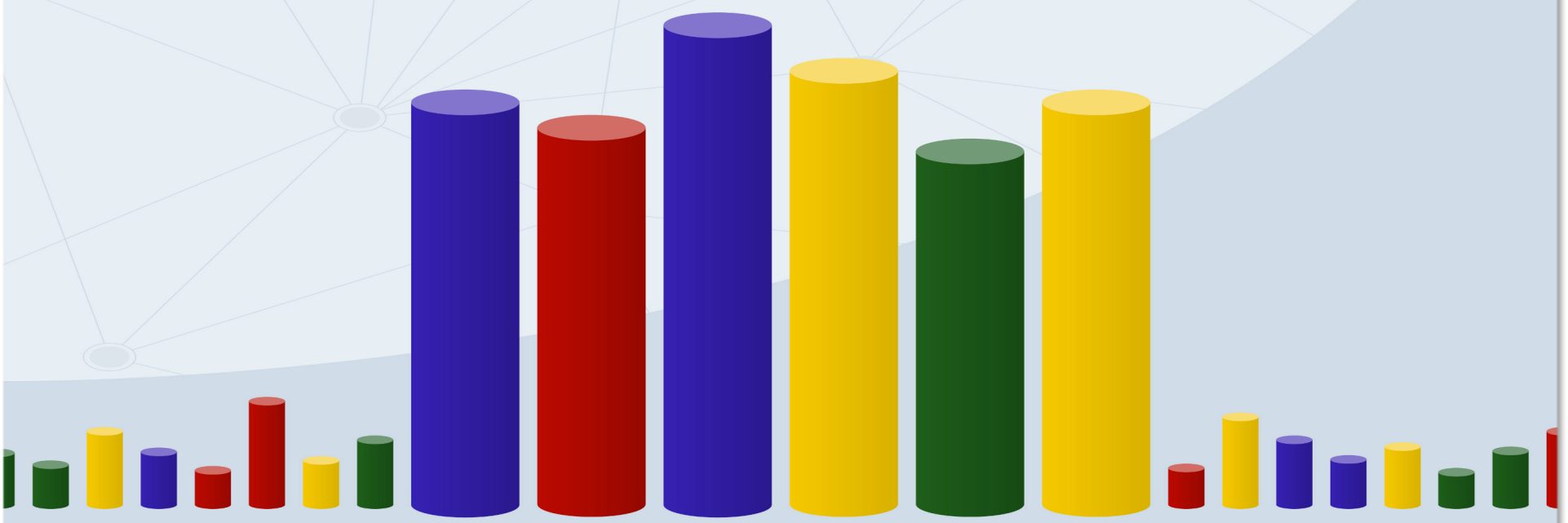
Cold Spring Harbor Laboratory

Simons Center for Quantitative Biology

2020 SCQB ANNUAL REPORT



Cover Image: Interpretable neural networks for genomics, credit Peter Koo (In Press at *Nature Machine Intelligence*).

LETTER FROM THE CHAIR

AMONG ITS OTHER ADVANTAGES, computational and mathematical research has the virtue of being able to be done almost anywhere. Indeed, the work that we do in the SCQB is sometimes better done in a quiet home than in a bustling workplace, free from the distractions of meetings, lectures, and frequent travel. As a result, while 2020 was not without challenges for researchers at the SCQB, the inconveniences we experienced were relatively mild overall, and they have been at least partly offset by opportunities for increased productivity.

Adam Siepel

It is true that we have missed our regular face-to-face interactions with our colleagues, our travel to scientific meetings, and the social events at CSHL. On the other hand, owing in part to increased time for writing, 2020 was an exceptionally good year for the Center in terms of publications and grants, with more than $8M in new awards (p.14) and over 40 publications and preprints (p.10). In addition to major research grants from the National Institutes of Health, National Science Foundation, the Simons Foundation and other foundations, we recently obtained a half-million-dollar grant from the NIH to improve our high-performance computing capabilities, including both new graphical processing units (GPUs) and large-memory computers.

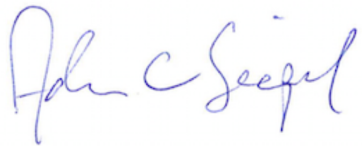
Owing to the pandemic, we have taken a hiatus from faculty recruiting, and hiring of postdocs and staff has somewhat slowed. Instead, we have focused on helping our recent hires settle into life at CSHL. Indeed, they are off to an outstanding start: Peter Koo has already taken two new PhD students and hired two postdocs as well as a programmer; similarly, Hannah Meyer's group has grown to four and Saket Navlakha's to five. To help fuel these growing groups, we recently initiated a new post-doctoral program in machine learning designed to support quantitative scientists who wish to transition into biology (p. 8). At the same time, several former postdoctoral associates took advantage of a less frantic schedule to wrap up their work at CSHL and move on to new jobs, predominantly in industry, including Maggie Crow (Genentech), Hussein Hejasi (Jansen Pharmaceutical), Niklay Rozhkov (Biogen), and Noah Dukler (Arpeggio Biosciences). (Sara Ballouz is the exception, remaining in academia; p. 9). In addition, the QB group awarded two new PhDs in 2020, to Elizabeth Hutton and Kristina Grigaityte (p. 8).

