Introduction to Statistical Analysis: a regression-from-the-outset approach

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Preface

0.1 Target

The target is graduate students in population health sciences in their first year. Concurrently, they take their first courses on epidemiologic methods. The department is known for its emphasis on quantitative methods, and students' ability to carry out their own quantitative work. Since most of the data they will deal with are non-experimental, there is a strong emphasis on multivariable regression. While some students will have had some statistical courses as undergraduates, the courses start at the beginning, and are pitched at the Master's level.

In the last decade, the incoming classes have become more diverse, both in their backgrounds, and in their career plans. Some of those in the recently begun MScPH program plan to ~~me~~ consumers rather than producers of research; previously, the majority of students pursued a thesis-based Masters that involved considerable statistical analyses to produce new statistical evidence.

0.2 Topics/textbooks

For the **first term** course 607, recent choices have been *The Practice of Statistics in the Life Sciences* by Baldi and Moore, and *Stats* by de Veaux, Velleman and Bock. Others that have been recommended are the older texts by Pagano and Gauvreau, and by Rosner. Some of us have also drawn on material in *Statistics* by Freedman, Pisani, Purves and Adkikari, and *Statistical Methods in Medical Research*, 4th Edition_ by Armitage,Berry, and Matthews.

The newer books have tried to teach the topic more engagingly, by starting with where data come from, and (descriptively) displaying single distributions, or relationships between variables. They and the many others then typically move on to Probability; Random Variables; Sampling Distributions; Confidence intervals and Tests of Hypotheses; Inference about/for a single Mean/Proportion/Rate and a difference of two Means/Proportions/Rates; Chi-square Tests for 2 way frequency tables; Simple Correlation and Regression. Most include a (or point

to an online) chapter on ~~Non-Parametric Tests.~~ They typically end with tables of probability tail areas, and ~~critical values.~~

Bradford Hill's *Principles of Medical Statistics* followed the same sequence 80 years ago, but in black type in a book that measured 6 inches by 9 inches by 1 inch, and weighed less than a pound. Today's multi-colour texts are 50% longer, 50% wider, and twice as thick, and weigh 5 pounds or more.

The topics to be covered in the **second term** course include multiple regression involving Gaussian, Binomial, and Poisson variation, as well as (possibly censored) time-durations – or their reciprocals, event rates. Here is is more difficult to point to one modern comprehensive textbook. There is pressure to add even more topics, such as ~~correlated data, missing data, measurement error~~ etc. top the second statistics course.

0.3 Regression from the outset

It is important to balance the desire to ~~cover more of these regression-based topics with having a good grounding, from the first term, in the basic concepts that underlie all statistical analyses.~~

The first term *epidemiology* course deals with proportions and rates (risks and hazards) and – at the core of epidemiology – comparisons involving these. Control for confounding is typically via odds/risk/rate differences/ratios obtained by standardization or Mantel-Haenszel-type summary measures. Teachers are reluctant to spend the time to teach the classical confidence intervals for these, as they are not that intuitive and – once students have covered multiple regression – superceded by model-based intervals.

~~One way to synchronize with epidemiology, is to teach the six separate topics Mean/Proportion/Rate and differences of two Means/Proportions/Rates in a more unified way by embedding all 6 in a regression format right from the outset, to use generalized linear models, and~~ to focus on all-or-none contrasts, represented by binary 'X' values.

This would have other benefits. ~~As of now, a lot of time in 607 is spent on 1-sample and 2-sample methods (and chi-square tests) that don't lead anywhere (generalize).~~ Ironically, the first-term concerns with equal and unequal variance tests are no longer raised, or obsessed about, in the multiple regression framework in second term.

The teaching/learning of statistical concepts/techiques is greatly enriched by real-world applications from published reports of public health and epidemiology research. In 1980, a first course in statistics provided access to 80% of the articles in NEJM articles. This large dividend is no longer the case – and even less so for journals that report on non-experimental research. The 1-sample and 2-sample methods, and chi-square tests that have been the core of first statistics courses are no longer the techniques that underlie the reported summaries in

the abstracts and in the full text. The statistical analysis sections of many of these articles do still start off with descriptive statistics and a perfunctory list of parametric and non-parametric 1 and 2 sample tests, but most then describe the multivariable techniques used to produce the reported summaries. [Laboratory sciences can still get by with t-tests and 'anova's – and the occasional ancova'; studies involving intact human beings in free-living populations can not.] Thus, if the first statistical course is to to get the same 'understanding' dividend from research articles as the introductory epidemiology course does, that first statistical course needs to teach the techniques that produce the results in the abstracts. Even if it can only go so far, such an approach can promote a regression approach right from week one, and build on it each week, rather than introduce it for the first time at week 9 or 10, when the course is already beginning to wind down, and assignments from other courses are piling up.

0.4 Parameters first, data later

When many teachers and students think of regression, they imagine a cloud of points in x-y space, and the least squares fitting of a regression line. They start with thinking about the data.

A few teachers, when they introduce regression, do so by describing/teaching it as **an equation that connects parameters**, constructed in such a way that the parameter-constrast of interest is easily and directly visible. Three such teachers are Clayton and Hills 1995, Miettinen1985, and Rothman 2012. In each case, their first chapter on regression is limited to the parameters and to undersatnding what they mean; data only appear in the next chapter.

There is a lot to commend this approach. It reminds epidemiologists – and even statisticians – that statistical inference is about parameters. Before addressing data and data-summaries, we need to specify what the estimands are – i.e, what parameter(s) is(are) we pursuing.

It is easy and tempting to start with data, since the form of the summary statistic is usually easy to write down directly. It can also be used to motivate a definition: for example, we could define an odds ratio by its empirical computational form ad/bc. However, this 'give me the answer first, and the question later' approach comes up short as soon as one asks how statistically stable this estimate is. To derive a standard error or confidence interval, one has to appeal to a sampling distribution. To do this, one needs to identify the random variables involvced, and the parameters that determine/modulate their statistical distributions.

~~Once students master the big picture (the parameter(s) being pursued), the task of estimating them by fitting these equations to data is considerably simplified, and becomes more generic.~~ In this approach more upfront thinking is devoted to the parameters – to what Miettinen calls the design of the study object –

with the focus on a pre-specified 'deliverable.'

0.5 Let's switch to "y-bar", and drop "x-bar".

The prevailing practice, when introducing descriptive statistics, and even to 1 and two sample procedures, is to use the term x-bar ($\bar{x}$) for an arithmetic mean (one notable execption is de Veaux at al.) This misses the chance to prepare students for regression, where E[Y|X] is the object of interest, and the X-conditional Y's are the random variables. Technically speaking, the X's are not even considered random variables. Elevating the status of the Y's and explaining the role of the X's, and the impact of the X distributions on precision might also cut down on the practice of checking the normality of the X's, even though the X's are not random variables. They are merely the X locations/profiles at which Y was measured/recorded. When possible, the X distribution should be determined by the investigators, so as to give more precise and less correlated estimates of the parameters being pursued. Switching from $\bar{x}$ to $\bar{y}$ is a simple yet meaningful step in this direction. JH made this switch about 10 years ago.

0.6 Computing from the outset

In 1980, most calculations in the first part of 607 were by hand calculator. Computing summary statistics by hand was seen as a way to help students understand the concepts involved, and the absence of automated rapid computation was not considered a drawback. However, doing so did not always help students understand the concept of a standard deviation or a regression slope, since these formulae were designed to minimize the number of keystrokes, rather than to illuminate the construct involved. For example, it was common to rescale and relocate data to cut down on the numbers of digits entered, to group values into bins, and use midpoints and frequencies. It was also common to use the computationally-economical 1-pass-through-the-data formula for the sample variance

$$s^2 = \frac{\sum y^2 - \frac{(\sum y)^2}{n}}{n-1},$$

even though the definitional formula is

$$s^2 = \frac{\sum (y-\bar{y})^2}{n-1}.$$

The latter (definitional) one was considered too long, even though having to first have to compute $\bar{y}$ and then go back and compute (and square) each $y - \bar{y}$ would have helped students to internalize what a sample variance is.

When spreadsheets arrived in the early 1980s, students could use the built-in mean formula to compute and display $\bar{y}$, another formula to compute and

display a new column of the deviations from $\bar{y}$, another to compute and display a new column of the squares of these deviations, another to count the number of deviations, and a final formula to arrives at s^2. ~~The understanding comes from coding the definitional formula, and the spreadsheet simply and speedily carries them out, allowing to user to see all of the relevant components, and from noticing if each one looks reasonable.~~ Ultimately, once students master the concept, they could move on to built-in formulae that hide (or themselves avoid) the intermediate quantities.

Few teachers actually encouraged the use of spreadsheets, and instead promoted commercial statistical packages such as SAS, SPSS and Stata. Thus, the opportunity to learn to 'walk first, run later' afforded by spreadsheets was not fully exploited.

RStudio is an integrated environment for R, a free software environment for statistical computing and graphics that runs on a wide variety of platforms. Just like spreadsheet software, one can use R not just as a calculator, but as a *programmable* calculator, and by programming them, learn the concepts before moving on to the built-in functions. There is a large user-community and a tradition of sharing information and ways of doing things. The graphics language contains primitive functions that allow customization, as well as higher-level functions, and is tighly integrated with the statistical routines amd data frame functions. R Markdown helps to foster reproducible research. Shiny apps allow interactivity and visualization, a bit like 'what-ifs' with a spreadsheet.

It takes practice to become comfortable with R. Gor those less mathematical, it is somewhat more cryptic than, and not quite as intuitive as, other packages. For the last several years, the department has offered a ~~13 hour course introduction to R in first term.~~ Initially the aim was to prepare students for using it in course 621 in second term, ~~but in the Fall 2018 and 2019 offerings of course 607, computing with R and use of R Studio became mandatory.~~ Just as the epidemiology material in the Fall is shared between 2 courses (601 and 602), the aim will be to also spread the statistics material over 607 and 613, and to integrate the two more tightly. As an example, the material on 'descriptive' (i.e., not model-based) statistics and graphical displays will be covered in 613, while 607 will begin with parameters and models. Rather than treat computing as a separate activity, exercises based on 607 material will be carried out as part of 613 classes/tutorials. The statistical material will be used to motivate the computer tasks.

0.7 Appendix:

[Still rough] History of current introductory biostatistics courses

The senior author first taught a 2-course sequence for first year graduate students in epidemiology in 1980, using Colton's Statistics in Medicine as the text for the introductory course (607). He developed his own notes for the second

course, which covered multiple regression for quantitative responses. Over the next 10 years, he continued to teach the first course – first from Colton, but latterly from Moore and McCabe (and undergraduate text) and with epi statistics from Armitage and Berry and some other fundamentals from Freedman (Statistics). Stan S taught the second (621 Data Analysis in the Health Sciences), mostly from Kleinbaum's Applied Regression Analysis and Other Multivariable Methods.

In the 1990s, Lawrence J taught 607, and Michal A 621. Neither used a required textbook. LJ ~~developed an extensive set of written notes~~ (still available on his website) (and contributed a chapter Introduction to Biostatistics: Describing and Drawing Inferences from Data book on Surgical Arithmetic) while MA used transparencies that were widely photocopied. 2000s Robert P 621? LJ 621

Meanwhile JH taught to summer students (mostly medical residents and fellows): 607 and a second course (678, Analysis of Multivariable Data). Both sets of content are available on JH's website. He last taught the Fall version of 607 in 2001, when LJ was on sabbatical.

