

**MthSc 985: Topics in discrete mathematical biology**  
**Fall Semester 2011**  
**Time: MWF 8:00-8:50am**  
**Location: Martin M-301**

**General information**

Instructor: Matt Macauley  
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Office: Martin O-325  
Office hours: (subject to change!) MWF 3:30–4:30 and by appointment  
Text: *Combinatorial Computational Biology of RNA: Pseudoknots and Neutral Networks*, by Christian Reidys.  
Web: I will post course material on my website and/or Blackboard.

**Learning Outcomes**

Finding good research problems is a challenge, even for the most experienced mathematicians. The course represents an introduction to a new active research area in the theory of RNA pseudoknot structures, in a non-traditional class setting. The author of our book, Christian Reidys, pioneered this subfield within the last decade and has carved a niche. In the process, he was honored as a Chang Jiang Scholar, the Chinese national research prize in mathematics. Reidys has written over fifty research articles on this topic with his collaborators (including 7 PhD students) at the Center for Combinatorics, at Nankai University. Reidys has written a book on this research, aimed at researchers and graduates students who are interested in learning about computational biology, RNA structures, and mathematics. The goal of this class is to learn about this new and exciting field.

The content of this research area is truly transdisciplinary, and draws from all five subfaculty research areas in the mathematical science department at Clemson. That said, *no one* (instructor included) will be fully prepared in terms of having a solid grasp on all of the prerequisites. However, the unique aspect is that the Clemson graduates students, who are required to take multiple courses in all five subfaculty areas, will have a more diverse and well-rounded background than any of the Clemson faculty! Examples of how various mathematical aspects of this research fall into the five subfaculty areas is given below:

**Algebra & Discrete Math:** Enumerative combinatorics, graph theory, group actions and Weyl groups.

**Analysis:** Singularity analysis, differential equations for generating functions.

**Computation:** Algorithm design, thermodynamic models for RNA pseudoknot structures.

**Operations Research:** Maximum weighted matching algorithms, dynamic programming.

**Probability & Statistics** Branching processes, central limit theorems for arcs in k-noncrossing structures.

We will take advantage of the diversity of the mathematical background and strengths of the students taking this class. *This course is not intended to be one faculty member teaching twelve graduate students, but rather, thirteen mathematicians with various backgrounds coming together to learn a new area of research.* As with any young field, there are surely many unexplored areas, loose ends, and good future research problems that we can discover, and one of our goals is to find and propose these problems. Everyone in this class will write a self-contained *research proposal*, that they could conceivably give to an incoming masters student or advanced undergraduate looking for a research project. Students will present their proposal in class, and are encouraged to pursue any research problems they find interesting. In addition, there will be a few (reasonable) homework assignments, because at this point in our careers, we all understand that it is simply not possible to truly learn mathematics by just watching and not doing.

This course is suitable for students who have a basic foundation at the undergraduate level in abstract algebra, complex analysis, differential equations, and probability theory (though a deficiency in one of these is not a problem). After successfully completing this course, a student will have knowledge of how discrete mathematical techniques have been applied to the field of biology, the challenges that still exist, and areas of active research. Though the plan is to spend the whole semester studying the combinatorics and computational biology of RNA, we may decide together that we have reached a natural stopping point, and move onto another topic in discrete mathematical biology, such as discrete modeling of biological networks, which is an active research area of several Clemson faculty members.

## Grading

Final grades will be determined by the following rubric:

Homework	20%
Midterm	15%
Participation	10%
Quizzes	10%
Research proposal	25%
Final exam	20%

## Attendance

Attendance is mandatory, and class participation (part of which is attendance) is 10% of your final grade. If you cannot make a class, please let the instructor know why. Student may leave if an instructor or guest lecturer does not show up after 10 minutes.

## **Laptops, cell phones, PDAs**

All use of cell phones, and typing on laptops is prohibited during lecture. Calculators, cell phones, laptops, and PDAs will not allowed during exams.

## **Academic integrity**

As members of the Clemson University community, we have inherited Thomas Green Clemson's vision of this institution as a high seminary of learning. Fundamental to this vision is a mutual commitment to truthfulness, honor and responsibility, As members of the Clemson University community, we have inherited Thomas Green Clemson's vision of this institution as a high seminary of learning. Fundamental to this vision is a mutual commitment to truthfulness, honor and responsibility, without which we cannot earn the trust and respect of others. Furthermore, we recognize that academic dishonesty detracts from the value of a Clemson degree. Therefore, we shall not tolerate lying, cheating, or stealing in any form."