

SEMINAR: Ecological & Population Genomics
BIOL 79302
CUNY Graduate Center, Fall 2012
Wednesdays 4:15 PM – 6:15 PM, Rm. 3308

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Seminar Description:

Recent technological advances have removed many of the obstacles to the collection of genome-scale sequence data for non-model organisms, but the application of these data to ecological and evolutionary questions is in its infancy. This seminar is aimed at students that do not necessarily have a strong background in molecular biology, but are conducting ecological or evolutionary research that may benefit from genomic approaches. The course will begin with discussions of the basic molecular biology and techniques needed to understand the primary literature. In the second part of the course, students will lead discussions of recent papers on selected topics from the growing ecological & population genomics literature (see schedule below). Readings will focus on non-model organisms when possible, because most EEB researchers work on species without reference genome sequences (although these gaps are being filled quickly!). In the second half of the semester, we will spend some time working in the GALAXY cloud-based platform (<https://main.g2.bx.psu.edu/>) on manipulating and analyzing next-gen genomic data. By the end of the seminar, students will be able to design studies that use genomic approaches to understand the evolution and ecology of wild populations.

Course Assessment:

Students will be assessed on their active participation in seminar discussions and their preparation for the one-two times that they will lead these discussions.

Required Readings:

For each seminar period we will read 2-4 new research papers, reviews, or textbook chapters on ecological and population genomics. These papers will be available as PDFs through the GC's library website, or will be made available by the instructor on the course BlackBoard site. The texts below are recommended references to familiarize oneself with basic genomic and computational issues:

Gibson, G., & S. V. Muse. 2009. A Primer of Genome Science, 3rd Edition. Sinauer, Sunderland, MA. **(not worth buying but OK reference from library!)**

Haddock, S., & C. Dunn. 2011. Practical Computing for Biologists. Sinauer, Sunderland, MA.

Course Schedule (NOTE: Subject to change if new papers of interest are published during the semester):

Weds	Discussion Topic	Readings (subject to change!)
08/29	Introduction to Population Genomics	Review of key concepts
09/05	Next-generation Sequencing—What's available?	(Metzker 2010; Glenn 2011) + Glenn (2012) updated tables & info on commercial seq services
09/12	Study Design, Data Processing, Alignment & Assembly	Fool's Guide to Population Genomics, (Gilad et al. 2009; Davey et al. 2011; Cahais et al. 2012)
09/19	Variant (i.e. SNP) Calling	(Bers et al. 2010; Nielsen et al. 2011; Altmann et al. 2012; MacArthur 2012)
09/26	NO CLASS	NO CLASS
10/03	Comparative Genomics	(Boyko et al. 2010; Kunstner et al. 2010; Elmer & Meyer 2011)
10/10	NO CLASS	NO CLASS
10/17	Population Genomic Structure / Intro. to Scans for Selection	(Liti et al. 2009; Gompert et al. 2010; Oleksyk et al. 2010)
10/24	Adaptive variation & gene discovery I	(Hoekstra & Coyne 2007; Hughes 2007; Halligan et al. 2010; Barrett & Hoekstra 2011)
10/31	Adaptive variation & gene discovery II	(Domingues et al. in press; Boyko et al. 2010; Hohenlohe et al. 2010; Jones et al. 2012)
11/07	Transcriptomics	(Elmer et al. 2010; Garber et al. 2011; Moya et al. 2012; Rosenblum et al. 2012)
11/14	WORKSHOP: GALAXY RNA-Seq analysis	(Trapnell et al. 2012)
11/21	Gene expression	(Wolf et al. 2010; Ometto et al. 2012; Oliver et al. 2012)
11/28	Env. Stress / Methylation	(Nätt et al. 2012; Liu et al. 2012; Smith et al. 2012)
12/05	Landscape Genomics	(Joost et al. 2007; Eckert et al. 2010; Manel et al. 2012)
12/12	Hybridization / Introgression	(Hohenlohe et al. 2011; Roesti et al. 2012; Twyford & Ennos 2012)

