



UNC  
GLOBAL

January 20, 2016

Administrative Board of the College of Arts and Sciences  
Office of General Education  
UNC-CH

Dear Colleagues,

### **UNC-Chapel Hill Summer Science program in Grenoble, BIOL 202**

The Department of Biology and the Study Abroad Office are seeking your approval to add a Biology course (BIOL 202) to the already existing UNC-CH Summer Science program in Grenoble. This program is a joint collaboration between the Joseph Fourier University (UJF) in Grenoble and UNC-CH. University Joseph Fourier currently offers a summer program with courses taught in English; one UNC course (CHEM 430), taught by a UNC faculty member, is in its second year. In the summer 2014, 16 UNC-CH students were on the CHEM 430 program and 18 UNC-CH students were enrolled for summer 2015. We now wish to add BIOL 202 to the present curriculum, starting summer 2017.

More information on the current UJF summer program can be found at the link below although it is important to note that the CHEM 430 is not mentioned here since we do not seek to recruit students from all over the world. The French students who join the course are selected by UJF.

<http://www.ujf-grenoble.fr/international/bachelor-summer-program>

#### *Rationale*

This program would extend the collaboration between these two universities under the existing MOU with the University of Grenoble. There is already a semester and year-long exchange in place and we have sent a number of semester and one year long student to UJF in Grenoble. This program contributes to our objective of offering more programs to science students, will follow the pattern of the current CHEM 430 program and we believe UNC-CH students will benefit from taking such a course in an international setting where they will be mingling with other French and international students. Lynn Neddo has visited the University in Grenoble on a number of occasions and Dr. Bob Miles recently completed a site visit as well.

#### *Description*

The UNC-CH Summer Science in Grenoble program is a six-week science and French language program. Students will take the UNC-CH faculty taught biology course as well as a French language course. Currently, along with the UNC-CH CHEM 430 course, there are two other science courses (Engineering: Introduction of Physical Computing; and Physics: Introduction to Large Scale Facilities) that are taught by University Joseph Fourier (UJF) professors. These courses are taught in English and are open to regular UJF students as well as international students. We expect that (as with the CHEM 430 course) at least two French students will take the course along with UNC students. The UNC-CH course would be open to other UNC system students (if needed to make the program financially viable), and also to a small number of UJF students.

### *Courses and Faculty*

All UNC-CH students will be registered for *BIOL 202: Molecular Biology and Genetics* (4 credits) taught in English by a UNC-CH faculty member. This course is part of the required curriculum for Biology and Chemistry students. Students will also take a French language course (3 credits) at the appropriate level based on a language test taken on arrival. Students with no prior French language will take the Elementary French course. These French courses, although language courses, also introduce students to local civilization and culture. Students also participate on a number of planned and guided excursions in the area.

### *Academic Requirements and Credit*

UNC students participating in this program will need to have a 2.7 GPA to be eligible and have completed their first year in order to apply for the program. There will be no language requirement. The UNC taught biology course will be awarded graded credit and thus the grade will be incorporated into the student's GPA. The French language course will receive TREQ credit and the student will need at least a grade of C in order for credit to transfer. The prerequisites are BIOL 101, CHEM 101 and CHEM 102. Students will receive 7 UNC credits in total.

An example of a course syllabus and faculty CV are attached in Appendices. This syllabus is for a semester course and is provided to give an overview of the course content.

### *Logistics, Health and Safety*

#### Facilities

This program will be offered on the campus of UJF, at the University of Grenoble, which is located on the outskirts of the city. It is easily reached by public transportation (both bus and tram) and students are often seen biking to campus.

#### Housing

Students will reside in a university residence arranged by UJF's international office.

Other activities

Summer is a wonderful time to be in Grenoble. There are planned cultural excursions, several festivals and opportunities to go hiking in the Alps.

Health and Safety

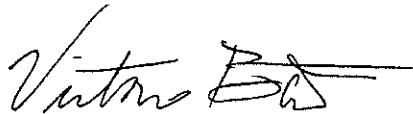
In France, health coverage is mandatory. Students are covered by UNC-Chapel Hill's insurance company, HTH. The University has an Inter-University Health Center which gives access to many free services including reception services, consultations and preventive medicine in the areas of general medicine, nursing care, gynecology, psychology, diet and nutrition, tobacco addiction, disabilities, etc.