Furthermore, the reach of QB across CSHL continues to grow through affiliated faculty in neuroscience, genomics, cancer, and other areas. Growth in the CSHL Cancer Center has been particularly pronounced this year. Three QB faculty members were invited to join the Cancer Center: McCandlish, Meyer, and Koo. In addition, I was asked to serve as co-leader (with Chris Vakoc) of the Cancer Genetics and Genomics Program, which has a growing emphasis on QB. At Director Dave Tuveson's initiative, the Cancer Center has further promoted QB through a round of pilot projects designed to promote collaboration between quantitative biologists and experimentalists, including seven projects on the topics ranging from basic molecular biology (Koo, McCandlish, Gillis) to immunology (Meyer) to applied cancer diagnostics (Krasnitz) and comparative genomics (Siepel).

Like thousands of other scientists around the world, some of us have been inspired by the pandemic to undertake research projects directly concerned with Covid-19. For example, Saket Navlakha's group used machine-learning methods to identify high-risk Covid patients from early patterns of disease progression (p. 4). In addition, my own group is studying the genome sequences of bats to better understand the likely source of the zoonotic transmission of CoV-2 to humans.

I recently had the opportunity to present a summary of our recent activities in QB to the CSHL Scientific Advisory Council. Viewing a slide on the involvement in QB across CSHL, one of them the neuroscientist Karel Svoboda noted that fully a third of the CSHL faculty is now either directly involved in QB or closely associated with it, making our program one of the largest and strongest among our peer institutions around the world. Clearly there is much more work to do, but it was a moment in which to savor how far we have come in just a few busy years.

Best Wishes for the New Year,



Adam Siepel, PhD, Chair
December 30, 2020

OVERVIEW

THE SIMONS CENTER FOR QUANTITATIVE BIOLOGY IS focused broadly on revealing how genomes work, how they evolve, and what makes them go wrong in disease. Investigators at the SCQB pursue diverse research interests in a wide variety of different areas, but our research continues to be permeated by four major themes: **Gene Regulation, Evolutionary Genomics, Genomic Disease Research, and Genomic Technology Development.**

GENE REGULATION

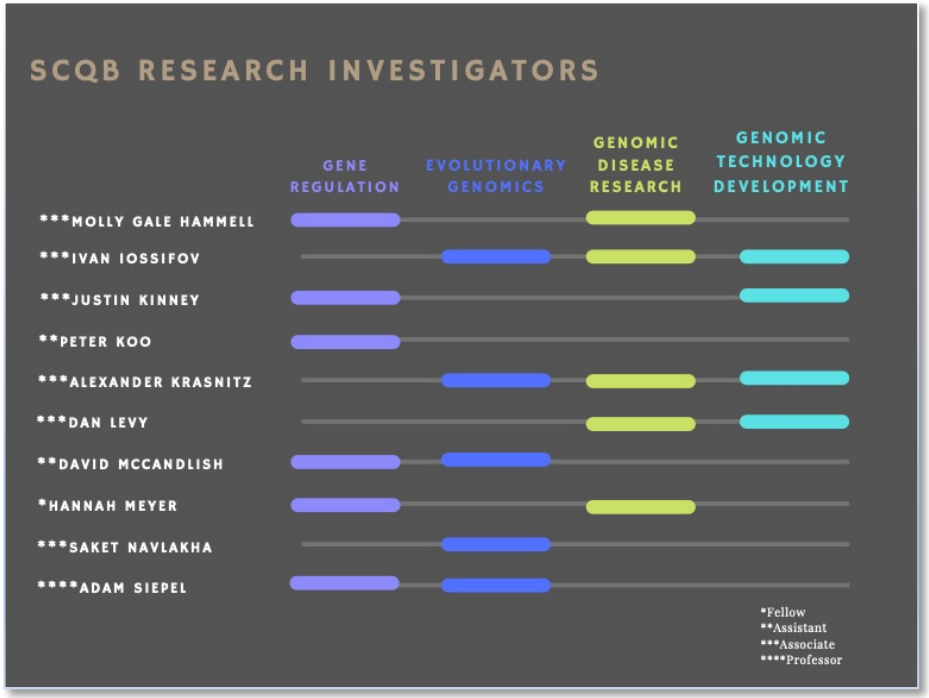
Several researchers at the SCQB are interested in developing both theoretical and experimental methods, along with computational and mathematical tools, for elucidating the relationship between biological sequences and biological functions ranging from gene expression to protein function. Ongoing studies in this area address the behavior of small noncoding RNAs, inference of gene regulatory networks, and the impact of transposable elements on gene expression. In addition, researchers at the SCQB are broadly interested in mathematical modeling of the regulation of gene expression in mammals, ranging from transcription factor binding and chromatin accessibility, to transcription initiation and elongation, to the determination of RNA stability.

