



THE Open Reading Frame

Newsletter of the
Genetics Section of the American Fisheries Society

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Candy Darter, Stoney Creek, VA

President’s Message

Tampa FL and I would like to thank everyone who made time in the busy conference schedule to attend the Section meeting. Member input and discussion during Section meetings helps the Section improve going forward. There was good discussion about the possibility of the Section helping to manage the [2018 Coastwide Salmonid Genetics Meeting](#) and it looks like the Section will help with meeting co-ordination. Please stay tuned for more information about student travel opportunities. We also discussed an addition to eligibility requirements for the Wright award that will be implemented in 2018. A revised application form will be added to the web site soon. Another outcome of the Section meeting to look for is a change to the Section’s website; we will be joining the AFS multi-site in the next few months to take advantage of additional features and increased security. Scott Bonar (AFS first vice-president) joined us to talk about some upcoming changes, most notably the change in publishers for AFS journals which will bring Society members free online access to all AFS journals. The Genetics Section sponsored symposia to honor the work of the work of two distinguished researchers; Dr. John Gold and the late Dr. Tim King. These symposia were well attended and the talks were excellent. The Section also co-sponsored a session with the new Imperiled Aquatic Species Section that drew a lot of interest. Please consider hosting symposium next year in Atlantic City. More details of the Section meeting can be found in the minutes (by Andrew Whiteley) located on the section website. Finally I would like to remind everyone to take a moment and renew their Society and Section dues if you have not done so already. The dues will help the Section to continue to offer travel grants to students.

Welcome to the fall edition of the Genetics Section newsletter. I hope everyone had a productive and safe summer. I would like to congratulate again our Phelps, Wright, and Early Career award winners and thank the members of those committees for their hard work making the selections. The Section was well represented at the annual meeting in

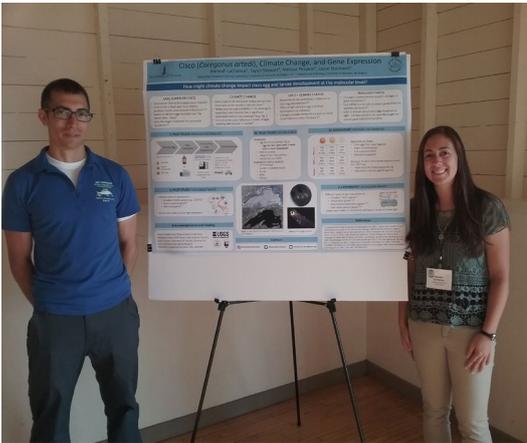
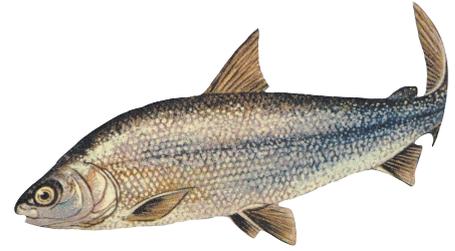


Dr. Wendylee Stott
AFSGS President

13th International Coregonid Symposium meeting recap

By Hannah Lachance

University of Vermont Master's student and AFSGS travel grant recipient



Jared Myers, USFWS and Hannah Lachance with Hannah's poster at the 13th International Coregonid Symposium

Thanks to the AFS Travel Award for Genetics Students I was able to experience the best conference I have attended to date! While conferences are always a wonderful opportunity to meet with and hear from a variety of fantastic researchers, the 13th International Coregonid Symposium was an exceptional gathering of world renowned professionals. My masters research aims to assess potential impacts of climate change on Lake Superior cisco (*Coregonus artedii*) egg development through gene expression analyses. Because my background is not in fisheries or the Great Lakes, the conference provided me with a thorough and insightful glimpse at research being conducted in my new field of study. My experience was heightened by the symposium's location in the beautiful town of Bayfield, WI, which sits right on the shores of my study system, Lake Superior. As I am based out of the University of Vermont, I had not had the chance to visit the lake that I had been reading so much about, and hope to help conserve. While the location, lodging, presentations, and events were all extremely

enjoyable, the highlight for me was hearing the feedback on my current and proposed work. Given how far removed I am from my study system and how new I am to coregonid and Great Lakes research, I sometimes felt isolated and unsure of how my project would be received by the scientific community. However, after presenting my current and proposed research at the symposium I was pleasantly surprised by the level of interest and excitement my project drew. This encouragement remains a nice reminder to reflect upon as I move forward with my masters. Overall, attending the Coregonid Symposium provided me with a means of meeting a friendly and brilliant community of scientists. Without the AFS Travel Award for Genetics Students I would have missed out on the opportunity of a life time. I am forever grateful for this award!

