HuGen2080 book

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Table of contents

Preface

This is a Quarto book created from markdown and executable code using Quarto within RStudio.

Book web site: https://danieleweeks.github.io/HuGen2080/

Book source code: https://github.com/DanielEWeeks/HuGen2080

Created by Daniel E. Weeks

Websites:

https://www.sph.pitt.edu/directory/daniel-weeks

To learn more about Quarto books visit https://quarto.org/docs/books.

1 Introduction

This is a Quarto book created from markdown and executable code using Quarto within RStudio.

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2 Logistics

2.1 GitHub: Set up an account

Please go to https://github.com and set up a GitHub account.

Choose your GitHub user name carefully, as you may end up using it later in a professional context.

2.2 GitHub Classroom

As GitHub Classroom will be used to distribute course materials and to submit assignments, it would be best if you get git working on your own computer. The easiest way to do this is to install RStudio, R, and git on your computer.

Please follow the detailed instructions in https://github.com/jfiksel/github-classroom-for-students

In particular, see Step 5 re generating an ssh key so you don't need to login every time.

3 Readings

3.1 Course Preparation

3.1.1 Required Readings

Background reading:
Ziegler and König - Chapter 1: Molecular Genetics
Ziegler and König - Chapter 2: Formal Genetics

3.1.2 Henry Stewart Talk:

Genotyping algorithms for genome wide association studies/ Dr. Vincent Plagnol

3.2 Models, Maps, and Markers

3.2.1 Learning Objectives

- To review basic genetic models
- To learn about genetic markers

3.2.2 Required Readings

Ziegler and König - Chapter 3: Genetic Markers
Ziegler and König - Chapter 5: Genetic Map Distances
Laird and Lange - Section 2.3: The biology underlying Mendelian inheritance (See errata)
Laird and Lange - Section 5.2 Genetic maps and marker maps

3.2.3 Recommended Problems:

(For understanding - not to be handed in)
Z&K 5.1
Z&K 5.2

3.2.4 Supplementary Readings

Elston RC (2000) Introduction and overview. Statistical methods in genetic epidemiology. Stat Methods Med Res 9:527-541

Chapters 1, 2, and 3: Laird NM, Lange C (2011) The Fundamentals of Modern Statistical Genetics. Springer.

3.2.5 Henry Stewart Talk:

Introductory genetics for statisticians/ Robert C. Elston.

3.3 Study Design Overview

3.3.1 Learning Objectives

- To learn the basic principles of study design for genetic studies
- To understand the vital importance of phenotype definition
- To understand the best sample selection strategies

3.3.2 Required reading:

Balding DJ. A tutorial on statistical methods for population association studies. Nature Reviews Genetics. Nature Publishing Group; 2006 Oct 1;7(10):781–791. DOI: https://doi.org/10.1038/nrg1916

3.3.3 Active Learning:

Intro to Unix & PLINK

3.3.4 Henry Stewart Talk:

Designing a genome-wide association study/ Dr. Chris Spencer

3.4 No class - Martin Luther King Day

3.5 Familial Aggregation: Recurrence Risk Ratios, Heritability

3.5.1 Learning Objectives

- To learn aggregation analysis
- To learn how to estimate recurrence risk ratios
- To review the concept of heritability

3.5.2 Active Learning:

Student Presentation

3.5.3 Required Readings

Ziegler and König - Chapter 6: Familiality, Heritability, and Segregation Analysis

3.5.4 Supplementary Readings

Chapter 4: Laird NM, Lange C (2011) The Fundamentals of Modern Statistical Genetics. Springer.

3.5.5 Henry Stewart Talk:

Heritability and its uses/ Doug Speed.

Inferring relatedness/ Prof. Emmanuelle Génin

3.6 Familial Aggregation: Segregation Analysis, Ascertainment

3.6.1 Learning Objectives

- To learn about segregation analysis
- To understand how to take ascertainment into account in the segregation models
- To formulate testable hypotheses about genetic models

3.6.2 Active Learning:

SOLAR heritability computer lab

3.6.3 Required Readings

Ziegler and König - Chapter 6: Familiality, Heritability, and Segregation Analysis

3.7 LOD scores: Model-based Linkage Analysis

3.7.1 Learning Objectives

- To learn how to compute LOD scores
- To learn about different map functions, and the distinction between genetic and physical maps
- To formulate testable hypotheses about linkage

3.7.2 Active Learning:

Student Presentation

3.7.3 Required Readings

Ziegler and König - Chapter 7: Model-based Linkage Analysis

3.7.4 Supplementary Readings

Chapters 5 and 6: Laird NM, Lange C (2011) The Fundamentals of Modern Statistical Genetics. Springer.