607: Tina 2006 - 201x Erica M; 20xx - Paramita SC. 2018, 2019 Sahir B 621: Aurelie Alexandra 2020 Shirin

Chapter 1

Introduction

1.1 Goals

Blah

1.2 Structure

Blah Blah

1.3 Attitudes, etc....

Blah Blah Blah

Part I

Part I

Chapter 2

Statistical Parameters

2.1 ~~Parameters~~

Parameter – A constant (of unknown magnitude) in a (statistical) model. [OSM2011, p60]

The parameters we will be concerned with

- μ The mean level of a quantitative characteristic, e.g. the depth of the earth's ocean or height of the land, or the height / BMI / blood pressure levels of a human population. [One could also think of mathematical and physical constants as parameters, even though their values are effectively 'known.' Examples where there is agreement to many many decimal places include the mathematical constant pi, the speed of light(c), and the gravitational constant G. The speed of sound depends on the medium it is travelling through, and the temperature of the medium. The freezing and boiling points of substances such as water and milk depend on altitude and barometric pressure]. At a lower level, we might be interested in personal characters, such as the size of a person's vocabulary, or a person's mean (or minimum, or typical) reaction time. The target could be a person's 'true score' on some test – the value one would get if one (could, but not realistically) be tested on each of the (very large) number of test items in the test bank, or observed/measured continously over the period of interest.

  Later on we will address ~~situations~~ where the mean μ is not the best 'centre' of a distribution, and why we might want to take some other feature, such as the median, or some other quantile, instead.

- π Prevalence or risk (proportion): e.g., proportion of the earth's surface that is covered by water, or of a human population that has untreated hypertension, or lacks internet access, or will develop a new health condition

over the next x years. At a lower level, we might be interested in personal proportions, such as what proportion of the calories a person consumes come from fat, or the proportion of the year 2020 the person spent on the internet, or indoors, or asleep, or sedentary.

- λ The speed with which events occur: e.g., earthquakes per earth-day, or heart attacks or traffic fatalities per (population)-year. At a lower level, we might be interested in personal intensities, such as the mean number of tweets/waking-hour a person issued during the year 2020, or the mean number of times per 100 hours of use a person's laptop froze and needed to be re-booted.

Each of these three parameters refers to a characteristic of the overall domain, such as entire surface of the earth, or the entire ocean, or population. There are no indicators for distinguishing among subdomains, so they refer to locations / persons not otherwise specified. We will drill down later.

Especially for epidemiologic research, and also more generally, one can think of π and λ as *parameters of occurrence*. [Although the word occurrence usually has a time element, it can also be timeless: how frequently a word occurs in a static text, or a mineral in a rock.] Prevalence is the proportion in a current state, and the 5-year risk is the expected proportion or probability of being in a new state 5 years from now. The parameter λ measures the speed with which the elements in question move from the original to the other state.

Even though the depths of the ocean, and blood pressures, are measured on a *quantitative* (rather than on all or none) scale, one can divide the scale into a finite number of bins/caterories, and speak of the prevalence (proportion) in each category. Conversely, one can use a set of descriptive parameters called quantiles, i.e, landmarks such that selected proportions, e.g., 0.05 or 5%, 25%, 50%, 75%, 95% of the distribution are to the left of ('below') these quantiles.

Occurence Parameters are not constants of nature [OSM1995]

> It has been noted in the philosophy of science that any science is concerned with functional relations of its objects (Friend and Feibleman, 1937). This proposition is quite evidently tenable for epidemiologic objects of research. Parameters of occurrence, such as the incidence rate for a particular illness, are not constants of nature. Rather, their magnitudes generally depend on — are functions of — a variety of characteristics of individuals — constitutional, behavioral, and/or environmental. Such relations, even if only remotely credible, are generally the objects of medical occurrence research. For example, one is quite usually interested in learning whether the rate of occurrence of some particular illness depends on (is related to or is a function of) gender — regardless of whether there is any express reason to surmise that it might be.
>
> EXAMPLE 1.5 The prevalence of any given blood type based on

the ABO antigen system„ while constant over gender and essentially constant over age, is not a constant of nature. It varies by ethnic groupings, for example. Thus the prevalence must be quantified in relation to—as a function of—ethnic group.

EXAMPLE 1.6. For the occurrence of various values of blood pressure among people, one descriptive parameter is the median of the pressure. (This is a value such that the prevalence of its exceedance is 50%.) This parameter, again, is not a constant of nature but depends on age and other characteristics of individuals. For the quantitative nature of the age relation of systolic blood pressure, a rule of thumb used to be that it is, in mm Hg, 100 plus age in years." This rule expresses a regression model - a **regression function** - of the form P = A + B x Age. In this example, P, the occurrence parameter, is the median of systolic blood pressure, A = 100 mm Hg, and B = 1 mm Hg/yr.

The characteristics on which the magnitude of an occurrence parameter depends (causally or otherwise) are **determinants** of the parameter. Thus, in the examples given above, ethnic grouping is a determinant of prevalence of any given blood type, and age is a determinant of the median of systolic blood pressure.

"Determinant" has no implication as to causality in science — any more than in everyday locution: the current age of a person is "determined" by his/her year of birth (noncausally), just as the expected outcome of a disease is "determined" by the treatment that is used (causally). The relation of an occurrence measure to a determinant, or a set of determinants, is naturally termed an occurrence relation or an occurrence function. These relations are in general the objects of epidemiologic research. [Even though the general inconstancy of occurrence parameters leads to the consideration of occurrence relations, this latter outlook affords only a partial accommodation of the inconstancy, because occurrence relations the degree also vary according to the type of individual. In particular, measures of a relation (Appendix 2) have determinants of their own.]

Before we start, a comment on terminology

Before we go on, we need to adopt sensible terminology for referring generically to the states, traits, conditions or behaviours whose category-specific parameter values are being compared. Following OSM (see above) we will use the term '**determinant**'. It has several advantages over the many other terms used in different disciplines, such as exposure, agent, independent/explanatory variable, experimental condition, treatment, intervention, factor, risk factor, predictor.

The main advantage is that it is broader, and closer to causally neutral in its connotaion. *Exposure* has environmental connotations, and technically refers to an opportity to injest or mentally take on board a substance or message.

Agent has causal connotations. The term *independent variable* suggests the investigator has control over it in a laboratory setting. The term *explanatory* is ambiguous as to the mechanism by which the parameter value in the index category got to be different from the value in the index category. Not all ~~contrasts are experimentally formed.~~ The term *factor*, and thus the term *risk factor*, are to be avoided because the word factor derives from the Latin *facere*, (the action of) doing, making, creating. *Predictor* makes one think of the future. The term *regressor* (or its shorthand, the 'X') won't be understood by lay people.

While the word 'determine' can suggest causality (e.g., demand determines the price), it also refers to 'fixing the form, position, or character of beforehand': two points determine a straight line; the area of a circle is determined by its radius. There is considerable philosophical debate as to whether something 'causes' something else. Some would argue that the extent to which genetics determines one's personality is a causal concept. Others argue that since one cannot cannot consider the alternative, ones biological sex or age can not be considered a causal determinant or a risk factor (in the strict causal meaning of the word). They prefer to refer to them as risk *indicators*.

We now move on to the parameter relations we will be concerned with, beginning with the simplest type.

2.2 Parameter Contrasts

In applied research, we are seldom interested in a single constant. Much more often we are interested in the contrast (difference) between the parameter values in different contexts/locations (Northern hemisphere vs Southern hemisphere), conditions/times (reaction times using the right versus left hand, or behaviour on weekdays versus weekends), or sub-domains or sub-populations (females vs males). Contrasts involving 'persons, places, and times' have a long history in epidemiology.

In this section, we will limit our attention to 'contrasts': a ~~comparison~~ of the parameter values between 2 contexts/locations/sub-populations. Thus (unlike in OSM's example 1.6) the parameter function has just 2 possible 'input' values. The next section will address more general parameter functions.

'Reference' and 'Index' categories

~~In many research contexts, the choice of 'reference' category (starting point, the category against which the other category is compared) will be obvious~~: it is the status quo (standard care, prevailing condition or usual situation, dominant hand, better known category). ~~The 'index' category is the category one is curious about and wishes to learn more about, by contrasting its parameter value with the parameter value for the reference category.~~

In other contexts, it is less obvious which category should serve as the reference and the index categories, and the choice may be merely a matter of

persepctive. If one is more famiar with the Northern hemisphere, it serves as a natural starting point (or 'corner' to use the terminology of Clayton and Hills, or reference category). The choice of reference category in a longevity contrast between males and females, or in-hospital mortality rates or motor vehicle fatality rates during weekends versus weekdays, might depend on what mechanism one wishes to bring out. Or one might close as the reference category the one with the larger amount of experience, or maybe the one with the lower parameter value, so that the 'index minus reference' difference would be a positive quantity, or the 'index: reference ratio' exceeds 1.

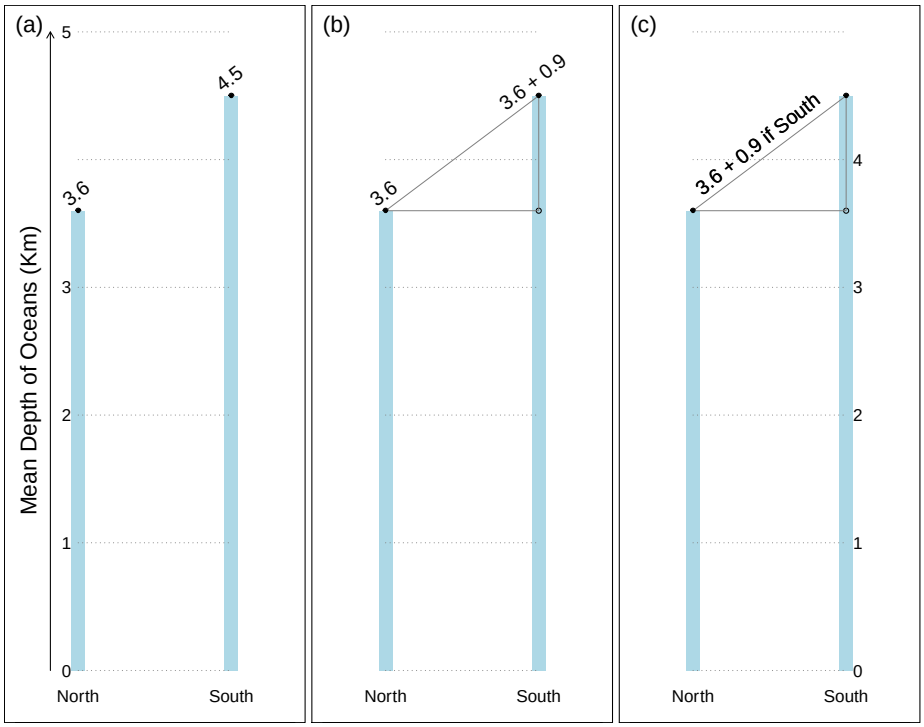
2.2.1 Parameter relations in numbers and words

~~To make this concrete,~~ we will use hypothetical (and very round) numbers and pretend we 'know' the true parameter values – in our example of the mean depth of the ocean in the Northern hemisphere (reference category) and Southern hemisphere (index category) – to be 3,600 metres (3.6Km) and 4,500 metres (4.5Km) respectively. Thus, the difference (South minus North) is 900 metres or 0.9Km.

If we wished to show the two parameter values graphically, we might do so using the format in panel (a), which shows the 2 hemisphere-specific parameter values – but forces the reader to calculate the difference.

Panel (b) follows a more reader-friendy format, where the difference (the quantity of interest) is isolated: the original 2 parameters are converted to 2 new, more relevant ones.

Panel (c) encodes the relation displayed in panel (b) in a **single phrase** that applies to **both** categories: Onto the 'starting value' of 3.8Km, one **adds** $\Delta\mu$ = 0.9 Km **only if** the resulting parameter pertains to the Southern hemisphere. The 0.9 Km is toggled off/on as one moves from North to South.