Genetics section awards



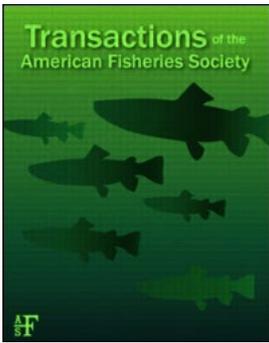
The **James E. Wright Graduate Award** is given in the memory of Jim Wright, one of the founders of fish genetics research and education in North America. The work of Jim Wright and his students combined classical chromosome studies with allozyme inheritance and helped shape our understanding of the salmonid genome. This award is presented annually at the Genetics Section Business Meeting during the AFS Annual Meeting to recognize excellence in graduate-level work in fisheries genetics, as well as assist graduate students with travel to the national meeting. Our awardees for 2017 include Matthew Snyder (left, with President Wendy Stott) from the University of Toledo and Zachary Robinson (right, with President Wendy Stott) from the University of Montana.



Continued on page 5

In case you missed it...

Recent genetics papers from AFS journals and beyond



Genomic analysis reveals genetic distinctiveness of the Paiute Cutthroat Trout *Oncorhynchus clarkii seleniris*. I.K. Saglam, D.J. Prince, M. Meek, *et al.* TAFS 146:1291-1302.

The time of origin and genetic diversity of three isolated Kokanee populations in Southwest Alaska. J.B Olsen, S.A. Pavey, J.L. Miller *et al.* TAFS 146:1212-1222.

Spatial and temporal genetic analysis of walleye *Sander vitreus* in the Ohio River. K.S. Page, R.D. Zweifel, W. Stott. TAFS 146:1168-1185.

Exploring the use of environmental DNA to determine species of salmon redds. B. Strobel, M.B. Laramie, D.S. Pilliod. NAMJFM 37:943-950.

Comparison of American Fisheries Society (AFS) standard fish sampling techniques and environmental DNA for characterizing fish communities in a large reservoir. C.R. Perez, S.A. Bonar, J.J. Amberg *et al.* NAMJFM 37:1010-1027.

Genetics and juvenile abundance dynamics show congruent patterns of population structure for depleted river herring populations in the Upper Chesapeake Bay. M.B. Ogburn, D.J. Hasselman, T.F. Shultz, *et al.* NAMJFM 37:1083-1092.

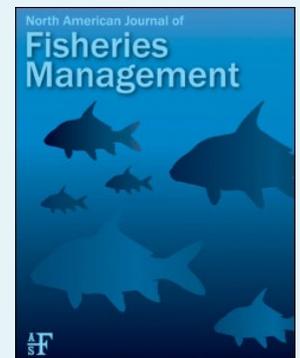


Photo USFWS Midwest / CC BY

Rapid, broad-scale gene expression evolution in experimentally harvested fish populations. S. Uusi-Heikkilä, T. Sävilämmi, E. Leader, *et al.* Molecular Ecology 26:3954-3967.

The K=2 conundrum. J.K. Jones, J.M. Miller, J.R. Dupuis, *et al.* Molecular Ecology 26:3594-3602.

