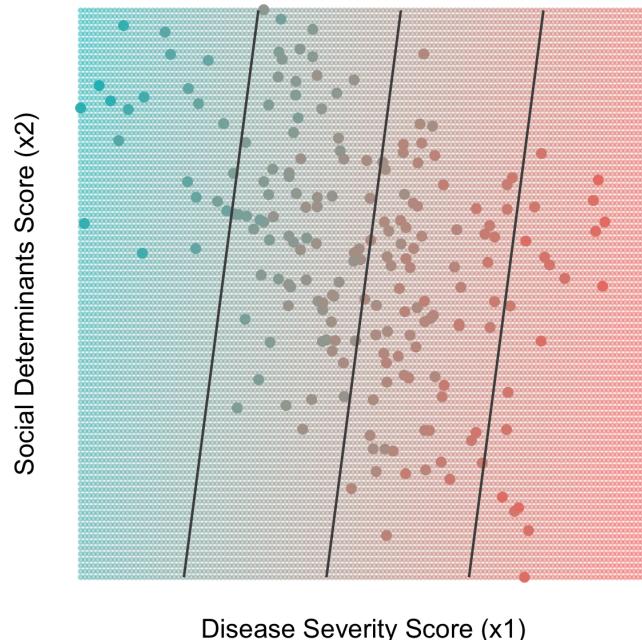
- How might you adapt KNN to deal with this problem?

- How might you adapt a decision tree to deal with this problem?
- How might you adapt logistic regression to deal with this problem? You'll have to "break the algorithm" a bit more this time.

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:

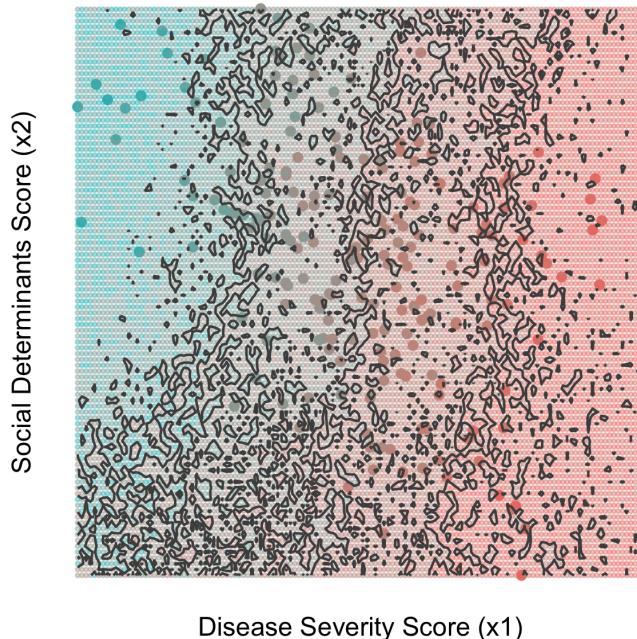


¹The terminology here is confusing. When we learn about generalized linear models in Chapter 6, you'll see why logistic regression has the word "regression" in its name even though it's a classification algorithm.

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.

3.2.2 K Nearest Neighbors (KNN)

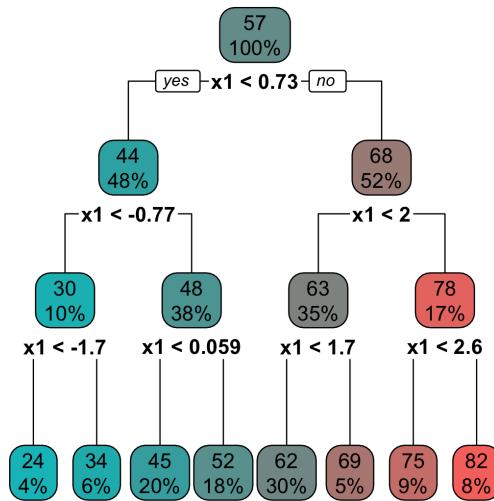
Regression using KNN works very similarly to KNN for classification. In classification, we allow the nearest K points to vote on the label of a new test point. In regression, we **interpolate** between the values of the surrounding points to come up with the value of y for a test point. Typically this 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:



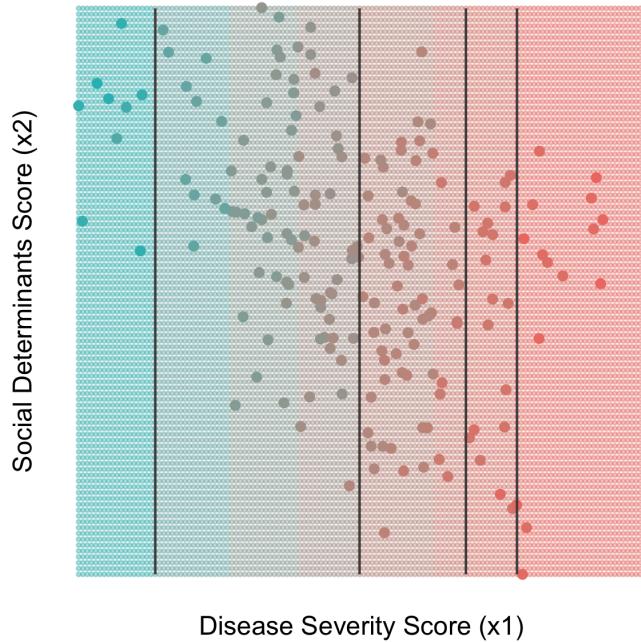
The contours are again drawn at the 25th, 50th, and 75th percentiles of the outcome, y . This looks like a bit of a mess compared to the linear regression plot, but at the same time, the KNN algorithm is able to capture arbitrarily complex relationships between x_1 , x_2 , and y that can be missed by 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 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. Of course, it would be difficult to climb such stairs, because they are not evenly spaced!

Question 3

What are the advantages and disadvantages of each of these three regression algorithms?

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 6) which make assumptions about the type of probability distribution followed by the outcome variable. Decision trees use a concept called **entropy** (see Chapter 11), whose mathematical formulation depends on the probability distribution underlying the outcome. Many **hypothesis tests** (see Chapter 8) 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.

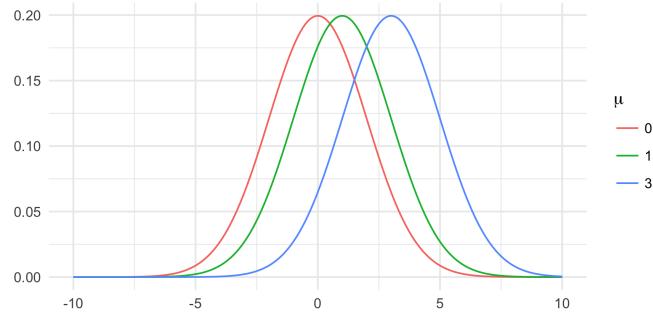
We use the notation $E[x|\theta]$ to refer to the **expected value**, or mean, of a distribution, given its parameter(s), θ . There can be more than one parameter, and it will not always be called θ ; this is just an example. We use the notation $\text{var}(x|\theta)$ to refer to the **variance**, or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