3.7.5 Henry Stewart Talk:

Linkage and sequence analysis in families/ Christopher Amos.

3.8 Non-parametric methods

3.8.1 Learning Objectives

- To learn how to carry out non-parametric linkage analyses
- To understand the motivation behind non-parametric linkage analysis approaches

3.8.2 Active Learning:

Merlin computer lab

3.8.3 Required Readings

Ziegler and König - Chapter 8: Model-free Linkage Analysis for Dichotomous Traits

3.8.4 Supplementary Readings

Shih MC, Whittemore AS (2001) Allele-sharing among affected relatives: non-parametric methods for identifying genes. Stat Methods Med Res 10:27-55

3.9 Association: Case/Control & Quantitative Traits

3.9.1 Learning Objectives

- To formulate testable hypotheses about association
- To understand and apply various case/control association tests
- To understand allele-based and genotype-based association tests, and trend tests.

3.9.2 Active Learning:

Student Presentation

3.9.3 Required Readings

Ziegler and König - Chapter 10: Fundamental Concepts of Association Analysis
Ziegler and König - Chapter 11: Association Analysis with Unrelated Individuals

3.9.4 Supplementary Readings

Chapter 7: Laird NM, Lange C (2011) The Fundamentals of Modern Statistical Genetics. Springer.

Cardon LR, Bell JI (2001) Association study designs for complex diseases. Nat Rev Genet 2:91-99.

Balding DJ (2006) A tutorial on statistical methods for population association studies. Nat Rev Genet 7:781-791

3.9.5 Henry Stewart Talk:

Introduction to genetic association analysis/ Jenny Barrett.

Statistical tests for association/ Dr. Andrew Morris

3.10 Association: Family-based and Haplotype-based

3.10.1 Learning Objectives

- To learn how to analyze family data for association
- To learn how to test haplotypes for association
- To understand sparsity issues involved in haplotyped-based tests

3.10.2 Active Learning:

PLINK computer lab

3.10.3 Required Readings

Ziegler and König - Chapter 12: Association Analysis in Families

3.10.4 Supplementary Readings

Chapter 9 & Chapter 10, Section 2: Laird NM, Lange C (2011) The Fundamentals of Modern Statistical Genetics. Springer.

Ott J, Kamatani Y, Lathrop M (2011) Family-based designs for genome-wide association studies. Nat Rev Genet 12:465-474

3.11 Multiple testing

3.11.1 Learning Objectives

- To understand how to adjust for multiple testing

3.11.2 Active Learning:

Student Presentation

3.11.3 Required Readings

Ziegler and König - Chapter 14, Section 14.4: Multiple Testing

3.11.4 Supplementary Readings

Chapter 10, Section 1: Laird NM, Lange C (2011) The Fundamentals of Modern Statistical Genetics. Springer.

3.11.5 Henry Stewart Talk:

Assessing significance in genome-wide studies/ Dr. David Evans

3.12 Power to detect Association: Linkage vs. Association

3.12.1 Learning Objectives

- To learn how to compute power for detecting association
- To compare and contrast linkage and association
- To understand the relative strengths and weaknesses of linkage and association tests

3.12.2 Active Learning:

Student Presentation

3.12.3 Supplementary Readings

Clerget-Darpoux F, Elston RC (2007) Are linkage analysis and the collection of family data dead? Prospects for family studies in the age of genome-wide association. Hum Hered 64:91-96

3.13 Rare variants

3.13.1 Learning Objectives

- To learn how to test rare variants for association
- To learn about burden tests, collapsing or grouping tests, weighted sum tests, and variable threshold tests.

3.13.2 Active Learning:

Student Presentation

3.13.3 Supplementary Readings

Asimit J, Zeggini E (2010) Rare variant association analysis methods for complex traits. Annu Rev Genet 44:293-308

Bansal V, Libiger O, Torkamani A, Schork NJ (2010) Statistical analysis strategies for association studies involving rare variants. Nat Rev Genet 11:773-785

3.14 Methods for correlated data: LME, GEE, Score

3.14.1 Learning Objectives

- To learn about linear mixed effects models, generalized estimating equations, and score tests
- To learn how to properly model relatedness while testing genetic hypotheses

3.14.2 Active Learning:

Student Presentation

3.14.3 Required Readings

Sul JH, Martin LS, Eskin E. Population structure in genetic studies: Confounding factors and mixed models. PLoS Genet. 2018; 14(12):e1007309. doi:10.1371/journal.pgen.1007309

3.15 Bayesian Methods in Human Genetics

3.15.1 Learning Objectives

- To learn about Bayesian methods in human genetics
- To understand Bayesian principles

3.15.2 Active Learning:

Student Presentation

3.15.3 Required Readings

Stephens M, Balding DJ. Bayesian statistical methods for genetic association studies. Nat Rev Genet. 2009 Oct;10(10):681-90. doi: 10.1038/nrg2615. Review. PubMed PMID: 19763151.