The U.S. Department of State considers France as a developed and stable democracy with a modern economy. Tourist facilities are widely available. Information is routinely shared between the United States and France in order to disrupt terrorist plotting, identify and take action against potential operatives, and strengthen our defenses against potential threats.

*Conclusion*

We hope this proposal has given a clear representation of the Summer Science program in Grenoble. We are enthusiastic about the opportunity this will give UNC-Chapel Hill science students to participate on a program where they will be able to receive credit for a required course in an international setting. We are happy to provide you with any additional information you might need to aid in your evaluations of this proposal.

Sincerely,



02/05/16

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Dr. Victoria Bautch, Professor and Chair, Department of Biology

Date



2.10.16

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Dr. Robert Miles, Associate Dean: Study Abroad and International Exchanges

Date

Appendices: Course syllabus and faculty CV

BIOL 202  
Molecular Biology & Genetics  
Alain Laederach  
alain@unc.edu

Class Lectures: M,T,W,Th: 9:50-11:30  
Recitations: M & W 11:40-13:00

Prerequisites

BIOL 101 and CHEM 101, with a grade of C or better

Goals of the course

1. To provide you with the core principles of genetics and molecular biology
2. To gain higher level thinking skills
3. To gain a better understanding of human genetics and its impact on phenotype

## Course Learning Outcomes

Upon completion of the 202 course in Biology, a student should be able to:

(Skills):

- Build hypotheses to answer a specific scientific question, design an experiment using an appropriate technique/assay to answer the question, and predict results of their experiment.
- Give examples of how advances in genetics and molecular biology, from the discovery of DNA's structure to sequencing individual genomes, have changed the world (examples include recombinant insulin, personalized medicine, transgenic crops)

(Concepts):

- Explain the term "allele" for a single gene at a population, organismal, cellular, and molecular level; explain how dominance and recessiveness are expressed at these levels.
- Explain how genetic variation comes from in a population (e.g. from meiosis, mutation, and epigenetic changes).
- Predict genotypic and phenotypic ratios of offspring in defined genetic crosses and work these problems in reverse (when given data about offspring, determine the genotypes and phenotypes of the parents).
- Deduce modes of inheritance (example: autosomal dominance, x-linked recessive) from genetic pedigrees and explain how incomplete penetrance and variable expressivity complicate these analyses.
- Distinguish single gene traits from polygenic traits and the influence of the environment on traits.
- Explain how DNA is replicated normally and abnormally and how these concepts are utilized in the polymerase chain reaction (PCR).
- Compare and contrast the consequences of germline errors during meiosis (such as non-disjunction, and translocations) and somatic errors during abnormal mitosis (such as non-disjunction and cancer)
- Explain the flow of genetic information, based on the central dogma- from DNA to proteins and how mutations are carried through this flow of information.
- Describe the nature of the genetic code
- Describe the general organization of prokaryotic and eukaryotic genomes, including the identification and significance of the different parts of a gene (e.g. regulatory/non-regulatory, exons/introns; transcription start site; translation start site; UTRs)
- Explain how a gene can be regulated transcriptionally and post-transcriptionally and how this leads to limited expression under different conditions (such as in different environments, during the course of development, or disease conditions)
- Predict the outcome of experimental manipulations in genes (e.g. GFP-tagging to investigate gene expression)
- Describe the basic steps in gene cloning (restriction, ligation, etc.)
- Design a transgenic animal/bacteria, where a protein of interest is specifically produced
- Explain the significance of research in genetic model organisms to understand fundamental biological phenomena.

## Expectations

The course is composed of four class meeting and two recitation sessions each week. This is NOT a class for passive learners. You are expected to be actively engaged in this course

through class discussions, class activities and pre- as well as post-lecture assignments and readings.

It is expected that you will spend several hours reading/working problems associated with each class. If you stay on top of your reading and homework, there will be no need to cram for an exam. Practice, practice, practice. Do problems that are assigned and then do others that are not assigned! Use the internet or other textbooks in the library to find more problems if you run out from your textbook.

### Textbook

Klug et al.: Essentials of Genetics 8<sup>th</sup> Edition

The textbook is available in the bookstore. This text comes with a web-based software package called MasteringGenetics that will be the medium through which you will be quizzed and receive short pre-lecture and post-lecture assignments. The package also includes an interactive eBook. There are also other purchase options of the textbook (e.g. you can buy a used textbook and a stand-alone MasteringGenetics package). For a detailed description of all the purchase options, please check Sakai under "Syllabus"

### Recitations

During recitations, the Professor will lead you through activities or problem solving practices. This course is a 4 credit hours course, and the recitations are not simply "going over the material that was learned in class", but rather a core component of the course. Some of the material covered in recitations will be supplemental to the one discussed in class. There will be no make-up opportunities for in-class assignments if you do not attend a recitation.