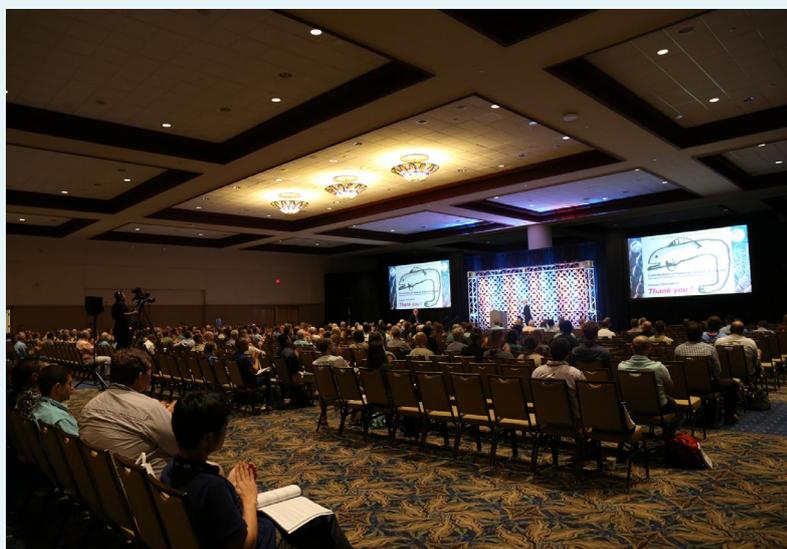
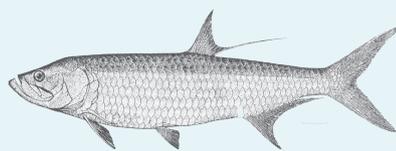
Applications of random forest feature selection for fine-scale genetic population assignment. E.V.A. Sylvester, P. Bentzen, I.R. Bradbury, *et al.* Evolutionary Applications. In Press.

Predicting the genetic impact of stocking in brook charr (*Salvelinus fontinalis*) by combining RAD sequencing and modeling of explanatory variables. Létourneau, J., Ferchaud, A.-L., Le Luyer, J., *et al.* Evolutionary Applications. In Press.

Genome scale assessment of a species translocation program. C.M. Dresser, R.M. Ogle, B.M. Fitzpatrick. Conservation Genetics 18:1191-1199.

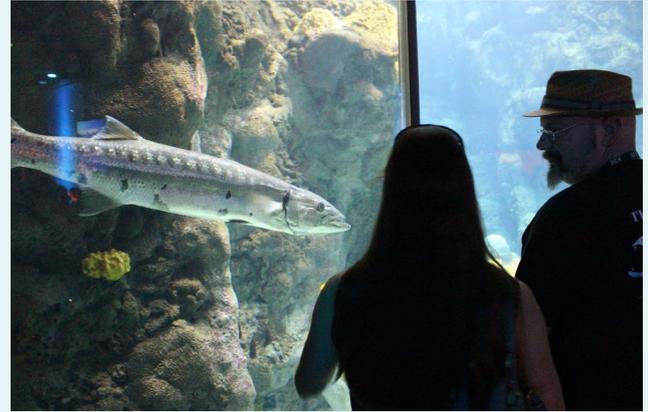
Effects of sampling close relatives on some elementary population genetics analyses. J. Wang. Molecular Ecology Resources. In Press.

Sights from the AFS Annual Meeting



Photos provided by AFS Flickr Photostream

Sights from the AFS Annual Meeting



Photos provided by AFS Flickr Photostream

Genetics section awards

Continued from page 2



The Genetics Section Early Career Award is given annually and recognizes the contribution of early-career researchers to the field of fisheries genetics. The goal of this award is to promote innovative and particularly applicable genetics research, increase interest in fisheries genetics careers, and enhance professional connections among fisheries geneticists. Our awardee for 2017 is Dr. Jean-Sébastien Moore, Assistant Professor in the Département de Biologie at Université Laval, Quebec, Canada (pictured at left). [Learn more about Dr. Moore's research here.](#)

The Stevan Phelps Memorial Award was created in 2000 as a perpetual memorial to Steve who died from cancer in 1999. The award, honoring Steve's strong commitment to publication of applied genetic research in fisheries, will be given annually for the best genetics paper published in an AFS journal the preceding year. Selection is typically made by the Phelps Award Committee in mid-June of each year. Our awardees for 2017 include Patrick W. DeHaan, Brice A. Adams, Paul D. Scheerer, and Brian L. Bangs for their paper, "[Influence of Introduction History on Genetic Variation in Introduced Populations: A Case Study of Oregon Chub](#)" in the *North American Journal of Fisheries Management*.