3.15.4 Supplementary Readings

Wakefield J. Bayes factors for Genome-wide association studies: Comparison with P-values. Genetic Epidemiology. 2009;33(1):79–86. DOI: https://doi.org/10.1002/gepi.20359

3.16 Review for Mid-term exam

3.17 Mid-term exam

3.18 Gene x Gene interaction, vQTLs

3.18.1 Learning Objectives

- To learn how to test for gene x gene interaction
- To formulate testable hypotheses about gene x gene interaction

3.18.2 Required Readings

Cordell HJ (2009) Detecting gene-gene interactions that underlie human diseases. Nat Rev Genet 10:392-404

3.18.3 Supplementary Readings

Gilbert-Diamond D, Moore JH (2011) Analysis of gene-gene interactions. Curr Protoc Hum Genet Chapter 1:Unit1 14

3.19 Gene x Environment interaction

3.19.1 Learning Objectives

- To learn how to test for gene x environment interaction
- To formulate testable hypotheses about gene x environment interaction

3.19.2 Active Learning:

Student Presentation

3.19.3 Required Readings

Thomas D (2010) Gene–environment-wide association studies: emerging approaches. Nat Rev Genet 11:259-272

3.19.4 Supplementary Readings

Chapter 10, Section 3: Laird NM, Lange C (2011) The Fundamentals of Modern Statistical Genetics. Springer.

Ottman R (1990) An epidemiologic approach to gene-environment interaction. Genet Epidemiol 7:177-185

3.19.5 Henry Stewart Talk:

Statistical issues in epidemiologic studies of gene-environment interaction/ Peter Kraft, Donna Spiegelman.

GxE interactions in genome-wide association studies/ David V. Conti.

3.20 Spring Recess

3.21 Spring Recess

3.22 Special Topic Lecture by Chris McKennan

3.23 Fine mapping

3.23.1 Learning Objectives

- To learn how to carry out fine mapping
- To understand and apply conditional tests of association

3.23.2 Active Learning:

Student Presentation

3.23.3 Required Readings

Schaid DJ, Chen W, Larson NB. From genome-wide associations to candidate causal variants by statistical fine-mapping. Nature Reviews Genetics. Nature Publishing Group; 2018 Aug 29;19(8):491–504. DOI: https://doi.org/10.1038/s41576-018-0016-z

3.23.4 Supplementary Readings

Cano-Gamez E, Trynka G. From GWAS to Function: Using Functional Genomics to Identify the Mechanisms Underlying Complex Diseases. Front Genet. 2020;11:424. PMID: 32477401 PMCID: PMC7237642 DOI: https://doi.org/10.3389/fgene.2020.00424

3.24 Meta analysis

3.24.1 Learning Objectives

- To learn about the different types of meta analysis.
- To understand the assumptions made by meta analysis.

3.24.2 Required Readings

Ziegler and König - Chapter 14, Section 14.5: Accumulating Data from Genome-wide Association Studies

3.24.3 Henry Stewart Talk:

Winner's curse, replication and meta-analysis/ Frank Dudbridge.

Meta-analysis in genome-wide association studies: application to type 2 diabetes/ Dr. Eleftheria Zeggini

3.25 Methods for multivariate phenotypes

3.25.1 Learning Objectives

- To learn about methods for analyzing multivariate phenotypes
- To learn how to properly account for correlation among phenotypes

3.25.2 Active Learning:

Student Presentation

3.26 Heritability from GWAS

3.26.1 Learning Objectives

- To learn how to estimate heritability using unrelated samples.
- To understand polygenicity.

3.26.2 Active Learning:

Student Presentation

3.26.3 Henry Stewart Talk:

Heritability and its uses/ Doug Speed.

3.27 LDscore regression

3.27.1 Learning Objectives

- To understand the principles of LDscore regression
- To understand polygenicity.

3.27.2 Active Learning:

Student Presentation

3.28 Mendelian Randomization

3.28.1 Learning Objectives

- To understand the basic principles of Mendelian Randomization.
- To formulate testable hypotheses about causation using Mendelian Randomization approaches.

3.28.2 Active Learning:

Student Presentation

3.28.3 Henry Stewart Talk:

Causal inference in genetic epidemiology: Mendelian randomization and beyond / Krista Fischer.

3.29 Genetic Risk Scores & Polygenic Risk Scores & Genomic Prediction

3.29.1 Learning Objectives

- To understand how to construct and use genetic risk scores.
- To understand the limits of genomic predication.