### Class and Recitations Attendance

Students are expected to attend and participate in class meetings and recitations. While the course follows the textbook, some of the material discussed in lecture may not be found in the text. You are responsible for all material and announcements made in lectures. You are not responsible for material that was not covered in class, unless it was specifically assigned (see detailed schedule for assigned readings).

## Assignments

During the summer session you will have pre-class, in-class, and post-class assignments.

- The pre-class assignments will be based on assigned readings from the textbook. The assignments will be given via the MasteringGenetics system (see above).
- In-class assignments will include Polleverywhere (see below) and other activities.
- Post-class assignments will include assigned homework problem sets, MasteringGenetics, and occasionally Peerwise assignments (see below).

All assignments due dates appear on the detailed schedule. Updates will be announced on Sakai. You are responsible for submitting the assignments on time. There will be no "second chances" in this case.

## Polleverywhere

In this class you will use a polling system to answer questions that we pose during class. You can submit your responses using a laptop or other mobile device with a WiFi connection, such as an iPod Touch or an iPad. Before you can participate, you'll need to create an account. For instructions on how to register to Polleverywhere, please follow the guidelines found on Sakai under the Resources folder.

## PeerWise

One of your assignments during the summer session will be to create multiple choice questions that address the material we learn. Asking questions and evaluate your peers' questions has been shown to be an invaluable tool in developing deep learning. Posting and reviewing questions will be done through an interactive system called PeerWise. Instructions on how to register and how to use PeerWise will be given during the summer session

## Grading

The material taught in class meetings and labs will be tested separately but the grades are combined for the final course grade. Your grade for this course will be determined as follows:

3 midterm exams = (21% each = 63%)

1 semi-cumulative final exam (21%)

MasteringGenetics assignments (6%)

Recitations (10%)

Grades will not be assigned for individual exams, only points; you will be able to see how you did from a posted distribution of scores after each test. Final grades will be assigned on the total number of points for the entire summer session: A 93-100; A- 90-92; B+ 87-89; B 83-86; B- 80-82; C+ 77-79; C 73-76; C- 70-72; D+ 66-69; D 60-65; F <60

A curve will be used ONLY if the class grade average is <75. Exam questions will be taken from class meetings and assigned readings. Exams must be taken on the dates indicated; no makeup exams except in special circumstances, i.e. medical or family emergency documented in writing.

THE PROFESSOR RESERVES THE RIGHT TO MAKE CHANGES TO THE SYLLABUS, INCLUDING PROJECT DUE DATES AND TEST DATES. THESE CHANGES WILL BE ANNOUNCED AS EARLY AS POSSIBLE

Schedule For a detailed schedule, including assigned readings, assignments, recommended readings, and objectives, check the lecture schedule under the Sakai "Syllabus" folder

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| Topics and exams:   |
| Structure and function of genes and genomes   |
| Genetic variation – from genotype to phenotype  |
| DNA replication   |
| Genetic variation arises by mutation  |
| Genetic variation arises by chromosomal rearrangements                                |
| Gene dosage   |
| Exam I (Lectures 1-6)   |
| Personal genomics   |
| The flow of genetic information - Transcription                                       |
| Gene expression – The making of a transcript  |
| Gene expression – Translation and the nature of the genetic code                      |
| Revisiting alleles and mutations  |
| Exam II (Lectures 9-14)   |
| Regulation of gene expression in prokaryotes I  |
| Regulation of gene expression in prokaryotes II                                       |
| Regulation of gene expression in eukaryotes I   |
| Regulation of gene expression in eukaryotes II – Epigenetics and alternative splicing |
| Regulation of gene expression in eukaryotes III - miRNAs                              |
| Exam III (Lectures 16-20)   |
| Recombinant DNA technology I  |
| Recombinant DNA technology II   |
| How genes affect phenotypes – transmission genetics I                                 |
| Gene interactions   |
| Pedigrees   |



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| Molecular genetics of Cancer |
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| Cumulative Final Exam (9:00-12:00) |
|------------------------------------|

February 2, 2016

### **a) Personal**

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Associate Professor  
Biology Department  
University of North Carolina, Chapel Hill  
Chapel Hill, NC 27599  
[alain@unc.edu](mailto:alain@unc.edu)  
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### **b) Education**

1999-2003 **Iowa State University**, (ISU) Ph.D. Bioinformatics and  
Computational biology program and Chemical Engineering Department, (Amy  
Andreotti and Peter Reilly, PI).

