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THE TENTH ANNUAL

Harvard Undergraduate Research Opportunities in Science (HUROS) Fair

ABSTRACTS

November 14, 2019
Harvard University

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Welcome to the 2019 Harvard Undergraduate Research Opportunities in Science (HUROS) Fair

What is HUROS?

The HUROS is a poster session where Harvard's science research groups explain their research to undergraduates and discuss possible undergraduate research projects.

What is Science Research?

Contemporary research in the sciences spans boundaries across traditional disciplines such as biology, chemistry, mathematics, statistics, physics, astrophysics, earth and planetary sciences, psychology, medical sciences, computer science, and engineering. For example, some researchers employ computational and chemical techniques to elucidate the structures of biological molecules; others strive to solve an engineering challenge with inspiration from a biological organism; and yet others investigate stem cells with a goal of developing therapies for human diseases.

What is the purpose of the HUROS?

This purpose of HUROS is to:

- ⇒ Provide a time and space for researchers from all of the Harvard's campuses and Harvard-affiliated research laboratories to speak in person with Harvard undergraduates interested in science research.

- ⇒ Connect research mentors with undergraduates interested in joining a lab or research group.

- ⇒ Promote Harvard programs, offices and organizations that administer fellowships, funding programs, and summer research internships that encourage undergraduate research and organize research conferences.

Which groups are here today?

The 2019 poster session includes researchers from the Faculty of Arts & Sciences, School of Engineering and Applied Sciences, Harvard Medical School, Harvard School of Dental Medicine, Harvard School of Public Health, Massachusetts General Hospital, McLean Hospital, Brigham and Women's Hospital, Boston children's Hospital, and more. We are grateful for the participation of these research groups and their support of undergraduate research.

Some of the other nearly 2,000 research labs at Harvard may have research opportunities for undergraduates, but are not able to attend the 2019 fair. See our website at http://lifesciences.fas.harvard.edu/harvard-affiliated-labs for more comprehensive listings of research areas and laboratories at Harvard. If you need help navigating your research path, you can set up an individual meeting with the Science Undergraduate Research Advisor, Dr. Anna Babakhanyan (ababakhanyan@fas.harvard.edu).

How do I navigate the HUROS?

Introduce yourself to the poster presenters and ask them to explain their research. Think about their research, hot it may relate to what you already know and ask questions.

Most of the posters are organized alphabetically by last name to encourage you to browse a number of different research areas. You may discover a new area or approach that captivates your interest. Finally, we have number of informational tables that provide information regarding summer research opportunities and funding.

Who sponsors the HUROS?

The Science Education Office in the Division of Science and the Office of Undergraduate Research and Fellowships (URAF) jointly sponsor this conference. We also thank the Harvard College Undergraduate Research Association (HCURA) for their participation.

Science Research Opportunities for Undergraduates: FAQs

lifesciences.fas.harvard.edu/research

Where can I do research?
There are nearly two thousand science research laboratories at Harvard. They are located not only at the Cambridge campus (Faculty of Arts & Sciences and School of Engineering and Applied Sciences), but also at Harvard Medical School, Harvard School of Public Health, and Harvard-affiliated hospitals and research institutions. See a list at http://lifesciences.fas.harvard.edu/harvard-affiliated-labs.

When can I start an independent research project in a laboratory or research group?
Most students dedicate the first semester of their first year getting acclimated to college life, college courses, and extracurricular activities. Some students join a lab the second semester of their first year or the summer after first year, while many others begin independent research during their sophomore year. Some students may start even later; however, if you intend to complete a senior thesis, plan to join a research group at the latest by the beginning of your junior year.

How can I find a research group to join?
A good place to start is to peruse the information in the Research tab of the Science Education website at http://lifesciences.fas.harvard.edu. Go to *Harvard-affiliated Labs* in the Research tab to find links to Harvard-affiliated research groups. For personalized advice, the Science Undergraduate Research advisor, Dr. Anna Babakhanyan (ababakhanyan@fas.harvard.edu) is here to help you define your research interests, find prospective labs, create a science-focused resume, write letters of inquiry to faculty, prepare for meetings with professors, and discuss funding or course credit options.

Do I need previous experience doing research?
You don't necessarily need previous experience to join many of Harvard's research labs. Most research groups are willing to train and mentor undergraduates who have limited previous lab or field research experience. Over time you will gain the skills and knowledge you need

for an independent project. Also, most students acquire basic laboratory skills in the laboratory sections of their science courses, and these help you transition into a research environment.

Can I earn course credit for term-time lab research?
Yes. The requirements for course credit vary among the different science and engineering concentrations, so it's best to contact a Concentration Advisor for specific details. The contact information for each of the Concentration Advisors is on the Life Sciences Education website in the Concentrations tab. For other concentrations, please contact the respective department.

Can I be paid for doing research during the summer or term-time?
Yes, but note that you can't simultaneously get paid and earn course credit for your research. For summer research, there are many sources of funding. Go to http://lifesciences.fas.harvard.edu and select *Research Opportunities* in the Research tab to see a list of funding opportunities. Notable funding sources include the Harvard College Research Program (HCRP) and the Faculty Aide Program. In addition, if you are eligible for the Federal Work-Study Program, you can qualify for term-time and summer research funding.

For more information or to make an appointment:
Please contact the Science Undergraduate Research Advisor, Dr. Anna Babakhanyan at ababakhanyan@fas.harvard.edu to schedule an advising meeting. She can help prepare for the interviews, provide information about funding and help with fellowship proposals and more.

Visit the Science Education Website at:
http://lifesciences.fas.harvard.edu/harvard-affiliated-labs

Index of Posters by Research Area

(numbers represent poster numbers and NOT page numbers)

Abbreviations

BCH: Boston Children's Hospital

BCMP: Dept. of Biological Chemistry & Molecular Pharmacology, HMS

BIDMC - Beth Israel Deaconess Medical Center, HMS

BME: Biomedical Engineering

BWH: Brigham and Women's Hospital

CCB: Chemistry and Chemical Biology

CPB: Chemical and Physical Biology

CSB: Computational and Systems Biology

HDRB: Human Developmental and Regenerative Biology

HEB: Human Evolutionary Biology

HMS: Harvard Medical School

HSPH: Harvard School of Public Health

HST: Health Sciences and Technology

IDI: Infectious Disease and Immunology

MCB: Molecular and Cellualr Biology

MEEI: Massachusetts Eye and Ear Infirmary

MGH: Massachusetts General Hospital

MGH/HST Athinoula A. Martinos Center for Biomedical Imaging,
Massachusetts General Hospital, Harvard Medical School

OEB: Organismic and Evolutionary Biology

PSYCH: Psychology

NB: Neurobiology

SCRB: Stem Cell and Regenerative Biology

Poster Abstracts

Note: *posters are arranged by the faculty/Principal Investigator last name, see map for poster location.*

Poster 1. Surgical Molecular Imaging Laboratory: Bench to Bedside Approaches to Advance Brain Tumor Treatment

Presenters: Amanda Clark, Sylwia Stopka
Principal Investigator: Nathalie Agar, Nathalie_Agar@dfci.harvard.edu
Dept. of Neurosurgery, BWH, HMS
60 Fenwood Rd. Room 8022 Boston, MA. 02115
https://agarlab.bwh.harvard.edu/

Cancer therapeutics have improved dramatically over the last decade, but many of these advances have not translated into improved outcomes for patients with brain tumors. Cancers of the brain and central nervous system (CNS) represent a diverse array of tumor types with more than 120 histologically or molecularly distinct types, which represents one of the challenges to successful treatment. A second challenge to the successful treatment of brain and CNS tumors is the blood-brain barrier (BBB), which is a combination of physical and biochemical barriers that regulate the passage of molecules, including therapeutics, into and out of the brain, thus impacting therapeutic efficacy. The Surgical Molecular Imaging Laboratory uses a combination of novel imaging techniques and both targeted and untargeted molecular biology approaches to investigate drug distribution and response in brain tumors, such as glioblastoma, diffuse intrinsic pontine glioma, and pediatric low grade astrocytomas. For example, in patient-derived xenograft models of glioblastoma, we showed that a targeted anti-cancer therapeutic (Erlotinib) displayed heterogeneous drug distribution within tumors with limited drug penetration at the proliferative tumor edge. Furthermore, a drug dose-dependent response was observed in the cell signaling network and transcriptome of the tumors. These results suggested that erlotinib's failure in treating brain tumors could be due to the combination of lower drug concentration and availability at the tumor edge which highlights the importance of understanding drug delivery and distribution to improve treatment of brain tumors.
Number of hours per week: Negotiable
Requirements: No prior research experience is required.

If interested email: Nathalie_Agar@dfci.harvard.edu

Poster 2. Increasing Ube3a in substance P (Tac1+) or progesterone receptor (Pgr+) expressing neurons of VMHvl heightens aggression

Presenters: Yi Nong, Morgane Boillot
Principal Investigator: Matthew Anderson,
mpanders@bidmc.harvard.edu
Department of Neurology and Pathology, BIDMC
330 Brookline Avenue, Boston, MA 02115, USA

Heightened aggression is a common comorbidity of autism spectrum disorder (ASD).Yet the molecular and neuronal circuit mechanisms underlying the ASD-associated aggression remains unknown. Here we reported that transgenic Ube3a mice (Ube3a2x mice, modeling ASD due to maternal 15q11-13 triplication) display increased Aggression. We also found that increasing UBE3A in glutamatergic neurons of ventral lateral subdivision of ventral medial hypothalamus (VMHvl) is sufficient to elevate aggression. We further define the neuronal subpopulation in VMHvl where increased Ube3a heightens aggression. To explore the role of Pgr+, Tac1+ or Oxtr+ neurons in regulating aggressive behavior, we applied Cre-targeted chemogenetics and stereotactically injected AAV-hSyn-DIO-hM3D(Gq)-mCherry virus into VMHvl of Pgr-Cre, Tac1-Cre or Oxtr-Cre male mice. Four weeks after the virus injection, we found that administering CNO dramatically increases attack behavior in VMHvl Tac1+ and Pgr+ neurons with a smaller effect when targeted to Oxtr+ neurons. Thus, chemogenetic activation of Tac1+, Pgr+, or Oxtr+ VMHvl neurons is sufficient to increase aggression. To determine the neuronal subpopulations in VMHvl where increased Ube3a in these neurons heightens aggression, we stereotactically injected AAV-hSyn-DIO-Ube3a virus into VMHvl of Pgr-Cre, Tac1-Cre or Oxtr-Cre male mice. We found that increasing Ube3a in Tac1+ or Pgr+, but not in Oxtr+ neurons increases aggression. Further, when co-injecting inhibitory AAV-DIO-hM4D(Gi)-mCherry viruses with AAV-hSyn-DIO-Ube3a viruses into VMHvl of Tac1-Cre mice, CNO reversed the heightened aggression due to increased Ube3a in Tac1+ neurons. The results indicate increasing Ube3a in the Tac1+ or Pgr+ expressing subset of neurons in VMHvl increases aggression.
Number of hours per week: 6-10 hours/week
Requirements: none
If interested email: mpanders@bidmc.harvard.edu

Poster 3. Role of vascular smooth muscle cells in stroke outcome
Presenters: Dmitriy Atochin,
Principal Investigator: Dmitriy Atochin, atochin@cvrc.mgh.harvard.edu
Cardiovascular Research Center, Cardiology, MGH, HMS
MGH, 149 East, 13th street, CVRC, 4th floor, Charlestown, MA 02129,
http://cvrc.massgeneral.org/faculty/dmitriy-atochin-phd/

Recent works highlight the therapeutic potential of targeting cyclic guanosine monophosphate (cGMP)-dependent pathways in the context of brain ischemia/reperfusion injury (IRI). Although cGMP-dependent protein kinase I (cGKI) has emerged as a key mediator of the protective effects of nitric oxide (NO) and cGMP, the mechanisms by which cGKI attenuates IRI remain poorly understood. We used a novel, conditional cGKI knockout mouse model to study its role in cerebral IRI. We assessed neurological deficit, infarct volume, and cerebral perfusion in tamoxifen-inducible vascular smooth muscle cell-specific cGKI knockout mice and control animals. Stroke experiments revealed greater cerebral infarct volume in smooth muscle cell specific cGKI knockout mice than in all control groups. Our results identify a protective role of cGKI in vascular smooth muscle cells during ischemic stroke injury. Moreover, this protective effect of cGKI was found to be independent of gender and was mediated via improved reperfusion. These results suggest that cGKI in vascular smooth muscle cells should be targeted by therapies designed to protect brain tissue against ischemic stroke.
Number of hours per week: negotiable
Requirements: none
If interested email: atochin@cvrc.mgh.harvard.edu