2.2.2 Parameter relations in symbols, and with the help of an index-category indicator

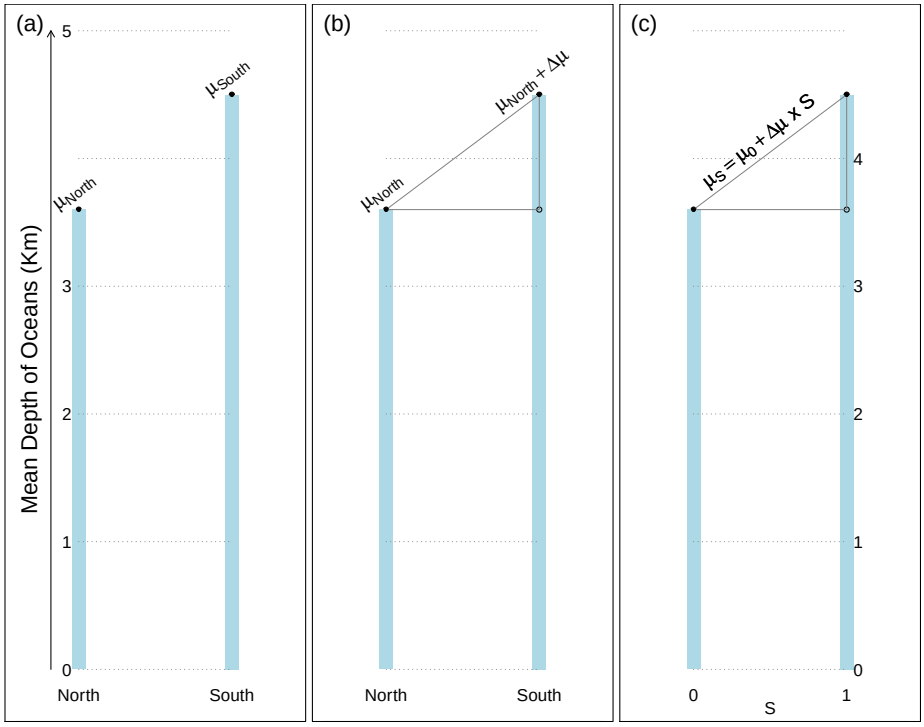
Panels (a) and (b) in the following figure repeat the information in panels (a) and (b) in the preceding Figure, but using Greek letters to symbolically represent the parameters. Just to keep the graphics uncluttered, the labels North and South are abbreviated to N and S and used as subscripts. Also, for brevity, the expression $\Delta\mu$ denotes $\mu_S - \mu_N$.

The relation encoded in a single phrase shown in the previous panel (c) has a compact form suitable for verbal communication. The representation can be adapted to be more suitable for computer calculations. (The benefit of doing this will become obvious as soon as you try to learn the parameter values by fiiting these models to actual data.) Depending on whether the hemisphere in question is the northern or southern hemisphere, the expression/statement 'the specified hemisphere is the SOUTHERN hemisphere' evaluates to a (logical) FALSE or TRUE. In the binary coding used in computers, it evaluates to 0 or 1, and we call such a 0/1 variable an 'indicator' variable.$\hat{}$

> $\hat{}$ In 'better families' we speak of INDICATOR variables, not DUMMY variables.
> The International Statistical Institute's Dictionary of Statistical Terms objects to the name: the term is 'used, rather laxly, to

> denote an artificial variable expressing qualitative characteristics ….
> [The] word 'dummy' should be avoided.'
> Miettinen's Epidemiological Research: Terms and Concepts:-
> Indicator variate – A variate with 0 and 1 as its (only) realizations, with realization 1 indicating something particular. (Examples: Y = 1 indicating membership in the case series of person-moments and X1 = 1 indicating index category of the etio-genetic determinant in an etiogenetic study – in the logistic model for the object of study.)
> Dummy variate (synonym: indicator variate) – See 'Indicator variate' in section II – 2. Note: This term is a misnomer: there is nothing dummy about an indicator variate.
> We encourage you to use, in your coding, **meaningful variable names** such as `i.South` or `i.Southern` (where `i` stands for indicator of) or `i.Male`. Don't use the name `sex` or `gender`, where the coding is not self evident. If you think `i.Male` is over doing it, then use `Male`.

In panel (c) in the following figure, just to keep the graphics uncluttered, the name of the indicator variable SOUTHERN is abbreviated to S, and μ_S is shorthand for the μ cooresponding to whichever value (0 or 1) of S is specified (we could also write it as $\mu|S$, or μ 'given' S.) Thus, the symbol μ_0 refers to the μ when $S = 0$, or in longerhand, to $\mu \mid S = 0$.



What does the equation in panel (c) remind you of?

Probably the equation of a line. In high school you may have learned it in the form $A + B \times X$ that Miettinen used to describe the relation between median blood pressure and age.

Today, in statistics, these equations are referred to as **regression equations**, and the statistical model is called a regression model. The term 'regression' is unfortunate, since it bears little relation to the original application. It concerned the phenomenon of 'reversion' first described by Charles Darwin. Following his first studies of the sizes of the 'daughter' seeds of sweet peas, his nephew Francis Galton, described the tendency:

> offspring did not tend to resemble their parent seeds in size, but to be always more mediocre ('middling', or closer to the mean) than they — to be smaller than the parents, if the parents were large; to be larger than the parents, if the parents were very small (Galton 1886)

One of the ***first 'regression' lines fitted to human data*** is Galton's line depicting the 'rate of regression on hereditary stature' where, using the term 'deviate' where today we would use 'Z-scores.'

> The Deviates of the Children are to those of their Mid-Parents as 2 to 3. (Galton, 1886)

Because he used z scores (so the means in the parents and in the children were both 0) the equation of the line simplified to

$$\mu(\text{Z-score in children of parents with mean z}) = 0 + (2/3) \times z$$

But don't we need a ~~*cloud of points* to have a regression line~~?

Although many courses and textbooks introduce regression concepts this way, the answer is **NO.** There is nothing in the regression formulation that specifies at which 'X' values the mean Y values at these X values are to be determined. Unlike many textbboks that start with Xs on a 'continuous' scale, and then later have to deal with a 2-point (binary) X, we are starting with this simplest case, and will move 'up' later.

We are doing this for a few reasons: in epidemiology, the first and simplest contrasts involve just two categories, the reference category and the index category; a simple subtraction of 2 parameter values is easier to do and to explain to a lay person; and there is no argument about how the function behaves at the values between 0 and 1. There are no parameter values at Male = 0.4 or Male = 1.4, they are only at Male=0 and Male=1.

In addition, it is easier to learn the fundamental concepts and principles of regression if we can easily 'see' what exactly is going on. Fewer blackbox formulae mean more transparency and understanding.

Once we see how to represent parameter values in two determinant-categories, we can easily extend it to more than two, such as the ethnic groups in example 1.5 above.
As we will see later on, when we have a value for a dental health parameter (eg the mean number of decayed, missing and filled DMF teeth) at X = 0 parts per million of fluoride in the drinking water, and another parameter value at X = 1 parts per million, we can only look at these 2 parameter values. If this is not enough, we would need to have (obtain) parameter values at the intermediate fluoride levels, or levels beyond 1 ppm, to trace out the full parameter relation, namely how the mean-DMF varies as a function of fluoride levels. If we have large numbers of observations at each level, then the DMF means will trace out a smooth curve. If data are limited, and the trace is jumpy/wobbly, we will probably resort to a sensible smooth function, the coefficients of which will have to be estimated from (fitted to) data.

This discussion leads on naturally to situations where the parameter varies over quantitative levels of a determinant - a topic considered in the next section.

~~But meantime, we need to answer this question: why limit ourselves to subtraction? why not consider the ratio of the two parameters, rather than their difference?~~

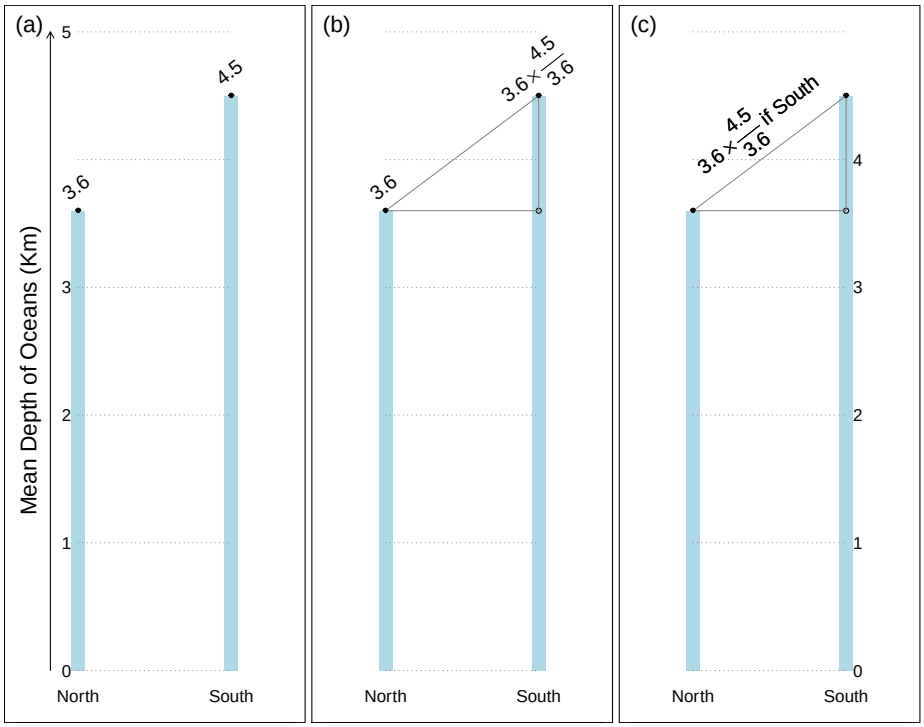
Relative differences (ratios) – *in numbers first*

A ratio can be more helpful than a difference, especially if you are don't have a sense of how large the parameter value is even in the reference category. As an example, on average, how many more red blood cells do men have than women? or how much faster are gamers' reaction times compared with nongamers?

Recall our hypothetical mean ocean depths, 3.6 Km in the oceans in the Northern hemisphere (reference category) and 4.5Km in the oceans of the Southern hemisphere (index category). Thus, the S:N (South divided by North) ratio is 4.5/3.6 or 1.25.

Panel (a) leaves it to the reader to calculate the ratio of the parameter values. In panel (b) the ratio (the quantity of interest) is isolated: again, the original 2 parameters are converted to 2 new, more relevant ones.

Again, panel (c) shows a single master-equation that applies to both hemispheres by togging off/on the ratio of 4.5/3.6.



Relative differences (ratios) – expressed in *symbols* and with the help of the *index-category indicator*

To rewrite these numbers in a symbolic equation suitable for a computer, we again convert the logical 'if South' to a numerical Southern-hemisphere-indicator, using the binary variate S (short for Southern) that takes the value 0 if the Northern hemisphere, and 1 if the Southern hemisphere.

But go back to some long-forgotten mathematics from high school to be able to tell the computer to toggle the ratio off and on. Recall '**powers**' of numbers, where, for example, 'y to the power 2', or y^2 is the square of y. The two powers we exploit are 0 and 1. 'y to the power 1', or y^1 is just y and 'y to the power 0', or y^0 is 1.