1993-1998 **EPFL (Swiss Federal Institute of Technology), Lausanne**, B.Sc.  
Chemical Engineering

1993 **Washington International School**, International Baccalaureate

### **c) Professional Experience**

01/2011- present **University of North Carolina, Chapel Hill**,  
Assistant Professor, Biology Department (3 years, 4 months).

04/2008-12/2010 **University at Albany/Wadsworth Center**,  
Assistant Professor, Department of Biomedical Sciences (2 years 9  
months)

08/2003-03/2008 **Stanford University**, Post-Doctoral Fellow,  
Department of Genetics (4 years, 7 months)

09/1999-05/2003 **Iowa State University**, Graduate Student Assistant,  
Department of Bioinformatics and Computational Biology (3 years, 9  
months)

### **d) Honors**

2004-2007 **Damon Runyon Cancer Research Foundation** fellow,  
"Elucidating the molecular mechanisms of RNA folding: a combined modeling  
and experimental study".

1999-2002 **National Science Foundation (USA)** IGERT fellow in  
bioinformatics is a full three-year graduate scholarship including stipend.

2003 **Zaffarano Prize** for Graduate Research ISU top honor for graduate  
student research awarded based for the most distinguished publication record.

## **e) Bibliography and products of scholarship**

### *Refereed Publications*

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50. Solem A, Laederach A. (2015) RNA folding: A clear path to RNA catalysis. *Nat Chem Biol.* Nov 17;11(12):906-8.
49. Lackey L, McArthur E, Laederach A. Increased Transcript Complexity in Genes Associated with Chronic Obstructive Pulmonary Disease. (2015) *PLoS One.* Oct 19;10(10):e0140885.
48. Blanco MR, Martin JS, Kahlscheuer ML, Krishnan R, Abelson J, Laederach A, Walter NG. (2015) Single Molecule Cluster Analysis dissects splicing pathway conformational dynamics. *Nat Methods.* Nov;12(11):1077-84.
47. Solem AC, Halvorsen M, Ramos SB, Laederach A. (2015) The potential of the riboSNitch in personalized medicine. *Wiley Interdiscip Rev RNA.* Sep-Oct;6(5):517-32.
46. Kutchko KM, Sanders W, Ziehr B, Phillips G, Solem A, Halvorsen M, Weeks KM, Moorman N, Laederach A. (2015) Multiple conformations are a conserved and regulatory feature of the RB1 5' UTR. *RNA.* Jul;21(7):1274-85.
45. Corley M, Solem A, Qu k, Chang H, Laederach A. (2015) Detecting riboSNitches with RNA folding algorithms: A genome-wide benchmark. *Nucleic Acids Res.* Feb 18;43(3):1859-68.
44. Ramos SB, Laederach A. (2014) Molecular biology: A second layer of information in RNA. *Nature.* 505(7485): 621-2.
43. Schlatterer JC, Martin JS, Laederach A, Brenowitz M. (2014) Mapping the kinetic barriers of a Large RNA molecule's folding landscape. *PLoS One.* 9(2):e85041.
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41. Ritz J, Martin JS, Laederach A. Evolutionary evidence for alternative structure in RNA sequence co-variation. (2013) *PLoS Comput Biol.* 2013;9(7):e1003152.