4.2 Normal Distribution

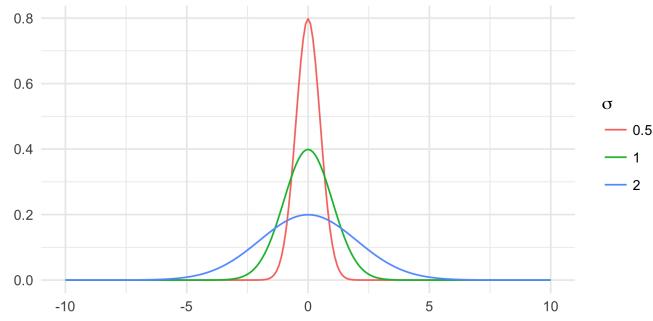
Also called the **Gaussian distribution**, the normal distribution is probably the most well-known continuous probability distribution. It has the following properties:

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

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 1

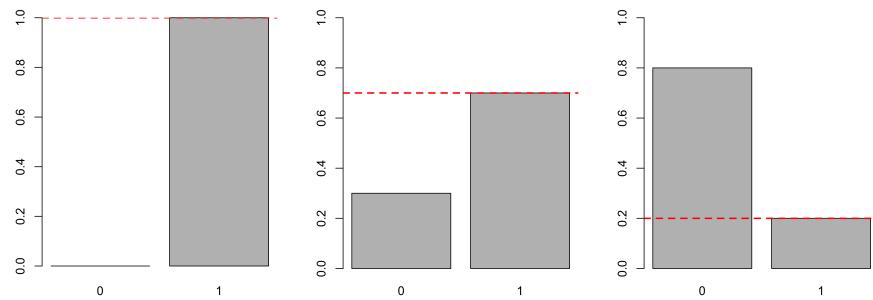
List 5 random variables from medicine or biology that should follow normal distributions.

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 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 $x \in \{0, \dots, n\}$:

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

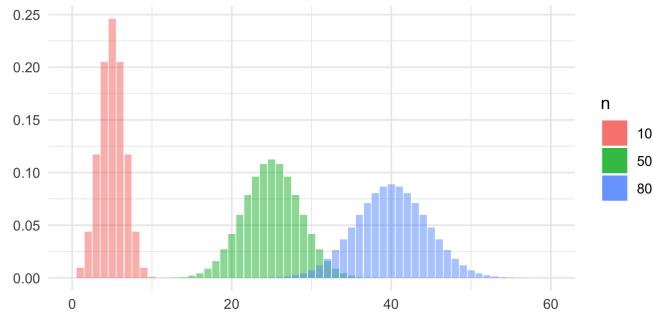
where the notation $\binom{n}{x}$ is defined as:

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

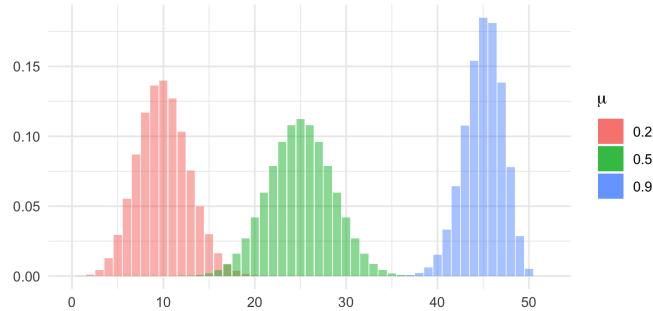
This notation denotes the number of ways it is possible to choose x things out of a group of n things, where the ordering doesn't matter. The exclamation point denotes the **factorial function**: $x! = x(x-1)(x-2)\cdots(2)(1)$.

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:

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



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



Question 3

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

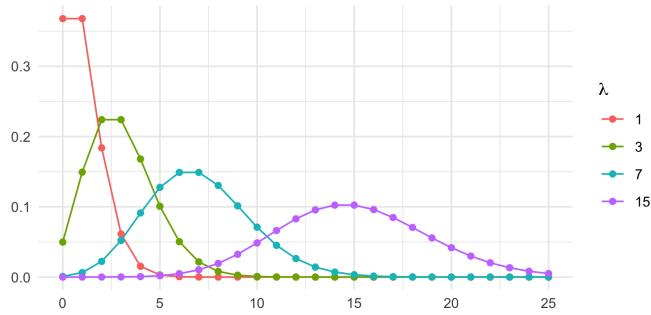
4.5 Poisson Distribution

The **Poisson distribution** is a discrete probability distribution that is often used to model 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.



Question 4

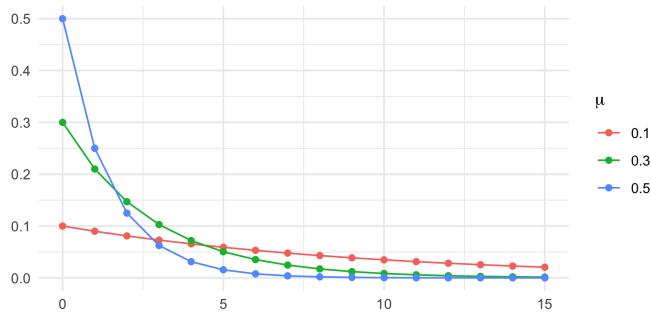
List 5 random variables from medicine or biology that should follow Poisson distributions.

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 5

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

4.7 Exponential

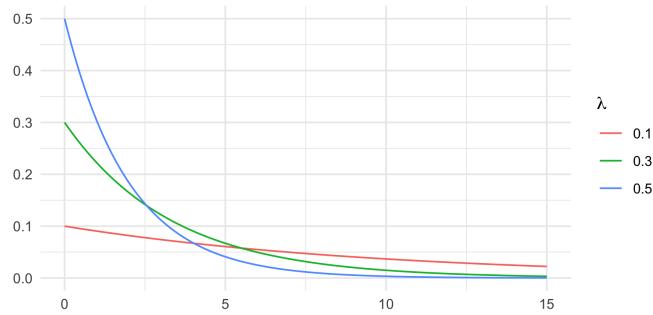
The **exponential distribution** is a continuous probability distribution that models waiting times between events that happen independently and continuously at a constant rate (Poisson process), as well as many other random variables². It has the following properties:

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

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.

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.



Question 6

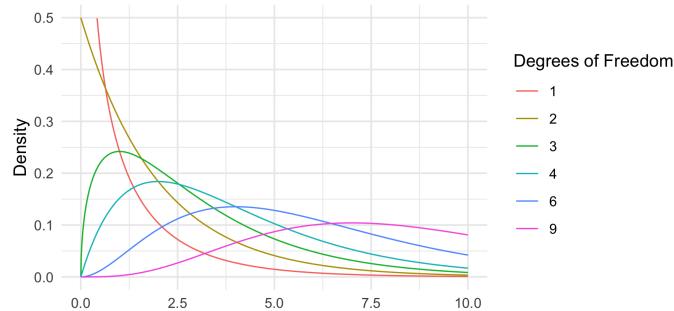
List 5 random variables from medicine or biology that should follow exponential distributions.