3.29.2 Active Learning:

Student Presentation

3.30 Special Topic Lecture by Lacey Heinsberg

3.30.1 Required Readings

Heinze G, Wallisch C, Dunkler D. Variable selection – A review and recommendations for the practicing statistician. Biometrical Journal. 2018;60(3):431–449. DOI: https://doi.org/10.1002/bimj.201700067

3.31 Special Topic Lecture by Jenna Carlson

3.32 Review for final exam

3.33 Final exam

4 Statistical Notation

4.1 Sums

$$\sum_{i=1}^{3} X_i = X_1 + X_2 + X_3 \tag{4.1}$$

Example:

The equation

$$\hat{p} = \frac{\sum_N Cr(r-1)}{\sum_N Cr(s-1)} \tag{4.2}$$

would be more clearly written as

$$\hat{p} = \frac{\sum_{i=1}^{N} C_i r_i (r_i - 1)}{\sum_{i=1}^{N} C_i r_i (s_i - 1)} \tag{4.3}$$

4.2 Products

$$\prod_{i=1}^{3} X_i = X_1 \times X_2 \times X_3 \tag{4.4}$$

4.3 Likelihood

Based in part on my class notes from the 1988 UCLA Biomathematics 207 A course "Theoretical Genetic Modeling" taught by Dr. Susan Hodge.

The likelihood $L(Hypothesis\ H|Data\ D)$, given a specific model, is proportional to $P(D|H)$ with the constant of proportionality being arbitrary.

As such, the likelihood is a function of the hypothesis, not of the data.

As Etz (2018) states:

"The likelihood of a hypothesis (H) given some data (D) is the probability of obtaining D given that H is true multiplied by an arbitrary positive constant K: $L(H) = K \times P(D|H)$. … For likelihood, the data are treated as a given, and the hypothesis varies." (Etz, 2018, p. 60)

Etz A. Introduction to the Concept of Likelihood and Its Applications. Advances in Methods and Practices in Psychological Science. SAGE Publications Inc; 2018 Mar 1;1(1):60–69. DOI: https://doi.org/10.1177/2515245917744314

4.4 Conditional Probability

1. Definition:

$$P(A|B) = \frac{P(A \cap B)}{P(B)} \tag{4.5}$$

2. Let $S = \bigcup\limits_{i=1}^{n} A_i$ and $A_i \cap A_j = \emptyset$ for $i \neq j$. Then $P(B) = \sum\limits_{i=1}^{n} P(B|A_i)P(A_i)$
3. $P(A|B) = \frac{P(B|A)P(A)}{P(B)}$
4. Bayes Rule

Let $S = \bigcup\limits_{i=1}^{n} A_i$ and $A_i \cap A_j = \emptyset$ for $i \neq j$. Then $P(A_j|B) = \frac{P(B|A_j)P(A_j)}{\sum\limits_{i=1}^{n} P(B|A_i)P(A_i)}$

5. Intermediate Conditioning

$$P(A|B) = \sum_i P(A|X_i, B)P(X_i|B) \tag{4.6}$$

6. $P(A|B, C) = \frac{P(B|A,C)P(A|C)}{P(B|C)}$

7. $P(A,B|C) = P(A|B,C)P(B|C)$

8. If A_i are mutually exclusive and exhaustive, then

$$P(A_j|B,C) = \frac{P(B|A_j,C)P(A_j|C)}{\sum_i P(B|A_i,C)P(A_i|C)} \tag{4.7}$$

5 GitHub

5.1 GitHub Introduction lecture

Here's a recording of this lecture (32 minutes 8 seconds):

Recording

5.2 GitHub Introduction slides

PDF slide set

6 Git Commands

6.1 git - best practices

pull - work - commit - pull - push

- `git pull`
- Make changes
- `git commit` your changes to your local repository
- `git pull` the latest remote changes to your local repository
- `git push` your changes.

Pay attention to any error messages.

6.2 Outline of essential Git commands

Here's an outline of essential Git commands, initially created by ChatGPT:

6.2.1 Initialization and Configuration

- `git init`: Initializes a new Git repository in the current directory.
- `git config`: Configure Git settings.

6.2.2 Basic Workflow

- `git add`: Stage changes.
- `git commit -m "message"`: Commits staged changes with a descriptive message.

6.2.3 Remote Repositories

- `git clone`: Clones a remote repository to your local machine.
- `git push`: Send local changes to remote repository.
- `git pull`: Retrieve changes from remote.
- `git remote`: Manage remote repositories.