40. Chen C, Mitra S, Jonikas M, Martin J, Brenowitz M, Laederach A. Understanding the role of three-dimensional topology in determining the folding intermediates of group I introns. *Biophys J*. 2013 Mar 19;104(6):1326-37.
39. Ritz J, Martin JS, Laederach A. (2012) Evaluating our ability to predict the structural disruption of RNA by SNPs. *BMC Genomics*. 13 (Suppl 4):S6 (06/18).
38. Sansone SA, Rocca-Serra P, Field D, Maguire E, Taylor C, Hofmann O, Fang H, Neumann S, Tong W, Amaral-Zettler L, Begley K, Booth T, Bougueleret L, Burns G, Chapman B, Clark T, Coleman LA, Copeland J, Das S, de Daruvar A, de Matos P, Dix I, Edmunds S, Evelo CT, Forster MJ, Gaudet P, Gilbert J, Goble C, Griffin JL, Jacob D, Kleinjans J, Harland L, Haug K, Hermjakob H, Ho Sui SJ, Laederach A, *et al.* (2012) Toward interoperable bioscience data. *Nat Genet*. 2012 Jan 27;44(2):121-6.
37. Martin JS, Halvorsen M, Davis-Neulander L, Ritz J, Gopinath C, Beauregard A, Laederach A. (2012) Structural effects of linkage disequilibrium on the transcriptome. *RNA*. Jan;18(1):77-87.
36. Pelleymounter LL, Moon I, Johnson JA, Laederach A, Halvorsen M, Eckloff B, Abo R, Rossetti S. (2011) A novel application of pattern recognition for accurate SNP and indel discovery from high-throughput data: targeted resequencing of the glucocorticoid receptor co-chaperone FKBP5 in a Caucasian population. *Mol Genet Metab*. 2011 Dec;104(4):457-69.
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32. Sanders, W. and Laederach A. (2011) Membrane RNAs in bacteria. *Mol. Microbiol*. 79(1) 1-2.
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27. Simmons K., Shcherbakova I., Martin J., Laederach A. Rapid quantification and analysis of kinetic •OH radical footprinting data using SAFA. (2009) *Methods in Enzymology*, 468, 47-66.
26. Martin J., Simmons K., Laederach A. Exhaustive enumeration of kinetic model topologies for the analysis of time-resolved RNA folding. (2009) *Algorithms*, 2, 200-214
25. Shcherbakova I., Mitra S., Laederach A., Brenowitz M. (2009) Energy barriers, pathways, and dynamics during folding of large, multidomain RNAs. *Curr. Opin. Chem Biol.* 12(6) 655-666.
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23. Mitra S, Shcherbakova IV, Altman RB, Brenowitz M, Laederach A. (2008) High-throughput single-nucleotide structural mapping by capillary automated footprinting analysis. *NAR*, 36(11):e63.
22. Laederach A, Das R, Vicens Q, Pearlman SM, Brenowitz M, Herschlag D, Altman RB. (2008) Semiautomated and rapid quantification of nucleic acid footprinting and structure mapping experiments. *Nat Protoc.* 3(9):1395-401.
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11. Aikens C.L., Laederach A. & Reilly P. J. (2004) Visualizing complexes of phospholipids with *Streptomyces* phospholipase D by automated docking. *Proteins* 1, 27-35.
10. Allen M.J., Laederach A., Reilly P. J., Mason R.J. & Voelker D.R. (2004) Arg343 in human surfactant protein D governs discrimination between glucose and N-acetylglucosamine ligands. *Glycobiology* 14, 693-700.
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8. Laederach, A., Cradic, K. W., Fulton, D. B. & Andreotti, A. H. (2003). Determinants of intra versus intermolecular self-association within the regulatory domains of Rlk and Itk. *J Mol Biol* 329, 1011-1020.
7. Laederach, A. & Reilly, P. J. (2003). Specific empirical free energy function for automated docking of carbohydrates to proteins. *J Comput Chem* 24, 1748-1757.
6. Laederach, A., Andreotti, A. H. & Fulton, D. B. (2002). Solution and micelle-bound structures of tachyplesin I and its active aromatic linear derivatives. *Biochemistry* 41, 12359-12368.

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2. Rockey, W. M., Laederach, A. & Reilly, P. J. (2000). Automated docking of  $\alpha$ -(1 $\rightarrow$ 4)- and  $\alpha$ -(1 $\rightarrow$ 6)-linked glucosyl trisaccharides and maltopentaose into the soybean beta-amylase active site. *Proteins* 40, 299-309.  
Laederach, A., Dowd, M. K., Coutinho, P. M. & Reilly, P. J. (1999). Automated docking of maltose, 2-deoxymaltose, and maltotetraose into the soybean  $\beta$ -amylase active site. *Proteins* 37, 166-175.
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### *Invited Presentations*

July 2015 Invited Speaker, Benasque Computational RNA meeting, Benasque, Spain.