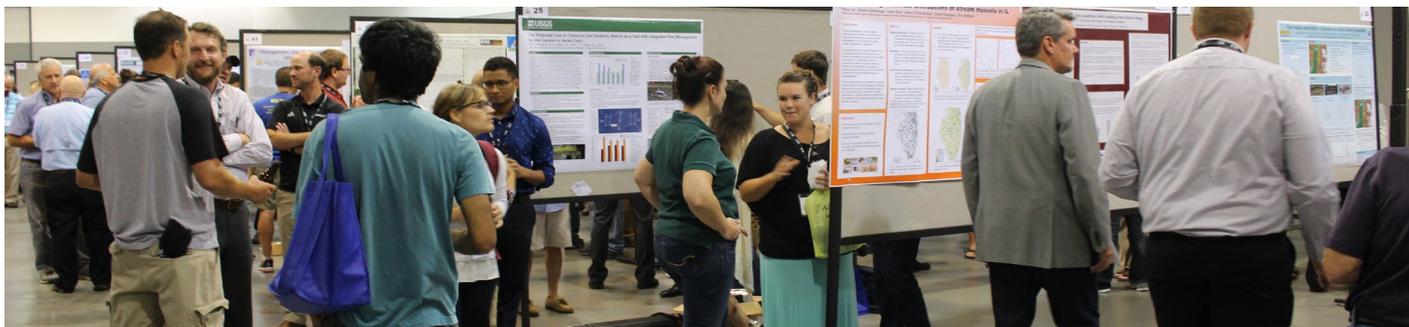


Photo by Beth Beard, AFS

Calendar

January 2018

3rd - 6th *Meeting*: Population Genetics Group. Bristol, UK.

3rd - 7th *Meeting*: The Society for Integrative and Comparative Biology Annual Meeting. San Francisco, CA.

5th - 9th *Meeting*: 150 Years of The American Naturalist. Asilomar, California.

19th *Symposium Proposal Deadline*: American Fisheries Society Annual Meeting

February 2018

6th - 8th *Meeting*: 76th Annual Stream Restoration Symposium, Stevenson, WI

11th - 16th *Meeting*: 2018 Ocean Sciences Meeting. Portland, Oregon.

22nd *Abstract Deadline*: Ecological Society of America Annual Meeting

March 2018

15th: *Grant deadline*: Sigma Xi Grants-in-Aid of Research

16th: *Abstract Deadline*: American Fisheries Society Annual Meeting

23rd - 25th *Meeting*: American Genetics Association's Evolutionary Quantitative Genetics in the Wild, Toronto

June 2018

18th - 21st *Meeting*: Coastwide Salmon Genetics Meeting, Mukilteo, WA

18th - 21st *Meeting*: 9th International Charr Symposium, Duluth, MN

18th - 22nd *Meeting*: International Association for Great Lakes Research Annual Conference, Toronto, ON

July 2018

15th - 19th *Meeting*: 13th International Congress on the Biology of Fish, Calgary, AB

August 2018

5th - 10th *Meeting*: Ecological Society of America Annual Meeting, New Orleans, LA

5th - 10th *Meeting*: 67th Annual International Conference of the Wildlife Disease Association. St. Augustine, FL.

19th - 22nd *Meeting*: Joint Congress on Evolutionary Biology, Montpellier, France

19th - 23th *Meeting*: American Fisheries Society Annual Meeting, Atlantic City, NJ

September 2018

24th - 27th *Meeting*: ICES Annual Science Conference, Hamburg, Germany

To find dates and information for AFS chapter meetings, visit fisheries.org/about/units/chapters/



Now Open **Hutton Student and Mentor** **Applications for Summer 2018**

More information at hutton.fisheries.org



Jobs

Graduate student positions

Ph.D. and M.S. positions in marine population genomics or eDNA.

Fish Ecology and Evolution in the Gaither Lab at UCF The Gaither Lab at the University of Central Florida (UCF) Department of Biology is recruiting highly motivated and independent graduate students in marine population genomics and evolution for Fall 2018. My lab uses RADSeq, whole genome re-sequencing, and targeted capture approaches to study coral reef and deep-sea fishes. We have new projects coming online involving eDNA techniques. Students will have access to a fully equipped genomics lab and a high powered computing cluster. Applicants should have completed a degree in a biological science. Computational skills or a desire to learn bioinformatics is a must. Ability to pursue independent research and excellent writing and fluency in English is expected. Interested students are encouraged to email Michelle Gaither at michellergaither@gmail.com with the subject line UCF_Graduate_Positions. Please include a brief description of your research interests and experience and a CV in your email. Note that the deadline for applications to UCF Biology is January 15th. To learn more about UCF Biology graduate programs go to <https://sciences.ucf.edu/biology/graduate-program/>. Contact Michelle Gaither at michellergaither@gmail.com.

