



HCGS

Hubbard Center for Genome Studies

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Issue 9



NEWSLETTER

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Happenings at HCGS: Fall 2015

The fall semester starts off with a bang! GEN 712/812 (Introduction to Programming for Bioinformatics) focuses on learning Python. (Instructors: Dr. Fescha Abebe-Akele and Dr. W. Kelley Thomas).



Full class!



The 2015-2016 Saul O Sidore Memorial Lecture Series

This year's theme is Personal Genomic Medicine: social, ethical, and scientific implications. The first speaker in the series is Dr. Jane Foster from McMaster University. Her lecture "Gut Feelings: How the microbiome influences behavior" takes place on October 14 at 3pm in the MUB Theaters.

HCGS

Student:

Joseph Sevigny

Hello all. I am a first year graduate student here at UNH, currently working on



my Masters in Genetics under the guidance of Kelley Thomas. I first became interested in working with Kelley and his HCGS lab group as an undergraduate at New England College. At New England College, I began working with NH-INBRE, and later as a lab tech, studying circadian rhythms using the model organism *Melibe leonina*. Throughout the project we collaborated with the HCGS team to sequence *Melibe's* genome. We used this data to drive our research: we located genes related to the circadian clock, developed antibodies for *in situ* hybridization experiments, and used the mitochondrial DNA to investigate the phylogenetic relationships of Gastropods ([see 2015 publication](#)). I quickly fell in love with the genomics and bioinformatics component of our research and am very glad to find a home here at HCGS working under the guidance of the skilled bioinformaticians and geneticists. My current research focus is studying metazoan mitochondrial DNA evolution and mito-metagenomics. When I am not doing research you can find me fishing or kayaking down at one of the ponds or rivers in Newmarket.

We are pleased to announce the 2015 Dartmouth Symposium for the Life Sciences, Signal Transduction in Development and Disease, to be held on Tuesday October 6 in Oopik Auditorium, Class of 1978 Life Sciences Center.

Discover how the study of cell signaling has revolutionized our understanding of animal development and provided strategies for the treatment of human diseases.

The full day program will feature the following seven speakers: They will be speaking about:

Signal Transduction in Development and Disease

- Kathryn Anderson, Ph.D. Professor and Chair of Developmental Biology Program, Sloan-Kettering Institute
- Yashi Ahmed, M.D., Ph.D. Associate Professor of Genetics, Geisel School of Medicine at Dartmouth College
- Jayaraj Rajagopal, M.D. Center for Regenerative Medicine, Massachusetts General Hospital
- Jean-Paul Vincent, Ph.D. Group Leader, The Francis Crick Institute
- Denise Montell, Ph.D. Duggan Professor of Molecular, Cellular and Developmental Biology, University of California, Santa Barbara
- Michael Cole, Ph.D. Professor of Pharmacology and Toxicology, and of Genetics, Geisel School of Medicine at Dartmouth College
- James Bradner, M.D. Associate Professor, Dana-Farber Cancer Institute, Harvard Medical School

Admission is free, and refreshments and lunch will be provided. We welcome the attendance of all faculty, physicians, researchers, post-docs, graduate students and undergraduate students interested in the life sciences. We hope to see you there!

This month we had the opportunity to host Francesca Leasi from the Smithsonian Institution. Here is what she had to say:

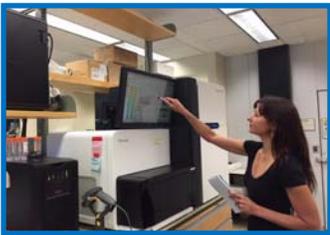
My name is Francesca Leasi (<http://invertebrates.si.edu/leasi.htm>) and I am a postdoctoral fellow at Smithsonian National Museum of Natural History, under the program Global Genome Initiative (<http://www.mnh.si.edu/ggi/>). My research project focuses on the genome investigation of neglected microscopic organisms living in the marine sediments (meiofauna).

Along with Prof. W. Kelley Thomas and his staff, we aim to address how the genomes of these microinvertebrates change in time and at different ecological conditions. This is a novel and important topic, especially for such organisms that represent one of the most diverse ecological communities. Nonetheless, working on tiny animals, which mostly lack published genome references, is very challenging.

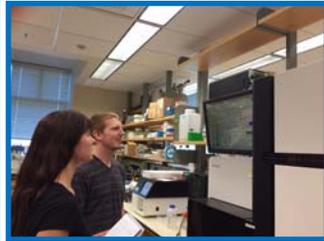
I had the luck and the pleasure to spend one week learning genomics techniques and data analysis under the guide of Stephen Simpson for lab work, Jordan Ramsdell for bioinformatics, and the continuous supervision of W. Kelley Thomas and Krystalynne Morris. Besides the extremely nice and comfortable working environment, I was impressed about the high quality of facilities and expertise. We succeeded in achieving genomic information from those critters more than my highest expectations and hopes. We now are analyzing data and start accomplishing the first important results.

I am very glad and excited about our ongoing collaboration and look forward to being back to UNH for additional work and to improve my skills.

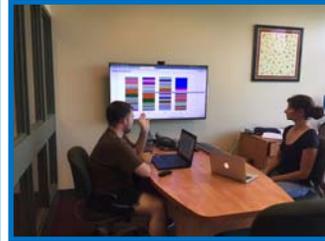
Francesca watching her run.



Steve and Francesca check out the Hi Seq 2500.



Jordan showing Francesca the QIIME pipeline.



Kelley sitting in on the tutorial.



DNA gives us the tool to go back through the generations to find out details about the very earliest days of our species and where we all came from.

—Spencer Wells

Publications: If you have any publications resulting from data generated by the HCGS that you would like to have listed here, please send the citation to Cynthia.Wiggin@unh.edu. **Please acknowledge our NSF MRI Grant in your publications: NSF DBI-1229361.**

Abebe-Akele F., Tisa L.S., Cooper V.S., Hatcher P.J., Abebe E., Thomas W.K., Genome sequence and comparative analysis of a putative entomopathogenic *Serratia* isolated from *Caenorhabditis briggsae*. BMC Genomics. 2015 Jul 18;16:531. doi: 10.1186/s12864-015-1697-8.