4.8 Chi-Squared Distribution

How this distribution arises:

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,

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

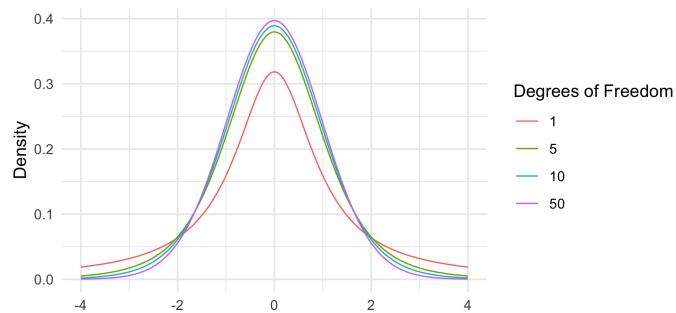
is a generalization of the factorial function to complex numbers. For any positive integer n , $\Gamma(n) = (n-1)!$.

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:

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

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

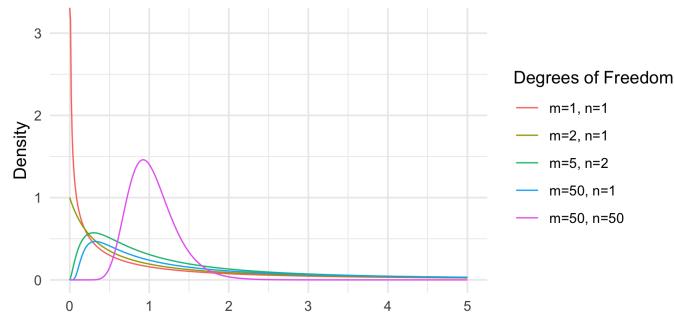
$$\text{var}(x|k) = \begin{cases} \frac{k}{k-2} & k > 2 \\ \infty & 1 < k \leq 2 \\ \text{undefined} & \text{otherwise} \end{cases}$$

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 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.

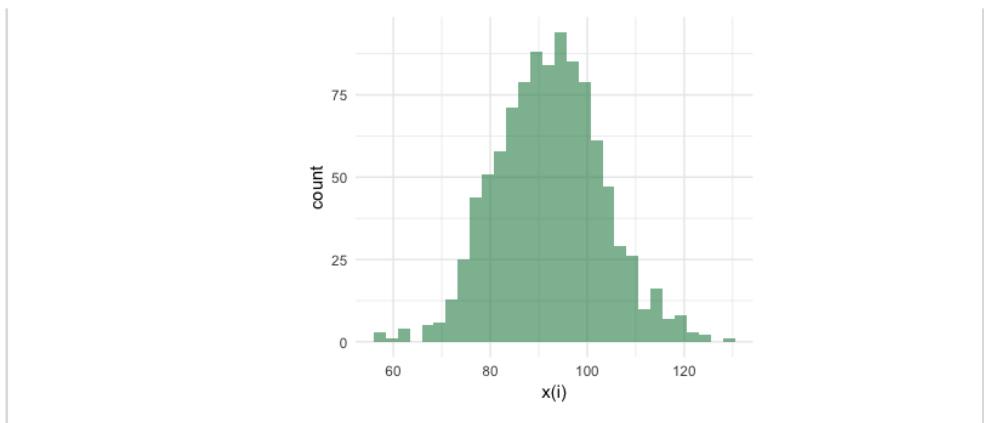
You have data from the late 1800s over the course of 20 years. Let $x^{(i)}$ be the number of people killed in year i .

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

Maximum Likelihood Estimation

Maximum likelihood (ML) is the most widely used technique for fitting data to probability distributions. In this technique, we choose parameter value(s) for a probability distribution that maximize the probability, or **likelihood**, that it generated our observed data.

5.1 Likelihood

If we draw independent¹ samples from the same distribution, $p(x|\theta)$, the **joint 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 typically view this thing as a function of θ :

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

¹Independent sampling just means that the values of different samples do not depend on each other.

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 use the logarithm of the likelihood, which we call the **log-likelihood**, because it has some nice properties, including allowing us to work with 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 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)**.

We will now go through a bunch of examples of how to find the MLEs of the probability distributions we saw in Chapter 4.

5.2 Bernoulli MLE

First, write down the log-likelihood.

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

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 estimate either way.

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

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

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

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

5.3 Binomial MLE

Here we assume m (the number of trials) is a known quantity. First, write down the log-likelihood.

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

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

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

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

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

5.4 Normal MLE

First, 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 , take the derivative of the log-likelihood with respect to μ :

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

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 , take the derivative of the log-likelihood with respect to σ :

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

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

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

5.5 Poisson MLE

First, write down the log-likelihood.

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

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

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

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

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

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 really small.

5.6 Geometric MLE

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

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

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

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

5.7 Exponential MLE

First, write down the log-likelihood.

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

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

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

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

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

5.8 Summary

Why is maximum likelihood estimation useful? When we are fitting a regression model or summarizing some data, we often want to represent that data using a **model**, a simplified representation of the properties of the data and/or how they were generated. A probability distribution is one type of model. Maximum likelihood estimation is one way to go from data to model.

The table below contains a summary of the MLEs of various parameters from different 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}^+

5.9 Discussion Questions

In Chapter 4, we examined several examples of experimental conditions and discussed which probability distribution(s) best modeled each one. Here we calculate the maximum likelihood estimates of the parameters of these distributions, based on data.

1. What distribution should you use to model these data? Calculate the MLE(s) for the parameter(s) of this distribution.
2. 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 deaths in year i .

What distribution should you use to model these data? Calculate the MLE(s) for the parameter(s) of this distribution.

3. What distribution should you use to model these data? Estimate the MLE(s) for the parameter(s) of this distribution.

Chapter 6

Generalized Linear Models

DRAFT

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. A linear function of the predictors (a.k.a. covariates, again see Chapter 2), x_1, \dots, x_p , explains where the mean of that distribution is, but there is still some random spread around that mean due to factors that aren't modeled, plus noise.

Today, we will focus on three classes of GLM: **linear regression**, which models data where the outcome, y , is numeric ($y \in \mathbb{R}$); **logistic regression**, in which the outcome is binary ($y \in \{0, 1\}$), and **loglinear (Poisson) regression**, in which the outcome is a positive integer, or count ($y \in \{0, 1, 2, \dots\}$).

6.1 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.). That 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.
- We assume that the predictors are fixed and known, and thus have no error associated with their measurements (Bayesian versions of these models relax this assumption).
- We assume that the predictors enter the model as a linear combination (this is what makes these “linear models”).
- We assume that the n samples in our dataset are collected independently, so that the errors of the n responses are uncorrelated. (Another way of thinking about this is that the outcomes are drawn iid from the relevant distribution.)
- We assume that the predictors are not collinear. If they are, it can lead to model instability even if the model appears to predict the outcome well.

6.2 Modeling the Outcome

6.2.1 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 way.

Outcome Distribution: Normal In linear regression, we assume that the outcome, y , is normal. 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 $y \in \mathbb{R}$.

6.2.2 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.

Outcome Distribution: Bernoulli In logistic regression, we assume that the outcome, y , is either 0 or 1. We model it using the Bernoulli distribution, 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 $y \in \{0, 1\}$.

6.2.3 Loglinear (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.

Outcome Distribution: Poisson 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 $y \in 0, 1, 2, \dots$

6.3 Modeling the Predictors

All of the models 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 denote the vector of predictors by x , 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:

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

6.4 Linking the Predictors to the Outcome

All of the models we see today model the **expected value** of the outcome, $E[y]$ as some function of this linear combination of predictors. The function that relates the two is called the **link function**. Different types of regression use different link functions.