Reading List

- Altmann A, Weber P, Bader D, Preuß M, et al. (2012) A beginners guide to SNP calling from high-throughput DNA-sequencing data. *Human Genetics*, 1–14.
- Barrett RDH, Hoekstra HE (2011) Molecular spandrels: tests of adaptation at the genetic level. *Nature Reviews Genetics*, **12**, 767–780.
- Bers NEMV, Oers KV, Kerstens HHD, Dibbitts BW, et al. (2010) Genome-wide SNP detection in the great tit *Parus major* using high throughput sequencing. *Molecular Ecology*, **19**, 89–99.
- Boyko AR, Quignon P, Li L, Schoenebeck JJ, et al. (2010) A Simple Genetic Architecture Underlies Morphological Variation in Dogs. *PLoS Biol*, **8**, e1000451.
- Cahais V, Gayral P, Tsagkogeorga G, Melo-ferreira J, et al. (2012) Reference-free transcriptome assembly in non-model animals from next-generation sequencing data. *Molecular Ecology Resources*.
- Davey JW, Hohenlohe PA, Etter PD, Boone JQ, et al. (2011) Genome-wide genetic marker discovery and genotyping using next-generation sequencing. *Nature Reviews Genetics*, **12**, 499–510.
- Domingues VS, Poh Y, Peterson BK, Pennings PS, et al. (in press) Evidence of adaptation from ancestral variation in young populations of beach mice. *Evolution, Evolution*.
- Eckert AJ, Bower AD, GONZÁLEZ-MARTÍNEZ SC, Wegrzyn JL, et al. (2010) Back to nature: ecological genomics of loblolly pine (*Pinus taeda*, Pinaceae). *Molecular Ecology*, **19**, 3789–3805.
- Elmer KR, Fan S, Gunter HM, Jones JC, et al. (2010) Rapid evolution and selection inferred from the transcriptomes of sympatric crater lake cichlid fishes. *Molecular Ecology*, **19**, 197–211.
- Elmer KR, Meyer A (2011) Adaptation in the age of ecological genomics: insights from parallelism and convergence. *Trends in Ecology & Evolution*, **26**, 298–306.
- Garber M, Grabherr MG, Guttman M, Trapnell C (2011) Computational methods for transcriptome annotation and quantification using RNA-seq. *Nature Methods*, **8**, 469–477.
- Gilad Y, Pritchard JK, Thornton K (2009) Characterizing natural variation using next-generation sequencing technologies. *Trends in Genetics*, **25**, 463–471.
- Glenn TC (2011) Field guide to next-generation DNA sequencers. *Molecular Ecology Resources*, **11**, 759–769.
- Gompert Z, FORISTER ML, FORDYCE JA, NICE CC, et al. (2010) Bayesian analysis of molecular variance in pyrosequences quantifies population genetic structure across the genome of *Lycæides* butterflies. *Molecular Ecology*, **19**, 2455–2473.
- Halligan DL, Oliver F, Eyre-Walker A, Harr B, et al. (2010) Evidence for pervasive adaptive protein evolution in wild mice. *PLoS Genetics*, **6**, e1000825.
- Hoekstra H, Coyne J (2007) The locus of evolution: Evo devo and the genetics of adaptation.

Evolution, **61**, 995–1016.