Poster 4. Deep Residual Auto-Encoders for Expectation Maximization-based Dictionary Learning
Presenters: Bahareh Tolooshams
Principal Investigator: Demba Ba
Crisp Lab. MD 140. 33 Oxford St. Cambridge,
https://crisp.seas.harvard.edu

Principal component analysis, dictionary learning, and auto-encoders are all unsupervised methods for learning representations from a large amount of training data. In all these methods, the higher the dimensions of the input data, the longer it takes to learn. We introduce a class of neural networks, termed RandNet, for learning representations using

compressed random measurements of data of interest, such as images. RandNet extends the convolutional recurrent sparse auto-encoder architecture to dense networks and, more importantly, to the case when the input data are compressed random measurements of the original data. Compressing the input data makes it possible to fit a larger number of batches in memory during training. Moreover, in the case of sparse measurements, training is more efficient computationally. We demonstrate that, in unsupervised settings, RandNet performs dictionary learning using compressed data. In supervised settings, we show that RandNet can classify MNIST images with minimal loss in accuracy, despite being trained with random projections of the images that result in a 50% reduction in size. Overall, our results provide a general Principald framework for training neural networks using compressed data.
Number of hours per week: 15hr/week for upperclassmen, full time in the summer.
Requirements: Prefer Seniors.
If interested email: btolooshams@seas.harvard.edu

Poster 5. Qualitative and Quantitative MRI Study of Infant Corpus Callosum Following Surgery and Critical Care for Long-Gap Esophageal Atresia

Presenters: Chandler Mongerson, Dusica Bajic
Principal Investigator: Dusica Bajic, dusica.bajic@childrens.harvard.edu
Boston Children's Hospital Department of Anesthesiology, Critical Care and Pain Medicine 300 Longwood Avenue, Bader 3 Boston, MA 02115
http://www.childrenshospital.org/research/researchers/b/dusica-bajic

Previous studies in pre-term infants report white matter abnormalities of the corpus callosum (CC) as an important predictor of neurodevelopmental outcomes. Our cross-sectional cohort study aimed to determine qualitative and quantitative CC size in critically ill infants following surgical and critical care for long-gap esophageal atresia (LGEA) – in comparison to healthy infants using brain MRI. Non-sedated brain MRI was acquired in full-term (n=13) and premature (n=13) patients following treatment for LGEA, and controls (n=20) <1 year corrected age. Neuroradiologist performed qualitative evaluation of T1-weighted images. ITK-SNAP was used for 2-D and 3-D manual CC segmentations that allowed for quantification of CC size. Qualitative MRI analysis indicated underdeveloped CC in both full-term and premature patients in comparison to controls. Our study showed decreased

absolute ($F(2,42)=20.40$, $p<0.001$) and normalized ($F(2,42)=16.61$, $p<0.001$) CC volumes following complex perioperative treatment for long-gap esophageal atresia in both full-term and premature patients, suggesting delayed or diminished CC growth in comparison to controls, with no difference between patient groups. 2-D surface area analysis should not substitute time-consuming 3-D volumetric analysis of CC. Future research should look into neurodevelopmental outcomes and a role of the CC as an early marker of neurodevelopment in this unique infant population.
Number of hours per week: Working and studying in research is an opportunity to express passion for medical studies. I encourage students to create their own schedule and routines that will lead to a successful accomplishment of research competencies (data presentation in oral and written forms as abstracts, posters, and/or manuscripts).
Requirements: none
If interested email: dusica.bajic@childrens.harvard.edu

Poster 6. Association of Anesthesia and Sedation Exposure with Brain MRI in Critically Ill Infants
Presenters: Jason Shen
Principal Investigator: Dusica Bajic, Dusica.Bajic@childrens.harvard.edu
Department of Anesthesiology, Critical Care and Pain Medicine, BCH
1 Autumn Street, 3rd Floor AU 388.1 Boston, MA 02115,
http://www.childrenshospital.org/research/departments-divisions-programs/departments/anesthesiology/meet-the-team

Previously, we reported smaller total brain volumes in critically ill full-term and premature infants following perioperative critical care for long-gap esophageal atresia (LGEA; n=13/group). Our present study investigated the relationship between anesthesia and postoperative sedation with brain MRI measures. Our secondary outcome measures were length of muscle relaxation, antibiotic, and total parenteral nutrition (TPN) administration (days). Brain MRI was obtained following treatment for LGEA. Neuroradiologists reported clinically relevant findings. We quantified normalized brain volumes (%intracranial volume). Clinical measures were obtained from patients' charts: number of anesthesia events, cumulative MAC anesthesia hours, days of postoperative sedation (viz. intubation length), paralysis, antibiotic use, and TPN administration. Pearson's correlation coefficient was used to measure linear associations between variables. We report positive association

between age and anesthesia exposure for both infant groups. There was no association for number of anesthesia events with number of MRI findings or normalized brain volume in either group. However, cumulative anesthesia exposure was associated with increased number of MRI findings in full-term infants and smaller normalized brain volume in premature infants. Length of sedation for intubation (days) showed positive association with number of MRI findings and negative association with normalized brain volume only in premature infants. There were no associations between length of paralysis, antibiotic use, or TPN administration with brain MRI measures in either group. Reported associations do not represent causative relationships. Future studies should evaluate other measures of care to better understand intrinsic disease and treatment impact for life-saving LGEA repair.
Number of hours per week: 40 hours/week for summer.
Requirements: none
If interested email: Dusica.Bajic@childrens.harvard.edu

Poster 7. Identifying "control stations" of cancers to develop targeted therapies

Presenters: Vajira Weerasekara
Principal Investigator: Nabeel Bardeesy
bardeesy.nabeel@mgh.harvard.edu
Massachusetts General Hospital Cancer Center
185 Cambridge St. CPZN 4100, Boston, MA 02114

Tumor suppressor LKB1 is a major mediator of cellular metabolism and stress response. However, it has not being clearly understood how loss of LKB1 leads to tumorigenesis. While number of studies point towards altered metabolism as a candidacy for tumor initiation in this context, nodes which deregulated upon LKB1 loss to drive such alterations remains unknown. My aim is to identify these regulatory nodes where LKB1 composes its tumor suppressor function at sub-organelle level. Identification of these "control stations", would allow us to successfully develop targeted therapies for LKB1 mutant cancers, which currently lack successful treatment strategies. Bardeesy lab had allowed me to device a multifaceted approach to tackle my question of interest. I have successfully applied bioinformatics, state-of-the-art imaging technologies, metabolomics and mouse genetics approaches to query my hypotheses in the perspective of cancer biology. This project will allow one to learn, understand and apply Biochemistry, Cell Biology,

Genetics and Computational Biology to unravel complex questions of cancer.
Number of hours per week: Hours can be negotiable depending on your academic term and year
Requirements: No prior research experience is required
If interested email: vweerasekara@mgh.harvard.edu and bardeesy.nabeel@mgh.harvard.edu

Poster 8. A novel class of activatable alkylating compound targets IDH mutated biliary cancer

Presenters: Shi Lei
Principal Investigator: Nabeel Bardeesy
bardeesy.nabeel@mgh.harvard.edu
MGH/HMS/Broad Institute
185 Cambridge Street, Boston, 02114, http://www.mghbardeesylab.com/

Cholangiocarcinoma is an epithelial malignancy of the biliary tract with poor prognosis that has been steadily rising incidence over the past several decades. Gain-of-function hot-spot mutations in the isocitrate dehydrogenase gene (IDH) are among the most common genetic alterations in these tumors. The mutant IDH enzyme produces high levels of the oncometabolite 2-hydroxyglutarate (2HG), which perturbs epigenetic control and leads to cell differentiation defect. We sought to uncover novel synthetic lethal therapeutic interactions in IDH1m comparing the sensitivity of IDH1m and IDH wild type cancer cells to extensive drug libraries. Among the most selective and potent hits in IDH1m cells was an orphan compound that we found leverage the defective differentiation state of IDH1m tumor cells and induce specific cytotoxicity. Associated with the differentiation defect, IDHm cells express high levels of SULT1A1 gene product, which is required for activation of the compound to alkylate cellular molecules and induce cell death. In result of the compound treatment, we observed DNA damage responses followed by apoptosis in these cells. Furthermore, in silico search and functional validation experiments revealed an extensive series of small molecules that share unifying chemical moieties and are cytotoxic to IDH1m cells. Thus, we have uncovered a novel class of Sult1a1 activatable alkylating compound leveraging the unique state of IDH1 mutated cholangiocarcinoma cells and demonstrated the potential of such compounds as a selective therapeutic strategy.
Number of hours per week: negotiable

Requirements: passion for science and sense of responsibility
If interested email: lshi7@mgh.harvard.edu and bardeesy.nabeel@mgh.harvard.edu

Poster 9. High-Field Neuroimaging of the Human Spinal Cord
Presenters: Robert Barry
Principal Investigator: Robert Barry, Robert.Barry@mgh.Harvard.edu
Brain & Spinal Cord Laboratory Athinoula A. Martinos Center for Biomedical Imaging, MGH/Harvard
149 13th Street, Charlestown, MA, 02129, fMRIresearch.com (and also martinos.org)

Magnetic resonance imaging of the human brain and spinal cord at an ultra-high magnetic field of 7 Tesla offers new opportunities to visualize structures with high spatial resolution and enhanced conspicuity, and to detect brain function and networks with greater sensitivity. This poster will highlight some of the technical challenges and recent advancements in functional imaging of the human brain and spinal cord at 7 Tesla, and present how this research may translate to the clinic to facilitate a more complete understanding of biological processes and etiologies of central nervous system diseases such as multiple sclerosis, amyotrophic lateral sclerosis, and spinal cord injury.
Number of hours per week: Negotiable for each individual student.
Requirements: Prior research experience is not necessary, though some programming skills and/or experience with data entry would be helpful.
If interested email: Robert.Barry@mgh.Harvard.edu

Poster 10. Cs6 clusters: evidence for a role of novel proteoglycan structures in experience-dependent clustered plasticity
Presenters: Gabriele Chelini
Principal Investigator: Sabina Berretta, sberretta@mclean.harvard.edu
McLean Hospital - Harvard Medical School
115 Mill street. Belmont, MA 02478

The mechanisms underlying experience-dependent learning arguably represent a major challenge for neurobiology. Elegant studies shifted the focus from single synaptic mechanisms to coordinated changes involving several synapses onto neighboring dendritic stretches. Recent findings from our group and others have shown a novel structure, i.e. CS6 clusters, enriched in 6-sulfated chondroitin sulfate proteoglycans (CS6-

CSPGs), potentially relevant to this mechanism. On the basis of their molecular composition we postulated that CS6 clusters may correspond to transient microenvironment contributing to coordinated synaptic plasticity. To test this hypothesis, we focused on the mouse barrel cortex (BC) and used a combination of somatosensory manipulations, immunohistochemistry and high resolution microscopy. Electron microscopy observation showed that CS6 clusters result from the accumulation of CS6-CSPG in the synaptic cleft and in astrocytes end-feet contacting synaptic terminals, within a segregated microenvironment. In naïve home-caged animals, we found that dendritic spine morphology within CS6 clusters is consistent with ongoing synaptic strengthening. Further evidence showed that unilateral sensory stimulation results in a significant increase of CS6 clusters in the corresponding BC, while, conversely, sensory deprivation induced a significant decrease in the number of clusters in the same brain region. Finally, numbers CS6 clusters in BC were positively correlated to the expression of the ARC protein, a key molecular player in experience-dependent plasticity. Together, these findings indicate that CS6 clusters form in response to specific stimulation with cellular and molecular characteristics consistent with locally coordinated plasticity, potentially corresponding to transient, multi-synaptic memory engrams.
If interested email: sberretta@mclean.harvard.edu