Oct. 2014 Invited Seminar Speaker, Carnegie Mellon University, Biology Department and Computational Biology Program Seminar Series

Dec. 2013 Invited Seminar Speaker, UT Austin, Biochemistry Department seminar series

Sept. 2013 Invited Seminar Speaker, Purdue University, Biochemistry Department Seminar Series

Nov. 2012 Invited Speaker at "Nucleic Acids Zing Conference" Xcaret, Mexico  
"Genomics of structured RNAs and their role in human disease"

Oct. 2012 Invited Speaker at "GSB Opening Symposium" Chapel Hill, NC  
"Genomics of RNA and Disease"

Oct. 2012 Invited Speaker at "Computational Biology Seminar Series at Berkeley" Berkeley CA "Genomics of RNA, SNPs and Disease"

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- Oct. 2012 Invited Speaker at "Asilomar Conference on Signals and Processing," Asilomar, CA "Genomics of RNA and Disease"
- July 2012 Invited Speaker at "RNA Benasque" Conference, Benasque, Spain "Evaluating our ability to predict deleterious RNA SNPs"
- June 2012 Invited Speaker at "Nucleic Acid Enzymes" FASEB meeting, Snowmass Village, Colorado. "Genomics of RNA and Disease."
- April 2011 Invited Speaker, Barbados, Bellairs workshop on integrative approaches for modeling biological complexes (McGill University)
- March 2011 Invited Speaker, University of Rochester Biology, Department Seminar Speaker, "Disease associated mutations and RNA."
- Feb. 2011 Invited Speaker, University of Missouri, Biochemistry Department Seminar Speaker, "Disease associated mutations and RNA."
- Jan. 2011 Invited Speaker, Pacific Symposium on Biocomputing RNA Ontology Meeting, "Organizing SNRNASM data."
- Nov. 2010 Invited Speaker, CUNY Hunter, New York, Chemistry Department Seminar Speaker, "Disease associated mutations and RNA."
- July 2009 Invited Speaker: RNA Bioinformatics Workshop, Benasque, Spain, "Disease-associated mutations and their effect on RNA structure."
- March 2009 Invited Speaker, Williams College, Williamstown Ma., Physics Department. "The Physics and Kinetics of RNA folding"
- July 2008 Invited Speaker: RNA Ontology Consortium meeting, Berlin, Germany, "Chemical mapping nomenclature standardization."
- Sept. 2007 Invited Speaker: Boston College Mathematical Biology, Boston, Ma. "Kinetics of RNA Folding."
- June 2006 Ribosome Meeting, Cape Cod. Invited Speaker "Kinetic Assembly pathways of 16S rRNA."
- Nov. 2006 Invited Panelist: EAST Alliance in Science and Technology Conference, "Science, Technology, Engineering, and Mathematics Education."
- Sept. 2006 Invited Speaker: Gerhard Wagner lab, Harvard Medical School, Boston, Ma. "RNA Folding and Kinetics."
- June 2006 Invited Speaker: RNA Ontology Consortium meeting, Seattle, Wa. "Standardizing RNA experiment nomenclature."



## f) Teaching activities

### *Undergraduate Teaching*

Fall 2015 UNC-Chapel Hill, Biol 528L "Systems Biology of Genetic Regulation" 4 credit Qbio lab course, 19 undergraduate students registered.

Fall 2014 UNC-Chapel Hill, Biol 528L "Systems Biology of Genetic Regulation" 4 credit Qbio lab course, 22 undergraduate students registered.

Fall 2013 UNC-Chapel Hill, Biol 528L "Systems Biology of Genetic Regulation" 4 credit Qbio lab course, 16 undergraduate students registered.

Fall 2013 Peter Fan, Honors Carolina Contract Student Project

Fall 2013 Jay Zhang, Honors Carolina Contract Student Project

Fall 2012 UNC-Chapel Hill, Biol 528L "Systems Biology of Genetic Regulation" 4 credit Qbio lab course, 11 undergraduate students registered.

Fall 2011 UNC-Chapel Hill, Biol 527L "Systems Biology of Genetic Regulation" 4 credit Qbio lab course, 10 undergraduate students registered.

### *Undergraduate Research Mentorship*

2013-2014 Charles Czysz, Undergraduate Research (Biol 395) and summer intern, currently a graduate student in the BCB program at Univ. of Chicago.

2013-2014 Kevin Currin, Undergraduate Research (Biol 395) and summer intern, currently a UNC-PREP scholar.