6.4.1 Linear Regression

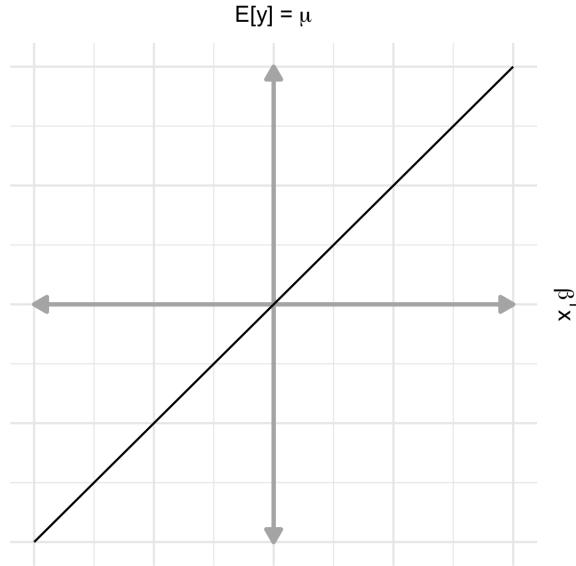
In linear regression, the mean of the outcome distribution, which is normal, can be any real number. We therefore use the **identity link**, setting $E[y]$ directly equal to the linear combination of predictors. Since the outcome is normal, we know that $E[y] = \mu$, the mean of the normal distribution.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

$$E[y] = \mu = \beta^T x \quad (6.1)$$

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.



6.4.2 Logistic Regression

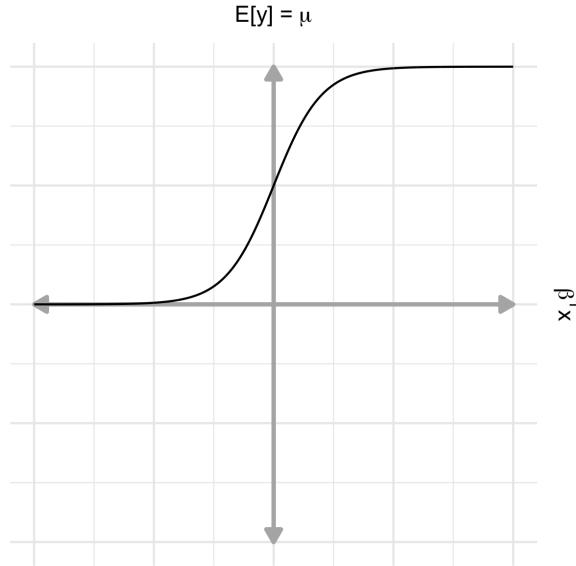
In logistic regression, the mean of the outcome distribution, which is Bernoulli, is a probability. It must therefore be a real number between 0 and 1. No matter how large or small $\beta^T x$ gets, the value of $E[y] = \mu$ cannot be outside this range. We therefore apply the **logistic function**,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

$$E[y] = \mu = \frac{1}{1 + \exp(-\beta^T x)} \quad (6.2)$$

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**.



6.4.3 Loglinear (Poisson) Regression

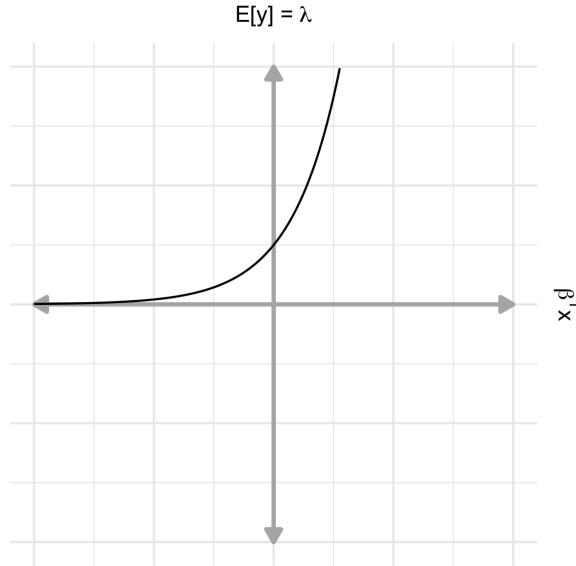
In Poisson regression, the mean of the outcome distribution, which is Poisson, is the expected value of a count. It must therefore be a real number greater than or equal to zero. In particular, no matter how small $\beta^T x$ gets, the value of $E[y] = \lambda$ cannot be negative. We therefore exponentiate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

$$E[y] = \lambda = \exp(\beta^T x) \quad (6.3)$$

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**.



6.5 Fitting 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.

6.5.1 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 6.1 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: $\sum_{i=1}^n (y^{(i)} - \beta^T x^{(i)})^2$.

6.5.2 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.

6.5.3 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.

Chapter 7

Fitting and Interpreting GLMs

DRAFT

We've seen the definition of GLMs and a lot of the math behind them in Chapter 6. Now it's time to talk about how to fit them in R and/or Python and how to interpret the model output.

Example: Linear Regression

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).

Fitting in R

To fit the model in R, you would use the `lm` command, which fits a linear regression model using ordinary least squares. Basically this package finds the analytical solution that maximizes the likelihood for linear regression, so it is taking advantage of the fact that such an analytical solution exists.

The commands for fitting the model are:

```
d <- read.csv("lecture-2-data/linear-small-cities-data.csv")
m <- lm(MORT ~ PRECIP + EDUC + NONWHITE + NOX + SO2, data = d)
summary(m)
```

The output of that last `summary` command is:

```
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 *** 
---
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
```

Fitting in Python

In Python, the `sklearn` package has a linear regression model. You fit it using the following commands:

```
from sklearn import linear_model
import pandas as pd

d = pd.read_csv("lecture-2-data/linear-small-cities-data.csv")
y = d[["MORT"]]
X = d[["PRECIP", "EDUC", "NONWHITE", "NOX", "SO2"]]
lr = linear_model.LinearRegression()
lr.fit(X, y)
lr.coef_
```

The output is somewhat less thrilling than R's:

```
array([[ 1.40734044, -14.80139073,    3.19909076,   -0.10796976,
        0.35517618]])
```

but you will notice that the coefficients are identical to those found by R. There are just a lot fewer model diagnostics, etc. If you want something that more closely approximates R's output, you can use the `statsmodels` package in Python. The commands there are:

```
import statsmodels.api as sm

d = pd.read_csv("lecture-2-data/linear-small-cities-data.csv")
y = d[["MORT"]]
X = d[["PRECIP", "EDUC", "NONWHITE", "NOX", "SO2"]]
X = sm.add_constant(X) # <- manually add the intercept
lr = sm.OLS(y, X)
results = lr.fit()
print(results.summary())
```

and the output looks like this:

OLS Regression Results						
	MORT	R-squared:	0.675			
Dep. Variable:		OLS	Adj. R-squared:	0.644		
Model:			F-statistic:	22.39		
Method:	Least Squares		Prob (F-statistic):	4.41e-12		
Date:	Tue, 17 Oct 2017		Log-Likelihood:	-298.78		
Time:	22:37:41		AIC:	609.6		
No. Observations:	60		BIC:	622.1		
Df Residuals:	54					
Df Model:	5					
Covariance Type:	nonrobust					
	coef	std err	t	P> t	[0.025	0.975]
const	995.6365	91.641	10.865	0.000	811.907	1179.366
PRECIP	1.4073	0.689	2.042	0.046	0.026	2.789
EDUC	-14.8014	7.027	-2.106	0.040	-28.891	-0.712
NONWHITE	3.1991	0.622	5.141	0.000	1.951	4.447
NOX	-0.1080	0.135	-0.800	0.427	-0.379	0.163
SO2	0.3552	0.091	3.905	0.000	0.173	0.538
Omnibus:		2.519	Durbin-Watson:			1.375
Prob(Omnibus):		0.284	Jarque-Bera (JB):			1.861
Skew:		0.136	Prob(JB):			0.394
Kurtosis:		3.819	Cond. No.			1.79e+03

Example: Logistic Regression

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.

