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When Solving an Equation Means Solving a Crime

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Introduction

One of the challenges when learning statistics is becoming comfortable analyzing situations using mathematical models. Students have seen some algebraic modeling; for instance, in algebra they may determine a linear pricing structure or model the trajectory of a ball using a quadratic equation. It is a difficult departure for students to design their own models for data. They are given freedom to explore potential alternatives, and are released from the stricture of a perfect fit to a textbook correct answer, but this can be terrifying. It is like going from painting-–by-–number to mixing your own palette and creating an original work.

In order for students to fully examine the implications of a situation, they must be willing to make assumptions that are possibly incorrect. They need to argue both sides of a case, asserting one hypothesis, while collecting evidence against it. This is not unlike the process of examining the evidence of a crime. That process is familiar to most of us, having been widely fictionalized in books, movies and television. It is not only a great analogy to prepare students for inference, but holds a great deal of interest for most students.

The purpose of this unit is to identify the specific types of data that are collected in crime scene investigations, present the relevant background or biology involved, and use this knowledge and statistical tools to create theories and hypothesis about the solutions to crimes. This setting frees students to inhabit the place of mystery and to feel comfortable in not knowing an exact answer. We will be poised together on the edge of discovering the answer to a riddle about a crime. My goal is that students learn to see mathematics as the tool to predict answers about which no one owns the truth.

Physical evidence of a crime

Physical evidence is collected at the scene of a crime. It can be compared to known evidence or classified by type and assigned a probability using data. It can identify a victim or tie a suspect to the scene of the crime. This evidence may be blood, bones, fingerprints, or hair. From most of these pieces of evidence, there may be the potential to extract and test DNA. Once collected and analyzed, these pieces of evidence speak most loudly through statistical analysis. Tremendous stores of data exist to analyze evidence; databases of fingerprints, probability models based on sizes of specific bones, DNA databases. The purpose of this unit will be to inform the presentation of statistics to students by utilizing actual data sets related to the human body and judging ""evidence"" according to the probabilities predicted in these data sets.

Our culture is saturated with television, movies and books that make these forms of evidence anecdotally familiar to students; fingerprints, skeletal remains, blood typing, and DNA. As each segment is introduced, students should be polled and pre-–assessed about their knowledge in these areas. The lessons will build on that pre-–knowledge and clarify important misconceptions. We will do a preview of the specific technology, looking at the biology, particular cases involving that evidence and the data that is available to work with. We will follow this with a look at the statistical tools that are available to calculate or estimate probabilities. Lastly, we will perform an investigation on some collected or created evidence. I will present this paper in the same format, breaking the work into the areas that we will cover and presenting background, mathematics and lab.

Bones

A mass grave is exhumed in Argentina by a team of forensic anthropologists. These scientists sift through bones for the identities of the desaparecidos, ""the disappeared ones."" [1] This horrific scene has been played out again and again, from Serbia, to Rwanda, to the site of the fallen Twin Towers. Forensic techniques have identified bodies to bring closure to bereaved families, and to be used as criminal evidence at trial. How are the age, gender and appearance of a person revealed by the shape and size of their bones? Do bones have important differences in size, appearance and composition? What can we learn about how to narrow our search for answers using statistical measures?

Types of information from bones

Bones can reveal much about a victim. Location of discovery, level of decay, size and shape are all useful indicators. Finding an intact skeleton, one can use the height to predict the age or gender using tables of normal curves. This particular concept requires little or no background knowledge and there is excellent data available through the United States Government''s Centers for Disease Control (CDC) site in The National Health and Nutrition Examination Survey (NHANES) [2] . An example introducing the use of the normal distribution in calculating percentiles will be included in the lessons for this unit.

In order to carefully determine the age of a victim, an X-–ray of the bones may be helpful. As a person grows, their long bones grow outward at the ends, called the epiphysis. Before the bones are fully developed, there is an area that is more cartilage than bone. The size of that area shrinks as the person ages. An X-–ray can be useful to measure the size of the area known as the epiphyseal plate. If the person is fully grown, the plate is simply a line. The measure of the epiphyseal plate can be compared to sample distributions in order to estimate the age of the skeleton. [3] Additionally, the numbers of permanent teeth in a skull are an indication of the age of the individual.

