Biology 484/584 - Molecular Evolution
Winter 2018

Professor: Matthew Barber, mfbarber@uoregon.edu
- Office hours: Tuesday and Thursday 3:20 - 3:50 (Straub 251) and Friday 10:00 - 10:30 AM (Pacific 321)

GE: Allison Fuiten, afuiten@uoregon.edu
- Office hours: Thursday 10:00 - 11:00 AM (Onyx 360)

Time and Location: Tuesday and Thursday 2:00 - 3:50 PM, Straub 251

Email: Please include “Bio484” in the subject line, so your email can be attended to in time. I will try to answer your email in a timely manner; however I do not often check our email in the evenings or during weekends.

Website: Syllabus, course materials, assignments and grades will be posted to the course Canvas site.

Textbook: There is no required textbook for this course. A recommended textbook (Molecular and Genome Evolution, Dan Graur) is available for purchase at the Duck Store. One copy is on reserve at the Science Library. Required readings will be drawn from primary journal articles and will be posted on Canvas.

Required supplies: Please bring 4x6 inch index cards to write ‘minute-papers.’

Course Description:
In this course we will explore how evolution occurs on a molecular scale. Guided largely by discussion of primary literature, students will gain an understanding of the forces and mechanisms by which genes, proteins, and genomes change over time. As an upper-level course, students will both assimilate and apply knowledge in molecular evolution to evaluate and propose new areas of investigation in the field. We will cover classical studies as well as recent research using modern genetic, computational and molecular approaches. Topics include mutation, genetic drift, tests of natural selection, molecular phylogenetics, genomics, evolution of protein function, gene regulation, and chromosome evolution.

Learning Goals:
Upon completing this course, students will be able to:
1. Understand molecular processes that contribute to evolutionary change.
2. Describe techniques used to study molecular evolution.
3. Synthesize, present, and critique primary research in the field of molecular evolution.
4. Use primary literature to propose an original research project in the area of molecular evolution.

Evaluation:

1. Questions before class (20%)
   - Questions for required readings will be posted on Canvas, answers must be submitted before each class.
2. Leading class discussion (15%)
   - Beginning in the second week, students will introduce the paper(s) for discussion using a Powerpoint (or similar) presentation. A rubric and guidelines for presentations will be provided.
3. Minute-papers (10%)
   - At the end of each class, students will be asked to write a short (1-3 sentence) answer to specific prompts relating the the discussion that day.
4. Abstract on paper topic (15%)
   - Students will prepare and submit a proposed topic for their final paper mid-way through the course. Instructions will be posted on Canvas.
5. Lab activity (10%)
   - We will dedicate one class to a 'lab' activity performing analyses using DNA sequence.
6. Final paper (30%)
   - The paper will consist of a literature review on a topic of interest in molecular evolution, as well as a short proposal of original work in this field.

Total: 100%

Class preparation:
It is expected that you complete assigned readings and review any posted sources before attending class. Please bring a copy of the papers (preferably a hard copy) to be discussed in class. Canvas question responses are due by noon before lecture. Students are responsible for bringing index cards for minute papers.

General policy on missed assignments:
Assignments must be turned in on time. The grading system is designed to allow some flexibility if you miss class or a homework assignment. If you anticipate an extended absence please contact the instructor.

No Extra Credit:
There will be no opportunities for extra credit. Please do not ask for exceptions.

Classroom etiquette:
Please arrive on time. Lectures and discussions begin promptly on the hour. Please do not leave early as this is disruptive to everyone. If you have an unusual circumstance and must leave early, please inform the instructor, and sit near the exit so your leaving is not disruptive. Finally, please be respectful of your fellow students.

Academic Integrity:
You are expected to do your own work on homework, class presentations, and papers. Academic misconduct, including cheating and plagiarism, will not be tolerated. You are encouraged to discuss

ideas with other students and study together, but do not copy someone else's work or allow anyone to copy yours. All students are expected to conform to the Student Conduct Code. Please note that Instructors are required to file a written report of any academic misconduct with the Director of Student Conduct and Community Standards.

Inclusive Learning:
In this class we aim to build an inclusive learning environment. We understand that our members represent a rich variety of backgrounds and perspectives. We are committed to providing an atmosphere for learning that respects diversity. While working together to build this community we ask all members to:

- be open to the views of others.
- honor the uniqueness of their colleagues.
- appreciate the opportunity that we have to learn from each other.
- value each other's opinions and communicate in a respectful manner.
- keep confidential discussions that the community has of a personal (or professional) nature.

