

# STAT 474/574 Biostatistics, Spring 2017

Lecturer: James Degnan

Office: SMLC 342

Office hours: MW 12:00-1:00 or by appointment

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**Please include STAT474 or STAT574 in the subject line of the email to make sure I don't overlook your email.**

Textbook: *Survival Analysis Techniques for Censored and Truncated Data* 2nd edition, by John P. Klein and Melvin L. Moeschberger

Assessment: Grading will be based homework (roughly 5 assignments in the semester) (40%), three in-class tests (20% each).

We will mostly use R for computing in class. Solutions to homework can be done in any software package, but it will be easier for me to grade and give partial credit for homework done in R.

## Homework

For turning in computer-based homework, **turn in all computer code used as an appendix only. Do not include computer code as part of your solutions.** Figures and tables can be generated from computer output, but solutions must be discussed separately from the output, and the results in the Figures and Tables should be cited in the homework solutions. This will be discussed further in class.

Late homework will be penalized 10% per day. All homework must be printed (not emailed) and turned in either in class or to my office. Sliding homework under the office door is acceptable.

## Disability statement

If you have a documented disability that will impact your work in this class, please contact me to discuss your needs. Youll also need to register with the Accessibility Resource Center in 2021 Mesa Vista Hall (building 56) across the

courtyard east from the SUB.

## Learning outcomes

We'll cover mostly topics from the listed book, with additional topics from biostatistics toward the end of the class. Items may include (but won't be limited to):

- Survival functions (and relationship to CDF)
- Hazard functions
- Censoring
- Maximum Likelihood estimation of the survival function
- Nonparametric estimation (particularly Kapan-Meier)
- Proportional Hazards models
- Genome-Wide Association tests
- Multiple testing issues and false discovery rates

By the end of the class, the goal is that you will be able to:

- identify the type of censoring used in a study (e.g., left versus right-censoring)
- analyze survival data using nonparametric and parametric methods using software
- formulate an appropriate model for particular survival problems
- interpret survival and hazard functions
- formulate and test hypotheses appropriate for survival data
- explain the difference between controlling for type I error and controlling the false discovery rate
- apply different mutliple testing procedures
- interpret results of genome-wide association studies
- interpret and summarize research papers using techniques discussed in class