The School of Biological Sciences at Washington State University invites motivated applicants for graduate training and research in ecology & evolutionary biology.

Research opportunities in both plant and animal systems are diverse. Research focus areas include disease and community ecology, ecosystem ecology, evolutionary genetics, ecological and evolutionary physiology, genomics, evolutionary theory, and phylogenetics and systematics. The following is a brief sketch of our faculty active in these areas: Jesse Brunner: Disease ecology; Jeremiah Busch: Population genetics, plant evolution; Patrick Carter: Quantitative genetics, animal physiology; Omar Cornejo: Genomics, host-pathogen evolution; Erica Crespi: Animal developmental physiology; Wes Dowd: Animal evolutionary physiology; Mark Dybdahl: Evolutionary ecology, adaptation, phenotypic plasticity; Dave Evans: Ecosystem ecology and nutrient cycling; Richard Gomulkiewicz: Evolutionary genetics and theory; Joanna Kelley: Genomics, adaptation to extreme environments; Eric Roalson: Plant phylogenetics and systematics; Elissa Schwartz: Disease dynamics and

virus-host interactions; Andrew Storfer: Landscape genomics, disease evolution; Heather Watts: Animal behavior and physiology; For more information on specific research areas in evolution and ecology, please visit their websites, available via sbs.wsu.edu<<http://sbs.wsu.edu>> Our graduate training program offers many opportunities for excellence. Every SBS student is fully funded with generous stipends through teaching or research assistantships, accompanying tuition waivers, and health benefits. Plus, SBS endowments provide over \$100,000 per year in student awards to facilitate research, training, and professional travel. PhDs receive up to \$10,000 in guaranteed support for research-related travel and MS students receive up to \$5,000 in guaranteed support. The campus houses outstanding facilities, including plant and animal growth chambers, managed field sites, a modern genomics core, stable isotope facility, and a campus-wide computer cluster. Washington State University is located in Pullman, WA, a friendly mid-sized town on the rolling hills of the unique Palouse region in eastern Washington. The campus is only eight miles from the University of Idaho in Moscow, ID. The two towns and campuses provide an academically and culturally rich community. The area offers great parks, bike paths, restaurants, farmer's markets and unbeatable opportunities for recreation in the adjacent mountains and rivers. For more information regarding the Graduate School applications at WSU, see: gradschool.wsu.edu<<http://gradschool.wsu.edu>> If you have any questions regarding the application process, please contact: Jenny Davis. The deadline for application of prospective students is January 10, 2018, but students are encouraged to apply anytime.

The Department of Ecology and Evolutionary Biology at the University of Connecticut (UConn) invites applications from prospective graduate students (M.S. and Ph.D.) to begin in Fall 2017.

Research in the department includes a wide range of topics in ecology, evolutionary biology, systematics, computational biology, global change biology and conservation biology in a highly collaborative environment at a leading public research university. Applicants should demonstrate a strong commitment to and potential for academic work in ecology and evolutionary biology. Applications from individuals of groups historically underrepresented in STEM fields are particularly encouraged with scholarships available from the university to promote a diverse and inclusive academic community. We will start reviewing applications on December 15th 2017. The on-line application process requires submission of the formal graduate school application, transcripts, GRE scores (general test required, biology GRE recommended), three letters of reference, a personal essay, and, for non-native speakers of English, TOEFL or IELTS scores. Inquiries For general inquiries about the application procedure, please contact the admissions coordinator, Madeline Hennessey. Specific questions about research directions, please contact potential advisers directly.

AFS Genetics Section Job Board

For additional job postings, be sure to watch the job board on the Section website

genetics.fisheries.org/jobs

Graduate student positions

Continued

Master's position in the Larson Lab using genomics to study connectivity and species diversity in the Boardman River, MI

