EEB504: Understanding Molecular Genetics from an Evolutionary Perspective

Instructor: Dr. Michael Gilchrist

    Office Hours: Tuesday 11:00am-12:30pm and by appointment

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Time & Location: M 4:40-5:30, 113 Ayers

Required Textbook: Lynch, M. (2007). *Origins of Genome Architecture.* Available in the UT Bookstore.

Credit Hours: 1 S/U

Course Overview

The central goal of this course is to examine our current understanding of molecular genetics within the well developed framework of population genetics. Using the required text as our guide, we will focus on understanding the four fundamental forces that can affect molecular evolution (natural selection, genetic drift, and mutation) and, in turn, the importance of each of these forces in explaining genome scale patterning.

Course Structure

Each week the course will meet to discuss the assigned reading. The goal is to create a welcoming and engaging environment in which students are free to pose and answer questions in a constructive manner. To help guide the students in the readings during the semester, each Thursday the instructor will post a set of questions on the course's Blackboard site. Additionally, each week a new forum will be added on the Piazza hosted Discussion Board (which is accessible through the course's Blackboard (Bb) site). Students are each expected to post at least two questions or observations on the week's reading by 5pm the Sunday class and respond to at least two other students' postings by noon on Monday. Often students can answer another students question based on their previous coursework or research, which is great. However, in order to help deepen student understanding of the material, at least one of your responses should include at least one citation of a paper from the literature. Below are an exemplar student question and response from a previous course.

Question: Lynch contends that the evolution of sex may be a result of "small population size" (pg. 97), however, the explanation offered is very brief. What additional support is there for the "small population size" as a driving force for evolution of sex over adaptive arguments such the benefit of more accurate DNA replication and DNA repair during recombination?

Response: A recent review, "The evolution of sex: empirical insights into the roles of epistasis and drift" by de Visser & Elena (2007, Nature Review Genetics 8: 139-149) argues that for sex to be beneficial linkage disequilibrium should be negative, or certain allele combinations being present in a population at lower rates than expected by chance. This would be a result of directional selection and drift, and negative epistasis. Since smaller populations are more likely to experience drift, as Lynch mentions, I think it could be argued that sex evolved in the smaller populations as a way to counter balance the effects of drift.

Assigned Readings

Assigned readings are either taken from Lynch (2007) or the literature and, as a result, are often quite technical. Students should expect to spend the readings to take an hour and a half or more. References for all readings are available below and papers from the literature will be posted on Blackboard.

Student Expectations and Assessment

It is explicitly assumed that students are enrolled in the course because they are interested in the topic, want to learn more about it, and are willing to engage in thoughtful discussion. Students are *not* expected to be experts in either molecular biology or population genetics, but instead have some exposure to one of these areas and an interest in the other. All students are expected to:

- Carefully read each week's readings.

- Post two questions or observations from the readings by 5pm Sunday.

- Respond to two other students' postings by noon on Monday.

- Actively participate in all classroom discussions.

Course Schedule

Date	Topic	Reading
Aug 24	Introduction & Overview	Lynch Ch 13: Genomfart*
Aug 31	Allele Fixation: The Math	Ch 4: Why Population Size Matters (through p. 83)
Sep 7	Labor Day Holiday	
Sep 14	Allele Fixation: The implications	Ch 4: Why Population Size Matters (p. 83-100)
Sep 21	Codon Usage Bias as a Case Study (Skype)	Sella and Hirsh (2005) & Shah and Gilchrist (2011)
Sep 28	Variation in Genome Structure	Lynch Ch 2: Genome Size and Organismal Complexity
Oct 5	The Structure of the Human Genome	Lynch Ch 3: The Human Genome
Oct 12	The ENCODE controversy (O'Meara)	Consortium (2012); Pennisi (2012); Graur et al. (2013)
Oct 19	Transposable Elements: Parasitic DNA	Lynch Ch 7: Mobile Genetic Elements p. 174-191 & Levin and Moran (2011)
Oct 26	Junk DNA & Craniofacial Development in Mice	Nobrega et al. (2004); Attanasio et al. (2013)
Nov 2	Criticisms of Lynch	Lynch and Conery (2003); Whitney and Garland (2010); Whitney et al. (2011)
Nov 9	No Class	
Nov 16	Genome Gain & Loss	Lynch Ch 8: Genomic Expansion by Gene Duplication
Nov 23	Case Studies: Coelocanth & Octopus Genomes	Amemiya et al. (2013); Albertin et al. (2015)
Nov 30	Pushing the Limits: Ocean microbes	Biller et al. (2014)

* Yes, the chapter is entitled "Genomfart". It's apparently Swedish for "the way forward."

References

Albertin, C. B., O. Simakov, T. Mitros, Z. Y. Wang, J. R. Pungor, et al. 2015. The octopus genome and the evolution of cephalopod neural and morphological novelties. Nature 524:220–224.

Amemiya, C. T., J. Alfoldi, A. P. Lee, S. Fan, H. *et al.* et al. 2013. The african coelacanth genome provides insights into tetrapod evolution. Nature 496:311–316.

Attanasio, C., A. S. Nord, Y. Zhu, M. J. Blow, Z. Li, et al. 2013. Fine tuning of craniofacial morphology by distant-acting enhancers. Science 342.

Biller, S. J., F. Schubotz, S. E. Roggensack, A. W. Thompson, R. E. Summons, et al. 2014. Bacterial vesicles in marine ecosystems. Science 343:183–186.

Consortium, E. P. 2012. An integrated encyclopedia of dna elements in the human genome. Nature 489:57–74.

Graur, D., Y. Zheng, N. Price, R. B. R. Azevedo, R. A. Zufall, et al. 2013. On the immortality of television sets: function in the human genome according to the evolution-free gospel of encode. Genome Biology and Evolution .

Levin, H. L. and J. V. Moran. 2011. Dynamic interactions between transposable elements and their hosts. Nature Reviews Genetics 12:615–627.

Lynch, M. 2007. The Origins of Genome Architecture. Sinauer.

Lynch, M. and J. S. Conery. 2003. The origins of genome complexity. Science 302:1401–1404.

Nobrega, M. A., Y. Zhu, I. Plajzer-Frick, V. Afzal, and E. M. Rubin. 2004. Megabase deletions of gene deserts result in viable mice. Nature 431:988–993.

Pennisi, E. 2012. Encode project writes eulogy for junk dna. Science 337:1159–1161.

Sella, G. and A. E. Hirsh. 2005. The application of statistical physics to evolutionary biology. Proceedings of the National Academy of Sciences of the United States of America 102:9541–9546.

Shah, P. and M. A. Gilchrist. 2011. Explaining complex codon usage patterns with selection for translational efficiency, mutation bias, and genetic drift. Proceedings of the National Academy of Sciences of the United States of America 108:10231–10236.

Whitney, K. D., B. Boussau, E. J. Baack, and T. Garland. 2011. Drift and genome complexity revisited. Plos Genetics 7.

Whitney, K. D. and T. Garland. 2010. Did genetic drift drive increases in genome complexity? Plos Genetics 6.

Note: Syllabus may be revised at instructor's discretion.

November 2, 2015