A single bone can be used to predict the height of an individual, again using sample data. Students can practice this by creating a sample using the NHANES data. Students can use linear regression techniques to predict height from the length of a single bone, see the lessons area for this example. Regression can also be used to predict weight based on skeletal evidence. Using X-‐rays of the femur, the weight of an individual is correlated with the diameter of the femur. [4]

Perhaps we have found only a piece of the person''s pelvis. Can we determine gender? We have seen that predicting gender using height alone can be inaccurate. There is a generous overlap between height that is predictably male and that is predictably female. In the lessons, we will look at gender differences in bones. Students will look at an image of the pelvis and identify key parts of the bones. [5] Using another distribution, students will predict the person''s gender based on the associated probabilities in the study. [6] The skeleton is a long lasting piece of our equipment. Using the bones to estimate time of death is not a very useful indicator. Once the soft tissue of our body has decayed, in a time span between two and eight months, our bones will remain fairly intact for a long period of time. Carbon dating can be used, or age can be estimated by using historical artifacts found at the site.

Blood

Blood evidence can be used to identify an unknown victim, comparing the blood type of the body to the recorded blood type of possible missing persons. If blood spatters or stains are left at the scene by a perpetrator, blood typing can help to narrow a field of suspects. In order to understand what a blood type is, students will need an overview of the type of cells found in blood and an introduction to the immune system.

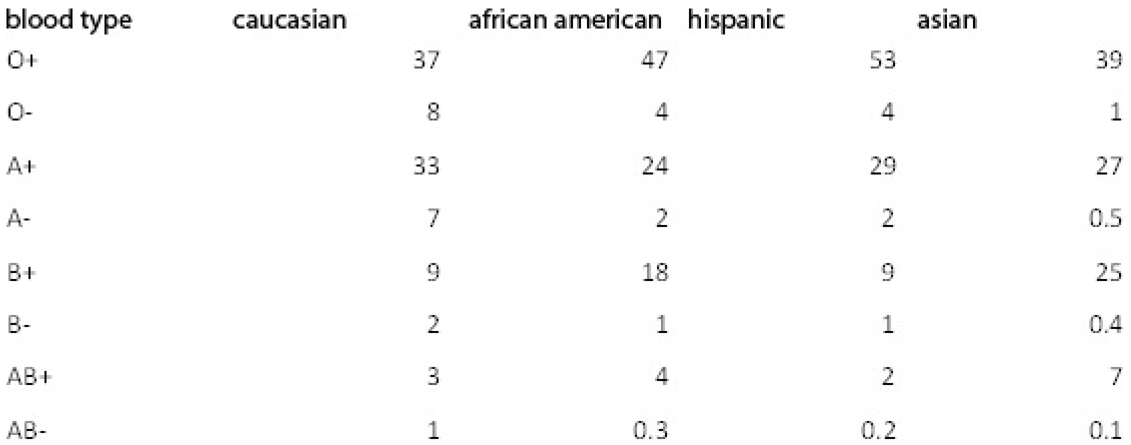
Blood is composed of liquids and solids that are pumped by the heart through the body''s network of veins and arteries. The liquid part of blood is called plasma, and the solids are made of blood cells: red cells, white cells, and platelets. Platelets are cell-‐like structures, formed in bone marrow, that help repair damage to blood vessels by creating clots to seal holes and allow the body to heal. Platelets and red blood cells have no nucleus and no DNA. White blood cells are active in fighting infections, attacking foreign cells and eating dead cells and bacteria. One of the ways that these white blood cells fight infections is to create proteins called antibodies. These antibodies have [7] special shaped receptors that will attach to a foreign object entering the blood. This object -‐ whether cell, chemical, bacteria or virus, has a specific epitope (think ""key"") that fits a specific antibody (think ""lock""). Once the antibody attaches to the antigen it may neutralize the object or identify the object as trouble, for other cells to destroy.

Red blood cells have antigens on their surface. It is these antigens that determine blood types. There are combinations of antigens that create even more complexity in the distribution of blood groups. The basic groups are called A, B, AB and O. They are known as (+) or (-‐) depending on the presence or absence of the antigen called Rh factor.

Each type has an attached probability, making a rather straightforward probability distribution, with slight variations across racial categories.

Introducing the lesson, students can play a blood typing game at the Red Cross website [8] or Nobel Prize website [9] . Both of these interactive games allow students to see the medical application of blood typing, where correct matching of antigen types is necessary for healthy outcomes. Once students see why and how blood is typed, we can apply it to forensics by observing the probability distribution of specific blood types.

Figure BLOOD TYPE BY RACE [10]



blood type	caucasian	african american	hispanic	asian
O+	37	47	53	39
O-	8	4	4	1
A+	33	24	29	27
A-	7	2	2	0.5
B+	9	18	9	25
B-	2	1	1	0.4
AB+	3	4	2	7
AB-	1	0.3	0.2	0.1

There are so many ways that this can be used in the statistics curriculum, that it is a great topic to explore early and often. Shown above is a great two-–way table that provides insight when examined in two directions. This table can be used in a discussion of independence. This distribution can also be revisited later in the course as we meet the chi-–square distributions.