Poster 11. Ver-Eat-Tas: Generating an evidence base to reduce our collective food print for a more sustainable and equitable future
Presenters: Stacy Blondin
Principal Investigator: Stacy Blondin, blondin@post.harvard.edu
Harvard TH Chan School of Public Health
677 Huntington Ave, Boston, MA, https://dining.harvard.edu/about-huds/sustainability/ver-eat-tas

In order to nourish nearly 10 billion people by 2050, we need to collectively consume more sustainable diets – patterns of eating that promote human health, food security, social justice, cultural diversity, and environmental and economic well-being for present and future generations. While we o¬ften receive messages about how our food choices affect our health and taste buds, we rarely receive information about the environmental, economic, and ethical implications of our choices. VerEatTas is an initiative developed by researchers at the Harvard T.H. Chan School of Public Health, the Harvard University

Climate Change Solutions Fund, and the Office for Sustainability in collaboration with Harvard University Dining Services. The goal of VerEatTas is to provide greater transparency about the food choices we make on campus every day with the goal of improving our collective dietary sustainability. We are looking for students to help with data analysis and visualization for data on undergraduates' dietary intake and food waste. There may also be opportunities for original research, including designing and running studies. We are open to hourly, stipend, or research for credit options (8-10 hours/week, immediately or beginning in the spring term). Please contact Stacy Blondin at sblondin@hsph.harvard.edu to learn more!
Number of hours per week: 8-10 hours/week, spring term
Requirements: Data analysis experience
If interested email: blondin@post.harvard.edu

Poster 12. Uncovering the molecular pathway controlling transcriptional memory during differentiation and stress
Presenters: Carlos Perea-Resa, Michael Blower
Principal Investigator: Michael Blower, blower@molbio.mgh.harvard.edu
Molecular Biology Department- MGH Genetics Department, HMS
Simches Research Center 185 Cambridge St, 6th floor 02114 Boston (MA), https://molbio.mgh.harvard.edu/laboratories/blower

Every cell division chromosomes segregate from mother to daughter cells. However, how cells maintain gene expression programs across generations is poorly understood. In addition, how adjustments to the gene expression program are regulated during cell differentiation or in response to stress conditions, is not known. In the Blower lab we are currently studying the role of cohesin ring complex on those important processes. Cohesin regulates several aspects of RNA Pol II-mediated transcription and sister chromatid cohesion by forming loops of chromatin. We have recently discovered that a pool of cohesin is safeguarded across mitosis and plays a critical role in re-establishing gene expression in G1. Using human cells as a model organism in combination with CRISPR/Cas9 technology and cell cycle synchronization methods, we aim to uncover the role of cohesin and its regulators in gene expression dynamics across mitosis, during differentiation, and in various stress conditions. Understanding those processes could aid the development of therapies for a group of

diseases caused by mutations on genes encoding cohesin subunits or its regulators commonly known as cohesinopathies.
Number of hours per week: 10 hours/week would be optimal, negotiable.
Requirements: Attending 2-3 days/week would be optimal for cell culture maintenance.
If interested email: perearesa@molbio.mgh.harvard.edu and blower@molbio.mgh.harvard.edu

Poster 13. PD-1 ablation mediates anti-tumor immunity by regulating metabolism-driven lineage fate commitment and function of myeloid cells during emergency myelopoiesis

Presenters: Laura Strauss
Principal Investigator: Vassiliki Boussiotis, vboussio@bidmc.harvard.edu
Beth Israel Deaconess Medical Center
330 Brookline Avenue Room Dana 513-517

PD-1, a T cell checkpoint receptor and target of cancer immunotherapy, is also expressed on myeloid cells. We examined how PD-1 regulates the response of myeloid progenitors to cancer-driven emergency myelopoiesis and their function on anti-tumor immunity. We determined that GMP myeloid progenitors that expand during cancer-driven emergency myelopoiesis express PD-1. PD-1 was also expressed on tumor-infiltrating myeloid cells, including M-MDSC and PMN-MDSC, CD11b+F4/80+ macrophages and CD11c+MHCII+ dendritic cells (DC) in tumor-bearing mice, and MDSC in cancer patients. PD-1 ablation in PD-1 KO mice or treatment with PD-1 blocking antibody prevented GMP accumulation and MDSC generation and resulted in increase of effector monocytes, macrophages and DC. We generated mice with conditional targeting and selective elimination of PD-1 in myeloid or T cells. Compared to T cell-specific, myeloid cell-specific PD-1 ablation more effectively decreased tumor growth in three different tumor models. During cancer-driven emergency myelopoiesis only myeloid-specific PD-1 ablation prevented accumulation of GMP, skewed the myeloid cell fate commitment from MDSC to effector monocytes, macrophages and DC, and induced TEM cells with improved functionality. In response to growth factors of emergency myelopoiesis, PD-1-deficient myeloid progenitors displayed elevated mTORC1 activity, enhanced glucose uptake and mitochondrial biogenesis, and activation of cholesterol synthesis. As cholesterol induces proinflammatory differentiation of myeloid cells toward effector monocytes, macrophages and DC, and amplifies TLR

signaling, our findings suggest that metabolic reprogramming of emergency myelopoiesis and differentiation of effector myeloid cells, thereby reprogramming T cell responses, might be a key mechanism by which PD-1 blockade mediates anti-tumor function. Number of hours per week: Hours of work are negotiable depending on the needs and schedule of each individual student.
Requirements: Students at all levels are welcome. Prior experience is a plus.
If interested email: vboussio@bidmc.harvard.edu

Poster 14. Reverse Engineering and Reconstructing the Lung
Principal Investigator: Douglas Glenn Brownfield
brownfield@hsph.harvard.edu
MIPS Program, Department of Environmental Health, HSPH
665 Huntington Avenue, Building 1, Room G03, Boston, MA 02115,
https://www.hsph.harvard.edu/douglas-brownfield/

The Brownfield lab reverse-engineers developmental processes for the rational synthesis of tissues and organs. With this approach, we seek to understand how tissues are constructed during development, maintained in adulthood, and disrupted in disease. To reverse-engineer a tissue's construction, we utilize single-cell transcriptomics, microfabricated 3D organotypic culture, and genetically-engineered mouse models in order to 1) enumerate the cellular and microenvironmental components that comprise a tissue, 2) reconstruct each component's assembly during development, and 3) rationally reconstruct assembly processes in culture with a higher degree of extrinsic control. Focusing on the lung, Dr. Brownfield has charted the cellular and transcriptional program that underlies alveolar epithelial cell fate selection in the mouse lung (Treutlein and Brownfield et al., Nature, 2014), which has been credited as the first use of single-cell transcriptomics in a developing tissue. Harnessing this reconstruction (a genome-wide map wherein changes in gene expression are charted with single—cell resolution), we have identified the long-sought signal that selects (and surprisingly maintains throughout life) alveolar epithelial cell fate. In a similar manner, the lab will determine how the remaining cell types and microenvironmental components of the lung are assembled as well as employ microfabrication techniques to reconstruct assembly processes with a greater degree of extrinsic control. Finally, the lab hopes to translate its findings into molecular, cellular, and tissue therapies for treating lung

diseases such as bronchopulmonary dysplasia, pulmonary fibrosis, chronic obstructive pulmonary disease, and emphysema.
Number of hours per week: 6-10 hrs/week for Freshmen and Sophomores, 15-20 hrs/week for juniors and seniors.
Requirements: No prior research experience is required to apply. Students with interests or skills in 3D printing, device design, or programming are encouraged to apply.
If interested email: brownfield@hsph.harvard.edu

Poster 15. Operations Supported by Ketamine Anesthesia in Resource-limited Settings: Surgeons' Perceptions and Recommendations

Presenters: Daniela Suarez-Rebling
Principal Investigator: Thomas F. Burke, tfburke@partners.org
Division of Global Health Innovation, Massachusetts General Hospital
125 Nashua Street, Suite 910, mghglobalhealth.org

Background: Ketamine's wide safety margin has led to its use as a sole anesthetic agent in resource-limited settings. However, there are few recommendations on approaches to associated intraoperative challenges. The objective of this study was to gain surgeons' perceptions on performing operations supported by ketamine and to recommend best practices and techniques. Methods: A qualitative study was conducted using semi-structured interviews of surgeons experienced with performing operations supported with ketamine as the sole anesthetic agent. Interviews continued until thematic saturation. Open-response data was analyzed using thematic analysis as well as iterative group discussions about emergent themes. Results: Sixteen surgeons were interviewed regarding their operative experiences supported by ketamine across 12 countries. Surgeons universally felt that ketamine is safe, saves lives, and that they would administer it to a loved one in support of an operation if no anesthetist was available. Although lack of muscle relaxation with ketamine may require additional strategies to gain exposure, few surgical technical changes are necessary. While ketamine side effects are manageable, a single provider must always be dedicated to ketamine administration and patient monitoring. Surgeons should advocate for global policies, training and access. Conclusion: Ketamine is safe, can provide increased access to emergency and essential surgery, and requires few operative technical changes. Global standards on Ketamine training and use should be established.

Number of hours per week: Depends on arrangement with each individual student.
Requirements: Interest in global health is required.
If interested email: dsuarez-rebling@mgh.harvard.edu and tfburke@partners.org

Poster 16. High-index dielectric metasurfaces for enhanced magneto-optics
Presenters: Maryna Meretska
Principal Investigator: Federico Capasso, capasso@seas.harvard.edu
SEAS 9 Oxford st., room 125B room 125B,
https://www.seas.harvard.edu/capasso/

Magneto-optic (MO) non-reciprocal devices have a wide range of applications ranging from current sensors to integrated devices such as isolators and circulators. Recent advances in nanophotonics, specifically metasurfaces, and material science allow us to rethink the design of such devices. Due to the directionality of MO interactions, this effect can be enhanced when light is cycled multiple times through the same material volume. In the past, plasmonic nanoparticle resonances have been used to achieve this. These particles suffer from excessive losses and therefore did not result in useful devices. To mitigate losses while ensuring small device sizes, this project instead will employ Kerker resonances in high-index dielectrics, which have been recently studied in the emerging field of metasurfaces.
Number of hours per week: 15-20 hours/week
Requirements: Knowledge of LabView is preferred. This project requires student to work on the setup.
If interested email: mmeretska@seas.harvard.edu and capasso@seas.harvard.edu

Poster 17. Identifying a Causal Variant in the GDF5-UQCC1 Locus Underlying Human Developmental Dysplasia of the Hip
Presenters: Pushpanathan Muthuirulan, Mary Broker
Principal Investigator: Terence Capellini, tcapellini@fas.harvard.edu
Department of Human Evolutionary Biology, Harvard University, Cambridge, MA, USA
Developmental and Evolutionary Genetics Laboratory, Department of Human Evolutionary Biology, FAS/Harvard University, Peabody Museum, 5th Floor, 11 Divinity Avenue, Cambridge, MA 02138,

https://projects.iq.harvard.edu/evolutionary_genetics/people/terence-d-capellini-phd

Developmental dysplasia of the hip (DDH) is an abnormality of the hip joint resulting in an increased risk for joint dislocation with prevalence of 1 per 1000 live births. While partially heritable, the genetic mechanisms underlying DDH remain unknown. Growth differentiation factor 5 (GDF5) is the most reproducibly associated locus with DDH. Here, we have elucidated the regulatory control of the GDF5 gene during embryonic development, and found one on/off switch “GROW1” that modulates activity in the hip joint. We also identified a specific human mutation (G to A) residing within the GROW1 enhancer that modulates GDF5 activity. Loss of the GROW1 enhancer and its variant significantly lowers GDF5 expression in mice and humans. We next found a major hindlimb transcription factor, PITX1 bound at this variant position in both human and mouse chondrocytes. To move towards the demonstration of direct causality, we genetically engineered a mouse containing the single human risk base-pair change and identified that the human risk variant decreases PITX1 binding in vivo. Phenotyping of mice harboring DDH variant revealed hip-joint alterations in the directions of effects of DDH patients. These observations suggest the role of PITX1-mediated functional effects on the regulatory risk variant during DDH development.
Number of hours per week: It is negotiable, and depends on arrangement with each individual student
Requirements: none
If interested email: tcapellini@fas.harvard.edu