If there are aspects of the instruction or design of this course that result in barriers to your participation, please let us know as early as possible, in person or via email. You may also wish to contact Accessible Education Services in 164 Oregon Hall, by phone at (541) 346-1155 or uoaec@uoregon.edu. We welcome the chance to help you learn, and will work with you to make it a positive experience.

Schedule:

Note: papers denoted with a * will be the focus of student-led discussion.

Date	Subject	Papers
1/9	Molecular genetics background, course logistics	-
1/11	Population genetics background, demonstration on paper presentations	-
1/16	The neutral theory of molecular evolution	Kimura 1968*, King and Jukes 1969*, Kimura and Ohta 1974 [1–3]
1/18	Nearly neutral theory, molecular clock	Ohta 1973, Ohta and Gillespie 1996, Peterson 2004* [4–6]
1/23	Positive selection, adaptive evolution	Yang and Bielawski 2000, Sawyer 2005* [7,8]
1/25	Polymorphism and divergence	McDonald and Kreitman 1991*, Fay Wyckoff Wu 2002 [9,10]

1/30	Linkage and recombination	Begun 1992*, Coop 2008 [11,12]
2/1	Phylogenetics	Simion 2017*, Felsenstein 1981 [13,14]
2/6	Comparative genomics	Pease 2016* [15]
2/8	Population genomics	Myers 2005*, Myers 2010* [16,17]
2/13	Gene duplication, fusion, loss	Force 1999*, Hittinger 2007 [18,19]
2/15	Lab activity	N/A
2/20	Evolution of protein function	Bridgham 2006, Bridgham 2010* [20,21]
2/22	Evolution of protein function (part 2)	Barber 2014*[22]
2/27	Evolution of gene regulation	Wallbank 2016*, Wittkopp 2012 [23,24]
3/1	Evolution of gene regulation (part 2)	Chuong 2016*, Chuong 2017 [25,26]
3/6	Microbial evolution - bacterial and archaea	Fox 1977*, Woese and Fox 1977*, Woese 2002, Waldor 1996 [27–30]
3/8	Eukaryotic genome evolution	Fontaine 2015* [31]
3/13	Sex chromosomes	Vicoso 2013*, Bachtrog 2014 [32,33]
3/15	Molecular evolution in action	Levy 2015*, Venkataram 2016 [34,35]

Citations:

1. Kimura M. Evolutionary rate at the molecular level. Nature. Nature Publishing Group; 1968;217: 624–626.

2. King JL, Jukes TH. Non-Darwinian evolution. Science. American Association for the Advancement of Science; 1969;164: 788–798.

3. Kimura M, Ohta T. On some principles governing molecular evolution. Proceedings of the National Academy of …. 1974. Available: http://www.pnas.org/content/71/7/2848.short

4. Ohta T. Slightly deleterious mutant substitutions in evolution. Nature. Nature Publishing Group; 1973;246: 96–98.

5. Ohta T, Gillespie JH. Development of Neutral and Nearly Neutral Theories. Theor Popul Biol. 1996;49: 128–142.

6. Peterson KJ, Lyons JB, Nowak KS, Takacs CM, Wargo MJ, McPeek MA. Estimating metazoan divergence times with a molecular clock. Proc Natl Acad Sci U S A. 2004;101: 6536–6541.

7. Yang Z, Bielawski JP. Statistical methods for detecting molecular adaptation. Trends Ecol Evol. Elsevier Ltd; 2000;15: 496–503.

8. Sawyer SL, Wu LI, Emerman M, Malik HS. Positive selection of primate TRIM5α identifies a critical species-specific retroviral restriction domain. Proc Natl Acad Sci U S A. National Academy of Sciences; 2005;102: 2832–2837.

9. McDonald JH, Kreitman M. Adaptive protein evolution at the Adh locus in Drosophila. Nature. Nature Publishing Group; 1991;351: 652–654.

10. Fay JC, Wyckoff GJ, Wu C-I. Testing the neutral theory of molecular evolution with genomic data from Drosophila. Nature. Nature Publishing Group; 2002;415: 1024–1026.

11. Begun DJ, Aquadro CF. Levels of naturally occurring DNA polymorphism correlate with recombination rates in D. melanogaster. Nature. 1992;356: 519–520.

12. Coop G, Wen X, Ober C, Pritchard JK, Przeworski M. High-resolution mapping of crossovers reveals extensive variation in fine-scale recombination patterns among humans. Science. 2008;319: 1395–1398.

13. Simion P, Philippe H, Baurain D, Jager M, Richter DJ, Di Franco A, et al. A Large and Consistent Phylogenomic Dataset Supports Sponges as the Sister Group to All Other Animals. CURBIO. Elsevier; 2017;27: 958–967.