Blood typing can only narrow probabilities to 1%, in the case of a very rare AB-– blood. That is not a small enough probability to base a criminal case on, although it often is used as crucial evidence. The unambiguous nature of physical evidence is very powerful. Unlike witness testimony, it has the backing of scientific fact, even if that fact is a probability. One example that students can examine is the Kenneth Waters trial for the 1980 murder of Katerina Brow. Blood evidence, along with testimony of his former girlfriends led to his conviction. Eighteen years later, DNA testing of the same blood evidence did not match Mr. Waters. The hard work of his sister Betty Ann Waters to free her brother, and his wrongful incarceration are the subject of the film Conviction.

Students will watch and discuss the film. Prior to screening, we will recreate the trial of Mr. Waters. Students will work in groups as the defense and as the prosecution. The evidence available at the trial will be available to use as students create their arguments. A third group will play judge and jury. Students should present the evidence and the jury should come to a decision. After the trial we will look at the Innocence Project page about Kenny Waters and view the film. [11]

DNA

Why is DNA a more powerful measure of identity than blood type? Blood matches a single protein attribute of the blood sample giving us a single probability of a match, while DNA uses multiple tags. A good analogy is cards. If I have a 2 of Hearts and I am trying to make a ""pair"" in a card game, I need to find either a 2 of Clubs, Spades or Diamonds. I have 3 chances in the 51 cards left, that gives me about a 6% chance. Now, if I want to get four of a kind, I have to multiply all of the probabilities as I pick the cards up. The probability of 4 of a kind is (3/51)x(2/50)x(1/49) = 0.005 %. The probability of making 3 matches drops to a thousandth of the probability of making one match.

DNA fingerprinting is a complex process that can yield extremely strong physical evidence. The probability of getting a match drops dramatically by looking at multiple distinctive areas within the DNA code of a sample. These areas within the DNA are called loci. These loci have been established by genetic researchers and with the United States Federal Bureau of Investigation (FBI) into a system called the Combined DNA Index System

(CODIS). Depending on the lab and the specific requirements of the test, two sets of DNA will be compared for matches on 7-–13 loci. A match on all 13 strands is a very powerful match indeed.

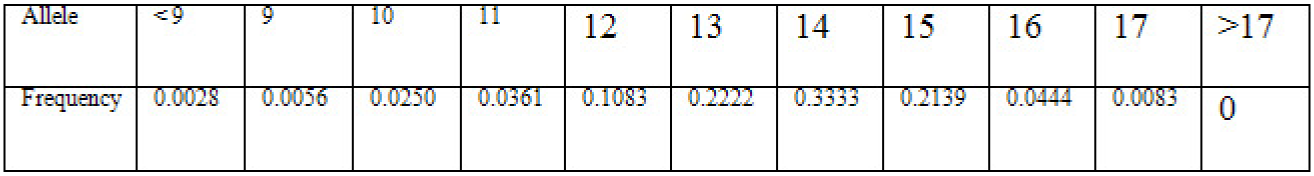
DNA is a tremendously long chain of bonded pairs (base pairs) of nucleic acids. These base pairs have distinct combinations and patterns that create a code. Areas of the chain are partitioned into genes which are specific portions of the chain that can produce a particular protein. The idea of ""mapping the genome"" is the concept that people can attach specific meaning to the codes of portions of this chain. Each person has their own expression of that gene, called their genotype. By understanding the purpose of a piece of the chain, we can notice the similarities and differences in genotypes that create variation in protein production, and in turn variation in anatomy.

About 2% of the total sets of base pairs have been sequenced to attach meaning about their genes. The rest are sometimes referred to as ""junk DNA."" Within the junk, there are curious areas that have stutters of combinations of base pairs. In other words, the combinations go into a sequence of repeating themselves. These areas are called short tandem repeat loci or STR.

Between individuals, each STR can exhibit a variable number of repeats of DNA code. An allele is a specific length of repeats that the locus can take on. There are a small number of alleles for each locus. The genotype of each person at the locus is a pair of two alleles, one from the mother and one from the father.