Description and responsibilities: The USGS Wisconsin Cooperative Fishery Research Unit at UW-Stevens Point is looking for a MS student to conduct genomics research on fish populations from the Boardman River near Traverse City, MI. This research is part of the FishPass project, a large collaborative effort to explore fish passage solutions that restore connectivity for native species while blocking invasive species, such as sea lamprey. The Union Street dam on the Boardman River is 150 years old, and fish populations below the dam have been isolated from above dam populations since its completion. The successful candidate will use restriction site-associated (RAD) sequencing to collect genetic data on five fish species sampled above and below the Union Street Dam to determine if these populations are significantly differentiated and/or show differences in diversity. Additionally, the student will collect eDNA samples from existing monitoring sites and pair these data with traditional surveys to determine the utility of eDNA metabarcoding for investigating species diversity and distribution patterns in this system. Genetic samples from white sucker, smallmouth bass, walleye, yellow perch, and rock bass as well as water samples for the eDNA portion of this project are being collected by the Michigan Department of Natural Resources and other local agencies and fieldwork for the student will be minimal. However, the student will likely be asked to help with sample collection one to two times per summer. Laboratory work will consist of constructing RAD and amplicon sequencing libraries to send out for high-throughput sequencing. Bioinformatic analysis will involve using programs such as STACKS to analyze RAD data and working with Linux based pipelines to analyze eDNA data. Qualifications: B.S. in biology, fisheries, or a related field, GPA of 3.0+, and GRE of 300+. Background in genetics is preferred but not required. Previous experience with fieldwork and analysis of genomic data is desirable. Salary: \$16,000 per year (2 yr) plus health insurance and tuition waiver. Closing date: March 1, 2018. Starting date: Position will start in September 2018 but there may be an opportunity to work in the Larson Lab during summer 2018

before the position starts. Contact: Please send CV, transcript copies, GRE scores, and names and contact information for 3 references to Wes Larson (Wes.Larson@uwsp.edu). Web Links: <https://larsonlab.wordpress.com/> https://www.coopunits.org/Wisconsin_Fish/People/Wes_Larson/index.html

An M.S. Graduate Research Assistantship is available in the Welsh Lab in Conservation Genetics at West Virginia University. Starting date of January 2018 is preferred but will consider May 2018. Application review will begin November 6 and continue until the position is filled. Interested individuals should send a letter of interest, CV, unofficial copies of transcripts and GRE scores, and contact information for three references to Dr. Amy Welsh at amy.welsh@mail.wvu.edu.

Postdoc positions

Bioinformatics and Environmental Genomics

Project length: 2 years, renewable for 3rd year Approx. start date: February 1st, 2018 Location: McGill University, Montreal, QC Summary of Project: The Postdoctoral Fellow will be involved in long-term and highly replicated laboratory and field experiments on the effect of multiple stressors on the structure and function of aquatic communities. The research will involve developing and implementing bioinformatic tools for analysing metabarcoding and metagenomics data sets and assessing biodiversity trends for broad taxonomic groups (bacterial, phytoplankton, zooplankton). The fellow will compare biodiversity estimates obtained from traditional sampling techniques with estimates based on refined metabarcoding approaches to describe the biodiversity of contaminated aquatic habitats and will characterize genomic responses to selection. The project involves the biodiversity group at McGill University and collaborators from the Biodiversity Institute of Ontario (BIO), University of Guelph, University of Quebec at Montreal and University of Montreal. Research Objectives/Sub-Objectives: 1) Develop sensitive metabarcoding bioinformatics protocols to describing aquatic communities; 2) Investigate the impact of multiple stressors on complex aquatic communities; 3) Characterize genomic responses to selection. Methodology: 1) Use high-throughput sequencing to develop metabarcoding and metagenomics protocols for describing aquatic communities in complex environmental samples; 2) Validate protocols; 3) Apply protocols on highly replicated field experiments. Expertise and Skills Needed: Experience with next generation sequencing or very-large sequence data and related bioinformatics / computational / programming skills is required. Familiarity with one or more of the following would be an advantage: genomics, phylogenetic analyses, genome evolution / programming language (R/Unix/Python or Perl).

Continued on next page

Please send information on symposia, jobs, articles, and calendar events to jared.homola@maine.edu to see it in the next newsletter!