Poster 18. From Molecular Biomarker to Clinical Quantification
Presenters: Iris Zhou
Principal Investigator: Peter Caravan, caravan@nmr.mgh.harvard.edu
Athinoula A. Martinos Center for Biomedical Imaging, Institute for Innovation in Imaging, Department of Radiology, MGH, HMS
Building 149, Room 2301 13th Street Charlestown, MA 02129 USA,
http://caravanlabmgh.weebly.com/

The mission of Caravan Lab is to invent, develop, and apply molecular imaging probes (MRI, PET, CT, optical) to diagnose, stage, and guide treatment of human disease, particularly in the areas of fibrosis. Over half of all deaths are caused by diseases that have some fibrotic component. Chronic diseases of the heart (cardiomyopathies, coronary

disease), arteries (atherosclerosis), liver (hepatitis B, C, steatohepatitis), kidney (diabetic nephropathy), lung (pulmonary fibrosis), and many cancers all result in fibrosis/scarring of the tissue, which is characterized by excess deposition of extracellular matrix proteins, primarily type I collagen. Our group have recently demonstrated that molecular imaging based on collagen-targeted either positron emission tomography (PET) or magnetic resonance imaging (MRI) molecular probes may serve as promising alternatives with better sensitivity in detecting early fibrosis and potentially in distinguishing new, active fibrosis from stable disease in animal models of pulmonary fibrosis. PET offers exquisite sensitivity to interrogate molecular processes while MRI can provide multiple readouts of morphology, physiology, and metabolism. However, their application to lung imaging has been historically limited because of low proton density and the fast signal decay due to susceptibility artefacts at air-tissue interfaces for MRI, while PET quantification remains challenging due to respiratory motion, attenuation and regional variations in tissue, air and blood fractions. We aim to address these challenges by developing and validating a quantitative PET-MRI lung imaging tool to accurately measure morphological, physiological and molecular information from the patients with pulmonary fibrosis, enabling a more precise capturing of the extent of disease activity.
Number of hours per week: 15-20/week
Requirements: prior research experience is preferred but not required
If interested email: iris.zhou@mgh.harvard.edu and caravan@nmr.mgh.harvard.edu

Poster 19. Examination of a Novel Emerging Immune Checkpoint In Kidney Transplant Recipients
Presenters: George Kavalam, Sudipta Tripathi
Principal Investigator: Anil Chandraker, achandraker@bwh.harvard.edu
Transplantation Research Center, 221 Longwood Ave, LM 316

Introduction: The balance between T-cell immunoglobulin and immunoreceptor tyrosine-based inhibitory motif domain (TIGIT) and its co-receptor CD226 function as an ‘immune checkpoint’ with immunomodulatory functions in both T and NK cells. Immunomodulation is mediated through the balance of TIGIT/CD226 binding with the ligands CD155/CD112. Interaction of CD226 with the ligands CD155 and CD112 co-stimulates T cell, whereas TIGIT exerts the opposite effect and inhibits T cell response. This ligand/receptor network plays an important

role in various autoimmune diseases and cancer, but its role in transplantation remains unclear. We examined the expression levels of TIGIT, CD226 and their ligands CD155 and CD112 in kidney transplant recipients (KTR) and healthy controls (HC) to understand the relevance of TIGIT/CD226 co-signaling in transplantation. Methods: Blood samples were collected from HC and KTR and cell surface expression of CD226, TIGIT, CD155 and CD112 on peripheral T and NK cells were determined by flow cytometry. Results: We observed that in the KTR group both T and NK cell populations showed a significant decrease in TIGIT and an increase in CD226 expression compared to HC. Interestingly, in the KTR CD4+ T cells showed a significant increase in CD226 expression whereas CD8+ T cells showed a significant decrease in TIGIT expression. Both these changes lead to an increase in IFN-γ production and a pro-inflammatory environment. The predominant peripheral CD16+ NK cells also showed an inflammatory phenotype with both increased CD226 expression and decreased TIGIT expression and also showed a significant increase in the expression of both the ligands CD155 and CD112 in comparison to HC. Conclusions: Increased expression of CD226 in both T and NK cells and increased expression of its ligands CD155 and CD112 on NK
Number of hours per week: Negotiable
Requirements: Prior knowledge of basic cell culture techniques will be helpful but not essential.
If interested email: stripathi@bwh.harvard.edu and achandraker@bwh.harvard.edu

Poster 20. Characterization of oxycodone self-administration and withdrawal-associated negative affect in male and female rats
Presenters: Suman Guha, Nick Constantino
Principal Investigator: Elena Chartoff, echartoff@mclean.harvard.edu
McLean Hospital Basic Neuroscience Division
McLean Hospital 115 Mill Street MRC 215 Belmont, MA 02478,
https://www.chartofflab.com/

Opioid Use Disorder (OUD) is characterized by initial abuse, a transition from impulsive to compulsive drug-taking behavior, and emergence of withdrawal-associated negative affective states that promote relapse. There are documented sex differences in each phase of OUD. Here, we used a rat model of prescription OUD: oxycodone self-administration (SA), to delineate putative sex differences in acquisition and escalation

of drug-taking; abstinence induced withdrawal signs; and incubation of craving as measured by post-abstinence drug-seeking behavior. Adult male and female Sprague-Dawley rats learned to self-administer 0.06 mg/kg of oxycodone per infusion on an FR1 schedule of reinforcement for 8 d of 1-h short-access, followed by 14 d of 6-h long-access (LgA) and 14 d of abstinence. On abstinence day 15, rats underwent 2 h of non-reinforced SA in the previously drug-paired chamber. To monitor motivational state and reward sensitivity in each rat throughout the different addiction-like phases, intracranial self-stimulation (ICSS) was conducted either 16-h or 2-h after each days' SA session. Both male and female rats acquired oxycodone SA and escalated drug intake during LgA. Pattern analysis showed that rats moved to a periodic pattern of drug intake during LgA that became more entrained over time. Both sexes reinstated drug-seeking after 14 d of abstinence. The ICSS test showed that 2-h post oxycodone SA, ICSS thresholds tended to increase in males, but not females, suggesting an anhedonia-like response. Interestingly, both sexes exhibited an increased incubation of oxycodone craving after abstinence. Our results provide a nuanced characterization of oxycodone SA in males and females that suggest sex differences in addictive-like behavior and hence suggest ultimately sex-dependent approaches to treatment.
Number of hours per week: Negotiable, depending on the student
Requirements: Willingness to handle rats for behavioral experiments. Experience with this is better, but not necessary.
If interested email: echartoff@mclean.harvard.edu

Poster 21. Immune tolerance as a novel strategy for ameliorating neurodegeneration in glaucoma

Presenters: Shuhong Jiang
Principal Investigator: Dong Feng Chen,
Dongfeng_Chen@meei.harvard.edu
Schepens Eye Research Institute, Massachusetts Eye and Ear, HMS
20 Staniford Street, Boston, MA 02114, http://schepens.harvard.edu/

Glaucoma is a globally unmet medical challenge, the most frequent neurodegenerative disease and a leading cause of irreversible blindness worldwide. The mechanism underlying neurodegeneration in glaucoma is not fully understood. Previous research in our lab provided the first convincing evidence demonstrating a link among microbiome, heat shock proteins (HSPs), T cell-mediated autoimmune responses and

neurodegeneration in glaucoma. We showed that elevated intraocular pressure – a known risk factor of glaucoma – induced T cell-mediated responses to HSP60, which contribute critically to neuron loss in the disease. The high degree of homology between microbial, mouse and human HSPs suggests that neuron loss in glaucoma can be caused by bacterial-primed memory T cells specific to commensal bacterial HSPs that cross-react with mouse or human HSPs via a mechanism of molecular mimicry. This has led to our hypothesis that immune tolerance to bacterial HSP60 attenuates neuron loss and ameliorates neurodegeneration or disease progression in glaucoma. Here we show that intranasal administration of low dose HSP60 induced immune tolerance and led to increased T regulatory cells in mice without affecting the basal level of visual acuity and contrast sensitivity. Induction of immune tolerance to bacterial HSP60 significantly attenuated neuron loss and improved retinal and visual function in a mouse model of glaucoma or ocular hypertension when compared to saline-treated control mice. These results present an attractive antigen-specific therapeutic strategy for the prevention of vision loss in glaucoma. The study also sheds light on our understanding of the pathogenesis of brain neurodegenerative disorders and lead to innovative intervention for the treatment of neurodegeneration affecting other parts of the central nervous system.
Number of hours per week: Number of hours per week depends on arrangement with each individual student.
Requirements: No prior research experience is required.
If interested email: Shuhong_Jiang@meei.harvard.edu and Dongfeng_Chen@meei.harvard.edu

Poster 22. Restoration of hearing by CRISPR/Cas9 mediated genome editing in the Pmca2 deafness mouse model by protein delivery

Presenters: Corena Loeb
Principal Investigator: Zheng-Yi Chen
Zheng-Yi_Chen@meei.harvard.edu
Harvard Medical School/Mass. Eye and Ear
234 Charles Street, Boston MA,
https://scholar.harvard.edu/chenlab/home

1 in 500 newborns suffers from genetic hearing loss, and hundreds of genes are likely to be responsible for genetic hearing loss when mutated.

CRISPR/Cas9-mediated genome editing presents an opportunity to develop new type of treatment for genetic hearing loss by permanent editing that targets the mutations to restore hearing. However, most CRISPR/Cas9 has been performed in germline or in vitro by viral vectors or DNA vectors, which raise long-term safety concerns. Further in vivo efficiency has been generally low. To develop CRISPR based gene therapy to treat genetic deafness we explored direct in vivo protein:RNA complex delivery into a genetic deafness mouse model, Oblivion (Obl), due to a mutation in the Pmca2 gene, and assess the effect on hearing restoration. Direct protein:RNA complex injection in vivo led to dramatic hearing recovery across most frequencies. Hearing recovery was the most significant in the middle frequencies, by as much as 45dB. Hearing recovery was gRNA specific and dose-dependent. Application of Cas9:gRNA resulted in rescue of inner ear hair cells, which are lost to the Pmca2 mutation. Auditory neurites were persevered after Cas9:gRNA delivery, whereas in the control Obl mice a majority of them underwent degeneration.
Number of hours per week: flexible
Requirements: Prior research experience in related fields
If interested email: Zheng-Yi_Chen@meei.harvard.edu

Poster 23. Developing Accessible Pathways to Care for Borderline Personality Disorder (BPD): Supplementing Specialist Treatments to Address Supply and Demand Gap
Presenters: Gabrielle Ilagan, Evan Iliakis
Principal Investigator: Lois Choi-Kain, lchoikain@partners.org
McLean Hospital; Harvard Medical School
115 Mill St., Mailstop 312, Belmont, MA 02478
https://www.mcleanhospital.org/biography/lois-choi-kain