Large samples of DNA have allowed probability distributions of the alleles to be determined and within these distributions, each allele has a specific likelihood to occur. In order to calculate the likelihood of a particular genotype, or combination of alleles, the probability of each allele is multiplied together. Lets say that a person has a genotype of 8,10, the 8 could be from the mother and 10 from father, or reversed. If the alleles are different, we multiply the individual probabilities together and then this number is multiplied by two because of the two ways in which it could occur. If the genotype is 12,12 with the same allele came from both parents, the probability is the square of the frequency of the allele.

The uniqueness of a person''s DNA follows from the extremely low probability that more than one person could have the same combinations along all loci compared. This is called a match probability. This probability is calculated using the product rule, and making the assumption that the loci are independent. Looking at one loci D8S1179, a sample of size 200 from the FBI was used to calculate these relative frequencies. The highest probability within this loci is for the individual to have 14 repeats, with a frequency of 0.3333. Taken together, the chance that the individual would display 14,14 at D8S1179 is $(0.3333)^2 = 0.1111$. About the highest probability at this locus would be a 15% chance with genotype 13,14 or 2(.2222)(.3333)= 15%



Allele	<9	9	10	11	12	13	14	15	16	17	>17
Frequency	0.0028	0.0056	0.0250	0.0361	0.1083	0.2222	0.3333	0.2139	0.0444	0.0083	0

[12] Some particular genotypes would have a lower probability, some perhaps higher. If we use this 15% probability as an example for all 13 loci, the match probability for this sample would be $1/.15^{13}$ because we would multiply the 15% chance of any particular genotype, with the same probability at 13 locations. This equates to about one in 1.5 trillion chance. Given the world population is only 9 billion it is extremely unlikely that more than one human would have this same combination of genotypes.

Students will be introduced to the science of the DNA testing, and its use in the courtroom through PBS video and online teaching resources. [13] Once DNA samples have been collected from the scene of a crime, the DNA sample must be copied and amplified to make it measurable. The process has several steps. First, the DNA is separated from the cell structure by using heat or chemicals. Next, specific enzymes are added to the DNA to cut the sample into fragments. The fragments with the loci that we wish to examine are amplified by making copies. This process is known as a Polymerase Chain Reaction or PCR. An enzyme that works with the fragment that we want copied is added to the DNA, and in a series of reactions, the number of copies is increased exponentially.

The DNA material is poured onto a laboratory gel, and electrical current is used to attract the chain of DNA through the gel. Depending on the weight of the specific allele, less repeats will be lighter, the fragments will travel more or less through the gel. The result is a length of DNA specific to the allele of the individual at the given loci. A set of these lengths is the DNA fingerprint. Depending on the number of matches, a probability of two sets of DNA matching is calculated by multiplying the probability of each allelic match.

We will create our own probability distributions of the major loci based on sample populations. [14,15] Students will have the opportunity to do a simulation to compare DNA strands "recovered from a crime scene" with the DNA strands of "subjects". Attention will be given to the exponential increase in probability as multiple markers match.

Fingerprints

A much older technology than DNA, often considered as specific and individualized as DNA, fingerprinting also uses the multiplication principle of probability to hone in on a certain match. Fingerprint probabilities can be less easy to pinpoint than DNA for a couple of specific reasons. One reason is that fingerprints collected from crime scenes are often imperfect. A second reason is that the probability of a match at a particular locus may not as easily quantified as it is in DNA. Loci in fingerprints are determined by gridding the image and matching areas on the grid. The match is visual and based on an expert''s judgment call. However, some experts argue that fingerprints are more reliable, matching as many as 36 loci, called minutiae.

In 2004 a tremendous error involving probabilities can be used as an example to illustrate how a one in a million chance can actually happen one in a million times. This can be used as an introduction to randomness and the law of large numbers.

On March 11, 2004, coordinated attacks on the commuter trains in Madrid, Spain, wounded approximately 200 people and killed 190. In a sweeping search for a fingerprint match to a print found on a bag of explosives, FBI investigators honed in on a lawyer in Oregon in the United States. His arrest was based on an absolute certainty among the investigators, all of whom were highly skilled, that they had found a perfect match of the print. They identified 15 areas of similarity. The problem here was that they did not limit their search to suspects. The unrestricted search in addition to the size of the database, turned up a virtual twin. The lawyer was released two weeks later when the Spanish police found a strong match with an Algerian suspect. [16]