Postdoc positions Continued

Experience working with aquatic organisms would be an asset. The candidate should have a PhD in evolution / genetics / computational biology, a good publication record and the ability to work well in a collaborative research environment. Applicants should send a curriculum vitae, short statements of research interests, and 3 representative publications to melania.cristescu@mcgill.ca. The application deadline is December 30, 2017. McGill University is strongly committed to diversity and equity within its community. The university is located in Montreal, a cosmopolitan city with great cultural and linguistic diversity. Melania E. Cristescu melania.cristescu@mcgill.ca

The Veeramah Lab at Stony Brook has an opening for a postdoctoral researcher to begin in December 2017 (later start dates may be negotiable). The successful applicant will lead a project that was recently funded by NIH for 5 years. Whole genome sequencing will be used to understand adaptation of marine Threespine Stickleback that have recently colonized freshwater lakes. We will study evolutionary trajectories of adaptive alleles by sequencing samples in time-series from young lake populations. The project will involve sample preparation for sequencing, population genetic analyses, and possibly sampling stickleback populations in Alaskan lakes. The successful applicant should have or will shortly obtain a PhD in the areas of population, evolutionary or anthropological genetics, while at least some computer programming experience (particularly in python, equivalent or lower level languages) is required. Prior experience analyzing 2nd generation sequencing data and/or modeling demographic scenarios with genetic data is desirable. Applications will be accepted until Dec 1st 2017. Applicants should submit a State employment application, cover letter, resume, two references and a one page research statement through the official online application: https://stonybrook.taleo.net/careersection/post_docs/jobdetail.ftl?job=1703191&tz=GMT-05%3A00 The official REF# is: 1703191 Queries regarding this position can be made by email to: krishna.veeramah@stonybrook.edu

The Larson and Stott Labs are hiring a postdoc position (position description available pending approval by HR) starting in spring 2018 focusing on population genomics in cisco, with opportunities for side projects. Please contact Wes Larson at Wes.Larson@uwsp.edu for details or to submit an application package.



Workshops

The Helsinki Summer School on Mathematical Ecology and Evolution 2018. We are glad to invite applications to the 2018 edition of The Helsinki Summer School on Mathematical Ecology and Evolution, an EMS-ESMTB School in Applied Mathematics. The school will be held between 19 and 26 August 2018 in Turku, Finland, and will be part of the EMS Year of Mathematical Biology <<http://euro-math-soc.eu/year-mathematical-biology-2018>>. The core program consists of five series of lectures: Karl Sigmund (University of Vienna): Evolutionary game theory Odo Diekmann; (Utrecht University): Renewal equations in population biology; Sebastian Schreiber (University of California, Davis): Coexistence in variable environments; Ellen Baake (University of Bielefeld): Probabilistic models and ancestral processes in population genetics; Mick Roberts (Massey University of New Zealand): Ecology of infectious diseases. All young researchers working in mathematical ecology can apply from all countries, especially from Europe and the Mediterranean. The school is aimed at graduate students of mathematics, but we also welcome students of biology with sufficient background in mathematics, as well as advanced undergraduates and postdocs. For more information and details of the application procedure, please visit the school's webpage <https://wiki.helsinki.fi/display/BioMath/>

The National Institute for Mathematical and Biological Synthesis (NIMBioS) is now accepting applications for its Tutorial, The Search for Selection, to be held June 18-22, 2018, at NIMBioS. Objectives: Biologists are obsessed (indeed, seduced) by the search for signatures of selection in organismal features of interest, ranging from specific traits to genome-wide signatures. A vast number of approaches have been suggested in this search for selection, including genomic-based signatures of recent or ongoing selection, tests based on either excessive amounts or nonrandom patterns of divergence (in both fossil sequences and functional genomics data) and the more classical Lande-Arnold fitness estimates (direct association of phenotypic values with fitness estimates) and their modern extensions (such as aster models). Given the breadth of such searches, a large amount of machinery has been developed, but is rarely presented in a unified fashion. This tutorial presents an integrated overview of all these approaches, highlighting common themes and divergent assumptions. The goal of this tutorial is to expose investigators from all branches of biology to this rich menagerie of tests. It is applicable for population geneticists, genome biologists, evolutionary ecologists, paleontologists, functional morphologists, and just about any biologist who ponders on how to formally demonstrate that a feature (or features) of interest might have been shaped by selection.