The Gunderson Personality Disorder Institute (GPDI) conducts research on the implementation of care for borderline personality disorder (BPD), a prevalent psychiatric disorder characterized by interpersonal sensitivity, affective instability and impulsivity. Our review assessed the supply of and demand for BPD treatments by estimating the total number of mental healthcare providers in 22 countries. The ratio of treatment-seeking patients with BPD to total providers ranged from 4:1 in Australia, the Netherlands, and Norway to 192:1 in Singapore. Upon including only providers certified in evidence-based treatments (EBTs) for BPD, ratios ranged from 49:1 in Norway to 148,215:1 in Mexico. Worldwide, there is

a shortage of providers available, much less specifically trained, to treat BPD. Thus, realistic treatment options apart from specialist EBTs must be considered, but unspecialized BPD care has been thought to be ineffective. We investigated this claim with a meta-analysis of outcomes in treatment as usual (TAU) groups of 16 trials of psychotherapies for BPD. For those in TAU, Hedges' g showed a small-to-moderate improvement in BPD symptoms (11 studies; g=0.371; 95% confidence intervals [CI: 0.246, 0.495]), small improvements in general psychopathology (14 studies; g=0.119; 95% CI [0.025, 0.214]) and global functioning (10 studies; g=0.254; 95% CI [0.123, 0.384]), and no effect for self-harm/suicidality (4 studies; g=0.003; 95% CI [–0.193, 0.199]). Hence, standard care may be a practical option, and a stepped care model with generalist treatments like Good Psychiatric Management (GPM) and its variants (e.g. GPM for Adolescents, developed by the GPDI lab) can also help meet the demand for BPD treatment. Taken together, these findings stimulate our ongoing research projects on a more accessible BPD treatment landscape.
Number of hours per week: 10 hours/week, negotiable
Requirements: Demonstrated interest in clinical work is recommended. Previous experience in literature review and statistical techniques relating to biomedical and psychological research is desired, but not required. Interest in any of the following ongoing project topics is a plus: the interplay of social cognitive, neuropsychological & attachment factors in BPD; generalist BPD treatments; brief treatment options for BPD; and a review and meta-analysis of smartphone-based interventions for BPD symptomatology
If interested email: gilagan@partners.org and lchoikain@partners.org

Poster 24. Characterization of RNA in Extracellular Vesicles and Applications to Reading Out the Brain
Presenters: Dima Ter-Ovanesyan,
Principal Investigator: George Church
Wyss Institute/Harvard
3 Blackfan Circle, Boston, MA 02115, http://arep.med.harvard.edu/

Exosomes are RNA-containing extracellular vesicles secreted by all cells. We set out to determine which RNAs are packaged into exosomes, and how the RNA profile of exosomes compares to that of donor cells. This question has been challenging to answer due to the difficulty in separating exosomes from Ribonucleoproteins (RNPs). We developed a

method to separate RNA inside exosomes from contaminating RNA using sequential enzymatic treatments with proteinase and RNAse. We applied this method to characterize the mRNA repertoire of exosomes from a variety of cell lines using RNA-Seq. We found that the mRNA profile of exosomes is highly correlated to that of cells. We then decided to build on this finding to develop a method to “read out” transcriptomes from human biological fluids. Using neurons as a proof of Principal, we developed a framework for identifying cell-type specific exosome markers, and applied it to immuno-isolate neuron-derived exosomes from cerebrospinal fluid (CSF) and blood. We are performing RNA-Seq on these exosomes to measure the neuronal transcriptome in humans. We hope these methods will have broad applicability in both diagnostics and the study of human biology.
Number of hours per week: Students are expected to work at least 15 hours per week, on average, during the semester, and full time during the summer. The length of the project is flexible. Although there is no obligation, we are interested in having students potentially continue on in our lab as Research Assistants after graduation for a year or two as a way to gain more research experience and make a larger contribution to the project.
Requirements: Molecular biology experience required. Experience with mammalian cell culture, RNA work, or protein biochemistry helpful but not required. Programming experience and computational skills analyzing high throughput sequencing data would also be helpful but are not required.
If interested email: dter@wyss.harvard.edu

Poster 25. Imaging metal content and stimulated secretion in the healthy and malignant secretory glands: from metallomics to molecular MRI

Presenters: Veronica Clavijo Jordan
Principal Investigator: Veronica Clavijo Jordan
MCLAVIJOJORDAN@MGH.HARVARD.EDU
Radiology - Harvard Medical School/Massachusetts General Hospital
149 13th St. Suite 2301, http://caravanlabmgh.weebly.com/

Metals play a crucial role in many cellular processes and are heterogeneously distributed within the cell and organs. In mitochondria, for example, iron–sulfur clusters act as redox catalysts in the electron transport chain and as catalytic sites in TCA cycle enzymes. Cellular

respiration, free radical detoxification, and cross-linking of collagen and elastin are regulated by copper-containing enzymes, and both iron and copper play critical roles in homeostasis of reactive oxygen species (ROS). In addition to its well-known structural role in zinc finger biochemistry, divalent zinc also serves as a regulatory messenger ion within cells and is stored and released along with hormones, enzymes, or metabolites released by secretory cells. Tissues such as the endocrine and exocrine pancreas, mammary glands, brain, and prostate are known to contain high levels of zinc, and zinc dysregulation is tightly linked to malignant transformations. Thus our lab has focused on characterizing the role of metal homeostasis by molecular imaging during cancer development in secretory organs such as the pancreas and prostate. We have been able to use metal sensitive MRI probes to detect the stimulated secretion of zinc, copper, and their ability to report early malignant changes in mouse models of pancreatic and prostate cancer. The emerging field of "metallomics" provides a new and innovative perspective to understand cancer development and response to therapy. By using our molecular imaging toolbox where we combine molecular MRI, PET/MRI, and synchrotron radiation x-ray fluorescence we can determine the metal dysregulation during onset of disease in order to intervene early, prevent further progression, and potentially promote cancer remission.
Number of hours per week: Negotiable.
Requirements: Needs to be willing to be exposed to animal models of cancer and imaging.
If interested email: MCLAVIJOJORDAN@MGH.HARVARD.EDU

Poster 26. Understanding—and Fixing—the Inner Ear
Presenters: David Corey
Principal Investigator: David Corey, dcorey@hms.harvard.edu
Department of Neurobiology, Harvard Medical School
Goldenson 443 220 Longwood Ave Boston, MA

We work on a fundamental problem in sensory neuroscience: how the vibration of sound is converted to an electrical signal by receptor cells of the cochlea. These cells, called hair cells for the tuft of mechanosensitive cilia on their top surface, open a set of ion channels when the cilia are moved by sound, and the resulting ionic current depolarizes the cells to initiate neurotransmitter release. We know many of the proteins in the mechanotransduction complex, but don’t know how

they connect to each other or how they change shape in response to mechanical force. Our work involves a combination of single-cell biophysics, cryo-electron microscopy and protein biochemistry; it has the ultimate goal of understanding the complex both structurally and biophysically, at an atomic level. All of these proteins are required for sensation of sound, and so it is not surprising that mutations in many of them cause hereditary deafness. We use mouse models of hereditary deafness, in which one or another gene for these proteins is nonfunctional, and we use new viral vectors to deliver replacement genes to the hair cells. In several of these models, we can rescue the deafness in mice. The ultimate goal will be to develop gene therapy methods for treating hereditary deafness in humans.
Number of hours per week: hour negotiable
Requirements: none, but prior laboratory experience preferred
If interested email: dcorey@hms.harvard.edu

Poster 27. HCF-1 regulates de novo lipogenesis through a glucose sensitive complex with ChREBP
Presenters: Dong Wook Choi
Principal Investigator: Nika Danial, Nika_Danial@dfci.harvard.edu
Department of Cancer Biology, Dana Farber Cancer Institute
360 Longwood Ave, Boston, MA 02215

Glucose metabolism provides both biosynthetic precursors and regulatory signals for de novo lipogenesis (DNL) — an anabolic process relevant for lipid/energy storage, mem- brane synthesis, and metabolic regulation at both cellular and organismal level. Carbo- hydrate Response Element Binding Protein (ChREBP) is a key transcriptional regulator of DNL in response to glucose- and high carbohydrate diet (HCD)-derived lipogenic sig- nals with important roles in both hepatic steatosis and cancer. Although several metabo- lites of glucose can activate ChREBP, the biochemical mechanisms underlying nutrient regulation of this transcription factor are still enigmatic. Here, we undertook unbiased proteomics analyses to compare the ChREBP-containing nuclear complexes in normal versus a genetic background in which glucose signals that normally activate ChREBP are blunted due to diminished hexokinase activity. This led to the discovery of the tran- scriptional co-regulator host cell factor 1 (HCF-1) as a novel ChREBP-interacting protein in a promoter complex that is assembled in a stepwise manner in response to lipogenic signals. Specifically, HCF-1 is O-

GlcNAcylated in response to glucose as a prerequisite for its binding to ChREBP and subsequent recruitment of OGT, ChREBP O-GlcNAcylation, and activation. Moreover, HCF-1:ChREBP complex resides at lipogenic gene pro- moters, where HCF-1 regulates H3K4 trimethylation to prime recruitment of the Jumonji C domain-containing histone demethylase PHF2 (KDM7C) for epigenetic activation of DNL genes. These findings define HCF-1's interaction with ChREBP as a novel mecha- nism whereby glucose signals are both relayed to ChREBP and transmitted for epigen- etic regulation of lipogenic genes.
Number of hours per week: It is negotiable
If interested email: Nika_Danial@dfci.harvard.edu

Poster 28. Undergraduate research opportunity to study knee osteoarthritis in the Quantitative Musculoskeletal Imaging Group Research (Q-MIG)
Presenters: Jeffrey Duryea, Rebecca Ramesbury
Principal Investigator: Jeffrey Duryea, jduryea@bwh.harvard.edu
Brigham and Women's Hospital, Thorn 333
https://www.brighamandwomens.org/radiology/research/quantitative-musculoskeletal-imaging-group-research-q-mig

Project description and duties: The candidate will work alongside the PI, a postdoc, and a Harvard medical student using Magnetic Resonance Imaging (MRI) data from one of the largest knee osteoarthritis (OA) cohorts in the world. The project will use highly efficient computer-based methods to automatically and quantitatively measure OA-related knee structures on MRI. The overall goal of this project is to examine the impact of structural changes on loss of cartilage and worsening of knee function. The results of this study will provide new insights into the prognosis, prevention and treatment of knee OA, with the ultimate goal of facilitating the development and assessment of highly needed disease-modifying drugs for OA. This is a multi-center collaboration. In our lab, the student will work specifically on computer assessment of bone and cartilage.
Number of hours per week: Terms and hours are negotiable. Preference will be given to students interested in working 12+ months to allow them to master techniques and produce results. During summers, students are encouraged to spend 10+ hours a week in the lab. During the school year, students are encouraged to attend lab meetings and spend time in

the lab as their schedule permits. Ideally the commitment should be at least 5 hours per week.
Requirements: Basic computer skills using the Windows operating system. No prior research experience is required.
If interested email: jduryea@bwh.harvard.edu

Poster 29. The effects of stress on olfaction in larval zebrafish
Presenters: Terzah Hill, Hanna Zwaka
Principal Investigator: Florian Engert, florian@mcb.harvard.edu
MCB 16 Divinity Avenue, https://www.engertlab.org/

Stress has a multitude of effects on our bodies. While prolonged stress is harmful and can decrease performance on tasks, intermediate stress levels can be beneficial for us. For example, we perform better on exams if we are a little stressed, or in the scope of this project, we are better at identifying specific odors. Despite a shared understanding of the behavioral effects of stress, little is known about how these changes are manifested in the brain. The larval zebrafish possess brains that share basic structures with humans and are optically accessible for whole-brain imaging at single cell resolution. Using calcium imaging, it is possible to identify the active brain regions during a stressful experience. More importantly, we show that in zebrafish larvae experiencing intermediate stress can also enhance performance. Our approach utilizes stress in free-swimming and head-fixed paradigms that allow us to image the behavior and brain while the animal is responding to a stimulus before and after stress. Here we show that a stress experience, induced by a shock, can induce a state-dependent modulation of olfaction in zebrafish larvae. Since increased locomotion during arousal increases odorant availability at the olfactory epithelium in free-swimming fish, we would expect results indicating a change in behavioral and neuronal response to odorants after stress. These findings would suggest that there is a reduction in sensory gain or amplification processes for olfaction during arousal or a low-stress state in order to maintain a normal dynamic sensory range. Stress can be beneficial, but prolonged stress can lead to an array of mental and physical health complications. Therefore, understanding the underlying neural circuitry of stress and its effects on behavior and sensory modulation is a critical field of research.
Number of hours per week: During the academic term Freshmen and Sophomores work ~10 hours/week, Juniors and Seniors ~20

hours/week. During the summer students can work up to 40 hours per week.
Requirements: none
If interested email: Zwaka@fas.harvard.edu and florian@mcb.harvard.edu

Poster 30. Genetic, functional, and computational approaches to dissecting cranial motor neuron development