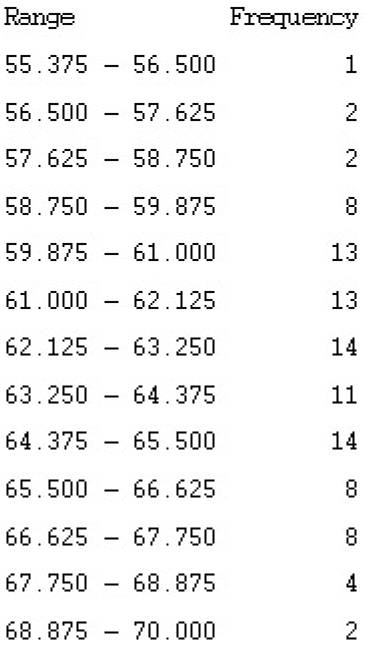
Lessons

Lessons with Bones

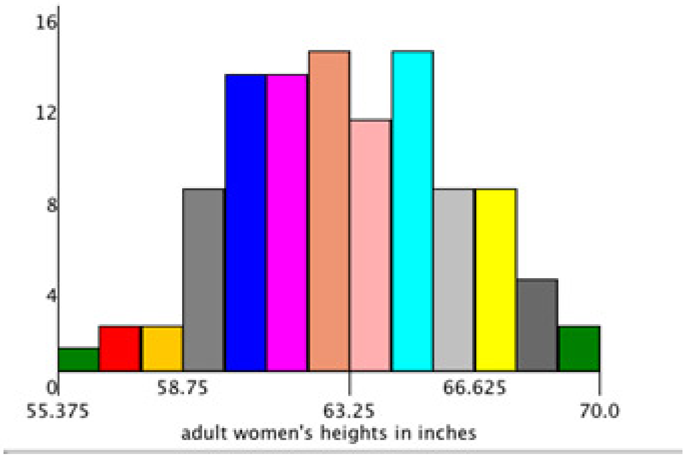
Height and Gender

Students will watch video from the National Institutes of Health, United States National Library of Medicine about the exhumation of bodies in Argentina and El Salvador. [17] Students will talk about the issues with a partner. Together they can make a list of known and unknown facts in the case. In regards to the skeletons, students should list the possible ways that they believe an archaeologist might begin to identify the remains of a particular individual.

Students can download data from the CDC website using data from the NHANES study [18] Using statistical software or a calculator, students will create a histogram for men and one for women that show the distribution of heights. Students should discuss shape, center and spread for the distributions. Students should determine the percentile rank of an individual in the data set. Percentile is a measure of location within an ordered distribution.

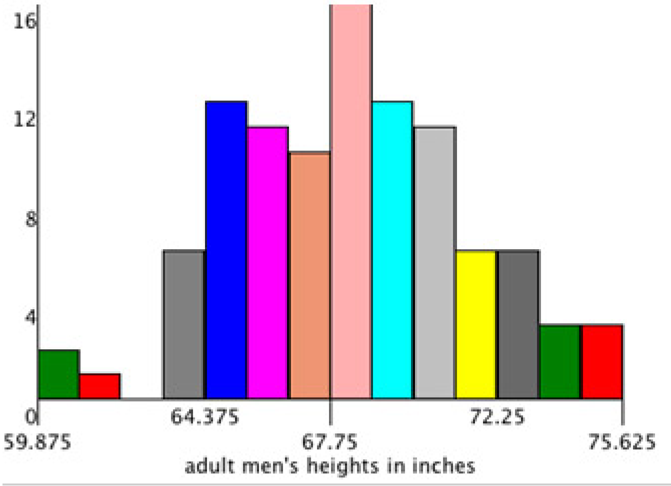


Range	Frequency
55.375 – 56.500	1
56.500 – 57.625	2
57.625 – 58.750	2
58.750 – 59.875	8
59.875 – 61.000	13
61.000 – 62.125	13
62.125 – 63.250	14
63.250 – 64.375	11
64.375 – 65.500	14
65.500 – 66.625	8
66.625 – 67.750	8
67.750 – 68.875	4
68.875 – 70.000	2



The distribution in the histogram is expressed in order from smallest to largest. The percentile is the ratio of the cumulative frequency of an individual divided by total number of individuals in the sample. For example, a skeleton that is 60.5 inches tall falls

59.875 – 61.000	2
61.000 – 62.125	1
62.125 – 63.250	0
63.250 – 64.375	6
64.375 – 65.500	12
65.500 – 66.625	11
66.625 – 67.750	10
67.750 – 68.875	18
68.875 – 70.000	12
70.000 – 71.125	11
71.125 – 72.250	6
72.250 – 73.375	6
73.375 – 74.500	3
74.500 – 75.625	3



within both distributions. However it is on the far low end of the men''s distribution, only 2/100 = .02 or 2% of men are at this height or smaller. For women the cumulative frequency at 60.5 inches 26/100 = .26 or 26%. There is a 26% chance of finding a female of this height but only a 2% chance of finding a male of this height.