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

LOW	Low birth weight (0 = birth weight ≥ 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

We would like to predict LOW based on all of the other covariates except BWT (why not use BWT?).

Fitting in R

To fit in R, we use the `glm` package, which fits GLMs using a numerical technique called Fisher scoring. The commands are:

```
d <- read.delim("lecture-2-data/logistic-lowbwt-data.tsv")
d$RACE <- as.factor(d$RACE) # <- ensure RACE is coded as factor, not number
m <- glm(LOW ~ AGE + LWT + RACE + SMOKE + PTL + HT + UI + FTV,
          family = "binomial", data = d)
summary(m)
```

The 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
---
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

```

Fitting in Python

You can use scikit-learn to fit logistic regression models as well. The commands are not nearly as straightforward:

```

from sklearn import linear_model, preprocessing
import pandas as pd

d = pd.read_table("lecture-2-data/logistic-lowbwt-data.tsv", sep="\t")
y = d[["LOW"]].values.ravel()
X = d[["AGE", "LWT", "RACE", "SMOKE", "PTL", "HT", "UI", "FTV"]]
X[["RACE"]] = X[["RACE"]].astype('category')

```

```

race_recoded = pd.get_dummies(X, columns=["RACE"])
X = X[["AGE", "LWT", "SMOKE", "PTL", "HT", "UI", "FTV"]].join(
    race_recoded.ix[:, 'RACE_2':])

lr = linear_model.LogisticRegression(C=100000.0, fit_intercept=True,
                                      penalty='l2', solver='liblinear', tol=0.00001)
lr.fit(X, y)
lr.coef_

```

But the end result is the same as what we got earlier in R:

```
array([-0.02952438, -0.01542876,  0.93984778,  0.54233679,  1.864694 ,
       0.76721899,  0.06538879,  1.27277704,  0.8812321 ])
```

where we must notice that the columns are in a different order:

```
array(['AGE', 'LWT', 'SMOKE', 'PTL', 'HT', 'UI', 'FTV', 'RACE_2', 'RACE_3'],
      dtype=object)
```

We can also do this in Python using statsmodels.

```

import statsmodels.api as sm

d = pd.read_table("lecture-2-data/logistic-lowbwt-data.tsv", sep="\t")
y = d[["LOW"]].values.ravel()
X = d[["AGE", "LWT", "RACE", "SMOKE", "PTL", "HT", "UI", "FTV"]]
X["RACE"] = X["RACE"].astype('category')
race_recoded = pd.get_dummies(X, columns=["RACE"])
X = X[["AGE", "LWT", "SMOKE", "PTL", "HT", "UI", "FTV"]].join(
    race_recoded.ix[:, 'RACE_2':])
X = sm.add_constant(X) # <- manually add the intercept
lr = sm.Logit(y, X)
results = lr.fit()
print(results.summary())

```

The results look like this:

Logit Regression Results						
Dep. Variable:	y	No. Observations:	189			
Model:	Logit	Df Residuals:	179			
Method:	MLE	Df Model:	9			
Date:	Wed, 18 Oct 2017	Pseudo R-squ.:	0.1423			
Time:	07:51:27	Log-Likelihood:	-100.64			
converged:	True	LL-Null:	-117.34			
		LLR p-value:	0.0001143			
	coef	std err	z	P> z	[0.025	0.975]
const	0.4806	1.197	0.402	0.688	-1.865	2.827
AGE	-0.0295	0.037	-0.798	0.425	-0.102	0.043
LWT	-0.0154	0.007	-2.229	0.026	-0.029	-0.002
SMOKE	0.9388	0.402	2.335	0.020	0.151	1.727
PTL	0.5433	0.345	1.573	0.116	-0.134	1.220
HT	1.8633	0.698	2.671	0.008	0.496	3.230
UI	0.7676	0.459	1.671	0.095	-0.133	1.668
FTV	0.0653	0.172	0.379	0.705	-0.273	0.403
RACE_2	1.2723	0.527	2.412	0.016	0.239	2.306
RACE_3	0.8805	0.441	1.998	0.046	0.017	1.744

Example: Poisson Regression

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 work or broken, 3 = both worn or broken)
WIDTH	Carapace width of the female crab (cm)
WEIGHT	Weight of the female crab (g)

Fitting in R

To fit in R, we again use the `glm` package. The commands are:

```
d <- read.table("lecture-2-data/poisson-crab-data.txt", head=TRUE)
m <- glm(satell ~ color + spine + width + weight, family = "poisson", data = d)
summary(m)
```

The 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
```

Fitting in Python

Right now scikit-learn does not allow you to use Poisson regression, but it looks like they're working on it:

The screenshot shows a Stack Overflow post with the following content:

- There is movement to implement generalized linear models with Poisson, gamma, and Tweedie error distributions in scikit-learn.
- 5 Statsmodels has implementations of generalized linear models with Poisson, Tweedie, and gamma error distributions.
- While I'm updating this answer, Spark ML also (experimentally) supports Poisson, Tweedie, and gamma distributions.

Below the list, there are standard Stack Overflow interaction buttons: share, cite, improve this answer, edited Sep 9 at 14:29, answered May 23 '16 at 17:09 by Neal, 168 views, 1 answer, 5 comments.

For now I would suggest using statsmodels. Here's how you'd do Poisson regression using that package:

```
import statsmodels.api as sm

d = pd.read_table("lecture-2-data/poisson-crab-data.txt",
                  sep=r"\s*", engine="python")
y = d[["satell"]].values.ravel()
X = d[["color", "spine", "width", "weight"]]
X = sm.add_constant(X) # <- manually add the intercept
lr = sm.Poisson(y, X)
results = lr.fit()
print(results.summary())
```

And here's the output:

```
Poisson Regression Results
```

Dep. Variable:	y	No. Observations:	173			
Model:	Poisson	Df Residuals:	168			
Method:	MLE	Df Model:	4			
Date:	Wed, 18 Oct 2017	Pseudo R-squ.:	0.08191			
Time:	07:50:24	Log-Likelihood:	-453.58			
converged:	True	LL-Null:	-494.04			
		LLR p-value:	1.102e-16			
-----	coef	std err	z	P> z	[0.025	0.975]
const	-0.3435	0.968	-0.355	0.723	-2.242	1.555
color	-0.1849	0.067	-2.780	0.005	-0.315	-0.055
spine	0.0400	0.057	0.704	0.482	-0.071	0.151
width	0.0275	0.048	0.574	0.566	-0.066	0.121
weight	0.0005	0.000	2.865	0.004	0.000	0.001

Chapter 8

Hypothesis Testing DRAFT

Hypothesis testing is the central idea underpinning most of the analysis you'll find in the clinical and biomedical research literature¹. There are multiple types of hypothesis testing, but the most common type is **null hypothesis testing**, most of the theory of which originated from the statistician R.A. Fisher. In null hypothesis testing, you create a model of how your data should look under default conditions, and then you look to see whether your data deviate appreciably from the model. You quantify your data's deviation from the model by calculating a **test statistic**. One can view this type of hypothesis testing as a form of **anomaly detection**.