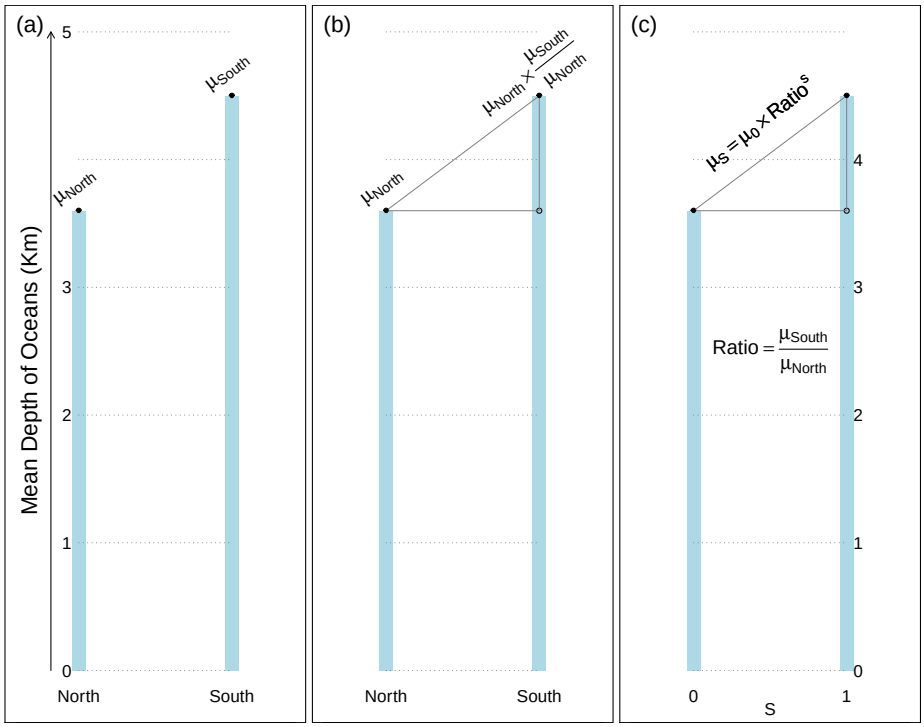
We take advantage of these to write

$$\mu_S = \mu \mid S \; = \mu_0 \; \times \; \left\{ \frac{\mu_{South}}{\mu_{North}} \right\}^S = \mu_0 \; \times Ratio^{\;S}.$$

You can check that it works for each hemisphere by setting $S = 0$ and $S = 1$ in turn.

Thus,

$$\log(y^S) = S \times \log(y)$$



Although this is a compact and direct way to express the parameter relation, it is not well suited for ~~fitting~~ these equations to data.

However, in those same high school mathematics courses, you also learned about **logarithms**. For example, that

$$\log(A \times B) = \log(A) + \log(B); \quad \log(y^x) = x \times \log(y).$$

Thus, we can rewrite the equation in panel (c) as

$$\log(\mu_S) = \log(\mu \mid S) \; = \underbrace{\log(\mu_0)}\; + \underbrace{\log(Ratio)}\times \; S.$$

This has the same 'linear in the two parameters' form as the one for the parameter difference: the parameters are $\underbrace{\log(\mu_0)}$ and $\underbrace{\log(Ratio)}$ and they are made into the following 'linear compound' or 'linear predictor' (see Remarks below) :

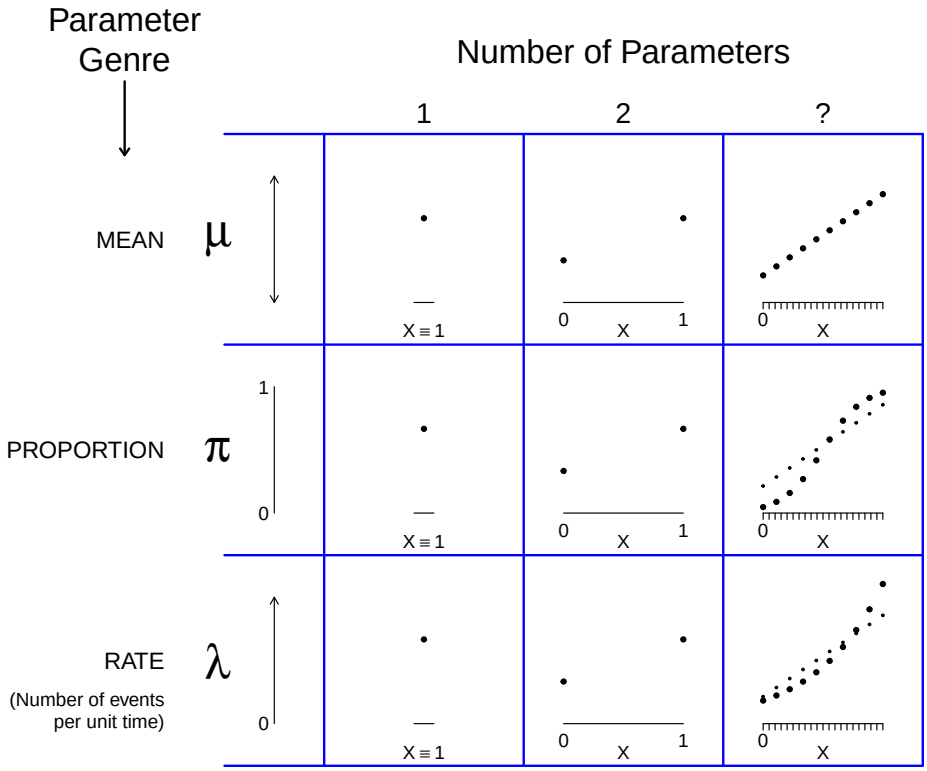
$$\log(\mu_S) = \log(\mu \mid S) \; = \underbrace{\log(\mu_0)}\times 1 \; + \underbrace{\log(Ratio)}\times \; S.$$

The course is concerned with using 'regression' software to 'fit'/'estimate' these 2 parameters from n depth measurements indexed by S.

2.3 Parameter functions

A very simple example of a function that describes how parameter values vary over quantitative levels of a determinant is the straight line shown in the upper right panel of the next figure. Here the determinant has the generic name X, and the equation is of the $A + B \times X$ or $B_0 + B_1 \times X$ or $\beta_0 + \beta_1 \times X$ straight line form. Miettinen used the convention that the upper case letters A and B are used to denote the (true but unknown) coefficient values, whereas the lower case leters a and b are used to denote their empirical counterparts, sometimes called estimated coefficients or fitted coefficients. This sensible and simple convention also avoids the need, if one uses Greek letters for the theoretical coefficient values, to put 'hats' on them when we refer to their empirical counterparts, or 'estimate/fit' them. Fortunately, journals don't usually allow investigators to use 'beta-hats'; but this means that the investigators have to be more careful with their words and terms.

As we go left to right in the following grid, the models become more complex. The simplest is the one of the left, in column 1, the one JH refers to as 'the mother of all regression models.' It refers to a *single* or *overall* situation/population/domain, so $X \equiv 1$, it takes on the value 1 in/for every instance/member. So the parameter equation is $\mu_X = \mu \mid X = \mu \times 1$. In column 2, there are 2 subdomains, indexed by the 2 values of the determinant (here generically called 'X'), namely $X = 0$ and $X = 1$. In the 3rd column, the number of of parameters is left unspecified, since the numbers of coefficients to specify a line/curve might vary from as few as 1 (if we were describing how the volume of a cube dependeds or, was is function of, its radius) to 2 (for a straight line that did not go through the origin, or for a symmetric S curve) to *more than 2* (e.g., for a non-symmetric S curve, or a quadratic shape).



A few more remarks on the panels in this Figure

- The 3 rows refer to the 3 core parameters we have given examples of above. All 3 are governed by the same principles, although there are more possibilities of different possible scales for some parameters.

- In setting (column) 1: there is just 1 parameter (value shown as a dot) corresponding to the 'overall' population or the entire domain. You can think of it as the limiting or 'degenerate' case of the columns to its right. One can still write it in a 'regression' model.

  It is of the form P(arameter) = B, involving no indicators for distinguishing among subdomains of the referent domain of the distribution, say adults not otherwise specified. [MSH2018, p63] It is sometimes referred to as a null or 'incercept only' regression model.

  We will exploit this idea to take a more holistic/general and economical approach to this introductory course. Many text-books/courses do not mention regression models until quite late, and spend a lot of time on '1-sample' (and even '2-sample') problems without pointing out that these are merely sub-cases of regression models. This 'silos' practice of promoting/learning a separate

software routine for dealing with a 1 sample problem, when one can get the same answer from a regression routine, leads to dead ends and wastes time.

Once we get to fitting/estimating a mean (or proportion or rate) parameter to/from data, we will encourage doing so within a regression framework.

- In setting (column) 2, there are 2 parameter values, one for the reference category and one for the index category of the determinant. As we have seen, how they relate to each other can be can be expressed in a number of different ways. A common and useful way is via a parameter equation that contains a parameter for the reference category and a comparative parameter (some measure of the difference between the two parameters) – the latter is often of most interest.

- In setting (column) 3, the parameter equation traces the parameter over a continuum of possible values of the determinant, using as many coefficients as are needed. In this particular diagram, the values of the determinant (X) are shown starting at X = 0, but this does not have to be. In data analysis, one often shifts the X origin, so that the 'intercept' makes more sense. For example, if one was plotting world temperatures, or ice-melting dates (see Chapter on Computning) against calendar year, it would be better to have the incercept refer to the fitted temperature for when the series begins, rather than when our current Western calendat begins (at the year 0 AD). Likewise, if we were describing the relation between ideal weight and height it is good to start near where people's heights are. Thus, '100 pounds for a **height of 5 feet**, with five additional pounds for each added inch of height' for women, and '106 pounds for a **height of 5 feet**, and six additional pounds for every added inch of height.' for men. Of course, if you wish, for women you could use the mathematically equivalent '-300 pounds for a **height of 0 feet**, with five additional pounds for each added inch of height' but it is not that easy to remember, and doesn't apply for much of the (unspecified) height range!

A few remarks on associated terminology

Instead of **'regression models'**, some textbooks and courses refer to **'linear models'** :

> **Linear model**: Formulation of the mean/'expectation' of (the distribution of) a random variate (Y) as a linear compound of a set $B_0, B_1, B_2, ...$ of parameters: as $B_0 + B_1X_1 + B_2X_2 + ...$ [Miettinen 2011, p54]

> **The meaning of 'linear'** in the ~~appellation~~ of this model has nothing to do with straight lines; it refers to the mathematical concept of '~~linear compound~~'; given ~~quantities~~ Q_1, Q_2, etc., a linear compound of these is the sum $C_1Q_1 + C_2Q_2 + ...$, where C_1 etc. are the 'coefficients' that define a particular linear compound of the set

> of quantities constituted by the Qs. So, the 'general linear model' is linear in the sense that the dependent parameter, M, is formulated as a linear compound of the independent parameters B0, B1, etc., the coefficients in this linear compound being 1, X1, etc. The model is, in this way, 'linear in the parameters.' [MSH2018, p65]

Statistics courses in the social sciences, the biological laboratory sciences, and other experimentally-based sciences, typically move on from 1- and 2-sample procedures (unfortunately, mainly focusing on statistical *tests*) to **'analysis of variance' models**

Miettinen explains an **'analysis of variance models** this way:

> In the 'analysis of variance model,' the random variate at issue – Gaussian – has a mean whose value depends on a *nominal-scale determinant*, a nominal scale being characterized by discrete categories without any natural order among them. The names of the (nominal) categories, some N in number, could be Category 1, Category 2, … , Category N. The term for the model is a misnomer. For, at issue is not analysis but synthesis of data, and the synthesis is not directed to learning about the variance of the random variate; it focuses on the mean, the relation of the mean to the (nominal-scale) determinant of it.
>
> A simple example of these models might address the mean of systemic blood-pressure – defined as the weighted average of the diastolic and systolic pressures with weights 2/3 and 1/3, respectively – in relation to ethnicity, represented by three categories. An 'analysis-of- variance' model would define a random variate (Y) as representing the numerical value of the pressure (statistical variates inherently being numerical) and having a Gaussian distribution with means M1, M2, and M3 in those ethnicity categories 1, 2, and 3, respectively, with the variance of the distribution invariant among them. The random variate (Y) is the '*dependent*' variate in the meaning that the value of its mean depends on ethnicity; and the ethnicity categories are represented in terms of suitably-defined '*independent*' – non-random – variates (Xs).
>
> The form of the 'analysis-of-variance' model in this simple example is: $M = B_0 + B_1X_1 + B_2X_2$, where M is the mean of Y and the two independent variates are indicators of two particular ones of the three ethnic categories. One possibility in this framework is to take X_1 and X_2 to be indicators of Category 2 and Category 3, respectively – an indicator variate being one that takes on the value 1 for the category it indicates, 0 otherwise.
>
> In terms of this model, B_0 is the value of M when $X_1 = X_2 = 0$, that is, for Category 1 (i.e., $B_0 = M_1$); and for Category 2 and Category 3 the values of M are represented by $B_0 + B_1$ and $B_0 + B_2$,

respectively (i.e., $M_2 = B_0 + B_1$, and $M_3 = B_0 + B_2$). Thus, the difference between M_1 and M_2 is represented by B_1; B_2 represents the difference between M_1 and M_3; and the difference between M_2 and M_3 is the difference between B_1 and B_2.