6.2.4 Status and Changes

- `git status`: Shows the current state of your working directory.
- `git diff`: Displays changes between working directory and the last commit.

6.2.5 History and Logs

- `git log`: View commit history.
- `git log --oneline`: Compact commit history.

6.2.6 Ignoring Files

- Create `.gitignore` file.

6.2.7 Branching

- `git branch`: List/create branches.
- `git checkout`: Switch branches.
- `git merge`: Merge branches.

6.2.8 Undoing Changes

- `git reset`: Unstage or reset changes.
- `git revert`: Create undoing commits.

6.2.9 Tagging

- `git tag`: Create and manage tags.

6.2.10 Stashing

- `git stash`: Temporarily store changes.

7 Basic Shell Commands

7.1 Acknowledgment and License

This chapter is a derivative of the Basic Shell Commands cheat sheet from the DEPRECATED-boot-camps/shell/shell_cheatsheet.md file created by Software Carpentry and is used under the Creative Commons - Attribution license CC BY 3.0

Minor section numbering and formatting changes were made here.

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7.2 Shell Basics:

Command	Definition
`.`	a single period refers to the current directory
`..`	a double period refers to the directory immediately above the current directory
`~`	refers to your home directory. *Note:* this command does NOT work on Windows machines (Mac and Linux are okay)
`cd ./dirname`	changes the current directory to the directory `dirname`
`ls -F`	tells you what files and directories are in the current directory
`pwd`	tells you what directory you are in (`pwd` stands for *p*rint *w*orking *d*irectory)
`history`	lists previous commands you have entered. `history	less` lets you page through the list.
`man` *cmd*	displays the *man*ual page for a command.

7.3 Creating Things:

7.3.1 How to create new files and directories..

Command	Definition
`mkdir ./dirname`	makes a new directory called dirname below the current directory. *Note:* Windows users will need to use `\` instead of `/` for the path separator
`nano filename`	if `filename` does not exist, `nano` creates it and opens the `nano` text editor. If the file exists, `nano` opens it. *Note: (i)* You can use a different text editor if you like. In gnome Linux, `gedit` works really well too. *(ii)* `nano` (or `gedit`) create text files. It doesn't matter what the file extension is (or if there is one)

7.3.2 How to delete files and directories...

7.3.2.1 *Remember that deleting is forever. There is NO going back*

Command	Definition
`rm ./filename`	deletes a file called `filename` from the current directory
`rmdir ./dirname`	deletes the directory `dirname` from the current directory. *Note:* `dirname` must be empty for `rmdir` to run.

7.3.3 How to copy and rename files and directories...

Command	Definition
`mv tmp/filename .`	moves the file `filename` from the directory `tmp` to the current directory. *Note: (i)* the original `filename` in `tmp` is deleted. *(ii)* `mv` can also be used to rename files (e.g., `mv filename newname`
`cp tmp/filename .`	copies the file `filename` from the directory `tmp` to the current directory. *Note: (i)* the original file is still there

7.4 Pipes and Filters

7.4.1 How to use wildcards to match filenames...

Wildcards are a shell feature that makes the command line much more powerful than any GUI file managers. Wildcards are particularly useful when you are looking for directories, files, or file content that can vary along a given dimension. These wildcards can be used with any command that accepts file names or text strings as arguments.

7.4.1.1 Table of commonly used wildcards

Wildcard	Matches
`*`	zero or more characters
`?`	exactly one character
`[abcde]`	exactly one of the characters listed
`[a-e]`	exactly one character in the given range
`[!abcde]`	any character not listed
`[!a-e]`	any character that is not in the given range
`{software,carpentry}`	exactly one entire word from the options given

See the cheatsheet on regular expressions on the second page of this PDF cheatsheet for more "wildcard" shortcuts.

7.4.2 How to redirect to a file and get input from a file ...

Redirection operators can be used to redirect the output from a program from the display screen to a file where it is saved (or many other places too, like your printer or to another program where it can be used as input).

CommandDescription	
`>`	write `stdout` to a new file; overwrites any file with that name (e.g., `ls *.md > mardkownfiles.txt`)
`>>`	append `stdout` to a previously existing file; if the file does not exist, it is created (e.g., `ls *.md >> markdownfiles.txt`)
`<`	assigns the information in a file to a variable, loop, etc (e.g., `n < markdownfiles.md`)

7.4.2.1 How to use the output of one command as the input to another with a pipe...

A special kind of redirection is called a pipe and is denoted by `|`.

CommandDescription	
|	Output from one command line program can be used as input to another one (e.g. ls *.md | head gives you the first 5 `*.md` files in your directory)

7.4.2.1.1 Example:

```
ls *.md | head | sed -i `s/markdown/software/g`
```

changes all the instances of the word `markdown` to `software` in the first 5 `*.md` files in your current directory.