- Hohenlohe PA, Amish SJ, Catchen JM, Allendorf FW, et al. (2011) Next-generation RAD sequencing identifies thousands of SNPs for assessing hybridization between rainbow and westslope cutthroat trout. *Molecular Ecology Resources*, **11**, 117–122.
- Hohenlohe PA, Phillips PC, Cresko WA (2010) Using Population Genomics to Detect Selection in Natural Populations: Key Concepts and Methodological Considerations. *International Journal of Plant Sciences*, **171**, 1059.
- Hughes A (2007) Looking for Darwin in all the wrong places: the misguided quest for positive selection at the nucleotide sequence level. *Heredity*, **99**, 364–373.
- Jones FC, Grabherr MG, Chan YF, Russell P, et al. (2012) The genomic basis of adaptive evolution in threespine sticklebacks. *Nature*, **484**, 55–61.
- Joost S, Bonin A, Bruford MW, Després L, et al. (2007) A spatial analysis method (SAM) to detect candidate loci for selection: towards a landscape genomics approach to adaptation. *Molecular Ecology*, **16**, 3955–3969.
- Kunstner A, Wolf JBW, Backstrom N, WHITNEY O, et al. (2010) Comparative genomics based on massive parallel transcriptome sequencing reveals patterns of substitution and selection across 10 bird species. *Molecular Ecology*, **19**, 266–276.
- Liti G, Carter DM, Moses AM, Warringer J, et al. (2009) Population genomics of domestic and wild yeasts. *Nature*, **458**, 337–341.
- Liu Y, Siegmund KD, Laird PW, Berman BP (2012) Bis-SNP: Combined DNA methylation and SNP calling for Bisulfite-seq data. *Genome Biology*, **13**, R61.
- MacArthur D (2012) Methods: Face up to false positives. *Nature*, **487**, 427–428.
- Manel S, Gugerli F, Thuiller W, Alvarez N, et al. (2012) Broad-scale adaptive genetic variation in alpine plants is driven by temperature and precipitation. *Molecular Ecology*, **21**, 3729–3738.
- Metzker ML (2010) Sequencing technologies - the next generation. *Nat Rev Genet*, **11**, 31–46.
- Moya A, Huisman L, Ball EE, Hayward DC, et al. (2012) Whole Transcriptome Analysis of the Coral *Acropora millepora* Reveals Complex Responses to CO₂-driven Acidification during the Initiation of Calcification. *Molecular Ecology*, **21**, 2440–2454.
- Nätt D, Rubin C-J, Wright D, Johnsson M, et al. (2012) Heritable genome-wide variation of gene expression and promoter methylation between wild and domesticated chickens. *BMC Genomics*, **13**, 59.
- Nielsen R, Paul JS, Albrechtsen A, Song YS (2011) Genotype and SNP calling from next-generation sequencing data. *Nature Reviews Genetics*, **12**, 443–451.
- Oleksyk TK, Smith MW, O'Brien SJ (2010) Genome-wide scans for footprints of natural selection. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **365**, 185–205.

- Oliver JC, Tong X-L, Gall LF, Piel WH, et al. (2012) A Single Origin for Nymphalid Butterfly Eyespots Followed by Widespread Loss of Associated Gene Expression. *PLoS Genet*, **8**, e1002893.
- Ometto L, Ross KG, Shoemaker D, Keller L (2012) Disruption of gene expression in hybrids of the fire ants *Solenopsis invicta* and *Solenopsis richteri*. *Molecular Ecology*, **21**, 2488–2501.
- Roesti M, Hendry AP, Salzburger W, Berner D (2012) Genome divergence during evolutionary diversification as revealed in replicate lake–stream stickleback population pairs. *Molecular Ecology*, **21**, 2852–2862.
- Rosenblum EB, Poorten TJ, Settles M, Murdoch GK (2012) Only skin deep: shared genetic response to the deadly chytrid fungus in susceptible frog species. *Molecular Ecology*, **21**, 3110–3120.
- Smith CR, Mutti NS, Jasper WC, Naidu A, et al. (2012) Patterns of DNA Methylation in Development, Division of Labor and Hybridization in an Ant with Genetic Caste Determination. *PLoS ONE*, **7**, e42433.
- Trapnell C, Roberts A, Goff L, Pertea G, et al. (2012) Differential gene and transcript expression analysis of RNA-seq experiments with TopHat and Cufflinks. *Nature Protocols*, **7**, 562–578.
- Twyford AD, Ennos RA (2012) Next-generation hybridization and introgression. *Heredity*, **108**, 179–189.
- Wolf JBW, BAYER T, HAUBOLD B, SCHILHABEL M, et al. (2010) Nucleotide divergence vs. gene expression differentiation: comparative transcriptome sequencing in natural isolates from the carrion crow and its hybrid zone with the hooded crow. *Molecular Ecology*, **19**, 162–175.