In this 'analysis-of-variance' framework it is feasible to accommodate, jointly, whatever number of nominal-scale determinants of the magnitude of the mean of the dependent variate. A simple example of this is the addition of the two categories of gender for consideration jointly with the three categories of ethnicity. These two determinants jointly imply a single nominal-scale determinant with six categories (as each of the three categories of ethnicity is split into two subcategories based on gender).

When involved in the definition of the independent variates is only a single determinant, the model is said to be for 'one-way analysis of variance'; with two determinants the corresponding term (naturally) is 'two-way analysis of variance'; etc.

2.4 Phraseology to avoid

~~It is quite common to hear a regression coefficient (fitted or theoretical) interpreted this way:~~

> ~~"For every 1 unit increase in X, the 'Y' parameter increases by β_X units."~~

or as follows

> "As (when) you increase X by 1 unit, you increase the Y parameter by β_X units."

We pick up this terminology very early, maybe even back in high school, and from other people around us. But, in interpreting the B = 1 mm Hg/yr in Miettenen's example (100 plus age in years), should we use such phrases?

Or, since you don't know the source of, or the data behind this rule, you can take a look at the distributions of some anthropometric chacacteristics (height, weight, forced expiratory volume, FEV) measured cross-sectionally, in different populations – Busselton, Australia and rural Southwest Ethiopia – in 1972 and 1992. By eye, try to estimate the slope you would get if you regressed the age-and sex-specific means or medians on the ages. and then summarize the gradient across age.

Remember that these these subjecsts aren't aging or going anywhere, and nobody was watching them age.

It is more accurate to say:

> People who were aged a+1 years at the time of the survey had heights/weights/FEVs that were t.tt units higher/lower than people who were aged a years.

or

> The mortality rate was u.uu units higher/lower (or u.u times higher/lower) in the experience in the index category than the reference category.

~~This way, you are telling the reader that this is a static source, and not a dynamic situation~~ where conditions are being manipulated by the investigators, or the subjects being watched as their ages go up [for many readers, the word 'increased' implies that some human force deliberately changed the dial, and turned the X up or down, as one could do with temperature or humidity in a laboratory.]

One of JH's favourite examples of people being misled into thinking that a cross-sectional dataset allows you to say that 'as people get older, they ...' is the McGill epidemiology department's studies, in the 1960s, on the health of the more than 10,000 millers and miners of asbestos. These workers were born between 1890 and 1920. In cross-sectional studies, there were gradients in mean height across attained age. It would be easy to give them a 'as people get older, they shrink in height' or they 'gain in height' interpretation. It is easy to overlook the fact that some of these were children and adolescents during the Depression.

Next Chapter

The next chapter will begin in the upper left corner of the grid, and address situations where the **estimand** (the parameter to be estimated) is μ. It will describe how we 'estimate' / 'fit' a single μ parameter from/to a finite number of observations, and how we quantify and report how far off the target our method of estimation can/might be.

2.5 SUMMARY

2.6 Exercises

So far, we have only dealt with equations involving a difference and the ratio of two μ parameters.

1. Extend the graphs and the equations (for the difference of means and the ratio of means) to the π parameter. Use as an example the proportions of the surfaces of the Northern (reference category) and Southern hemisphere (index category) covered by water, i.e, π_{North} and π_{South}. Use the hypothetical values $\pi_{North} = 0.65$ and $\pi_{South} = 0.75$.
2. Instead of focusing on the proportions covered by *water*, focus on the proportions covered by *land*.

- How does the **difference** of the two proportions relate to the difference calculated in 1?
- How does the **ratio** of the two proportions relate to the ratio calculated in part 1? i.e., is one the reciprocal of the other?
- Can you think of different scale, where the ratio when the focus is *land* IS just the reciprocal of the ratio when the focus is *water*.?
- If you can, show that the log of the ratio when the focus is *land* IS just the negative of the log of the ratio when the focus is *water*.?

3. Extend the graphs and the equations (for the difference of means and the ratio of means) to the λ parameter. Use as an example the mean number of earthquakes per year in the Northern (reference category) and Southern hemisphere (index category) , i.e, λ_{North} and λ_{South}. Use the hypothetical values $\lambda_{North} = 5.0$ and $\lambda_{South} = 7.5$

2.7 References

Olli S. Miettinen. Theoretical epidemiology: Principles of Occurrence Research in Medicine. Wiley, New York, 1985. Chapter 1: The study of occurrence patterns in medicine. Introduction.

David Clayton and Michael Hills. Statistical Models for Epidemiology. Oxford University Press, 1993. Chapter 22: Introduction to regression models.

Kenneth J. Rothman. Epidemiology: An introduction. Oxford University Press, 2012. Chaper 12: Using regression models in epidemiologic analysis.

Olli S. Miettinen, Johann Steurer, Albert Hofman. Clinical Research Transformed. Springer, 2019. Chapter 7: The Logistic Regression Model (The Precursors of the General Linear Model; The General Linear Model; The Generalized Linear Model; The Logistic Regression Model)

Chapter 3

The parameter μ

[and other location (and spread and shape) parameters]

3.1 Two genres

- Constants of Nature, not easily measured on a single try
- Centers of (infinite sized) biological (population) distributions

3.2 Fitting these to data / Estimating them from data

- Metrics (criteria) for measuring (best) fit

Chapter 4

The (proportion) parameter π

4.1 Example one

etc

4.2 Example two

etc

Chapter 5

The (event rate) parameter λ

5.1 Etc

-

5.2 ETC

-

Chapter 6

Contrast: 2 μ parameters

6.1 Estimand, estimator, estimate

Chapter 7

Contrast: 2 π parameters

7.1 Estimand, estimator, estimate

Chapter 8

Contrast: 2 λ parameters

8.1 Estimand, estimator, estimate

Part II

Part II

Chapter 9

Probability

9.1 Conditional – forwards

•

9.2 Conditional – reverse

- Application: medical diagnostic tests

Exercises: Efron, Monty Hall, Economist, Wald : CF screening

Chapter 10

Distributions /Random Variables

Chapter 11

Statistical Inference

11.1 2 schools

11.1.1 Bayesian

11.1.2 Frequentist

Part III

Part III

Chapter 12

Mathematics

12.1 Notation

- **Variables and Subscripts**
  Variable Y with n sample values denoted $y_1, y_2, ..., y_n$ in order of entry; The "1", "2", … are called subscripts or indices. We use the letter i (or j) and the range "1 to n" to denote the n different y values and refer to the value of the ith y as "y_i".
- **Summation**
  The term Σy (spoken: "sigma y" or "sum of y's") is used as a shorthand for the sum $y_1 + y_2 + \cdots + y_n$.

12.2 Powers, Logarithms and Anti–logarithms

- The term $y^{1/2}$ is shorthand for the square root of y or $\sqrt{y}$. Likewise, $y^{1/n}$ denotes the n-th root of y.
- $\ln(y)$ denotes the "natural log of y" or "log of y to the base e" i.e. $\log_e(x)$, where e is 2.718.
  Note: y must be positive; ln (y) ranges from -inf to +inf.

  ln (0.1) = -2.30; ln (1) = 0; ln (2) = 0.69; ln (10) =2.30
- $\ln(A \times B) = \ln(A) + \ln(B)$; $\ln(\frac{A}{B}) = \ln(A) - \ln(B)$
- $\exp(y)$ is shorthand for e^y or "exponential of y" or the natural anti-log of y. y ranges from -∞ to +∞. and $\exp(y)$ yields a positive value. eg. exp(-1) = 0.36; exp(0) =1; exp(.5) =1.64; exp(1) = 2.71…

Chapter 13

Computing Week 1

The **'computing' objectives** are to learn how to use `R` to put series of observations into vectors, and how to plot one series against another.

The **'statistical' objective** of this exercise is to understand the concept of a distribution of a numerical characteristic (here an amount of elapsed time), and the various numbers describing its 'central' location and spread, and other 'landmarks'. You will also be introduced (in the next section) to 2 functions that give a more complete description of a distribution.

13.1 Biological background

Later on we will examine climate trends using unusual datasets, which suggest that over the last few centuries, winter tends to end earlier, and plants tend to flower earlier.

One such dataset arose as part of a long-running contest, the Nenana Ice Classic More here

13.2 Statistical Task

You are asked to approximate and carefully examine the distribution of guesses in 2018, contained in the Book of Guesses for that year.

For now, we will measure the guesses (and eventually the actual time) as the numbers of days since the beginning of 2018. Thus a guess of Tuesday April 17 5:20 p.m. would be measured as 31 + 28 + 31 + 16 + (16 + 20/60)/24 = 106.6806 days since the beginning of 2018.

It would be tedious to try to apply optical character recognition (OCR) to each of the 1210 pages in order to be able to computerize all of the almost 242,000

guesses. Instead, you are asked to reconstruct the distribution of the guesses in two more economical ways:

1. By determining, for each of the 36 x 2 = 72 half-days days from April 10 to May 15 inclusive, the proportion, p, of guesses that are earlier than midnight on that date. [In `R`, if p = 39.6% of the guesses were below xy.z days, we would write this as pGuessDistribution(xy.z) = 0.396. Thus, if we were dealing with the location of a value in a Gaussian ('normal') distribution, we would write `pnorm(q=110, mean = , sd = )`] Once you have determined these 72 proportions (p's), plot them on the vertical axis against the numbers of elapsed days since the beginning of the year on the horizontal axis. Thus the horizontal axis runs from 92 + 10 = 102 days to 92 + 30 + 15 = 137 days.

2. By determining the 1st, 2nd, … , 98th, 99th percentiles. These are specific examples of 'quantiles', or q's. The q-th quantile is the value (here the elapsed number of days since the beginning of 2018) such that a proportion q of all guesses are below this value, and 1-q are above it. [In `R`, if 40% of the guesses were below 110.2 days, we would write this as qGuessDistribution(p=0.4) = 110.2 days. Thus, if we were dealing with the 40th percentile of a Gaussian distribution with mean 130 and standard deviation 15, we would write `qnorm(p=0.4, mean = 130, sd = 15).`] Once you have determined them, plot the 99 p's (on the vertical axis) against the 99 (elapsed) times on the horizontal axis.