Presenters: Arthur Lee, Julie Jurgens
Principal Investigator: Elizabeth Engle,
BCH, HMS, Broad Institute, Howard Hughes Medical Institute
Center for Life Sciences, Dept. of Neurology Boston Children's Hospital
CLS 14077 3 Blackfan Circle Boston, MA 02115
http://www.childrenshospital.org/research/labs/engle-laboratory/lab-members

The Lab of Elizabeth Engle, MD is a Howard Hughes Medical Institute lab based at Boston Children's Hospital and affiliated with the Broad Institute that uses clinical, genetic, 3D imaging, in vivo modeling, and computational approaches to study the biological processes that govern normal and aberrant development of the cranial motor neurons (cMNs). Dr. Engle is a physician-scientist and, as a pediatric neurologist, she discovered and/or clinically defined the genetic causes of a series of disorders affecting the cranial motor neurons called the congenital cranial dysinnervation disorders (CCDDs). The cMNs are a unique group of sensory and motor nerves that originate in the brainstem and project to the muscles of the eyes and face in a highly stereotyped (but incompletely understood) sequence during prenatal development. They control our ability to see, hear, taste, smell, move, and communicate. In patients, mutations in these genes can cause complex eye and facial movement disorders, deafness, loss of the ability to smell, and sucking and swallowing difficulties. The cMNs and the muscles they innervate also share unique but incompletely understood properties that make them resistant to neuro-degenerative disease (a phenomenon in the ALS field referred to as "selective vulnerability"). cMN function is exquisitely conserved throughout vertebrate evolution (from zebrafish, to mouse, to human patients), making them an attractive system that translates well to the clinic. Major projects in the lab include (1) identifying coding and noncoding pathogenic mutations from roughly 1000 whole genome sequences of CCDD patients; (2) mechanistic studies of these mutations

using vertebrate and stem cell model systems; and (3) single-cell functional genomic analysis of wildtype and mutant motor neurons (RNA-seq, ATAC-seq, ChIP-seq).
Number of hours per week: 10 (negotiable)
Requirements: none
If interested email: arthur@broadinstitute.org

Poster 31. Early Detection of Tumor Apoptotic Response to Oncolytic Virotherapy using Deep Learning based CEST Molecular Magnetic Resonance Imaging

Presenters: Or Perlman
Principal Investigator: Christian Farrar, cfarrar@nmr.mgh.harvard.edu
Harvard Medical School, Athinoula A. Martinos Center for Biomedical Imaging Massachusetts General Hospital 149 13th Street Charlestown, MA 02129, http://farrarlab.martinos.org

Background: Oncolytic virotherapy (OV) is a promising treatment for high mortality cancers. Non-invasive monitoring of OV would improve our understanding of the interactions between the virus and its tumor-host and help predict therapeutic response. Chemical exchange saturation transfer (CEST) MRI is a molecular imaging technique capable of detecting protein concentration and pH. However, clinical translation has been hindered by its qualitative nature and the long acquisition-times. The goal of this work was to develop a deep-learning-based CEST technique for quantitative and rapid imaging of OV treatment response. Methods: Two fast acquisition protocols (105s) were designed. The signals for 70M combinations of tissue parameters were simulated and used for training a deep neural-network, designed to output the quantitative CEST properties. Tumors were implanted in the brains of 16 mice, imaged prior to, 24h, and 48h post OV. The protocol was translated to a clinical MRI scanner and evaluated on a normal volunteer. Results: At baseline the semi-solid and amide proton concentrations were both decreased in the tumor, consistent with increased edema. The tumor amide proton exchange rate was increased, indicative of increased intracellular pH. Following OV, the core of the tumor presented significantly lower amide proton concentration and exchange rate. Both effects are indicative of apoptosis, as it is known to inhibit protein synthesis and decrease cytosolic pH. The normal volunteer scan yielded WM/GM exchange parameters in good agreement with literature values. Conclusions: The CEST technique successfully detected pH and

molecular concentration changes, potentially serving as important biomarkers for OV-induced apoptosis.
Number of hours per week: Number of hours per week is negotiable
Requirements: Basic programming experience (Matlab and/or python)
If interested email: cfarrar@nmr.mgh.harvard.edu

Poster 32. CRISPR/Cas9 gene-edited iPSC-derived RPE cells to model Age-Related Macular Degeneration

Presenters: Parthena Foltopoulou, Blanca Chinchilla
Principal Investigator: Rosario Fernandez-Godino,
Rosario_FernandezGodino@MEEI.HARVARD.EDU
Ocular Genomics Institute (Massachusetts Eye and Ear Infirmary; Harvard University).
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Age-related macular degeneration (AMD) is the most common cause of vision loss in elderly people in developed countries. AMD causes a loss of structure and function of the macula; the central region of the retina that provides detailed vision. The first clinical sign of AMD is the formation of deposits called drusen between the basal lamina of the retinal pigment epithelium (RPE) and the Bruch's membrane (BrM). The mechanisms for drusen biogenesis are not fully understood, but involve increased complement activation and abnormal extracellular matrix (ECM) turnover. Genetic variants in or near the complement genes are significantly associated with AMD, and active complement components have been found in drusen. Drusen is also characterized by alterations in the ECM turnover of BrM, which is controlled by matrix metalloproteinases (MMPs) and its inhibitors, secreted by the RPE. Dysregulation of the ECM turnover triggers complement activation and formation of drusen in early AMD. However, the specific factors and mechanisms that lead from ECM dysregulation to complement activation and drusen formation remain unclear. In our lab, we combine genome editing tools and cell biology to study the impact of each risk complement variant in the formation of sub-RPE deposits. Using CRISPR/Cas9 technology, we have engineered induced pluripotent stem cells (iPSC) to harbor a combination of risk alleles typically associated with AMD to understand their impact in the formation of drusen as well as in the response to complement-based therapies. Additionally, we have used

these models to develop new approaches such as ECM regulators for the treatment of AMD. Since there are not efficient therapies for the AMD, our in vitro model provides a valuable tool to study the pathogenesis of the disease and will help to find efficient treatments.
Number of hours per week: The students are required to come to the lab at least three times a week, a minimum of two hours each time. The length of the project can vary between 3-12 months.
Requirements: Students are required to have experience culturing cells. Molecular biology experience desired.
If interested email: Rosario_FernandezGodino@MEEI.HARVARD.EDU

Poster 33. 3D-printed ABCB5-positive stem cells for the treatment of corneal blindness

Presenters: Catherine Lee
Principal Investigator: Natasha Frank, nyfrank@bwh.harvard.edu
Division of Genetics, BWH, HMS, Transplant Research Program, BCH, HMS, Department of Medicine, VA Boston Healthcare System
164 Harvard New Research Building, 77 Avenue Louis Pasteur, Boston, MA 02115, http://franklab.bwh.harvard.edu

Limbal stem cells (LSC) continually repopulate the corneal epithelium. Patients with limbal stem cell deficiency (LSCD) are unable to regenerate the corneal epithelium, resulting in blindness due to an opaque cornea. A major barrier to the treatment of patients with bilateral LSCD is the shortage of donor tissue available for transplantation. We previously demonstrated that human ABCB5(+) LSC were capable of restoration of the corneal epithelium in an immunodeficient mouse model of LSCD. We found that ABCB5 is also expressed by multipotent dermal stem cells (DSC). We hypothesized that ABCB5+ DSC could provide an alternative source of stem cells for corneal epithelial regeneration and tested this by subjecting ABCB5(+) DSC to corneal differentiation conditions in vitro and saw significant induction of the corneal markers PAX6 and KRT12. Transplantation of human ABCB5+ DSC to immunodeficient recipient mice with mechanically induced LSCD resulted in clear corneas. Current work focuses on bioprinting of these cells in fibrin gel using a custom-designed droplet-based bioprinter and grafting to an immunodeficient mouse model of LSCD. Our results set the stage for the use of ABCB5+ DSC as an alternative autologous source of stem cells to regenerate the corneal epithelium in patients with bilateral LSCD.

Number of hours per week: 6-10 hours a week Freshmen and Sophmores 15-20 hours a week Juniors and Seniors 40 hours a week during the summer
Requirements: No prior research experience required.
If interested email: nyfrank@bwh.harvard.edu

Poster 34. Collective cell migration and energy metabolism
Presenters: Victor Tsuda, Stephen DeCamp
Principal Investigator: Jeffrey Fredberg, jfredber@hsph.harvard.edu
Harvard T.H. Chan School of Public Health
677 Huntington Ave, Boston, MA 02115,
https://www.hsph.harvard.edu/fredberglab/

From embryo development to cancer metastasis, epithelial cell layers dynamically rearrange and move as a single unit by undergoing collective cell migration. During collective migration, cells modulate their physical properties; migration speeds increase, traction stresses rise, and cell shapes elongate. These dynamical, mechanical and morphological changes require additional energy consumption and, therefore, must ultimately result from alterations in cell metabolism. However, the metabolic processes that energetically support collective cell migration remain unclear. Here we explore the collective migration of expanding epithelial cell layers while simultaneously extracting single-cell resolved metabolic data and characterizing canonical energy-producing pathways. Our findings indicate that collective cell migration requires significant alterations to the basal bioenergetic state of the cell. Therefore, when cell migration occurs, cells must undergo a metabolic switch.
Number of hours per week: 40 hours
Requirements: interest in physics and biology
If interested email: decamp@hsph.harvard.edu and jfredber@hsph.harvard.edu

Poster 35. Measuring vascular deficits by tracking blood through your body
Presenters: Blaise deB. Frederick, Lia M. Hocke
Principal Investigator: Blaise deB. Frederick,
bbfrederick@mclean.harvard.edu
McLean Hospital, Harvard Medical School

Opto-Magnetic Group (OMG), McLean Imaging Center, 115 Mill Street, Belmont MA 02478, https://www.nirs-fmri.net/home/the-group

We have developed a portable device to quantify peripheral blood flow delays non-invasively by correlating low-frequency oscillations (LFOs: 0.01 to 0.15 Hz), throughout the body. These low frequency variations are carried by the blood itself, and therefore show up at different parts of the body at specific times as the blood travels through the vasculature. By comparing the readings from multiple sensors at multiple peripheral locations (on the toes, fingers, and earlobes), we can detect and quantify delayed or altered blood flow in limbs affected by vascular insufficiencies, or any condition that alters circulation. In healthy subjects, the blood flow arrival time difference between fingers on opposite hands is generally less than 0.5 seconds. Delay between toes is of a similar magnitude due to the symmetry of the body. In addition, blood arrives in toes from 2-4 seconds after arrival in the fingers, with a weak dependence on subject height. In contrast, in a single subject who had had surgery on her femoral artery 2 years prior to the exam, blood arrived in the foot of the treated leg 6 seconds after arrival in the unaffected leg. In related cerebrovascular work in stroke patients, we found that occlusion in the carotid arteries can lead to blood flow arrival delays of up to 80-90 seconds in affected brain regions relative to the unaffected side of the brain, a difference which returns to near zero following revascularization surgery. We are currently optimizing our portable device for the diagnosis of Peripheral Artery Disease (PAD), a narrowing of peripheral arteries leading to inadequate limb bloodflow, and for use during procedures to restore vascular function. Quantitative measurement of blood flow delays can be used to rapidly and objectively assess circulatory health, even intraoperatively.
Number of hours per week: Negotiable - Depends on the arrangement with each individual student.
Requirements: Basic facility with either MATLAB or Python is required.
If interested email: lhocke@mclean.harvard.edu and bbfrederick@mclean.harvard.edu

Poster 36. Activating proteasomes to remove toxic proteins and combat neurodegenerative diseases**
Presenters: Galen Collins, Hyoung Tae Kim
Principal Investigator: Alfred Goldberg
alfred_goldberg@hms.harvard.edu

Harvard Medical School, Department of Cell Biology
240 Longwood Ave C-411 Boston, MA 02115,
https://proxy.qualtrics.com/proxy/?url=https%3A%2F%2Fagoldberg.med.harvard.edu%2F&token=dT8qp%2F9JR5uf89Gfd4axDh4kapcFgTe%2FYALK5g9ryhE%3D