EVOLUTIONARY GENOMICS

Other scientists at the SCQB develop theory and mathematics to address a number of open questions in evolutionary genetics, including the dynamics of evolution when mutation is rate-limiting or exhibits biased patterns, and the evolutionary implications of epistasis, i.e., interactions between mutations and genes. Additional studies at the Center use evolutionary methods to identify regulatory elements, to reconstruct early human history, and to estimate the fitness consequences of new mutations in the human genome. Researchers also use evolutionary signatures to aid in the identification of genes associated with autism spectrum disorder and employ phylogenetic methods to study the evolution of tumors.

GENOMIC DISEASE RESEARCH

Several researchers at the Center are trying to understand the genetics of autism spectrum disorder (ASD) through the analysis of large genomic data sets, while other researchers are developing mathematical and statistical tools to characterize the cellular composition, genomic disruptions, evolutionary history, and invasive capacity of malignant tumors. In addition, scientists at the Center are investigating the role of transposable element activation in neurodegenerative diseases, particularly amyotrophic lateral sclerosis (ALS) and frontotemporal dementia (FTD).



Researchers are also interested in diverse modeling and statistical inference problems having to do with cancer and immunology, often through consideration of single-cell sequencing data. A majority of the SCQB are active participants in the CSHL Cancer Center. Our faculty are represented across two of the three major Cancer Center programs: Cancer Genetics and Genomics (CGG) and Gene Regulation and Cell Proliferation (GRCP).

GENOMIC TECHNOLOGY DEVELOPMENT

Various research groups in the SCQB are working on the development of new DNA and RNA sequencing methods, single-cell genomic technologies, and cancer diagnostics. Our scientists have also pioneered the development of massively parallel reporter assays for characterizing the relationship between regulatory sequences and gene expression, including both transcription and RNA splicing.

COLD SPRING HARBOR LABORATORY was shut down except for essential operations from March to June 2020, and research activity in the SCQB was forced to proceed in virtual form, through heavy use of Zoom video conferencing and Slack workspaces. Some workers have now returned to their offices, but the majority continue to work from home. Despite these challenges, research at the SCQB has continued at full throttle, resulting in a number of major accomplisments this year. Selected projects are highlighted below.

How to tune out common odors and focus on important ones

Saket Navlakha

A dog with its nose buried in flowers is still able to notice odors from other plants and animals. Should a predator like a fox appear, the dog can suppress the signal of the flowers and amplify the scent of the predator, and then react appropriately. This adjustment is enabled by habituation, a form of simple memory that suppresses neural activity in response to repeated neutral stimuli. This process is critical in helping the dog guide attention toward the most salient and novel features in the environment.

Dogs have complex brains, so Associate Professor Saket Navlakha turned to the fruit fly olfactory system to understand how the simple fly brain learns to ignore prevalent odors to focus on newer but rarer odorants. In a recent study, Navlakha and postdoctoral researcher Yang Shen used a known connectivity map for the nearly 100,000 neurons in the fruit fly brain to understand the mechanisms the fly uses to solve the habituation problem from an algorithmic perspective.

The researchers found that odor habituation is driven by an important signal filtering process. When a fly detects an odor, a few select neurons (called Kenyon cells) respond to it. The pattern of firing in these responding neurons make up what's called the "tag" for the odor. If an odor is constantly present but conveys no urgent information to the fly, the neurons that make up the odor's tag will start to decrease their activity over time. This is the brain habituating to a background smell. An odor tag with fewer active neurons is less likely to elicit a response in an organism than an odor with lots of neuron activity. As a result, smells that are around all the time can be ignored in favor of a new odor that is faint but important. A fly brain suppresses responses to repeated odors, but the process can also be reversed if the odor becomes more rare or important to the fly. These findings may apply to dogs or humans, and could be used to train artificially intelligent machines.