1) locate the bin that your height is in and record the frequencies in that bin and every bin below. Add all of those frequencies together to get cumulative frequency.
2) Divide (cumulative freqency/total frequency). This is the probability that a human would be the size of your human or smaller, given that they are of the gender you are looking at.

Students can extend this to draw a normal probability plot and shade the height of their skeleton on the two curves. They can estimate the mean and standard deviation from the histograms or by using the original data. Students should calculate the percentile height for both woman and man. Using tracing paper, students should create a third graph that shows the intersection of the curves and shades the area of probability for the skeleton. Students should discuss the consequences of the incorrect decision. If they already know Type 1 and Type 2 errors, that can be discussed, otherwise this is an example of for-–shadowing of that topic. (see example for pelvis size below)

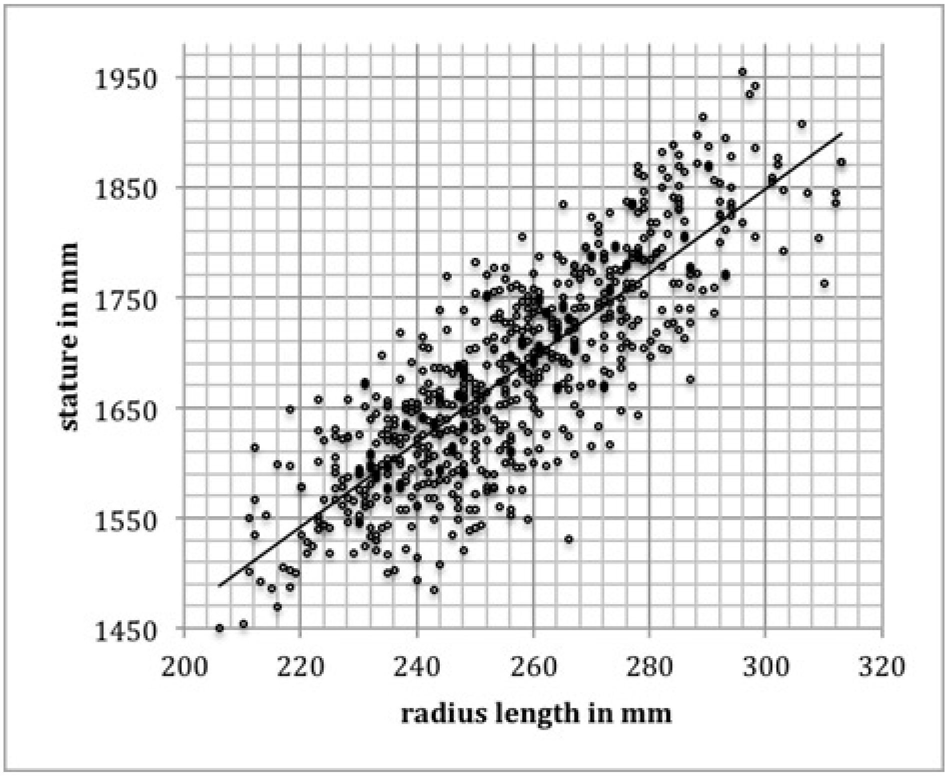
Predicting height from a single bone

How can we predict someone''s size based on that single bone? This has been done with regression equations based on data from many skeletons. [19] This lab will be performed when we are looking at regression and correlation. Students will identify the bone that they have been given and measure it using the NHANES study guidelines. Although NHANES was performed with live subjects, we will approximate using this data. Students will take random samples of 50 men and 50 women using the NHANES data. Using their sample, they will find a regression model for predicting height given the length of the bone that they have been given.

A bone has been discovered, and you have identified it as a human arm bone, a radius. Using this chart predict the height of the human, to whom this bone belonged.

Estimated height:____

How did you estimate the height (Describe your thought process)__________



This chart is created from a large sample of measurements of human bodies.

- Each dot represent one person, with their height measurement on the y-–axis and their radius measurement on the x-–axis.
- The black line is a model called a line of best fit and is used as a prediction tool. We use it to predict the persons''s _____________ in mm from their ___________ in mm.

Additional questions:

Slope can be determined using two points on a line, it describes the ratio (difference in y/difference in x).