The statisticians Jerzy Neyman and Karl Pearson instead favored the use of hypothesis testing as a **model comparison** tool. In their view, you would set up multiple different models and then quantify each model's fit to your data to choose the best one. Fisher hated this approach because it meant accepting one or more models as truth, when in reality it's impossible to account for all potential scenarios.

Most of the hypothesis tests we use today (T-tests, chi-squared tests, etc.) follow Fisher's approach. Likelihood ratio tests and Bayesian methods adhere more to the Neyman-Pearson philosophy.

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.

8.1 Basic Steps of a Hypothesis Test

1. *Create an initial research hypothesis.* A hypothesis is an assertion that is capable of being proved false, such as, “If the subject has this genetic mutation, his risk of developing cancer will increase.”
2. *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.” For some techniques, you also need to state an **alternative hypothesis**, which is the hypothesis that is contrary to the null².
3. *List statistical assumptions.* E.g. in **parametric** hypothesis testing methods, we assume the data follow some particular probability distribution under the null. **Nonparametric** methods do not make this assumption.
4. *Decide on an appropriate test and test statistic.* The **test statistic** quantifies the degree of deviation of your observed data from what you would expect under the null hypothesis³.
5. *Derive the distribution of the test statistic under the null.* This is called the **null distribution**.
6. *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, which is when you reject the null even if it is true (false positive result).
7. *Compute the observed value of the test statistic from the data.*
8. *Decide whether or not to reject the null hypothesis.*

²The alternative hypothesis is the hypothesis that is contrary to the null hypothesis. It is usually taken to be that the observations are the result of a real effect (with some amount of chance variation superposed). As mentioned above, there was a huge controversy between R.A. Fisher and Jerzy Neyman/Karl Pearson over the use of alternative hypotheses. Fisher said you shouldn't use them because rejecting the null doesn't mean accepting that there's a true effect. Neyman and Pearson thought you should use them because it gave statistical tests more power. Most of hypothesis testing ended up following Fisher's approach.

³Some 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.

8.2 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 $1 - \beta$.

8.3 The Z-Test

8.4 Student's T-tests

The T -test (actually a family of tests) deals with situations where you have data that are assumed to be normally distributed, and you want to draw a conclusion about the mean of that distribution.

8.4.1 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 . You can do this using a test statistic

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

which follows a T-distribution with $n - 1$ degrees of freedom under the null hypothesis that the means are the same. Here \bar{x} refers to the sample mean, and s refers to the sample standard deviation, which is the square root of the sample variance, s^2 :

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

8.4.2 One-Sample T-test vs. Z-test

A one-sample T-test looks a lot like a Z-test (example from slides). Here is the difference:

- A Z-test assumes that the population standard deviation, σ , is fixed and known with 100% certainty so that the test statistic follows a normal distribution.
- The T-test estimates the population standard deviation from the data. The sample variance follows a chi-squared distribution with $n - 1$ degrees of freedom, where n is the sample size. In this case, the test statistic follows a Student's T-distribution with $n - 1$ degrees of freedom.

If you have enough samples, 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.

8.4.3 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 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.

8.4.4 Two Independent Samples, Unequal Variance

Sometimes you have two independent samples but cannot assume the variances are equal. 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

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

8.4.5 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. You want to test whether the second set of values have changed relative to the first set of values.

8.5 Mann-Whitney Test

All of these variants of the T-test make assumptions about the normality of the data. Sometimes you want to compare the means of two groups but you aren't sure whether the normal assumption holds. In this case, you might want to try a **nonparametric** alternative to the two-sample T-test called the **Mann-Whitney Test**, or Wilcoxon Rank Sum Test.

Some interesting points about nonparametric tests:

- There are no distributional assumptions.
- Most nonparametric methods replace data by their ranks, which are invariant to any monotonic transformation of the data.
- Compare this to the T-test: If you use the log-transform of the data instead of the original values and do a T-test on them, the p -value can change. But with ranks that doesn't happen.
- Replacing the data by ranks also makes the test less sensitive to outliers.
- But remember, there is no free lunch: You will always lose power relative to a parametric test if you use the nonparametric alternative in a case where the distributional assumptions of the parametric test are true.

8.6 Pearson's Chi-Squared Test

Imagine you have data on two discrete covariates for a number of different subjects. You want to test whether the value of one covariate depends on

the value of the other. **Pearson's chi-squared test** is used to assess the independence of row and column values in contingency tables, provided the cell counts are high enough.

We make some assumptions:

- The data are sampled randomly from a fixed population where each member of the population has an equal probability of selection.
- 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.
- The observations are independent of each other. One observation should not be influenced in any way by the other observations taken before or after it.

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". This test statistic follows a chi-squared distribution with $(r - 1)(c - 1)$ degrees of freedom.

8.7 Fisher's Exact Test

For small sample sizes, the assumptions underlying Pearson's chi-squared test are no longer true. In these cases, it is common to replace the chi-squared test with something called **Fisher's Exact Test**, which calculates an exact p -value directly by considering every possible outcome.

Chapter 9

The Bias-Variance Tradeoff **DRAFT**

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.

9.1 Goodness of Fit vs. Generalizability

Training vs. test error

9.2 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.