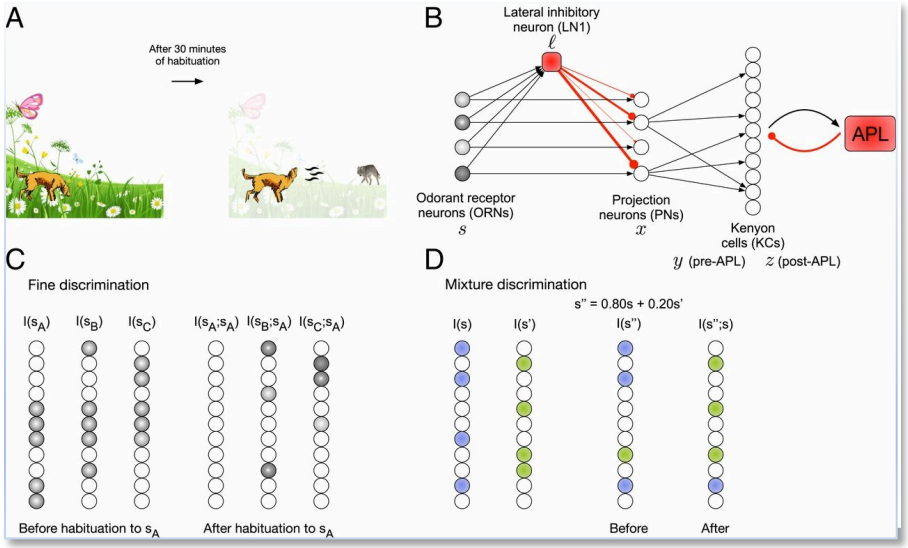


Illustration of the fruit fly olfactory circuit and two habituation-related problems. (A) Cartoon illustration of the effects of short-term habituation. (B) Overview of the fruit fly olfactory circuit. (C) Illustration of fine discrimination. (D) Illustration of foreground (mixture) discrimination.

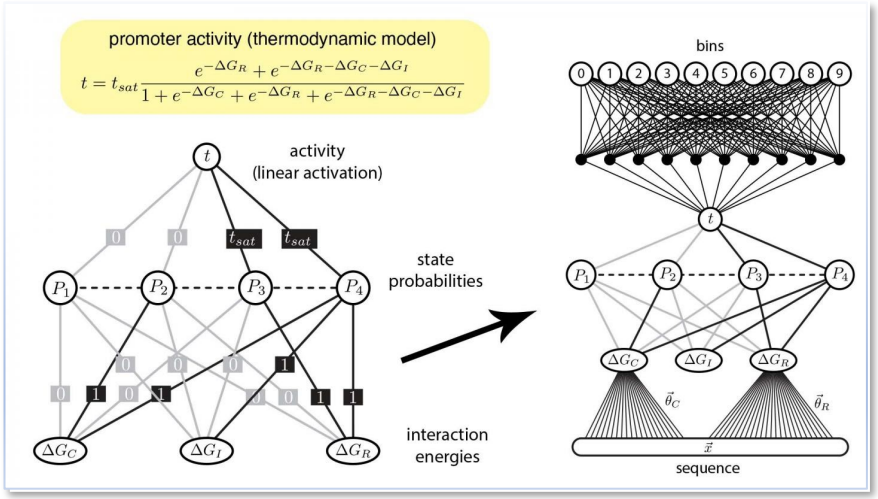
Yand Shen, Sanjoy Dasgupta, and Saket Navlakha, "Habituation as a neural algorithm for online odor discrimination" was published in *PNAS* on May 11, 2020.

Machine Learning Interprets Gene Regulation

Justin Kinney

Machine-learning (ML) algorithms are widely used to analyze the dizzying array of molecular signals that control how genes function, but these algorithms often produce complex "black box" models that are difficult for humans to understand. Associate Professor Justin Kinney and postdoc Ammar Tareen have a strategy to design ML models that are easier for biologists to interpret. Their models a type of artificial neural network (ANN), inspired by the way real neurons connect in the brain are used to analyze large data sets generated by "massively parallel reporter assays" (MPRA), which efficiently probe the downstream molecular effects of many thousands of variants in DNA sequences. Using MPRA data, Kinney and Tareen can train their ANNs to predict the precise DNA letters that regulate the expression of specific genes.

Cells don't need all proteins all the time. Instead, they rely on complex molecular mechanisms to turn on or off the genes that produce those proteins, as needed in



A mathematical thermodynamic model for gene regulation (top, left) is formulated as an artificial neural network (ANN) (bottom, left). Large DNA datasets are fed through the new ANN (right). The pattern of connections is presented in a way that is easy for biologists to interpret.

particular tissues or under particular conditions. When those regulations fail, disorder and disease usually follow.

Kinney and Tareen created custom ANNs that mathematically reflect principles biologists already use to understand the regulation of gene expression. As a result, they are able to force machine learning algorithms to interpret MPRA data in a way that biologists understand. These efforts highlight how modern, industrial AI technologies can be optimized for use in the life sciences. Having verified this new strategy to make custom ANNs, Kinney's lab is applying it in investigating a wide variety of biological systems, including key gene circuits involved in human disease.

Ammar Tareen and Justin B. Kinney, "Biophysical models of cis-regulation as interpretable neural networks" was posted to *bioRxiv* November 8, 2019 presented at the 1st Conference on Machine Learning in Computational Biology in Vancouver on December 13th.