2013 Emily Ajumobi, NIH E-MARC U-Star Summer Research fellow, currently a graduate student University of Washington, Health Informatics

2012-2013 Zack McCaw, Undergraduate Research (Biol 395) and summer intern, currently working at NIEHS.

2012-2013 Alex Smith, Undergraduate Research (Biol 395) and summer intern, currently a medical student at the University of Oklahoma

2011-2013 Chas Kissick, Undergraduate Research (Biol 395) and summer intern, currently working in an international biotech.

### *Graduate Student Mentorship*

2008-2013 Matt Halvorsen, Ph.D. BCB program, UNC-Chapel Hill, "Disease associated mutations and functional variants that significantly disrupt RNA structure," currently a post-doc at Duke University, David Goldstein Lab.

2012-2014 Wes Sanders, M.S. Biology, UNC-Chapel Hill, "Two Retinoblastoma associated Single Nucleotide Variants in RB1 form a RiboSNitch," currently working in UNC virology lab

2011-2012 Justin Ritz, M.S. Biostatistics, University of Albany, "Evolutionary Evidence for Alternative Structure in RNA Sequence Co-variation," currently statistical analyst, Harvard Medical School

2013- Katrina Kutchko, BCB Program, NSF graduate award fellowship recipient, "RNA structural elements as predictors of genetic regulation"

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2013- Chanin Tolson, BCB Program, "Visualization of the RNA structural ensemble and its thermodynamic consequences"

2013- Meredith Corley, BCB Program, "Allele-specific identification of RiboSNitches in high throughput sequencing data"

## **g) Grant Funding**

### *Awarded*

2015-2018 **NIH/NHGRI R01 Variation in Human Non-Coding Genomic Regions RFA-HG-13-013** "Predicting the causative SNPs in LD blocks by allele-specific structural analysis of the transcriptome" (P.I. Alain Laederach \$2,253,180, 25% Effort)

2012-2016 **NIH/NIGMS R01 Investigator Initiated PA**, "Structural and Functional Consequences of Disease SNPs in the Transcriptome," (P.I. Alain Laederach \$1,440,208, 25% Effort)

2012-2017 **NIH/NHLBI R01 Genetics of Pulmonary Disease RFA**, "Non-coding RNA structure change in Chronic Obstructive Pulmonary Disease," (P.I. Alain Laederach \$1,800,260, 30% Effort)

### *Completed*

2007-2013 **NIH/NIGMS K99/R00 Pathway to Independence Career Award**, "Multi-Scale Dynamic Modeling of RNA Folding and Assembly," (P.I. Alain Laederach \$833,454, 75% Effort).

2009-2011 **NIH/NIGMS R00 ARRA Administrative Supplement**, "Multi-Scale Dynamic Modeling of RNA Folding and Assembly," (P.I. Alain Laederach \$243,454, 10% Effort).

2009-2011 **NIH/NIMH R21 Genes, Environment Roadmap Initiative**, "Identifying Disease-Associated Mutations That Alter RNA Structure," (P.I. Alain Laederach \$470,718, 10% Effort).

## **h) Professional Service**

Nov. 2013 Co-chair of the "Bioinformatics and Computational Issues – RNA ontologies, databases, sequence analysis, annotations, structure prediction, and modeling." discussion at the NIGMS Workshop on RNA Structure, Function, and Targeting advisory council meeting.

Oct. 2013 Co-organizer North Carolina RNA Society biennial meeting, Tool and Target X, Chapel Hill North Carolina

June 2013 Organizer of "Tutorial on prediction of RNA secondary structure" at the 2013 annual meeting of the RNA society, Davos Switzerland.

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May 2012 Chair for “RNA-seq & computational structure prediction” Session at RNA 2012, Ann Arbor Michigan

June 2011 Chair for the “High-throughput methods” workshop at the 2011 RNA meeting in Kyoto, Japan.

May 2009 Chair for the “Methods for RNA 3D Modeling,” session at the 2010 RNA meeting Madison, WI

Peer Review for: *RNA*, *PLoS One*, *PLoS Computational Biology*, *Genome Biology*, *Nature*, *Nucleic Acids Research*, *RNA Biology*, *J. of Bacteriology*.

Grant reviews for: NIH NIGMS MSFD Study Section, 10/2014, NIH NIGMS ZGM1 R13 Study Section 07/2013, “Conseil franco-québécois de coopération universitaire (CFQCU),” US NSF, Foundation for Polish Science.