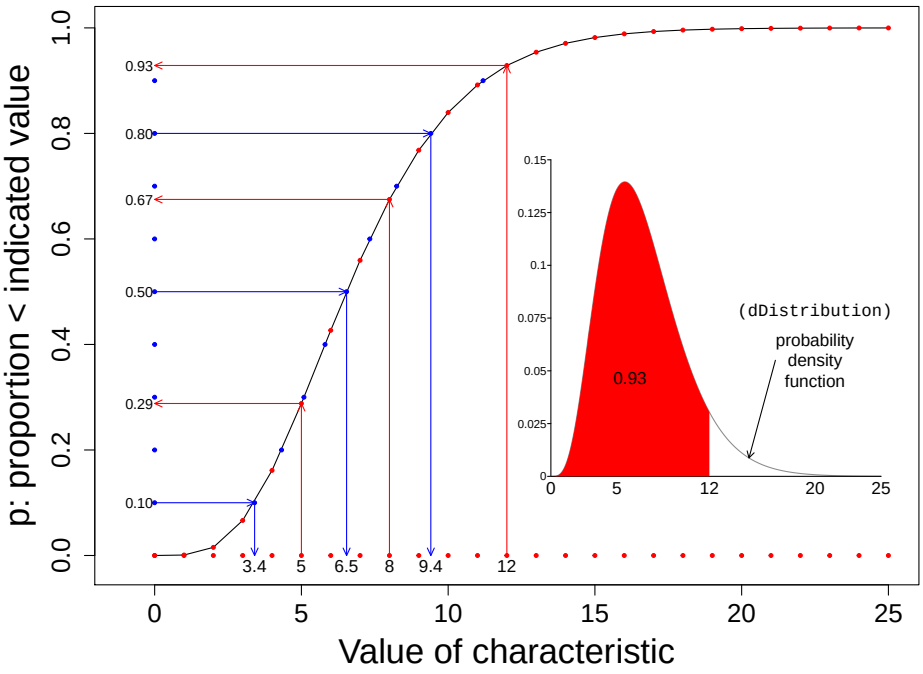
13.2.1 The p and q functions: an orientation

The '**p**' function tells us, for a given value of the characteristic, what **p**roportion of the distribution lies to the left of this specified value.

The '**q**' (or quantile) function tells us, for a given proportion p, what is the value of the characteristic such that that specified proportion p of the distribution lies to the left of this 'q' value.

In the plot below, the values of the **p** function are shown on the vertical axis, in red, against the (in this case, equally-spaced) values of the characteristic, shown on the horizontal axis. You enter on the horizontal axis, and exit with an answer on the vertical axis.

The **q** function (in blue) goes into the opposite direction. You enter at some proportion on the vertical axis, and exit with a value of the characteristic (a quantile) on the horizontal axis. In our plot, the proportions on the vertical axis are equally-spaced. Percentiles and quartiles are a very specific sets of quantiles: they are obtained by finding the values that divide the distribution into 100 or into 4.



13.2.2 Exercises

1. Once you have determined the 72 (cumulative) proportions (p's) associated with the 72 half-days, plot them on the vertical axis against the numbers of elapsed days since the beginning of the year on the horizontal axis. Thus the horizontal axis runs from 92 + 10 = 102 days to 92 + 30 + 15 = 137 days.

2. The 1st, 2nd, … , 98th, 99th percentiles are not so easy to determine since you have to locate the 2419th, 4839th, 7258t, … entries in the 1201-page Book of Guesses and plot the 99 p's (on the vertical axis) against the 99 (elapsed) times (q's) on the horizontal axis. Instead, use the first entry on each of pages 11, 21, … in this excerpt. Using a different colour, plot these slightly-more-dense quantiles on the horizontal axix against the following percentages:

```
entries = 200*seq(10,1200,10) + 1
percent = 100 * entries/241929
noquote( paste(head(round(percent,1),10),collapse="%, ") )
```

```
## [1] 0.8%, 1.7%, 2.5%, 3.3%, 4.1%, 5%, 5.8%, 6.6%, 7.4%, 8.3
```

```
tail(round(percent,1),10)
```

```
##  [1] 91.8 92.6 93.4 94.2 95.1 95.9 96.7 97.5 98.4 99.2
```

3. Compare the Q_{25}, Q_{50}, and Q_{75} obtained directly with the ones obtained by interpolation of the curve showing the results of the other method.

4. Compare the directly-obtained proportions of guesses that are before (the end of) April 20, April 30, and May 10 with the ones obtained by interpolation of the curve showing the results of the other method.

5. By successive subtractions, calculate the numbers of guesses in each 1/2 day bin, and make a histogram of them. From them, calculate the mean, the mode, and the standard deviation.

6. (For a future assignment, but you can start thinking about how) From a random sample of 100 guesses from the book, estimate how many guesses in the entire book are PM.

```
my.id = 800606
set.seed(my.id)
n = 50
sample.entry.numbers = sample(x = 1:241929, size=n)
sorted.sample.entry.numbers = sort(sample.entry.numbers)
head(sorted.sample.entry.numbers,10)
```

```
##  [1] 10542 17437 18351 21113 24086 28782 30055 32220 33162 36443
```

```
page.number = ceiling(sorted.sample.entry.numbers/200)
within.page = sorted.sample.entry.numbers-200*(page.number-1)
column.number = ceiling(within.page/100)
row.number = within.page - 100*(column.number-1)

dataset = data.frame(page.number,column.number,row.number)
head(dataset)
```

```
##   page.number column.number row.number
## 1          53             2         42
## 2          88             1         37
## 3          92             2         51
## 4         106             2         13
## 5         121             1         86
## 6         144             2         82
```

```
tail(dataset)
```

```
##    page.number column.number row.number
## 45        1087             1         80
## 46        1097             2          3
## 47        1121             1         16
## 48        1131             1         55
## 49        1175             2         52
## 50        1181             2         30
```

- How far off was the median guess in 2018 from the actual time? Answer in days, and (with reservations stated) as a percentage? {see the 2020 brochure }
- Why did the experts at the country fair do so much better?
- Where were the punters in 2019 with respect to the actual time?
- Instead of measuring the guessed times from the beginning of the year, suppose that, as Fonseca et al did, we measure the guessed times from the spring equinox in Alaska, i.e. from 8:15 a.m. on Tuesday, March 20, 2018, Alaska time. In this scale, compute the mean guess, and the SD of the guesses.
- Suppose, again, we measure the guessed times from the spring equinox, but in weeks. In this scale, compute the mean guess, and the SD of the guesses.

Some links on the 'Wisdom of Crowds'

https://www.technologyreview.com/s/528941/forget-the-wisdom-of-crowds-neurobiologists-reveal-the-wisdom-of-the-confident/

https://www.all-about-psychology.com/the-wisdom-of-crowds.html

http://galton.org/essays/1900-1911/galton-1907-vox-populi.pdf

- How much warmer/colder in Nov-April is Monreal than Nenana?

Chapter 14

Computing Week2

14.1 Ages of books

14.2 ngrams

14.3 Ice Breakup Dates

Here are some details on the Nenana Ice Classic More here

14.3.1 The ~~2018 Book of Guesses~~

We are keen to establish the distribution of guesses, with the guessed times measured from midnight on December 31, 2017. Thus a guess of April 06, at 5:15 p.m. would be measured as 31 + 28 + 31 + 5 + 12/24 + (5+ 15/60)/24 = 95.71875 days into the year 2018.

It would be tedious to apply optical character recognition (OCR) to each of the 1210 pages in order to be able to computerize all 240,000 guesses. Instead, you are asked to reconstruct the distribution of the guesses in two more economical ways:

- By determining, for (the beginning of) each day, from April 01 to June 01 inclusive, ~~the proportion,~~ p, of guesses that predede that date. [In `R', if p = 39.6% of the guesses were below 110 days, we would write this as pGuessDistribution(110) = 0.396. Thus, if we were dealing with the location of a value in a Gaussian ('normal') distribution, we would write`pnorm(q=110, mean = , sd =)‘] Once you have determined them, plot these 62 p's (on the vertical axis) against the numbers of elapsed days (90-152) on the horizontal axis.
- By determining the 1st, 2nd, … , 98th, 99th percentiles. These are

specific examples of 'quantiles', or q's. The q-th quantile is the value (here the elapsed number of days since the beginning of 2018) such that a proportion q of all values are below this value, and 1-q are above it. [In `R', if 40% of the guesses were below 110.2 days, we would write this as qGuessDistribution(p=0.4) = 110.2 days. Thus, if we were dealing with the 40th percentile of a Gaussian distribution with mean 130 and standard deviation 15, we would write`qnorm(p=0.4, mean = 130, sd = 15)'.] Once you have determined them, plot the 99 p's (on the vertical axis) against the 99 (elapsed) times on the horizontal axis.

- Compare the Q_{25}, Q_{50}, and Q_{75} obtained directly with the ones obtained by interpolation of the curve showing the results of the other method.
- Compare the directly-obtained proportions of guesses that are before April 15, April 30, and May 15 with the ones obtained by interpolation of the curve showing the results of the other method.
- By successive subtractions, calculate the numbers of guesses in each 1-day bin, and make a histogram of them. From them, calculate the mean, the mode, and the standard deviation.

To measure the spread of guesses, Galton, in his vox populi (wisdom of crowds) article, began with the interquartile range (IQR), i.e. the distance between Q75 and Q25, the 3rd and 1st quartiles. In any distribution, 1/2 the values are within what was called the 'probable error (PE) of the mean; i.e., it is equally probable that a randomly selected value would be inside or outside this middle-50 interval. Today, we use standard deviation (SD) instead of probable error. In a *Gaussian* distribution, some 68% of values are within 1 SD of the mean, whereas 50% of values are within 1 PE of the mean. We can use `R` to figure out how big a PE is in a Gaussian distribution compared with a SD. By setting the SD to 1, and the eman to 0, we have

```
Q75 = qnorm(p = 0.75, mean=0, sd=1)
round(Q75,2)
```

```
## [1] 0.67
```

i.e, a PE is roughtly 2/3rds of a SD.

- Galton – convert to SD.
- Geometric mean Amsterdam study
- How far off was the median guess in 2018 from the actual time? Answer in days, and (with reservations stated) as a percentage?
- Why did the experts at the country fair do so much better?
- Where were the punters in 2019 wrt the actual ?

https://www.technologyreview.com/s/528941/forget-the-wisdom-of-crowds-neurobiologists-reveal-the-wisdom-of-the-confident/

https://www.all-about-psychology.com/the-wisdom-of-crowds.html

http://galton.org/essays/1900-1911/galton-1907-vox-populi.pdf

[Nenana Ice Classic]

Tanana River

14.3.2 Trends over the last 100 years

fill in the data since 200x.

cbind with …

https://www.adn.com/alaska-news/2019/04/14/nenana-ice-classic-tripod-goes-down-setting-record-for-earliest-river-break-up/

time trends

morning vs afternoon ?

2019 extreme… how many SD's from the line?

- Where were the punters in 2019 wrt the actual ?

Sources:

1917-2003 data in textfile on course website;

http://www.nenanaakiceclassic.com/ for data past 2003

ascii (txt) and excel files with data to 2003

Working in teams of two …

*Create a dataframe containing the breakup data for the years 1917-2007. Possible ways to do so include: directly from the ascii (txt) file; from the Excel file

*From the decimal portion of the Julian time, use `R` to create a frequency table of the hour of the day at which the breakup occurred.

*From the month and day, use `R` to calculate your own version of the Julian day (and the decimal portion if you want to go further and use the hour and minute)

*Is there visual evidence that over the last 91 years, the breakup is occurring at an earlier date?

*Extract the date and ice thickness measurements for the years 1989-2007 from the website and use `your software of choice`R‘ to create a single dataset with the 3 variable, year, day and thickness. From this, fit a separate trendline for each year, and calculate the variability of these within-year slopes.

14.4 Galton's data on ~~family heights~~

These data were gathered to examine the relation between heights of parents and heights of their (adult) children. They have been recently 'uncovered' from the Galton archives. As a first issue, for this exercise, you are also asked to see whether the parent data suggest that stature plays "a sensible part in marriage selection".