Jesse Gillis

The Quadruplets That Aren't

Nine-banded armadillos have an unusual reproductive strategy. They always have litters of quadruplets, four genetically identical armadillo babies. Associate Professor Jesse Gillis and his colleagues decided to take advantage of that birth pattern to determine when random developmental noise starts leading to differences in the adult animals' physiology and behavior. They began by looking at a classic random process in genetics: the inactivation of an X chromosome where one of the two X chromosomes in females is randomly silenced in early embryonic development. Gillis' analysis found that X inactivation occurred when the armadillo embryos consisted of a mere 25 cells. And because the precise combination of 25 random maternal or paternal X selections was different in every embryo, it became a permanent "identifying signature" for each of the genetically identical members of the armadillo brood. The group then turned their attention to the 31 other pairs of chromosomes in the armadillos to see how much each contributes to overall gene expression.

Nine-banded armadillos always have litters of identical quadruplets. Researchers are now taking advantage of that system to study nongenetic sources of variation among individuals.

The researchers used a machine-learning method to estimate when those unique ratios became fixed in cell lineages. They estimated that this fixation happened when the embryos had just a couple of hundred cells, meaning that one cell early in development is the progenitor of millions of cells later in life. That one cell is instrumental in stablishing different patterns of gene expression in each armadillo embryo, influencing other developmental processes, and eventually yielding differences in traits. To determine what those downstream effects might be, Gillis and his team examined differences in overall gene expression. They found that armadillo siblings varied in their expression of about 500 to 700 of their 20,000 genes (although the scientists also expect that their analysis missed some fluctuations, so this might be an underestimate). Moreover, it wasn't always the same 700 genes or so that were affected in each litter, offering further evidence that randomness dictated the variation. Those gene expression differences, in turn, seemed to correlate with differences in a variety of traits, especially those associated with immune and hormonal processes. Most obviously, in one litter, some of the genes were associated with muscle growth and those siblings did indeed vary significantly in size. While further work is needed to confirm these associations, Gillis and his colleagues estimated that approximately 10% of the total variation they observed among the armadillos could be attributed to developmental noise.

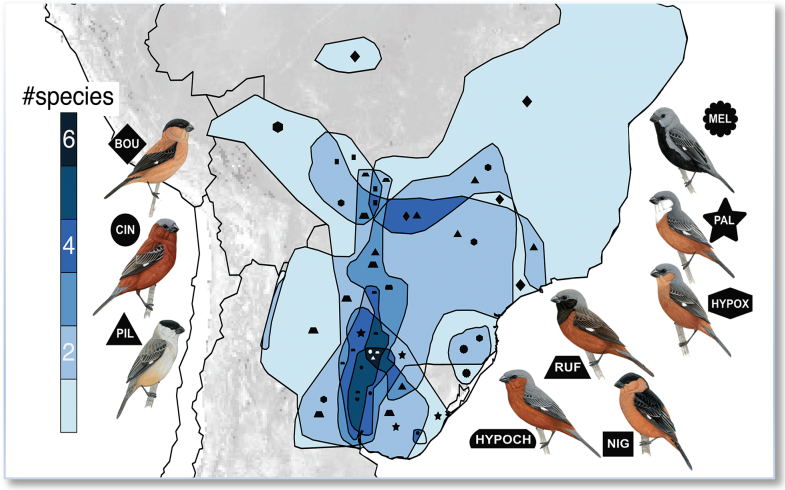
Sara Ballouz, Maria T. Pena, Frank M. Knight, Linda B. Adams, and Jesse A. Gillis, "The transcriptional legacy of developmental stochasticity" was posted to *bioRxiv* on December 12, 2019.

Birds of a feather *do* flock together

Adam Siepel

Nearly 200 years ago, Charles Darwin puzzled over the striking diversity among finch-like birds of the Galapagos Islands, and his observations helped him develop his theory of evolution by natural selection. Recently, biologists at Cornell University who study a related group of birds the finch-like capuchino seedeaters of South America called on Professor Adam Siepel's group to help deepen their understanding of the forces that cause organisms to separate into distinct species.

Capuchino seedeaters are of interest because they have diversified from their common ancestor relatively recently. The various species of seedeaters all resemble one another in body shape, but they differ in plumage and song. These differences are caused by large numbers of variations in only a few dozen spots in otherwise remarkably similar genomes. These small genetic "islands of differentiation" emerged at some point as these species evolved, but it is unclear exactly how or when this occurred.



In South America, different species of capuchino seedeaters live in overlapping territories. In some areas, as many as six different species live in the same places. Each species has a distinctive coloring and song. Illustration by Ben Wigler (CSHL) based on an illustration by Leonardo Campagna (Cornell University).

Two different genetic processes can create islands of differentiation: selective sweeps or a genetic incompatibility limiting the passage of specific segments of DNA within a population. Computational tools developed in Siepel's lab allowed his team, led by postdoc Hussein Hejase, to discriminate between these possibilities. Comparing the genomes of 60 birds from five species, they confirmed that most of the islands of differentiation that separate today's seedeater species arose due to selective sweeps. Siepel said the finding shows that even quite striking islands of genetic differentiation can be explained by selective sweeps that acted on newly emerging species.