14. Felsenstein J. Evolutionary trees from DNA sequences: a maximum likelihood approach. J Mol Evol. 1981;17: 368–376.

15. Pease JB, Haak DC, Hahn MW, Moyle LC. Phylogenomics Reveals Three Sources of Adaptive Variation during a Rapid Radiation. PLoS Biol. 2016;14: e1002379–24.

16. Myers S, Bottolo L, Freeman C, McVean G, Donnelly P. A fine-scale map of recombination rates and hotspots across the human genome. Science. 2005;310: 321–324.

17. Myers S, Bowden R, Tumian A, Bontrop RE, Freeman C, MacFie TS, et al. Drive against hotspot motifs in primates implicates the PRDM9 gene in meiotic recombination. Science. 2010;327: 876–879.

18. Force A, Lynch M, Pickett FB, Amores A, Yan YL, Postlethwait J. Preservation of duplicate genes by complementary, degenerative mutations. Genetics. 1999;151: 1531–1545.

19. Hittinger CT, Carroll SB. Gene duplication and the adaptive evolution of a classic genetic switch.

Nature. 2007;449: 677–681.

20. Bridgham JT, Carroll SM, Thornton JW. Evolution of hormone-receptor complexity by molecular exploitation. Science. 2006;312: 97–101.

21. Bridgham JT, Eick GN, Larroux C, Deshpande K, Harms MJ, Gauthier MEA, et al. Protein evolution by molecular tinkering: diversification of the nuclear receptor superfamily from a ligand-dependent ancestor. PLoS Biol. 2010;8. doi:10.1371/journal.pbio.1000497

22. Barber MF, Elde NC. Escape from bacterial iron piracy through rapid evolution of transferrin. Science. American Association for the Advancement of Science; 2014;346: 1362–1366.

23. Wallbank RWR, Baxter SW, Pardo-Diaz C, Hanly JJ, Martin SH, Mallet J, et al. Evolutionary Novelty in a Butterfly Wing Pattern through Enhancer Shuffling. PLoS Biol. 2016;14: e1002353–16.

24. Wittkopp PJ, Kalay G. Cis-regulatory elements: molecular mechanisms and evolutionary processes underlying divergence. Nat Rev Genet. 2011;13: 59–69.

25. Chuong EB, Elde NC, Feschotte C. Regulatory evolution of innate immunity through co-option of endogenous retroviruses. Science. 2016;351: 1083–1087.

26. Chuong EB, Elde NC, Feschotte C. Regulatory activities of transposable elements: from conflicts to benefits. Nat Rev Genet. 2017;18: 71–86.

27. Fox GE, Magrum LJ, Balch WE, Wolfe RS, Woese CR. Classification of methanogenic bacteria by 16S ribosomal RNA characterization. Proc Natl Acad Sci U S A. 1977;74: 4537–4541.

28. Woese CR, Fox GE. Phylogenetic structure of the prokaryotic domain: the primary kingdoms. Proc Natl Acad Sci U S A. National Academy of Sciences; 1977;74: 5088–5090.

29. Woese CR. On the evolution of cells. Proc Natl Acad Sci U S A. 2002;99: 8742–8747.

30. Waldor MK, Mekalanos JJ. Lysogenic conversion by a filamentous phage encoding cholera toxin. Science. 1996;272: 1910–1914.

31. Fontaine MC, Pease JB, Steele A, Waterhouse RM, Neafsey DE, Sharakhov IV, et al. Mosquito genomics. Extensive introgression in a malaria vector species complex revealed by phylogenomics. Science. 2015;347: 1258524.

32. Vicoso B, Emerson JJ, Zektser Y, Mahajan S, Bachtrog D. Comparative sex chromosome genomics in snakes: differentiation, evolutionary strata, and lack of global dosage compensation. PLoS Biol. 2013;11: e1001643.

33. Bachtrog D, Mank JE, Peichel CL, Kirkpatrick M, Otto SP, Ashman T-L, et al. Sex Determination: Why So Many Ways of Doing It? PLoS Biol. 2014;12: e1001899–13.

34. Levy SF, Blundell JR, Venkataram S, Petrov DA, Fisher DS, Sherlock G. Quantitative evolutionary dynamics using high-resolution lineage tracking. Nature. 2015;519: 181–186.

35. Venkataram S, Dunn B, Li Y, Agarwala A, Chang J, Ebel ER, et al. Development of a Comprehensive Genotype-to- Fitness Map of Adaptation-Driving Mutations in Yeast. Cell. Elsevier Inc.; 2016;166: 1585–1589.e22.