7.5 How to repeat operations using a loop...

Loops assign a value in a list or counter to a variable that takes on a different value each time through the loop. There are 2 primary kinds of loops: `for` loops and `while` loops.

7.5.1 For loop

For loops loop through variables in a list

```
for varname in list
do
    command1 $varname
    command2 $varname
done
```

where,

- `for`, `in`, `do`, and `done` are keywords
- `list` contains a list of values separated by spaces. e.g. `list` can be replaced by `1 2 3 4 5 6` or by `Bob Mary Sue Greg`. `list` can also be a variable:
- `varname` is assigned a value without using a `$` and the value is retrieved using `$varname`

–

```
list[0]=Sam
list[1]=Lynne
list[2]=Dhavide
list[3]=Trevor
.
.
.
list[n]=Mark
```

which is referenced in the loop by:

```
for varname in ${list[@]}
do
    command1 $varname
    command2 $varname
done
```

Note: Bash is zero indexed, so counting always starts at `0`, not `1`.

7.5.2 While Loop

While loops loop through the commands until a condition is met. For example

```
COUNTER=0
while [ ${COUNTER} -lt 10 ]; do
    command 1
    command 2
    COUNTER=`expr ${COUNTER} + 1`
done
```

continues the loop as long as the value in the variable COUNTER is less than 10 (incremented by 1 on each iteration of the loop).

- `while`, `do`, and `done` are keywords

7.5.2.1 Commonly used conditional operators

Operator	Definition
`-eq`	is equal to
`-ne`	is not equal to
`-gt`	greater than
`-ge`	greater than or equal to
`-lt`	less than
`-le`	less than or equal to

Use `man bash` or `man test` to learn about other operators you can use.

7.6 Finding Things

7.6.1 How to select lines matching patterns in text files...

To find information within files, you use a command called `grep`.

Example command	Description
`grep [options] day haiku.txt`	finds every instance of the string `day` in the file haiku.txt and pipes it to standard output

7.6.1.1 Commonly used `grep` options

	`grep` options
`-E`	tells grep you will be using a regular expression. Enclose the regular expression in quotes. *Note:* the power of `grep` comes from using regular expressions. Please see the regular expressions sheet for examples
`-i`	makes matching case-insensitive
`-n`	limits the number of lines that match to the first n matches
`-v`	shows lines that do not match the pattern (inverts the match)
`-w`	outputs instances where the pattern is a whole word

7.6.2 How to find files with certain properties...

To find file and directory names, you use a command called `find`

Example command	Description
`find . -type d`	`find` recursively descends the directory tree for each path listed to match the expression given in the command line with file or directory names in the search path

7.6.2.1 Commonly used `find` options

	`find` options
`-type [df]`	`d` lists directories; `f` lists files
`-maxdepth n`	`find` automatically searches subdirectories. If you don't want that, specify the number of levels below the working directory you would like to search
`-mindepth n`	starts `find`'s search `n` levels below the working directory

8 Ascertainment

8.1 Example

Burton et al (2000) provide the following example:

They simulated a population containing 4,800 sibships of size 3, with a total of 14,400 children, and 864 affected children. In this population, the prevalence of the disease is 864/14400, which equals 0.06:

```r
864/14400
```

```
[1] 0.06
```

In their simulation, they then sampled every family that contained one or more affected child, and ended up with this set of 813 families:

N Aff Children	N Sibships
1	763
2	49
3	1

Question 1: What is the prevalence in this sample of 813 families if we compute it without employing any ascertainment correction?

```r
# Edit/add R code here
```

Answer 1

The prevalence without any ascertainment correction is 864/(3*813) = 0.3542.

```r
# Total number of affecteds
763 + 2*49 + 3*1
```

```
[1] 864
```

```r
# Total number of children
3*813
```

```
[1] 2439
```

```r
# (Number of affecteds)/(Number of children)
864/(3*813)
```

```
[1] 0.3542435
```

Question 2: What is the prevalence estimate after correcting for ascertainment?

```r
# Edit/add R code here
```

Answer 2

Here we use the Li and Mantel (1968) formula
p = (R - J)/(T - J)
where

- R = the total number of affected siblings
- T = the total number of siblings
- J = the number of siblings with only one proband

In this case,

- R = 864
- T = 3 * 813 = 2439
- J = 763

So p = (R - J)/(T - J) = (864 - 763)/(2439 - 763) = 0.0603

```r
R = 864
T = 3 * 813
J = 763
(R - J)/(T - J)
```

```
[1] 0.06026253
```