For the purposes of this exercise, the parent data [see http://www.epi.mcgill.ca/hanley/galton] are in a file called parents.txt , with families numbered 1-135, 136A, 136-204 ({the heights of the adult offspring will be used in a future exercise)

Do the following tasks using `R`

1. Categorize each father's height into one of 3 bins (shortest 1/4, middle 1/2, tallest 1/4). Do likewise for mothers. Then, as Galton did [Table III], obtain the 2-way frequency distribution and assess whether "we may regard the married folk as picked out of the general population at haphazard".
2. Calculate the variance Var[F] and Var[M] of the fathers' [F] and mothers' [M] heights respectively. Then create a new variable consisting of the sum of F and M, and calculate Var[F+M]. Comment. Galton called this a "shrewder" test than the "ruder" one he used in 1.
3. When Galton first anayzed these data in 1885-1886, Galton and Pearson hadn't yet invented the correlation coefficient. Calculate this coefficient and see how it compares with your impressions in 1 and 2.

14.5 Temperature perceptions

Create 5 datasets from the questionnaire data on temperature perceptions etc.

(i) by importing directly from the Excel file applied to .csv version of Excel file);

(ii) by first removing the first row (of variable names) and exporting the Excel file into a 'comma-separated-values" (.csv) text file, then ...

reading the data in this .csv file via the INFILE and INPUT statements in a SAS DATA step,

[SAS] INFILE 'path' DELIMITER =","; INPUT ID MALE $ MD $ EXAM TEMPOUTC TEMPINC TEMPOUTF TEMPINF TEMPFEEL TIME PLACE $;

(iii) by reading the data in the text file temps_1.txt into

the SAS dataset via the INFILE and INPUT statements. Notice that the 'missing' values use the SAS representation (.) for missing values.

or the Stata dataset using the 'infile' command

(iv) by reading the data in the text file temps_2.txt via [in SAS] the INFILE and INPUT statements in a DATA step or [in Stata] the 'infix' command.

Here you will need to be careful, since 'free-format' will not work correctly (it is worth trying free format with this file, just to see what goes wrong!). When using the INFILE method, you can control some of the damage by using the 'MISSOVER' option in the INFILE statement: this keeps the INPUT statement from continuing on into the next data line in order to find the (in our example) 11 values implied by the variable list. JH uses this 'defensive' option in ALL of his INFILE statements.

(v) by cutting and pasting the contents of the text file temps_2.txt directly into the SAS or Stata program - in SASthe lines of data go immediately after the DATALINES statement, and there needs to be a line containing a semicolon to indicate the end of the data stream. In Stata, the lines of data go immediately after the infile or infix statement, and there needs to be a line containing the word 'end' to indicate the end of the data stream

This Cut and Paste Method is NOT RECOMMENDED when the number of observations is large, as it is too all too easy to inadvertently alter the data, and the SAS/Stata porogram becomes quite long and unwieldy. It is Good Data Management Practice to separate the program statements from the data.

[Run [in SAS] PROC MEANS [in Stata] the 'describe' command, on the numerical variables, and [in SAS] PROC FREQ or [in Stata] the 'tabulate' command, on the non-numerical variables, to check that the 5 datasets you created contain the same information. Also, get in the habit of viewing or printing several observations and checking the entries against the 'source'.

When using (i), have SAS show you the SAS statements generated by the wizard. Store these, and the DATA steps for (ii) to (v) in a single SAS program file (with suffix .sas).

Annotate liberally using comments:

in SAS, either begin with * ; or enclose with /* … */

in Stata ..begin the line with * or place the comment between /* and */ delimiters or begin the comment with // or begin the comment with ///

Q2

`Use one of these 5 datasets, and the appropriate [in SAS, PROCs (see Exploring Data under UCLA SA`

(i) list the names and characteristics of the variables

(ii) list the first 5 observations in the dataset

(iii) list the id # and the responses just to q3, w5 and q6, for all respondents, with respondents in the order: female MDs, male MDs, female non-MDs,

male non-MDs. Indicate the [sub-]statement that is required to reverse this order.

(iv) create a 2-way frequency table, showing the frequencies of respondents in each of the 2 (MD nonMD) x 2 (male female) = 4 'cells' (one defintion of an epidemiologist is 'an MD broken down by age and sex'). Turn off all the extra printed output, so that the table just has the cell frequencies and the row and column totals.

(v) compare the mean and median attitude to exams in MDs vs. non-MDs (hint: in SAS, the CLASS statement may help). Get SAS/Stata to limit the output to just the 'n', the min, the max, the mean and the median for each subgroup. And try to also get it to limit the number of decimal places of output (in SAS the MAXDEC option is implememnted in some procedures, but as far as JH can determine not in all)

(vi) compare the mean temperature perceptions (q6) of male and female respondents

(vii) [in SAS] create a low-res ('typewriter' resolution) scatterplot of the responses to q5 (vertical axis) vs. q4 (horizonatal axis), using a plotting symbol that shows whether the responsdent is a male or a female. If we have not covered how to show this '3rd dimension', look at the ONLINE Documentation file {the guide for most of the procedures covered in this set of exercises is in the Base SAS Procedures Guide; other procedures are in sthe more advanced 'STAT' module}. You can specify the variable whose values are to mark each point on the plot. See PLOT statement in PROC PLOT, and the example with variables height weight and gender. [in Stata] use the (automatically hi-res) graphics capabilities available from the 'Graphics' menu

[if SAS] Put all of the programs for Q1, and all of these program steps and output for Q2 in a single .txt file (JH will use a mono-spaced font such as Courier to view it – that way the alignment should be OK), with PROC statements interleaved with output, and a helpful 2-line title (produced by SAS, but to your specifications) over top of each output. Get SAS to set up the output so that there are no more that 65 horizontal characters per line (that way, lines won't wrap-around when JH views the material).

[if Stata] paste the results and graphics into Word.

NOTE: To be fair to SAS, it CAN produce decent (and even some publication-quality) graphics. See http://www.ats.ucla.edu/stat/sas/topics/graphics.htm

Then submit the text file electronically (i.e., by email) to JH by 9 am on Monday October 2.

14.6 Natural history of prostate cancer

Q1

The following data items are from an investigation into the natural history of (untreated) prostate cancer [report (.pdf) by Albertsen Hanley Gleason and Barry in JAMA in September 1998].

id, dates of birth and diagnosis, Gleason score, date of last contact, status (1=dead, 0=alive), and – if dead – cause of death (see 2b below). data file (.txt) for a random 1/2 of the 767 patients

1. Compute the distribution of age at diagnosis (5-year intervals) and year of diagnosis (5 year intervals). Also compute the mean and median ages at diagnosis.

2. For each of the 20 cells in Table 2 (5 Gleason score categories x 4 age-at-dx categories), compute the

a. number of man-years (M-Y) of observation

b. number of deaths from prostate cancer(1), other causes(2), unknown causes(3)

c. prostate cancer(1) death rate [deaths per 100 M-Y]

d. proportion who survived at least 15 years.

For a and b you can use the 'sum' option in PROC means; ie PROC MEANS data = … SUM; VAR vars you want to sum; BY the 2 variables that form the cross-classification. Also think of a count as a sum of 0s and 1s. For c (to avoid having to compute 20 rates by hand), you can 'pipe' i.e. re-direct the sums to a new sas datafile, where you can then divide one by other to get (20) rates. Use OUTPUT OUT = …. SUM= …names for two sums;

3. On a single graph, plot the 5 Kaplan-Meier survival curves, one for each of the 5 Gleason score categories (PROC LIFETEST .. Online help is under the SAS STAT module, or see http://www.ats.ucla.edu/stat/sas/seminars/sas_survival/default.htm. For Stata, see http://www.ats.ucla.edu/stat/stata/seminars/stata_survival/default.htm.

4. [OPTIONAL] In order to compare the death rates with those of U.S. men of the same age, for each combination of calendar year period (1970-1974, 1975-1979, …, 1994-1999) and 5 year age-interval (55-59, 60-64, … obtain

a. the number of man-years of follow-up and

b. the number of deaths.

Do so by creating, from the record for each man, as many separate observations as the number of 5yr x 5yr "squares" that the man traverses diagonally through the Lexis diagram [use the OUTPUT statement within the DATA step]. Then use PROC MEANS to aggregate the M-Y and deaths in each square. If you

get stuck, here is some SAS code that does this, or see the algorithm given in Breslow and Day, Volume II, page ____

Put all of the program steps and output into a single .txt file. JH will use a mono-spaced font such as Courier to view it – that way the alignment should be ok. Interleave DATA and PROC statements with output and conclusions, and use helpful titles (produced by SAS, but to your specifications) over top of each output. Get SAS to set up the output so that there are no more that 65 horizontal characters per line – that way, lines won't wrap-around even when the font used to view your file is increased. Show relevant excerpts rather than entire listings of datafiles. Annotate liberally. Submit the text file electronically (i.e., by email) to JH by 9 am on Monday Nov 7.

14.7 Serial PSA values

Q1

These two files contain PSA values [pre-] and [post-] treatment of prostate cancer *.

(a) Create a 'wide' PSA file of 25 log-base-2 PSA values per man (some will be missing, if PSA not measured 25 times). Print some excerpts.

(b)From the dataset created in (a), create a long file, with just the observations containing the non-missing log-base-2 PSA values [OUTPUT statement in DATA step]. Print and plot some excerpts.

(c) From the dataset created in (b), create a wide file [RETAIN, first. and last. helpful here; or use PROC TRANSPOSE]. Print some excerpts.

- The order of the variables is given in this sas program . Some of the code in the program may also be of help.

Put all of the program steps and output into a single .txt file. JH will use a mono-spaced font such as Courier to view it – that way the alignment should be ok. Interleave DATA and PROC statements with output and conclusions, and use helpful titles (produced by SAS, but to your specifications) over top of each output. Get SAS to set up the output so that there are no more that 65 horizontal characters per line – that way, lines won't wrap-around even when the font used to view your file is increased. Show relevant excerpts rather than entire listings of datafiles. Annotate liberally. Submit the text file electronically (i.e., by email) to JH by 9 am on Monday Nov 14.

14.8 Graphics

1a

Re-produce (or if you think you can, improve on) three of the graphs shown in "Examples of graphs from Medical Journals." These examples are in a pdf file on the main page. Use Excel for at least one of them, and R/Stata/SAS for at least one other. Do not go to extraordinary lengths to make them exactly like those shown – the authors, or the journals themselves, may have used more specialized graphics software. You may wish to annotate them by making (and sharing with us) notes on those steps/options that were not immediately obvious and that took you some effort to figure out. Insert all three into a single electronic document.

1b

Browse some medical and epidemiologic journals and some magazines and newspapers published in the last 12 months, Identify the statistical graph you think is the worst, and the one you think is the best. Tell us how many graphs you looked at, and why you chose the two you did. If you find a helpful online guide or textbook on how to make good statistical graphs, please share the reference with us. [The bios601 site http://www.epi.mcgill.ca/hanley/bios601/DescriptiveStatistics/ has a link to the Textbook by Cleveland and the book "R Graphics" by Paul Murrell.

If possible, electronically paste the graphs into the same electronic file you are using for 1a.

2

[OPTIONAL] The main page has a link to a lifetable workbook containing three sheets. Note that the 'lifetable' sheet in this workbook is used to calculate an abridged current life table based on the 1960 U.S. data. Use this sheet as a guideline, and create a current life-table ('complete', i.e., with 1-year age-intervals) for Canadian males, using the male population sizes, and numbers of deaths, by age, Canada 2001. [The calculations in columns O to W of the lifetable sheet are not relevant for this exercise]. Details on the elements of, and the construction of current lifetables can be found in the chapters (on website) from the textbooks by Bradford Hill and Selvin, and in the technical notes provided by the US National Center for Health Statistics in connection with US Lifetable 2000. See also the FAQ for 613 from 2005. The fact that the template is for an abridged life table, with mostly 5-year intervals, whereas the task is to construct a full lifetable with 1 year intervals, caused some people problems last year.. they realized something was wrong when the life expectancy values were way off!