Hussein A. Hejase, Ayelet Salman-Minko, Leonardo Campagna, Melissa J. Hubisz, Irby J. Lovette, Ilan Gronau, and Adam Siepel, "Genomic islands of differentiation in a rapid avian radiation have been drive by recent selective sweeps" was posted to the *Proceedings of the National Academy of Sciences* on December 1, 2020

SCQB members join the fight against Covid-19

This year, some of our members have redirected their expertise towards untangling aspects of Covid-19.

In particular, Associate Professor **Saket Navlakha** teamed up with researchers at the Memorial Sloan Kettering Cancer Center in order to better understand Covid-19 disease severity in cancer patients using machine-learning algorithms. This computational tool can be used to identify high-risk patients early in their disease progression, aiding in clinical decision-making and selecting treatment options.

Molecular analyses suggest that SARS-CoV-2 crossed into humans from an animal species, most likely a bat. Postdoc Armin Scheben in **Adam Siepel**'s lab, wants to know how it is that bats are able to tolerate so many viral infections without getting sick and dying. By studying the genome sequences of several species of bats, Scheben is gaining insights into antiviral immune responses that may ultimately shed light on the zoonotic transmission of Cov-2 to humans.

The Jamaican fruit bat.

Saket Navlakha, Sejal Morjaria, Rocio Perez-Johnston, Allen Zhang, and Ying Taur, "Projecting COVID-19 disease in cancer patients using purposefully-designed machine learning" was posted to *medRxiv* on August 25, 2020.

Armin Scheben, Olivia Mendivil-Ramos, Melissa Kramer, Sara Goodwin, Sara Oppenheim, Daniel J Becker, Michael C. Schatz, Nancy B. Simmons, Adam Siepel, and W. Richard McCombie, "Unraveling molecular mechanisms of immunity and cancer-resistance using the genomes of the Neotropical bats *Artibeus jamaicensis* and *Pteronotus mesoamericanus*" was posted to *bioRxiv* on September 9, 2020

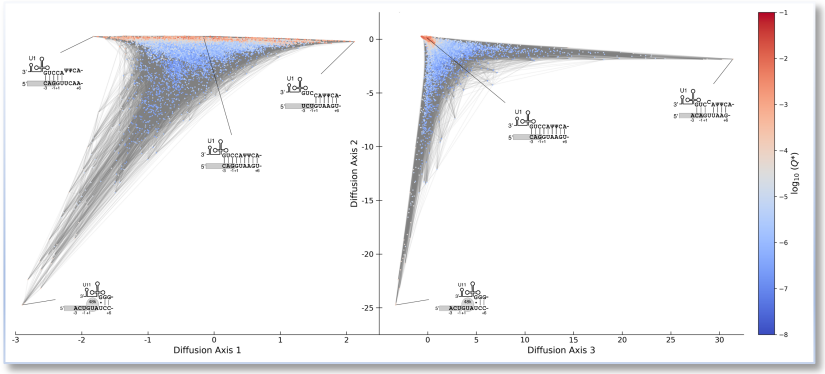
COLLABORATIONS

MEMBERS OF THE SCQB maintain close collaborative ties across CSHL and with other local area groups. This year, there has been a major effort to better integrate quantitative biology in cancer research at CSHL. In 2020, Assistant Professors David McCandlish, Peter Koo, and Fellow Hannah Meyer were added to the roster of the **CSHL Cancer Center**. Here we highlight two studies that are representative of our 2020 collaborative efforts with the Cancer Center.

David McCandlish and Justin Kinney apply computational methods to human cancer

David McCandlish

When **David McCandlish** and **Justin Kinney** spoke with Jason Sheltzer (CSHL Fellow and Cancer Center member) after a recent seminar, the researchers realized they might be able to apply computational methods already developed by McCandlish and Kinney to study human cancer, a major focus of Sheltzer's lab. McCandlish focuses on computational methods for modeling genetic interactions while, Kinney applies ideas from physics to estimating probability distributions. Fellow Jason Sheltzer wondered if they might



Visualization of the distribution of 5′ splice sites inferred by SeqDEFT.

be able to apply the surprising mathematical connections between these techniques to cancer. As detailed in a recent preprint, the team developed a method, called SeqDEFT (Density Estimation using Field Theory) to understand the accumulation of chromosomal abnormalities during cancer progression.

Wei-Chia Chen, Juannan Zhou, Jason M. Sheltzer, Justin B. Kinney, David M. McCandlish, "Non-parametric Bayesian density estimation for biological sequence space with applications to pre-mRNA splicing and karyotypic diversity of human cancer" was posted to *bioRxiv* on December 10, 2020.

Peter Koo applies deep-learning approach to pancreatic cancer in collaborative study

Peter Koo

Assistant Professor **Peter Koo** teamed up with Professor Chris Vakoc, co-leader of the Cancer Genetics and Genomics Program, to examine the interferon (IFN) transcriptional response and pancreatic cancer. The IFN response is a conserved pathway that protects organisms from pathogens and malignancy. Using a deep-learning approach, the team characterized the transcriptional function of ZBED2, a sequence-specific transcriptional repressor. Their findings suggest that high ZBED2 is acquired during pancreatic cancer progression to suppress the IFN response pathway and to promote lineage plasticity, a powerful contributor to the pathogenesis of human cancer.