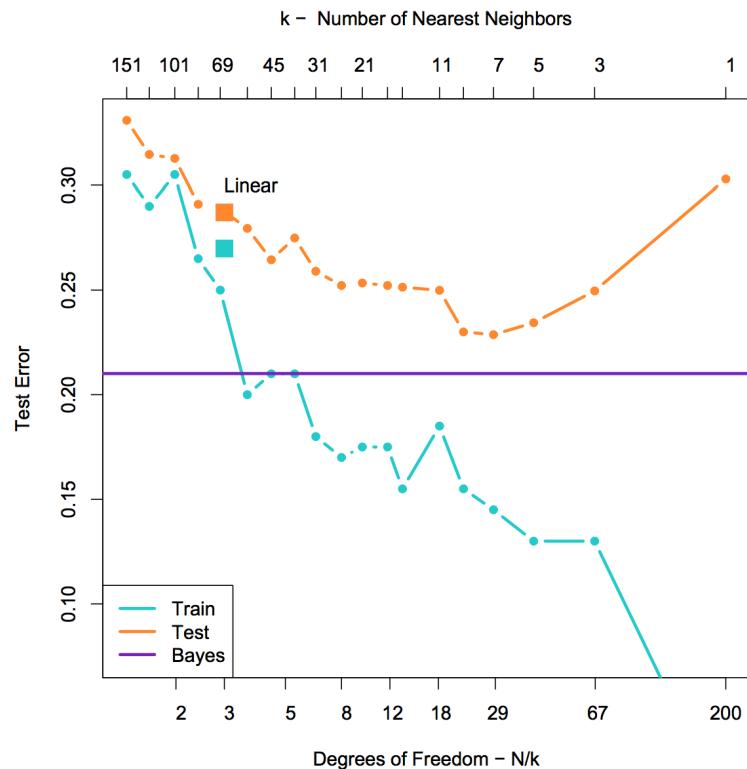
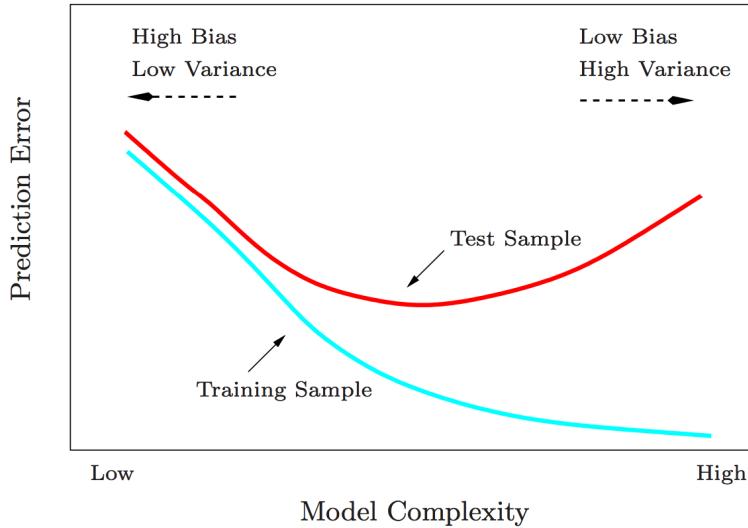
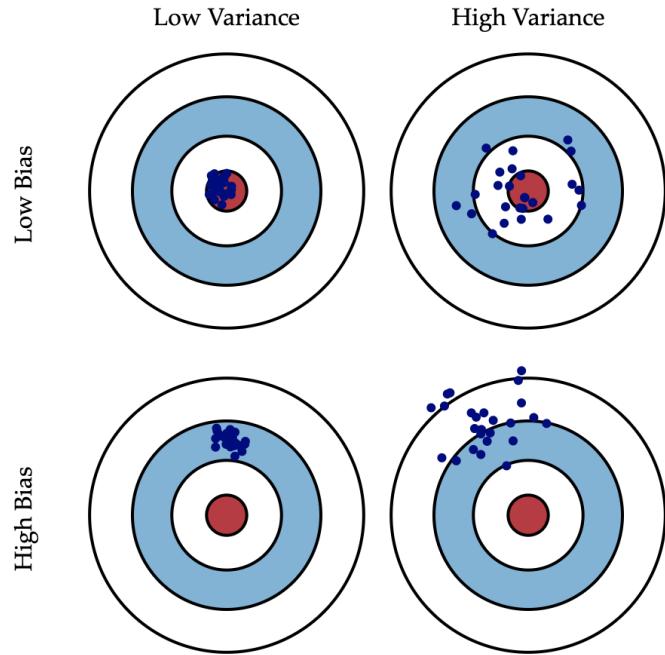


Illustration of training vs. test error as a function of model complexity, as well as the bias-variance tradeoff. From *Elements of Statistical Learning*, Figure 2.11.



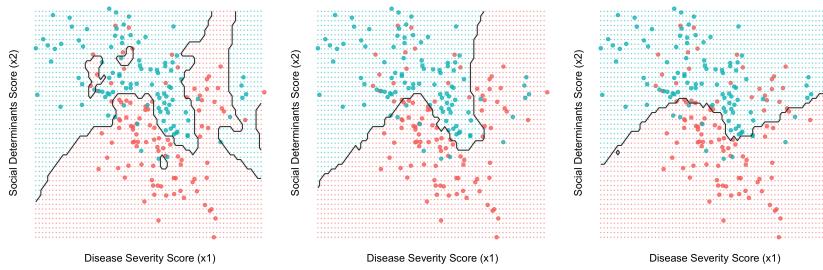
A graphical illustration of the difference between bias and variance. Think of each dot as representing a single test example evaluated under the same model trained on slightly different datasets. The center of the target is the prediction the model should make for that test example. In the case of high 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.



9.3 Overfitting vs. Underfitting

Question 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 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)?

Chapter 10

Lasso, Ridge, and Elastic Net

DRAFT

Sometimes when building regression models, you run into issues like the following:

- You have more predictors, p , than you have samples, n .
- Your predictors are highly correlated.

Both of these conditions can lead to models that are highly unstable. Maybe they fit your training data well, but if you change your training set even a tiny bit, the coefficients shift wildly. It becomes very hard to trust the coefficient values under these circumstances. One way to combat this is to introduce a **penalty** on the values of the coefficients. There are different types of penalty (see slides) that do different things. Relevant terms include: **ridge regression**, **Lasso**, and **elastic net**.

Chapter 11

Decision Trees DRAFT

Decision trees were developed as an alternative to neural networks in the 1970s. They can be used either for classification or regression. There are several algorithms for fitting decision trees, all of which are heuristic, because the general problem of learning an optimal decision tree for a dataset is NP-complete. All algorithms for tree learning are **greedy** and are not guaranteed to give the optimal solution.

11.0.1 Entropy and Information Gain

Today we will discuss the ID3 algorithm for building decision trees, which relies on the concepts of entropy and information gain. **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 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, 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 , as usual, is the probability the outcome is 1.

Let Y be the outcome variable of a training set. Let X be some other random variable defined over the training set. It could be one of the original predictors or some arbitrary combination of them. **Information gain** is defined as:

$$\begin{aligned} \text{Gain}(Y, X) &= H(Y) - \sum_x P(X = x) H(Y|X = x) \\ &= H(Y) - H(Y|X) \end{aligned}$$

It is a measure of how much our uncertainty in the value of Y is reduced by knowing X .

11.0.2 The ID3 Algorithm

Here is the algorithm:

1. Start with a single node representing the entire dataset.
2. At each current leaf node in the tree:
 - (a) Compute the information gain for each feature in turn.
 - (b) Split on the one with the highest information gain.
3. Return to Step 2. Stop the recursion when either the class distributions at the leaf nodes are entirely pure (all data points at a leaf have the same outcome class), or there are no more variables left to split on.

11.0.3 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 you use 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.

11.0.4 Numeric Predictors

So far we've also assumed that our predictors are discrete. But decision trees can handle numeric predictors as well. There are many different strategies for deciding on an optimal split for a predictor. Two simple ones:

- Split at the median or mean of the predictor.
- Order the datapoints on the value of the predictor and consider each possible split, looking for the one that gives the greatest information gain/standard deviation reduction. So for example, if you have a predictor called "age" and its values are 10, 11, 16, 18, 20, and 35, consider all $N - 1 = 5$ possible split points. (This is the approach used by C4.5, a successor to ID3.)

If you have a large dataset, the second option is probably not practical, but you can downsample your dataset first and then look for the optimal cut point(s).