What is the slope of the line?____

Estimate the linear equation of this line of best fit. (hint using a point from your previous calculation (x,y) and the slope m, that you calculated: m(x-–x)=(y-–y))

____

____

Describe in words what the slope means in this context:_________________________

____

Bones and Gender

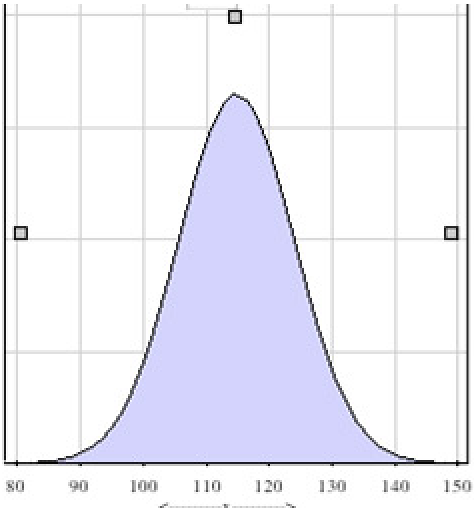
Using the tools at the same NLM/NIH website [20] , students will look at skulls for features that assist in deciphering the gender of its owner. The skull and the pelvis of an intact skeleton are often the most distinctive way to determine the gender of the individual.

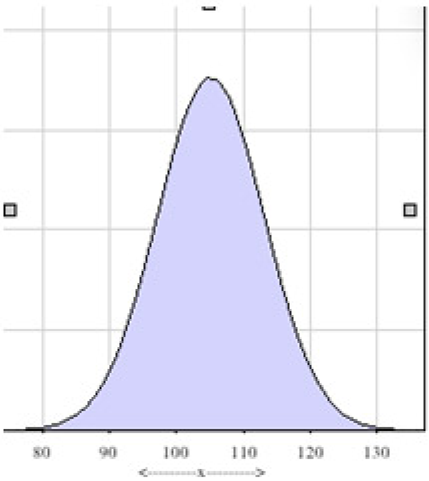
Using statistics from a study of sexual dimorphism in pelvis measurements [21] students can use the mean and standard deviations to graph normal curves of pelvis sizes. Students can view images from the study or use the online tool at the University of Wyoming [22] to see the pelvis, and what measurements are indicated.

Students will each get a paper cut-–out of a pelvis to measure. Using the images from the study, or online, students should identify the area to measure and accurately measure the individual bone that they have ""found."" The pelvis was discovered during an archeological dig at a Colonial home site in the northeastern United States. The normal curves that the students have produced can be used to indicate the likelihood that the pelvis is male or female.

For example, a student measures the anterior posterior distance of the pelvic outlet of their discovered pelvis. They find a measure of 122 mm. Using the normal curves shown below, where the female statistics are $\mu = 114.65$ and $\sigma = 9.18$ and the males are $\mu = 105.00$ and $\sigma = 8.05$. Students can mark the point at which a pelvis with measure of 122 mm would be found within the distributions. How likely is this a female? Using the z-–score formula we calculate z-–scores for our males and our females. Male: $Z = (x - \mu) / \sigma$ or $Z = (122 - 105)/8.05$ or 2.11. Female: $Z = (x - \mu) / \sigma$ or $Z = (122 - 114.65)/9.18$.

With a table of z-–values or our calculator we can determine that about 1.7% of men have a bone that size or larger and about 22 % of women have a bone that size or larger.

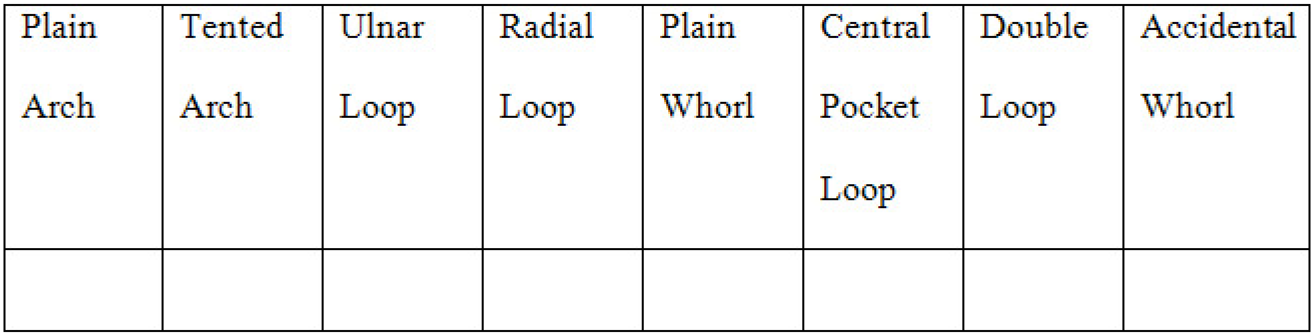




This becomes an easy bet that the bones belong to a woman.