Tim D. D. Somerville, Yali Xu, Xiaoli S. Wu, Diogo Maia-Silva, Stella K. Hur, Larissa M.N. deAlmeida, Jonathan B. Preall, Peter K. Koo, Christopher R. Vakoc "ZBED2 is an anatagonist of interferon regulatory factor 11 and modifies cell identity in pancreatic cancer" was posted to *Proceedings of the National Academy of Sciences* on May 8, 2020.

New York Genome Center

Ivan Iossifov

Several SCQB faculty members continue to have affiliations with the New York Genome Center (NYGC). Associate Professor **Ivan Iossifov** is core faculty member at the NYGC where his research focuses on large autism sequencing projects. Professor Adam Siepel continues to co-lead the **Population Genomics Working Group** at the NYGC, now with David Knowles, PhD, of the NYGC. Held virtually this year due to the Covid-19 pandemic, this group brings together leading population and statistical geneticists and focuses on human population genomics, statistical analyses, and applications to precision medicine.

Molly Gale Hammell

This year, Associate Professor **Molly Gale Hammell,** a member of the NYGC Center ALS Consortium, received NIH funding for her collaborative work with Hemali Phatnani (NYGC & Columbia University) to determine whether transposable elements are inducing neurotoxicity or neuroinflammation downstream of TDP-43 pathology in patients with frontotemporal dementia or Alzheimer's disease.

EDUCATION AND OUTREACH

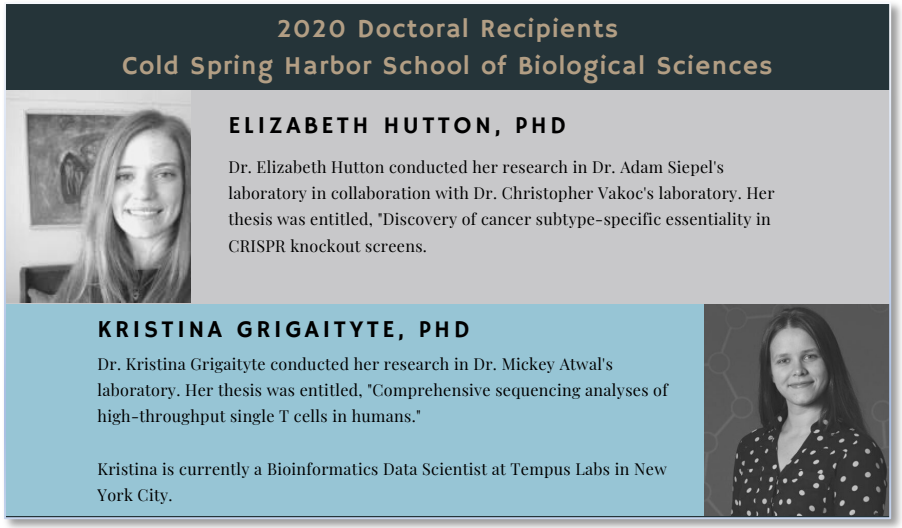
THE SCQB SERVES AS A HUB for research, training and education in the quantitative biological sciences. Students, postdocs, and staff are encouraged to participate in regular symposia, weekly informal gatherings, classes covering advanced quantitative material, and journal clubs focused on cutting-edge research.

PhD training program

Justin Kinney, Alex Dobin & Hannah Meyer

We continue to offer a broad training program in quantitative biology to PhD students through the **Cold Spring Harbor Laboratory School of Biological Sciences**. This program includes a **2.5-day QB Bootcamp** which introduces incoming students to Python programming and high-performance computing followed by a **22 lecture QB course** taught by a team of QB faculty. The lectures series focuses on a wide range of topics in **machine learning, algorithms, population genetics, functional genomics, image analysis and biophysics**.

QB course instructors include: Associate Professors **Justin Kinney** (lead instructor), Professor **Adam Siepel**, Assistant Professors **Alex Dobin**, **David McCandlish**, **Peter Koo**, CSHL Fellow **Hannah Meyer**, and Research Assistant Professor Jon Preall.



A FOCUS ON MACHINE LEARNING

The Center now has over a dozen faculty members who are doing research in **machine learning** (ML), with applications in neuroscience, genomics, plant biology, cancer, and other areas. Knowledge of machine learning is becoming essential to navigate the real-world complexities of biological data analysis. As a result, faculty in the Center have designed new and exciting opportunities for students and postdocs related to ML.

Independent study program for CSHL graduate students

Students who choose to pursue their research in the SCQB are now encouraged to participate in a newly initiated mentored independent study program. In this program, students work individually or in small groups with a supervising faculty member to design a program of directed reading in quantitative graduate-level course material. Students then pursue these studies in parallel with their thesis research throughout the remainder of their time in the CSHL School of Biological Sciences.