Since this is an exercise, and not a calculation for an insurance company that wants to have 4 sig. decimal places, don't overly fuss about what values of 'a' you use for the early years.. they don't influence the calculations THAT much: If you try different sets of values (such as 0.1 in first year and 0.5 thereafter) you will not find a big impact. But don't take my word for it .. the beauty of a spreadsheet is that you can quickly see the consequences of different assumptions or 'what ifs'.

[In practice, in order not to be unduly influenced by mortality rates in a single calendar year (e.g. one that had a very bad influenza season), current lifetables are usually based on several years of mortality data. Otherwise, or if they are based on a small population, the quantities derived from them will exhibit considerable random fluctuations from year to year]

Once you have completed the table, use the charting facilities in Excel to plot the survival curve for the hypothetical (fictitious) male 'cohort' represented by the current lifetable.

On a separate graph, use two histograms to show the distributions of the ages at death (i) for this hypothetical male 'cohort' and (ii) those males who died in 2001. To make it easy to compare them, superimpose the histograms or put them 'side by side' or 'back to back' within the same graph. Explain why the two differ in shape and location. Calculate/derive (and include them somewhere on the spreadsheet) the median and mean age at death in the hypothetical cohort and the corresponding statistics for the actual deaths in 2001.

14.9 Possible Body Mass Indices

This exercise investigates different definitions of Body Mass Index (BMI).

BACKGROUND: With weight measured in Kilograms, and height in metres, BMI is usually defined as weight divided by the SQUARE of height, i.e., BMI = Wt / (Height*Height), or BMI = Wt/(height**2) using, as SAS and several other programming languages do, the symbol ** for 'raised to the power of'. [NB: Excel uses ^ to denote this]

What's special about the power of 2? Why not a power of 1 i.e., Weight/height?

Why not 3, i.e., Weight/*(height**3) ? Why not 2.5 i.e. Weight/(height**2.5)?

One of the statistical aims of a transformation of weight and height to BMI is that BMI be statistically less correlated with height, thereby separating height and height into two more useful components height and BMI. For example in predicting lung function (e.g. FEV1), it makes more sense to use height and BMI than height and weight, since weight has 2 components in it – it is partly height and partly BMI. Presumably, one would choose the power which minimizes the correlation.

The task in this project is to investigate the influence of the power of height used in the ratio, and to see if the pattern of correlations with power is stable over different settings (datasets).

DATA: To do this, use 2 of the 6 datasets on the 678 webpage: [usernane is c678 and p w is H**J44]

- Children aged 11-16 Alberta 1985 (under 'Datasets')

- 18 year olds in Berkeley longitudinal study, born 1928/29 (under 'Datasets')
- Dataset on bodyfat – 252 men (see documentation) (under 'Datasets')
- Pulse Rates before and after Exercise – Australian undergraduates in 1990's (under 'Projects')
- Miss America dataset 1921-2000 (under 'Resources')
- Playboy dataset 1929-2000 (under 'Resources')

METHODS: First create each of the two SAS datasets, and if height and weight are not already in metres and Kg, convert them to these units. Drop any irrelevant variables. Inside each dataset, create a variable giving the source of the data (we will merge the two – and eventually all six– datasets, so we need to be able to tell which one each observation came from).

Combine the two datasets, i.e. 'stack' them one above the other in a single dataset. Print out some excerpts.

For each subject in the combined dataset, create 5 versions of < using the powers 1, 1.5, 2, 2.5 and 3.

Calculate the correlation between the 'BMI' obtained with each of these powers, and height. Do this separately for the observations from the two different sources (the BY statement should help here).

Report your CONCLUSIONS.

14.10 Galton

The objective of this exercise is to examine the relation between heights of parents and heights of their (adult) children, using recently 'uncovered' data from the Galton archives, You are asked to assess if Galton's way of dealing with the fact that heights of males and females are quite different produces sharper correlations than we would obtain using 'modern' methods of dealing with this fact. As side issues, you are also asked to see whether the data suggest that stature plays "a sensible part in marriage selection" and to comment on the correlations of the heights in the 4 {father,son}, {father,daughter}, {mother,son} and {mother,daughter} pairings.

BACKGROUND: Galton 'transmuted' female heights into their 'male-equivalents' by multiplying them by 1.08, and then using a single combined 'uni-sex' dataset of 900-something offspring and their parents. While some modern-day anayysts would simply calculate separate correlations for the male and female offspring (and then average the two correlations, as in a meta-analysis), most would use the combined dataset but 'partial out' the male-females differences using a multivariable analysis procedure. The various multivariable procedures in effect create a unisex dataset by adding a fixed number of inches to each female's height (or, equivalently, in the words of one of our female PhD students, by 'cutting the men down to size'). JH was

impressed by the more elegant 'proportional scaling' in the 'multiplicative model' used by Galton, compared with the 'just use the additive models most readiliy available in the software' attitude that is common today. In 2001, he located the raw (untransmuted) data that allows us to compare the two approaches.

DATA: For the purposes of this exercise, the data [see http://www.epi.mcgill.ca/hanley/galton] are in two separate files:

- the heights# of 205 sets of parents (parents.txt) with families numbered 1-135, 136A, 136-204
- the heights# of their 900-something* children (offspring.txt) with families numbered as above
- The data on eight families are deliberately omitted, to entice the scholar in you to get into the habit of looking at (and even double checking) the original data. Since here we are more interested in the computing part in this course, and because time is short, ignore this invitation to inspect the data – we already had a look at them in class. In practice, we often add in 'missing data' later, as there are always some problem cases, or lab tests that have to be repeated, or values that need to be checked, or subjects who didn't get measured at the same time as others etc.. JH's habit is to make the additions in the 'source' file (.txt or .xls or whatever) and re-run the entire SAS DATA step(s) to create the updated SAS dataset (temporary or permanent). If the existing SAS datset is already large, and took a lot of time to create, you might consider creating a small dataset with the new observations, and then stacking (using SE) the new one under the existing one – in a new file. SAS has fancier ways too, and others may do things differently!

If your connection is too slow to view the photo of the first page of the Notebook, the title reads

FAMILY HEIGHTS (add 60 inches to every entry in the Table)

METHODS/RESULTS/COMMENTS:

1. Categorize each father's height into one of 3 subgroups (shortest 1/4, middle 1/2, tallest 1/4). Do likewise for mothers. Then, as Galton did [Table III], obtain the 2-way frequency distribution and assess whether "we may regard the married fold as picked out of the general population at haphazard".
2. Calculate the variance Var[F] and Var[M] of the fathers' [F] and mothers' [M] heights respectively. Then create a new variable consisting of the sum of F and M, and calculate Var[F+M]. Comment. Galton called this a "shrewder" test than the "ruder" one he used in 1. (statistic-keyword VAR in PROC MEANS)

3. When Galton first anayzed these data in 1885-1886, Galton and Pearson hadn't yet invented the CORRelation coefficient. Calculate this coefficient and see how it compares with your impressions in 1 and 2.

4. Create two versions of the transmuted mother's heights, one using Galton's and one using the modern-day (lazy-person's, blackbox?) additive scaling [for the latter, use the observed difference in the average heights of fathers and mothers, which you can get by e.g., running PROC MEANS on the offspring dataset, either BY gender, or using gender as a CLASS variable]. In which version of the transmuted mothers' heights is their SD more simlar to the SD of the fathers? (statistic-keyword STD in PROC MEANS)

5. Create the two corresponding versions of what Galton called the 'mid-parent' (ie the average of the height of the father and the height of the transmuted mother). Take mid-point to mean the half-way point (so in this case the average of the two)

6. Create the corresponding two versions (additive and multiplicative scaling) of the offspring heights (note than sons' heights remain 'as is'). Address again, but now for daughters vs sons, the question raised at the end of 4.

7. Merge the parental and offspring datasets created in steps 4 and 6, taking care to have the correct parents matched with each offspring (this is called a 1:many merge).

8. Using the versions based on 1.08, round the offspring and mid-parent heighs to the nearest inch (or use the FLOOR function to just keep the integer part of the mid-parent height –you need not be as fussy as Galton was about the groupings of the mid-parent heights), and obtain a 2-way frequency distribution similar to that obtained by Galton [Table I]. Note that, opposite to we might do today, Galton put the parents on the vertical, and the offspring on the horizontal axis. (The MOD INT FLOOR CEIL and ROUND functions can help you map observations into 'bins' ; we will later see a way to do so using loops)

9. Galton called the offspring in the same row of his table a 'filial array'. Find the median height for each filial array, and plot it, as Galton did, against the midpoint of the interval containing their midparent – you should have one datapoint for each array. *Put the mid-parent values on the vertical, and the offspring on the horizontal axis. By eye, estimate the slope of the line of best fit to the datapoints. Mark your fitted line by 'manually' inserting two markers at the opposite corners of the plot. Does the slope of your fitted line agree with Galton's summary of the degree of "regression to mediocrity"? [Plate IX]* Note that Galton used datapoints for just 9 filial arrays, choosing to omit those in the bottom and top rows (those with the very shortest and the very tallest parents) because the data in these arrays were sparse. (By using the binned parental height in the CLASS statement in PROC MEANS or PROC UNIVARIATE, directing

the output to a new SAS dataset, and applying PROC PLOT to this new dataset, you can avoid having to do the plotting manually See more on this in the FAQ)

10. Plot the individual unisex offspring heights (daughters additively transmuted) versus the mid-parent height (mothers transmuted). OVERLAY on it, with a different plotting symbol, the corresponding plot involving the multiplicatively transmuted offspring values (on the parent-axis, stay with Galton's definition of a midparent). (see FAQ) Compare the two, and have a look at Galton's fitted ellipse, corresponding to a bivariate normal distribution [Plate X]) {here, again, we would be more likely to plot the parents' heights on the horizontal, and the offspring heights on the vertical axis}.

11. For each of the following 'offspring vs. mid-parent' correlations, use the 'mid-parent' obtained using Galton's multiplicative method. Calculate (a) the 2 correlations for the 2 unisex versions of the offspring data (b) the sex-specific correlations (i.e., daughters and sons separately) and (c) the single parent-offspring correlation, based on all offspring combined, and their untransmuted heights, ignoring the sex of the offspring. Comment on the correlations obtained, and on the instances where there are big disparities between them. [a PLOT, with separate plotting symbols for sons and daughters, might help in the case of (c)]

12. Calculate the 4 correlations (i) father,son (ii) father,daughter, (iii) mother,son and (iv) mother,daughter. Comment on the pattern, and on why you think it turned out this way.

Put all of the program steps and output into a single .txt file. JH will use a mono-spaced font such as Courier to view it – that way the alignment should be ok. Interleave DATA and PROC statements with output and conclusions, and use helpful titles (produced by SAS, but to your specifications) over top of each output. Get SAS to set up the output so that there are no more that 65 horizontal characters per line – that way, lines won't wrap-around even when the font used to view your file is increased. Show relevant excerpts rather than entire listings of datafiles. Annotate liberally. Submit the text file electronically (i.e., by email) to JH by 9 am on Monday October 30.

Chapter 15

Computing Week3

(Probabilities, evaluated by simulation)

15.1 Epidemics

15.2 Duplicate Birthdays

15.3 Lottery payoffs

15.4 Chevalier de Méré

15.5 Detecting a fake Bernoulli sequenece

15.6 Cell occupancy

15.7 Life Tables

15.8 Carrier Status (genetics)

15.9 Diagnostic and statistical tests

Chapter 16

DALITE

16.1 Aim

16.2 How it works