8.2 References

1. Burton PR, Palmer LJ, Jacobs K, Keen KJ, Olson JM, Elston RC. Ascertainment adjustment: where does it take us? Am J Hum Genet. 2000 Dec;67(6):1505–1514. PMID: 11078478 PMCID: PMC1287927 DOI: https://doi.org/10.1086/316899

2. Li CC, Mantel N. A simple method of estimating the segregation ratio under complete ascertainment. Am J Hum Genet. 1968 Jan;20(1):61–81. PMID: 5635671 PMCID: PMC1706251

3. Davie AM. The “singles” method for segregation analysis under incomplete ascertainment. Ann Hum Genet. 1979 May;42(4):507–512. PMID: 475337 DOI: https://doi.org/10.1111/j.1469-1809.1979.tb00683.x

9 Model-based Linkage Analysis

10 Maximum likelihood estimation

Suppose we have a phase-known family with 7 non-recombinant children and 1 recombinant child. The LOD score function for this family is then:

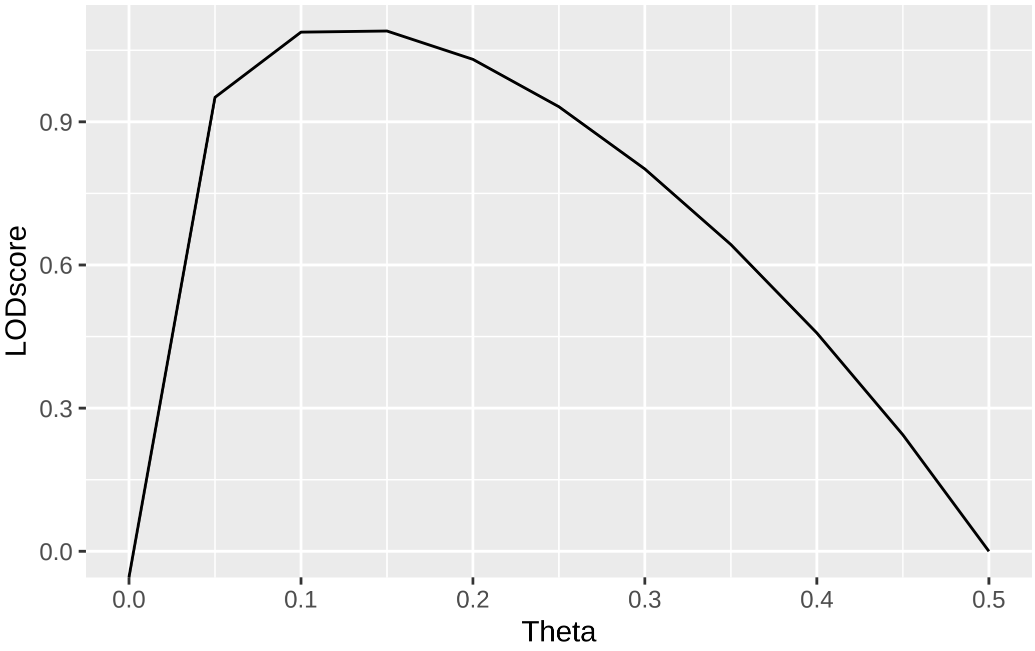
$$LOD(\theta) = log_{10}\frac{\theta(1-\theta)^7}{0.5^8} \tag{10.1}$$

We could then build up a LOD score table:

```r
library(pander)
library(ggplot2)
LOD <- function(theta) {log10((1/0.5^8)*theta*(1-theta)^7)}
thetas <- seq(0,0.5,0.05)
df <- data.frame(Theta=thetas,LODscore=NA)
for (i in 1:length(thetas) ) {
  df$LODscore[i] <- LOD(thetas[i])
}
pander(df)
```

Theta	LODscore
0	-Inf
0.05	0.9513
0.1	1.088
0.15	1.09
0.2	1.031
0.25	0.9316
0.3	0.801
0.35	0.6427
0.4	0.4574
0.45	0.244
0.5	0

```
ggplot(data=df,aes(x=Theta,y=LODscore)) + geom_line()
```



These results indicate that the LOD score takes its maximum at a value of theta (θ) that lies somewhere between 0.10 and 0.15.

We can find the maximum likelihood estimator of θ by using a much finer grid of theta values, or by using a numerical search, or by taking the derivative of the LOD score function with respect to θ, setting it to zero, and solving for θ.