Peter Koo

Assistant Professor **Peter Koo** launched an independent study course designed for Quantitative Biology (QB) track students at the CSHL School of Biological Sciences. Beginning in the summer and continuing over an eight-week period, nine CSHL graduate students participated in a self-study course working through the book "**Pattern Recognition and Machine Learning**" by Christopher Bishop. The course, co-instructed by Drs. **McCandlish**, **Kinney**, **Siepel,** and **Krasnitz**, covered topics in linear models, neural networks, kernel methods, graphical models, and sampling methods.

Opportunities for postdoctoral fellows

The SCQB launched a **Post-doctoral Training Program in Machine Learning** designed to support quantitative scientists who want to transition into biology, with a particular focus on machine learning and data science. Participating faculty include Alex Dobin, Tatiana Engel, Jesse Gillis, Molly Gale Hammell, Justin Kinney, Peter Koo, Alex Koulakov, David McCandlish, Hannah Meyer, Partha Mitra, Saket Navlakha, Adam Siepel, and Tony Zador.

AWARDS AND RECOGNITION

$500K NIH grant for Graphical Processing Units (GPUs) and large-memory nodes

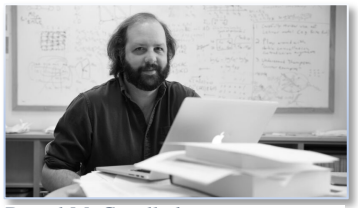
Members of the SCQB including **Adam Siepel**, **Alex Dobin, Molly Gale Hammell, Jesse Gillis, Justin Kinney, David McCandlish,** and **Tatiana Engel** were recently awarded a Shared Instrumentation grant from the NIH that will address two crucial limitations of the computing environment at CSHL: limited availability of Graphical Processing Units (GPUs) and large-memory compute nodes. Both GPUs and large-memory nodes are increasingly in demand to facilitate computations in many areas of biological research, including several of primary interest at CSHL, spanning genomics, quantitative biology, neuroscience, and structural biology. These new nodes will substantially enhance the overall computational infrastructure at CSHL, enabling a great deal of innovative research.

Tatiana Engel named 2020 Sloan Fellow

Tatiana Engel

Assistant Professor **Tatiana Engel** was named a 2020 Sloan Fellow. Engel is being honored for her work in the field of neuroscience. Her lab focuses on developing computational models of how populations of neurons in the brain give rise to cognition and how this neural activity is coordinated across different regions of the brain. The Sloan Fellowship is awarded by the Alfred P. Sloan Foundation to researchers in recognition of distinguished performance and unique potential to make substantial contributions to their field. Cold Spring Harbor Laboratory is home to six current and past Sloan Research Fellows, including Assistant Professor **David McCandlish** and Professor **Adam Siepel.**

David McCandlish receives grant from the John Templeton Foundation



David McCandlish

Assistant Professor **David McCandlish** received a grant from the Templeton Foundation for his work on the role of mutational biases in molecular adaption. The John Templeton Foundation serves as a philanthropic catalyst for discoveries relating to the deepest and most perplexing questions facing humankind.

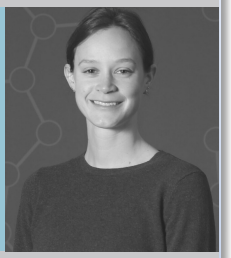
2020 SCQB Alumni

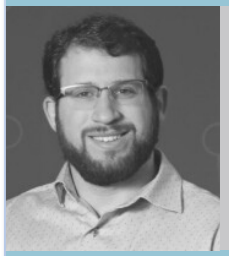
SARA BALLOUZ, PHD

Dr. Sara Ballouz, formerly of the Gillis Lab, is now a Group Leader at the Garvin-Weizmann Centre for Cellular Genomics in Sydney, Australia.

MAGGIE CROW, PHD

Dr. Maggie Crow, formerly of the Gillis Lab, is now a Bioinformatics Scientist at Genentech in San Fransisco, CA.



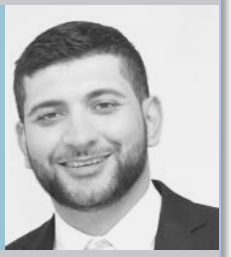


NOAH DUKLER, PHD

Dr. Noah Dukler, formerly of the Siepel Lab, is now a Bioinformatician at Arpeggio Biosciences in Boulder, CO.

HUSSEIN HEJASI, PHD

Dr. Hussein Hejasi, formerly of the Siepel Lab, is now a Scientist in Computational Genomics at Jansen Pharmaceutical Companies of Johnson & Johnson in Titusville, NJ.



NIKOLAY ROZHKOV, PHD

Dr. Nikolay Rozhkov, formerly of the Gale Hammell Lab, is now a Scientist II at Biogen in Boston, MA.