

Preface

This text is a result of many semesters of teaching introductory statistical courses to engineering students at Duke University and the Georgia Institute of Technology. Through its scope and depth of coverage, the text addresses the needs of the vibrant and rapidly growing engineering fields, bioengineering and biomedical engineering, while implementing software that engineers are familiar with.

There are many good introductory statistics books for engineers on the market, as well as many good introductory biostatistics books. This text is an attempt to put the two together as a single textbook heavily oriented to computation and hands-on approaches. For example, the aspects of disease and device testing, sensitivity, specificity and ROC curves, epidemiological risk theory, survival analysis, and logistic and Poisson regressions are not typical topics for an introductory engineering statistics text. On the other hand, the books in biostatistics are not particularly challenging for the level of computational sophistication that engineering students possess.

The approach enforced in this text avoids the use of mainstream statistical packages in which the procedures are often black-boxed. Rather, the students are expected to code the procedures on their own. The results may not be as flashy as they would be if the specialized packages were used, but the student will go through the process and understand each step of the program. The computational support for this text is the MATLAB[®] programming environment since this software is predominant in the engineering communities. For instance, Georgia Tech has developed a practical introductory course in computing for engineers (CS1371 – Computing for Engineers) that relies on MATLAB. Over 1,000 students take this class per semester as it is a requirement for all engineering students and a prerequisite for many upper-level courses.

In addition to the synergy of engineering and biostatistical approaches, the novelty of this book is in the substantial coverage of Bayesian approaches to statistical inference.




I avoided taking sides on the traditional (classical, frequentist) vs. Bayesian approach; it was my goal to expose students to both approaches. It is undeniable that classical statistics is overwhelmingly used in conducting and reporting inference among practitioners, and that Bayesian statistics is gaining in popularity, acceptance, and usage (FDA, Guidance for the Use of Bayesian Statistics in Medical Device Clinical Trials, 5 February 2010). Many examples in this text are solved using both the traditional and Bayesian methods, and the results are compared and commented upon.


This diversification is made possible by advances in Bayesian computation and the availability of the free software WinBUGS that provides painless computational support for Bayesian solutions. WinBUGS and MATLAB communicate well due to the free interface software MATBUGS. The book also relies on `stat` toolbox within MATLAB.

The World Wide Web (WWW) facilitates the text. All custom-made MATLAB and WinBUGS programs (compatible with MATLAB 7.12 (2011a) and WinBUGS 1.4.3 or OpenBUGS 3.2.1) as well as data sets used in this book are available on the Web:


<http://springer.bme.gatech.edu/>

To keep the text as lean as possible, solutions and hints to the majority of exercises can be found on the book's Web site. The computer scripts and examples are an integral part of the text, and all MATLAB codes and outputs are shown in **blue typewriter font** while all WinBUGS programs are given in **red-brown typewriter font**. The comments in MATLAB and WinBUGS codes are presented in **green typewriter font**.

The three icons , , and  are used to point to data sets, MATLAB codes, and WinBUGS codes, respectively.

The difficulty of the material in the text necessarily varies. More difficult sections that may be omitted in the basic coverage are denoted by a star, *. However, it is my experience that advanced undergraduate bioengineering students affiliated with school research labs need and use the “starred” material, such as functional ANOVA, variance stabilizing transforms, and nested experimental designs, to name just a few. Tricky or difficult places are marked with Donald Knut’s “bend” .

Each chapter starts with a box titled WHAT IS COVERED IN THIS CHAPTER and ends with chapter exercises, a box called MATLAB AND WINBUGS FILES AND DATA SETS USED IN THIS CHAPTER, and chapter references.

The examples are numbered and the end of each example is marked with .

I am aware that this work is not perfect and that many improvements could be made with respect to both exposition and coverage. Thus, I would welcome any criticism and pointers from readers as to how this book could be improved.

Acknowledgments. I am indebted to many students and colleagues who commented on various drafts of the book. In particular I am grateful to colleagues from the Department of Biomedical Engineering at the Georgia Institute of Technology and Emory University and their undergraduate and graduate advisees/researchers who contributed with real-life examples and exercises from their research labs.

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The book benefited from the input of many diligent students when it was used either as a supplemental reading or later as a draft textbook for a semester-long course at Georgia Tech: BMED2400 Introduction to Bioengineering Statistics. A complete list of students who provided useful comments would be quite long, but the most diligent ones were Erin Hamilton, Kiersten Petersen, David Dreyfus, Jessica Kanter, Radu Reit, Amoreth Gozo, Nader Aboujamous, and Allison Chan.

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