The vast majority of intracellular proteins in eukaryotes are degraded by the 60-subunit molecular machine called the proteasome. The proteasome specifically degrades proteins tagged with chains of ubiquitin. It is commonly believed that the rate of ubiquitination determines proteins' rates of degradation. However, we and other labs recently uncovered mechanisms of regulating proteasome function that alter the rate of intracellular protein degradation. Our lab is interested in how the proteasome and protein degradation is controlled in both normal and disease conditions. There is growing evidence in neurodegenerative diseases like Alzheimer's disease and Amyotrophic Lateral Sclerosis (ALS) that degradation by the proteasome is impaired and misfolded, toxic proteins accumulate and contribute to the pathogenesis and disease progression. Thus, enhancing the ability of the proteasome to destroy these toxic proteins has the therapeutic potential to combat these diseases. Our lab has uncovered several mechanisms that enhance proteasome function, including the binding of adaptor proteins to proteasomes and the phosphorylation of proteasome subunits. Excitingly, proteasome phosphorylation can be promoted by various pharmacological agents, and we've found that FDA-approved drugs that activate kinases improve mouse and zebrafish models of several neurodegenerative diseases.
Number of hours per week: Negotiable
Requirements: No prior research required
If interested email: galen_collins@hms.harvard.edu and alfred_goldberg@hms.harvard.edu

Poster 37. Molecular, Cellular and Genetics of Skeletal Homeostasis and its Regulation in Health and Disease
Presenters: Francesca Gori,
Principal Investigator: Francesca Gori
francesca_gori@hsdm.harvard.edu
Harvard School of Dental Medicine, 188 Longwood Ave, Boston MA

Our current projects can be subdivided into the following areas: 1) Wnt signaling and bone. As clearly shown for the Wnt signaling pathway, the study of rare genetic disorders of the skeleton can yield insights that fuel novel therapeutic approaches for the treatment of both rare disorders and common skeletal ailments. Ongoing studies on the role of Wnt signaling in skeletal stem cells, skeletal homeostasis and bone regeneration are part of the current focus of the lab. 2) Hippo signaling and bone. The Hippo signaling, involved in various mechanical cues with implications for cell fate, tissue development and homeostasis, has been recently implicated in bone biology. Crosstalk between the Hippo and the Wnt signaling has been reported. Ongoing studies in the lab focus on the role of Hippo and its potential interactions with Wnt signaling in the regulation of skeletal homeostasis. 3) Osteocytes and skeletal homeostasis. Osteocytes, the most abundant cells in bone, are embedded into bone and in intimate contact with the bone matrix. Ongoing studies explore the link between the matrix that surrounds the osteocytes and the way in which they regulate bone remodeling and/or mineral metabolism. 4) PTH signaling in skeletal stem cell fate decision. PTH is one of the few approved anabolic drugs for osteoporosis, a widespread chronic condition linked to aging with important health and socio-economic consequences. Osteoporosis and aging involve dysfunctions of cells in bone, often associated with decrease bone formation and increase in bone marrow adipose tissue (BMAT). In addition to increasing bone mass, PTH treatment represses BMAT, but the mechanisms by which this occurs are not known. Ongoing studies are focused to explore novel molecular pathways by which PTH regulates skeletal stem cell fate decision.
Number of hours per week: 6-20 hours/week during the academic term and 40 hours/week during the summer session.
Requirements: No prior intensive basic research experience is required
If interested email: francesca_gori@hsdm.harvard.edu

Poster 38. Tracking the neural dynamics and decoding the neural representations that support and structure spoken language
Presenters: David Gow, Olivia Newman
Principal Investigator: David Gow, gow@helix.mgh.harvard.edu
HMS, MGH Dept. of Neurology
65 Landsdowne Street, Cambridge MA , under construction

The Neurodynamics and Neural Decoding Group (Gow Lab) develops and applies sophisticated analytic tools to understand the mechanisms responsible for the lawful sound structure of spoken words and syllables (phonology). Our research examines the role of interactive pattern association mechanisms versus generative grammatical processes in shaping phonology and phonotactic processes. Our methods begin with the creation of high spatiotemporal resolution reconstructions of event-related brain activity based on the integration of magnetoencephalographic (MEG), electroencephalographic (EEG) and magnetic resonance imaging (MRI) data. We use machine learning techniques to determine what kinds of information are encoded in localized patterns of brain activation (neural decoding), and a technique called Granger Causation analysis to track patterns of directed information flow between these localized brain regions over large networks with millisecond temporal resolution. These methods address fundamental inferential limitations in cognitive neuroscience, linguistics, and cognitive psychology. We are looking for student researchers who are interested in advancing theory by helping design, implement and analyze new experiments aimed at testing bedrock premises of generative linguistics, classical computational accounts of cognition, and emergentist approaches inspired by connectionism and dynamic systems theory. While it is not a requirement, we would be extremely interested in working with students with fluency in Hebrew or Arabic to help us explore critical linguistic puzzles that are specific to the Semitic languages. We would also be very interested in working with students with strong coding skills (MatLab/Python) who might be interested in helping us develop, refine, and test our cutting-edge processing stream.
Number of hours per week: Minimum of 8 hours per week (academic year and summer), with maximum of 40 hours per week (summer only).
Requirements: No prior experience necessary, but background in experimental psychology or linguistics, and basic coding skills are highly desirable. Fluency in Hebrew or Arabic would be extremely interesting to us, but is not required.
If interested email: gow@helix.mgh.harvard.edu

Poster 39. Biodiversity Research with Anolis lizards in Jamaica
Presenters: Inbar Maayan
Principal Investigator: David Haig, dhaig@oeb.harvard.edu
Dept of Organismic & Evolutionary Biology, 26 Oxford Street, Cambridge MA, 02138, https://lososlab.oeb.harvard.edu

A key goal of evolutionary biology is to understand the factors that generate biodiversity and the mechanisms that maintain it. To study these questions in the wild, we use the species-rich group of lizards called anoles (genus Anolis), which are found throughout the New World tropics. Here, we focus on using Jamaica's anoles to explore drivers of biogeographic variation and steps along the speciation continuum. Six of the seven species occur solely in Jamaica, the descendants of a single population that arrived and diversified after the island re-emerged from the Caribbean Sea ca. 10 million years ago. Five species occur island-wide, each adapted to use a different part of the habitat. These species differ from each other in appearance, movement, color, behavior and many other traits. But despite decades of research that have made anoles a classic group for the study of ecology and adaptive evolution, the relationships among species in Jamaica remain poorly understood. The uncertainty of relationships among species is further complicated by the great diversity within species, and almost nothing is known about how different populations are related to each other. We integrate molecular, ecological, morphological and behavioral data to investigate how many species there are in Jamaica, how they are related to each other, whether they exhibit shared responses to geological features and environmental conditions, and what drove – and is driving – their evolution. In collaboration with Jamaican scientists and students, we travel to sites throughout the island to collect data from several populations of each of the six Jamaican anole species. This represents a great opportunity for students interested in the evolution of biodiversity to learn hands-on research skills – both in the field and in the lab – and to develop independent thesis projects.
Number of hours per week: negotiable; can range from 6-10 a week to ~70 during fieldwork in Jamaica
Requirements: No specific skills necessary, all training will be provided. However, curiosity for nature, perseverance, and a strong work ethic are highly encouraged.
If interested email: dhaig@oeb.harvard.edu

Poster 40. A longitudinal study of relationships between resting state functional connectivity and real-life functioning in early psychosis

Presenters: Shi Yu Chan
Principal Investigator: Mei-Hua Hall, mhall@mclean.harvard.edu
McLean Hospital

Admission Building S338 115 Mill Street Belmont, MA 02478,
https://www.mcleanhospital.org/biography/mei-hua-hall

There is large variability in the functional outcomes of psychosis patients, and the underlying neurobiological mechanisms contributing to varies outcome trajectories are not well understood. Resting state functional magnetic resonance imaging (rs-fMRI) has emerged as a useful technique to study functional connectivity (FC) between spatially distinct brain regions that are altered in psychiatric illnesses. In this study, we implemented a longitudinal study design, following early stage psychosis patients at two time-points for up to two years, to investigate 1) whether there are subgroups of patients who share similar clinical symptoms and functioning outcomes; 2) whether FC changes within the default mode network (DMN) link to each subgroup's outcome trajectory; 3) whether variability in DMN connectivity is significantly correlated with variability in clinical symptoms and functioning of individual patient. Clinical, MRI, functional data were collected from 36 early-stage psychosis (ESP) patients at both baseline and follow-up time points. Rs-fMRI data was collected on a Siemens 3T Tim Trio scanner. Clinical scales and functional outcome measures included the Positive and Negative Syndrome Scale (PANSS), and the Multnomah Community Ability Scale (MCAS). We applied unsupervised machine learning methods to empirically identify homogeneous subgroups of patients with distinct outcome trajectories. ROI-to-ROI analysis was used to characterize differences within the DMN among patients in each outcome trajectory. Correlation analysis was used to assess associations between FC and behavioural outcomes. We found that there are four distinct subgroups of patients; DMN connectivity were different between subgroups with different trajectories; and that changes of DMN significantly correlated with functioning.
Number of hours per week: between 8-10 hours/week, it is negotiable with each individual student
Requirements: basic statistical or biology knowledge
If interested email: mhall@mclean.harvard.edu

Poster 41. Cellular mechanisms involved in the subset distribution of lower GBA activity in idiopathic Parkinson's disease
Presenters: Ria Thomas
Principal Investigator: Penelope Hallett, phallett@mclean.harvard.edu
McLean Hospital / Harvard Medical School

Previous work in our lab determined that a subset of idiopathic Parkinson's disease (PD) patient fibroblasts phenocopied mitochondrial vulnerability observed in mutant LRRK2 PD fibroblasts (Smith G et al., 2016, Mol. Neurobiol.). We have previously shown that glucocerebrosidase (GCase) activity progressively declines with age, and is decreased in PD patient substantia nigra compared to healthy patients (Rocha E et al., 2015, Ann Clin Transl Neurol). To determine if PD patient fibroblasts could be stratified based on GCase activity, we used a large cohort of idiopathic PD-patient fibroblasts and measured basal levels of lysosomal GCase activity. Healthy subject-derived fibroblasts (n=14), idiopathic Parkinson's disease (PD) patient (n=32), and mutant GBA1 PD patient fibroblasts (n=8) lines were obtained from Coriell, and NINDS repositories. Sequencing of idiopathic PD patient lines were sequenced to confirm the absence of mutations in GBA1 and LIMP-2 genes. GCase activity was diminished in a subset of idiopathic PD-patient fibroblasts as determined by a Gaussian model. This mathematical modeling showed a significant bimodal distribution of GCase activity in human-derived fibroblasts, with approximately 35% of the cases at normal GCase activity compared to controls, and a separate group with approximately 50% GCase activity decline. Measurements of GBA mRNA or protein expression did not correlate with the GCase activity. We therefore explored LIMP-2 transporter levels, post-ER/ER distribution of GBA, and chaperone functions. Our findings will potentially help define the underlying mechanisms for subsets of patients that are vulnerable to glycolipid induced Parkinson's disease, in order to provide appropriate treatments aimed at causality.
Number of hours per week: to be negotiated with the student
Requirements: No prior research experience is required
If interested email: phallett@mclean.harvard.edu

Poster 42. Magnitude of A1C Improvement in Relation to Weight Loss after Intensive Lifestyle Intervention in Real-World Diabetes Practice: 13 Years of Observation

Presenters: Ahmed Eldib, Hannah Gardner
Principal Investigator: Osama Hamdy,
Osama.hamdy@joslin.harvard.edu
Joslin Diabetes Center/Harvard Medical School
One Joslin Place, Boston, MA 02215