Fingerprint Lesson

Fingerprints have several distinct categories, again with a specific probability distribution. Students will use a pre-–assessment exercise on the PBS website called *Whodunnit* . [23] Students will fingerprint themselves. A simple classroom method would be to rub a spot of pencil graphite on paper, rub their thumb on the spot and lift the print using scotch tape. Students can identify the types of fingerprint, and classify themselves according to the type they see on their fingers. Great images for these are available at the FBI website. [24] The class will create probability distribution as shown below:



Plain Arch	Tented Arch	Ulnar Loop	Radial Loop	Plain Whorl	Central Pocket Loop	Double Loop	Accidental Whorl

Students can ""blow up"" their fingerprints using an overhead projector. By projecting the image over a grid image, students can compare regions on the grid. Working in teams (Placeholder2), students should create maps of their fingerprints. The grid should have assigned coordinates and each block should be numbered. Using a random number generator, students can pick 4-–5 blocks to compare for similarities.

Appendix of standards

Common Core Standards for Mathematics (relevant standards included)

Summarize, represent, and interpret data on a single count or measurement variable

1. Represent data with plots on the real number line (dot plots, histograms, and box plots).
2. Use statistics appropriate to the shape of the data distribution to compare center and spread of two or more different data sets.
3. Interpret differences in shape, center and spread in the context of the data sets.
4. Use the mean and standard deviation of a data set to fit it to a normal distribution and to estimate population percentages. Recognize that there are data sets for which such a procedure is not appropriate. Use calculators, spreadsheets, and tables to estimate areas under the normal curve.

Summarize, represent, and interpret data on two categorical and quantitative variables

5. Summarize categorical data for two categories in two-–way frequency tables. Interpret relative frequencies

in the context of the data (including joint, marginal, and conditional relative frequencies). Recognize possible associations and trends in the data.

6. Represent data on two quantitative variables on a scatter plot, and describe how the variables are related.

> a. Fit a function to the data; use functions fitted to data to solve problems in the context of the data. Use given functions or choose a function suggested by the context.
> c. Fit a linear function for a scatter plot that suggests a linear association.

Interpret linear models

7. Interpret the slope (rate of change) and the intercept (constant term) of a linear model in the context of the data.

9. Distinguish between correlation and causation.

Making Inferences and Justifying Conclusions

Understand and evaluate random processes underlying statistical experiments

> 1. Understand statistics as a process for making inferences about population parameters based on a random sample from that population.
> 2. Make inferences and justify conclusions from sample surveys, experiments, and observational studies
> 3. Recognize the purposes of and differences among sample surveys, experiments, and observational studies; explain how randomization relates to each.
> 6. Evaluate reports based on data.

Conditional Probability and the Rules of Probability

Understand independence and conditional probability and use them to interpret data

> 1. Describe events as subsets of a sample space (the set of outcomes) using characteristics (or categories) of the outcomes, or as unions, intersections, or complements of other events (""or,"" ""and,"" ""not"").
> 2. Understand that two events A and B are independent if the probability of A and B occurring together is the product of their probabilities, and use this characterization to determine if they are independent.

3. Understand the conditional probability of A given B as P(A and B)/P(B), and interpret independence of A and B as saying that the conditional probability of A given B is the same as the probability of A, and the conditional probability of B given A is the same as the probability of B.
4. Construct and interpret two-–way frequency tables of data when two categories are associated with each object being classified. Use the two-–way table as a sample space to decide if events are independent and to approximate conditional probabilities.
5. Recognize and explain the concepts of conditional probability and independence in everyday language and everyday situations. Use the rules of probability to compute probabilities of compound events in a uniform probability model
6. Find the conditional probability of A given B as the fraction of B''s outcomes that also belong to A, and interpret the answer in terms of the model.
7. Apply the Addition Rule, P(A or B) = P(A) + P(B) – P(A and B)
8. Apply the general Multiplication Rule in a uniform probability model
9. Use permutations and combinations to compute probabilities of compound events and solve problems.

Using Probability to Make Decisions

Calculate expected values and use them to solve problems

1. Define a random variable for a quantity of interest by assigning a numerical value to each event in a sample space
2. Calculate the expected value of a random variable; interpret it as the mean of the probability distribution.
4. Develop a probability distribution for a random variable defined for a sample space in which probabilities are assigned empirically; find the expected value.
6. (+) Use probabilities to make fair decisions (e.g., drawing by lots, using a random number generator).
7. (+) Analyze decisions and strategies using probability concepts

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