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The intended audience is advanced graduate students, postdocs, and faculty with an interest in searching for targets of selection, be they particular genomic sequences or particular traits. Given the breadth of this topic, we expect students from functional genomics, population and evolutionary genetics, ecology, paleobiology, functional morphology, and statistics (as well as other fields). The background required is some basic introduction to population and/or quantitative genetics. Location: NIMBioS at the University of Tennessee, Knoxville Organizer: Bruce Walsh, Ecology & Evolutionary Biology, Univ. of Arizona For more information about the tutorial and a link to the online application form, go to <http://www.nimbios.org/tutorials/selection> Participation in NIMBioS tutorials is by application only. Individuals with a strong interest in the topic are encouraged to apply, and successful applicants will be notified within several weeks after the application deadline. NIMBioS will cover lodging (5 nights) and provide breakfast and lunch each day at NIMBioS. If needed, limited financial support for travel expenses is available. Application deadline: February 1, 2018 The National Institute for Mathematical and Biological Synthesis (NIMBioS) (<http://www.nimbios.org>) brings together researchers from around the world to collaborate across disciplinary boundaries to investigate solutions to basic and applied problems in the life sciences. NIMBioS is sponsored by the National Science Foundation, with additional support from The University of Tennessee, Knoxville.

University of Chicago Workshop on Molecular Evolution
Course Date: July 19 – July 29, 2018. Deadline: April 6, 2018; Tuition: \$2100.00; Room and Board: \$722.50. Directors: Joseph Bielawski, Dalhousie University; and Mark Holder, The University of Kansas. Course Description: MBL's Workshop on Molecular Evolution is the most prestigious workshop serving the field of evolutionary studies. Founded in 1988, it is the longest-running workshop of its kind, and it has earned worldwide recognition for its rich and intensive learning experience. Students work closely with internationally-recognized scientists, receiving (i) high-level instruction in the principles of molecular evolution and evolutionary genomics, (ii) advanced training in statistical methods best suited to modern datasets, and (iii) hands-on experience with the latest software tools (often from the authors of the programs they are using). The material is delivered via lectures, discussions, and bioinformatic exercises motivated by contemporary topics in molecular evolution. A hallmark of this workshop is the direct interaction between students and field-leading scientists. The workshop serves graduate

students, postdocs, and established faculty from around the world seeking to apply the principles of molecular evolution to questions of anthropology, conservation genetics, development, behavior, physiology, and ecology. The workshop also welcomes participants from federal agencies and science journalists. A priority of this workshop is to foster an environment where students can learn from each other as well from the course faculty. Content has been carefully selected to provide participants with the background and practical skills required by modern molecular datasets. The schedule addresses the following subject areas, with each subject having one or more exercises focused on practical data analysis and interpretation skills. An evolutionary perspective on molecular data: sequence matching; protein sequence versus protein structure; homology, orthology and paralogy; mathematical, statistical, and theoretical aspects of sequence database searches; multiple alignment; information resources Foundations of phylogenetic analysis: theoretical, mathematical, and statistical principles; sampling properties of sequence data; Maximum likelihood theory and practice; Bayesian analysis; hypothesis testing Species-level phylogenomics: species trees from gene trees; species delimitation; multi locus and SNP data; empirical examples. Deep phylogenomics: deep evolutionary relationships; lateral gene transfer; modeling approaches; topology testing; sequencing strategies. Foundations of population genetic analysis: neutral theory; coalescence theory; maximum likelihood and Bayesian estimation of population genetic parameters; empirical examples Population genomics: phylogeography; molecular ecology; next-generation population genetics; signatures of natural selection; natural populations of non-model organisms Comparative genomics: genome content; genome structure; gene and genome evolutionary dynamics; prediction of gene function. Molecular evolution integrated at organism and higher levels: population biology and ecology; natural selection; systematics and conservation. Molecular evolution integrated at lower levels: biochemistry; cell biology; physiology; natural selection; relationship of genotype to phenotype. As the course progresses, participants learn how to use the following software to address questions concerning the origins, maintenance, and function of molecular variation: ASTRAL, BEAST2, BEST, BPP, FASTA, FigTree, GARLI, MIGRATE, MAFFT, MP-EST, RaxML, RevBayes, PAML, PAUP*, Phybase, ipyrad and SVD Quartets. Students will have the opportunity to work with software on their own laptops as well receive training on how to use the same programs on a high performance computer.





Minutes from the Genetics Section's Annual Business Meeting are available by clicking here!

Comic



Comic by XKCD/ CC BY

Section officers, committees, and representatives

Section Officers

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Committees

Hall of Excellence

Robin Waples

James Wright Award

Amy Welsh
Andrea Schreier
Carol Stepien

Early Career Award

Helen Neville

Stevan Phelps Award

Ken Currens

Listserve

Andrew Whiteley

Membership

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Black Bass Symposium

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