R's Non-Linear Minimization `nlm` function can be used to do a numerical search, but it searches for a minimum of the function, not a maximum, so to use it, we need to define a different function that computes the negative of the LOD score:

```
negLOD <- function(theta) {
  -1*LOD(theta)
}
results <- nlm(negLOD,p=0.05)
```

```
Warning in LOD(theta): NaNs produced
```

```
Warning in nlm(negLOD, p = 0.05): NA/Inf replaced by maximum positive value
```

```
unlist(results)
```

```
      minimum      estimate      gradient          code    iterations 
-1.099206e+00  1.249995e-01 -2.653433e-07  1.000000e+00  6.000000e+00 
```

So our maximum likelihood estimate $\hat{\theta}$ is 0.1249995.

If we use the derivative approach, we'll find that the exact MLE $\hat{\theta}$ is the number of recombinants over the total number of children:

$$\hat{\theta} = 1/8 = 0.1250 \tag{10.2}$$

At this value of θ, the LOD score takes on its maximum value which is:

```
LOD(1/8)
```

```
[1] 1.099206
```

11 Summary

In summary, this book is a work in progress.

References

A Technical Details

A.1 Quarto

This book was build using Quarto.

A.1.1 Callout blocks

To hide a solution that then can be clicked to view, we use a `.callout-tip collapse="true"` callout block.

Here are some examples from the Quarto documentation:

> Note
>
> Note that there are five types of callouts, including: `note`, `tip`, `warning`, `caution`, and `important`.

> Warning
>
> Callouts provide a simple way to attract attention, for example, to this warning.

> This is Important
>
> Danger, callouts will really improve your writing.

> Tip With Title
>
> This is an example of a callout with a title.

> Expand To Learn About Collapse
>
> This is an example of a 'collapsed' caution callout that can be expanded by the user. You can use `collapse="true"` to collapse it by default or `collapse="false"` to make a collapsible callout that is expanded by default.

A.1.2 Adding a chapter

To add a new chapter to the book, make a Quarto file containing the chapter text and code. It should have only one top-level header at the beginning which will be the title of the chapter.

Then add it to the list of chapters in the `_quarto.yml` file.

A.2 Previewing the book

Type `quarto preview` in the Terminal window.

A.3 Deploying the book to GitHub Pages

Type `quarto publish` in the Terminal window.

A.4 Deploying the book to Netlify

Type `quarto publish netlify` in the Terminal window.

A.5 Multiple choice questions

To create multiple choice questions, use functions from the `webexercises` R package.

At installation, first do `add_to_quarto()` to add the needed files and setup to include webexercises in a quarto project.

The multiple choice question below is created by the inline R code

```
r longmcq(opts_ci)
```

What is true about a 95% confidence interval of the mean?

```
opts_ci <- c(
  answer = "If you repeated the process many times, 95% of intervals calculated in this wa
  "There is a 95% probability that the true mean lies within this range",
  "Approximately 95% of the data fall within this range"
)
```

- (A) If you repeated the process many times, 95% of intervals calculated in this way contain the true mean

- (B) There is a 95% probability that the true mean lies within this range

- (C) Approximately 95% of the data fall within this range

A.6 WebR: R in the browser

This Quarto book uses this WebR Quarto extension

https://github.com/coatless/quarto-webr

WebR makes installs a version of R that runs within the browser, and the Quarto extension makes it interactively available in `webr-r` chunks.

```
# Edit/add/try out R code here
```

To get this to work, the `_quarto.yml` had to be modified.

We added a 'resources' directive to copy over the java script files, which places them next to the 'index.html' file during deployment of the book:

```
project:
  type: book
  resources:
    - "webr-serviceworker.js"
    - "webr-worker.js"
```

We also enabled the `webr` filter:

```
filters:
    - webr
```

A.7 embedpdf Quarto extension

This book uses the `embedpdf` Quarto extension from https://github.com/jmgirard/embedpdf, which was installed via this command:

```
quarto add jmgirard/embedpdf
```

To embed a PDF, use code like this:

```
{{< pdf dummy.pdf width=100% height=800 >}}
```

However, the PDF embedding done this way did not work in Chrome.

Example:

So instead we used an iframe, which works on Chrome, Firefox, and Safari:

```
 <iframe width="100%" height="800" src="pdfs/GitHubIntro.pdf">
```

Note that for iframe embedding of Panopto video from the University of Pittsburgh, one needs to use a credentialless iframe.

B WebR - R in the web browser

This is a WebR-enabled code cell in a Quarto HTML document. As the WebR documentation states: “WebR makes it possible to run R code in the browser without the need for an R server to execute the code: the R interpreter runs directly on the user’s machine.”

```
# Edit/add code here
fit = lm(mpg ~ am, data = mtcars)
summary(fit)
library(ggplot2)
ggplot(mtcars, aes(x=am,y=mpg)) +
   geom_point() +
   geom_smooth(method="lm")
```

B.1 Link: WebR and `quarto-webr`.