What if the outcome is numeric? In that case, we can 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:

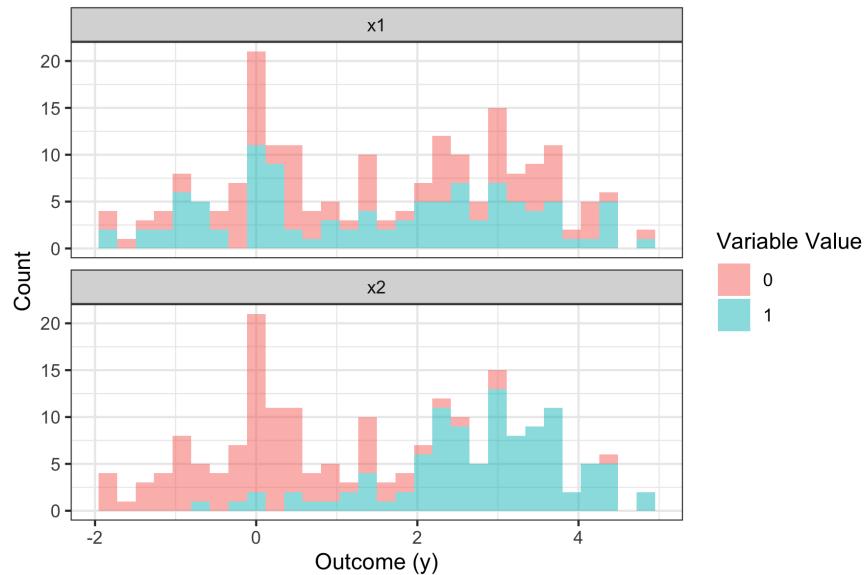
$$S(Y) = \sqrt{\frac{\sum_i (y^{(i)} - \bar{y})^2}{n - 1}}$$

where \bar{y} is the overall mean of the outcome. The procedure is identical to the ID3 algorithm (see Chapter 11) except you use conditional standard deviation instead of information gain to decide on features. We define

$$S(Y, X) = \sum_{x \in \text{Values}(X)} \frac{|Y(X = x)|}{|Y|} S(Y(X = x))$$

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.

For example, imagine you had a dataset similar in structure to our example, but instead of two real-valued predictors, you have two binary predictors, x_1 and x_2 . The decision tree algorithm could choose either one of them to split on first. Here are the distributions of outcome values associated with x_1 and x_2 .



Question 1

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?

Chapter 12

Random Forests **DRAFT**

A random forest is just a collection (or **ensemble**) of decision trees whose “votes” are uncorrelated. The trees vote to produce a final prediction.

Two details are important to the construction of random forests:

1. Each tree is built using a subset of training examples sampled with replacement from the original training set. This is called **bagging** (bootstrap aggregating). Typically around $2/3$ of training examples are used per tree. Note that bagging is a general-purpose procedure that can be used for other models besides random forests.
2. For each split, the tree considers not all m predictor variables, but only a randomly-chosen subset, usually of size approximately \sqrt{m} (for classification problems) or $m/3$ (for regression problems). This keeps you from building the same tree over and over again and ensures that the votes from different trees are uncorrelated.

Here are two bagged samples of size 6 from the dataset in Table ??.

ID	friends (X_1)	money (X_2)	free time (X_3)	happy (Y)
5	1	0	0	0
4	0	0	0	0
2	1	1	1	0
10	1	0	0	1
8	1	0	1	1
10	1	0	0	1

ID	friends (X_1)	money (X_2)	free time (X_3)	happy (Y)
5	1	0	0	0
6	0	0	0	0
2	1	1	1	0
5	1	0	0	0
9	0	0	1	1
7	1	2	1	1

Question 3.11: Use a random forest to fit the data from the low birth-weight example used in the logistic regression model, above. Use the following commands exactly as shown to ensure it all runs smoothly and you can view the output:

```

1 library(randomForest)
2 d <- read.delim("../data/logistic-lowbwt-data.tsv")
3 d$RACE <- as.factor(d$RACE) # <- ensure RACE coded as
   factor
4 d$LOW <- as.factor(d$LOW)    # <- ensure LOW coded as
   factor
5 r <- randomForest(LOW ~ AGE + LWT + RACE + SMOKE + PTL
   + HT + UI + FTV, data = d, ntree = 100, do.trace =
   TRUE)
6 plot(r)

```

The random forest will report a number called the **out-of-bag (OOB)** error as it runs. To calculate OOB error, the trees are allowed to vote on the points that were *not* used in their construction. This provides an ongoing estimate of the generalization error of the algorithm, so you can see if adding more trees is likely to help.

What is the (approximate) overall OOB error? What is it for the positive outcome class only? The negative outcome class only?

Chapter 13

Boosting DRAFT

Each decision tree within a random forest provides a full model of some subset of the training data. The trees are fully grown and have low bias - most of their generalization error comes from their high variance (they overfit to details of their individual training sets). Averaging the votes from the different trees reduces this variance and increases accuracy.

There is also a different approach, called **boosting**, that uses an ensemble of *biased* learners. As more learners are added, the importance of datapoints that have been previously misclassified is upweighted so that subsequent learners will “focus on” those points. Averaging the votes from the different classifiers reduces the overall bias and increases accuracy in a way distinct from bagging/random forests.

13.0.1 AdaBoost

The first boosting algorithm was called **AdaBoost**, which is what we will look at today. Assume we have a training set

$$\{(x^{(1)}, y^{(1)}), \dots, (x^{(n)}, y^{(n)})\}.$$

We will start by assuming a binary outcome, $Y \in \{1, -1\}$. The $x^{(i)}$ are feature vectors of length p . Assume we have p total classifiers (for example, one classifier based on each feature in your training data).

1. Initialize the observation weights to $w_i = \frac{1}{N}$ for $i = 1, \dots, N$.
2. For $m = 1, \dots, M$:
 - (a) Calculate the weighted errors of the available classifiers using the current training weights, w_i . Select the classifier $G_m(x)$ that minimizes the weighted training error.
 - (b) Compute

$$\text{err}_m = \frac{\sum_{i=1}^N w_i \cdot \mathcal{I}(y^{(i)} \neq G_m(x^{(i)}))}{\sum_{i=1}^N w_i}$$
 - (c) Compute voting weight for classifier m :

$$\alpha_m = \log \left(\frac{1 - \text{err}_m}{\text{err}_m} \right)$$
 - (d) Set

$$w_i := w_i \cdot \exp \left[\alpha_m \cdot \mathcal{I}(y^{(i)} \neq G_m(x^{(i)})) \right]$$
 for $i = 1, \dots, N$.
3. Output

$$G(x) = \text{sign} \left[\sum_{m=1}^M \alpha_m G_m(x) \right]$$

We will now apply AdaBoost to the “happiness” example.

13.0.2 Gradient Boosting

Jerome Friedman and Leo Breiman generalized AdaBoost into a general framework called **gradient boosting**. In this framework, of which AdaBoost is a subset, there are three components:

1. A loss function to be optimized.
2. Weak learners to make predictions.
3. An additive model that adds the contributions of different weak learners to minimize the loss function.

We don't have time to get into the details of the gradient boosting framework today, but its basic advantage is that it formulates the boosting process in such a way that any differentiable loss function can be used. In addition, although classification trees or regression trees are usually the weak learners (and technically, Friedman defined "gradient boosting" as a model that uses trees as learners) the framework is general enough to encompass other types of weak learners.

Chapter 14

Missing Data DRAFT

Chapter 15

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