The effect of Intensive Lifestyle Intervention (ILI) on A1C in real-world clinical practice is inconsistent and is frequently underestimated. It is also presumed that the magnitude of A1C improvement is solely dependent on the amount of weight loss. In this study we report the magnitude of A1C change in a large cohort of patients with diabetes who underwent ILI over 13 years in relation to their baseline A1C and the amount of weight loss. We evaluated 590 diabetic patients (age 52.5±11 yrs, 58.6% females, A1C 7.7±1.4%, weight 105.54±18.6 Kg, BMI 36.7±5.1 Kg/m2, diabetes duration 10.9±9.8 years, 83.7% with type 2 diabetes), who enrolled in the Weight Achievement and Intensive Treatment (Why WAIT) program, a 12-week multidisciplinary ILI designed for real-world clinical practice between September 2005 and May 2018. We stratified patients based on baseline A1C into three groups: group A with A1C >9% (16.95% of participants), group B with A1C from 8 to <9% (19.15% of participants), and group C with A1C <8% (63.9% of participants). After 12 weeks of intervention, body weight decreased by 8.5±4.6 Kg in group A, 8.0±4.6 Kg in group B, and 7.6±5.8 Kg in group C (p=0.22 between groups). A1C decreased by 2.5±1.3% in group A, 1.2±0.8% in group B and 0.5±0.6% in group C (p<0.001 between groups). Pairwise comparisons of A1C changes between groups showed that: group A had 1.3% greater A1C reduction than group B (p=0.0001) and 2% greater A1C reduction than group C (p=0.0001), while group B had 0.7% greater A1C reduction than group C (p=0.0001). Conclusion: ILI may decrease A1C by up to 2.5% in patients with diabetes. In patients with a similar magnitude of weight loss, A1C reduction was more prominent in those with higher baseline A1C levels. This will help clinicians to set their expectations for A1C reduction in response to ILI.
Number of hours per week: negotiable
Requirements: no prior research experience is required
If interested email: Hannah.gardner@joslin.harvard.edu and Osama.hamdy@joslin.harvard.edu

Poster 43. Branched flow and its different applications in Physics
Presenters: Alvar Daza
Principal Investigator: Eric Heller, eheller@fas.harvard.edu
Harvard Department of Physics, Department of Chemistry & Chemical Biology, Mallinckrodt Building, Cambridge, MA 02138, https://www-heller.harvard.edu/
When a wave or ray impinges on a weakly refracting medium, a tree-like pattern usually emerges. Some of these branches carry an unusual

energy density compared to "usual diffusion" and they can travel long distances too. Ocean tsunami waves are fearful examples of the power of this regime, but branched flow has also been reported in many other physical situations ranging different length scales: from the gravitational lensing of light by galactic clusters, to light being refracted by living tissue or electrons propagating in semiconductors. Currently the group is working on new applications of branched flow and, at the same time, trying to delve deeper into some of the basic features of this universal phenomenon.
Number of hours per week: Negotiable
Requirements: There are no specific requirements, although mathematical and computational skills can be helpful.
If interested email: adazaesteban@fas.harvard.edu and eheller@fas.harvard.edu

Poster 44. Personal space correlates with social motivation and connectivity between a peri-personal space monitoring network and the default mode network
Presenters: Sarah Zapetis
Principal Investigator: Daphne Holt, dholt@mgh.harvard.edu
Department of Psychiatry, Massachusetts General Hospital
149 13th Street, Charlestown, Boston, MA 02129,
https://holtlab.wixsite.com/esnlab

Background: Personal space, the distance that people comfortably maintain from others, is an automatic form of social communication that is altered in a number of neuropsychiatric disorders. However, the neurocognitive mechanisms underlying this association remain unknown. Methods: In 33 patients with schizophrenia (SCZ) and 36 demographically-matched controls (CON), social behaviors were measured using the Social Anhedonia Scale (SAS) and the Time Alone Questionnaire (TAQ). Personal space size and flexibility ("permeability") were measured using the classic Stop Distance Procedure. Resting state fMRI scans were acquired in both groups using a 3T Siemens MRI scanner and analyzed using Freesurfer 6. A region-of-interest (ROI) analysis was conducted using ROIs defined in an independent fMRI dataset in which activation in response to approaching versus withdrawing face stimuli was measured. The ROIs were then merged into two different networks: a peri-personal space monitoring network and the default mode network. Spearman's correlations were used to

analyze the relationships between the network-to-network connectivity and behavioral and personal space measures. Results: In the combined group of CON+SCZ (n=69), all four correlations between social behaviors and personal space measures were significant (all r's > 0.352, all p's < 0.003). In both groups separately, as well as in the combined group, network-to-network connectivity was negatively correlated with personal space permeability (all r's > -0.318, all p's < 0.05). Conclusions: A preference for greater personal space and/or a more rigid personal space boundary may represent markers of diminished social drive across a range of populations. Identifying the neural basis of this relationship may help us to understand the social deficits seen in schizophrenia.
Number of hours per week: minimum of 8 hours
Requirements: Prior experience with excel and SPSS would be favorable
If interested email: szapetis@mgh.harvard.edu and dholt@mgh.harvard.edu

Poster 45. Deep Learning in Medical Imaging: Opportunities and Challenges

Presenters: Ken Chang, Katharina Hoebel
Principal Investigator: Jayashree Kalpathy-Cramer, kalpathy@nmr.mgh.harvard.edu
QTIM lab, MGH/HMS MGH & BWH Center of Clinical Data Science
149 13th St, Charlestown, MA 01940, https://qtim-lab.github.io/

Deep learning is transforming all aspects of the medical imaging through the ability for improved quantification, detection and classification. Our lab applies deep learning to clinical applications in ophthalmology, radiology and oncology. Retinopathy of prematurity of retinopathy (ROP) is a leading cause of preventable childhood blindness worldwide. We have developed a deep-learning based classifier for disease severity. Large scale screening efforts are underway in many low and middle income countries. Working with collaborators in Thailand and India, we evaluating the algorithm in many populations. We are also developing models that incorporate clinical and imaging features to predict treatment requiring disease. Brain metastases and gliomas are common but deadly forms of brain tumors with very poor prognoses. There is great interest in developing a fully-automated, reproducible, and accurate method of assessing tumor volumes. Our lab has used deep learning algorithms to automatically segment brain tumors to aid in quantifying the tumor burden and assessing response. Our translational

research efforts are geared towards clinical deployment and validation of the tools Change detection is a common task in many clinical disciplines that utilize medical imaging. We are working on neural network architectures that assess change given a pair of images. These methods can be applied to longitudinal imaging to assess disease progression and response. Deep learning methods have numerous challenges including the need for large datasets, brittleness, bias and lack of transparency. We are working in developing fundamental algorithms to address including methods to reduce the annotation burden, methods to identify and mitigate bias, methods for domain adaptation and methods to improve the explainability of these models.
Number of hours per week: negotiable (10-40 depending on availability)
Requirements: Familiarity with Python is a requirement Familiarity with deep learning packages (Pytorch, tensorflow, keras) would be helpful
If interested email: kalpathy@nmr.mgh.harvard.edu

Poster 46. Perinatal immune alterations impact the developing brain, gastrointestinal system, gut microbiome and social behavior of offspring

Presenters: Evan Bordt
Principal Investigator: Marcy Kingsbury, ebordt@mgh.harvard.edu
Department of Pediatrics Lurie Center for Autism MGH, HMS
114 16th Street (Mail Stop 114-3400) Charlestown, MA 02129

The majority of early-onset neurodevelopmental disorders have increased prevalence in males, whereas many late-onset disorders are female-biased. A primary focus of the lab is on Autism Spectrum Disorders (ASD), a collection of complex neurodevelopmental disorders characterized by repetitive behaviors and alterations in sensory processing, social interaction and social communication. ASD occurs in ~1 in 59 children in the US, with a strong sex bias in prevalence (~3-4 males diagnosed to every female). The overarching focus of our lab is to study how immune challenges in the perinatal period impact microglial development in the brain and how this impacts neurodevelopmental disorders. We have found that there are dramatic sex differences in the developmental trajectories of microglia, and that early life immune challenges reveal further sex differences in these trajectories. We are also interested in gut microbiome-brain-immune interactions and whether early perturbations of the in utero or perinatal environment increase immune system dysfunction and/or inflammation within the brain and

gastrointestinal system during critical periods of development, leading to disease processes. To address these questions, we utilize several models of perinatal inflammation that result in sex-biased alterations in social and anxiety behaviors relevant for early-onset neurodevelopmental disorders. Mechanistically, we study whether perinatal changes in inflammatory signaling result in sex differences in mitochondrial function, neuroinflammation, gut inflammation, gut microbiome composition, and gut-brain axis communication.
Number of hours per week: negotiable and depends on the arrangement with the student
Requirements: None
If interested email: ebordt@mgh.harvard.edu

Poster 47. Genetic manipulations in the Fruit Fly Fight Club: similarities and differences in the intensity levels and circuitry involved in male and female aggression

Presenters: Rachel Monyak, Saheli Sengupta
Principal Investigator: Edward Kravitz, edward_kravitz@hms.harvard.edu
Dept. of Neurobiology, Harvard Medical School
220 Longwood Avenue, Boston, MA 02115
http://www.hms.harvard.edu/bss/neuro/kravitz/

Aggression is an essential innate behavior that is used across the animal kingdom to acquire food, territory and mates. We developed a fruit fly model system to study aggression using powerful genetic tools that allow us to: (i) reproducibly identify single neurons important in the behavior; and (ii) manipulate these neurons while animals are behaving. Male and female flies fight in same sex pairings with the males fighting at higher intensity and establishing hierarchical relationships and females fighting at lower levels and sharing resources. Animals learn during bouts and the outcomes of fights influence future behavior, with “winner” and “loser” effects seen. Neurohormones, including amines, peptides and classical transmitters, influence the behavior and are involved in the associated circuitry. By inbreeding winners of fights for 35 generations we generate “bullies” that fight at higher intensity levels and always win fights against the parent strain. Specific gene expression differences associated with this phenotype have been identified in the bullies. Serotonin facilitates going to higher levels of intensity in male fights, but is not required for aggression. Using an intersectional genetics approach, we found two pairs of serotonergic neurons responsible for the facilitation, and have

identified a “switch” mechanism downstream of the serotonergic neurons that is a key element in the facilitation. Using the same genetic approach in female flies, we have found small clusters of cholinergic neurons responsible for an uncommon transition to very high levels of aggression in females. Studies in our lab focus on uncovering circuit similarities and differences between male and female aggression. In the immediate future, we plan optogenetic studies of brain neuron function in freely moving flies.
Number of hours per week: Negotiable
Requirements: Introductory neurobiology and introductory genetics helpful, but not required
If interested email: edward_kravitz@hms.harvard.edu

Poster 48. Biological and Artificial Intelligence
Presenters: Mengmi Zhang
Principal Investigator: Gabriel Kreiman,
Gabriel.Kreiman@childrens.harvard.edu
Boston Children's Hospital and Harvard Medical School
Center for Life Sciences, 3 Blackfan Cir, Boston, MA 02115,
http://klab.tch.harvard.edu//#sthash.HHe6liaO.dpbs

Our lab is interested in elucidating how neural circuits compute and building biologically-inspired Artificial Intelligence. To this end, we combine behavioral measurements, invasive neurophysiological recordings in the human brain and computational neuroscience models. The main topics of investigation center around visual recognition, learning, and memory. Within visual recognition, current projects include studying the mechanisms of pattern completion, visual search, context and task dependence, spatiotemporal integration and building machines that can see and interpret the world the way we do. Within learning and memory, current projects include studying real life memories, understanding how medial temporal lobe circuits lead to memory consolidation, and building biologically plausible models for episodic memory formation.
Number of hours per week: it is negotiable, and depends on arrangement with each individual student
Requirements: none. All are welcome!
If interested email: Gabriel.Kreiman@childrens.harvard.edu

Poster 49. High throughput dynamic BH3 profiling identifies active cancer therapies in solid tumors

Presenters: Patrick Bhola
Principal Investigator: Anthony Letai, anthony_letai@dfci.harvard.edu
Dana-Farber Cancer Institute Harvard Medical School
200 Longwood Ave Boston MA 02115, https://letailab.dana-farber.org/

Despite decades of effort, individual tumor sensitivity to individual drugs is often not predictable based on biological hypotheses. Therefore, unbiased, non-hypothesis-driven high-throughput approaches to matching patient tumors to effective drugs are badly needed. Here we developed a method called high-throughput dynamic BH3 profiling (HT-DBP), a robust microscopy-based assay with single-cell resolution that enables chemical screens of hundreds to thousands of candidate drugs on freshy isolated tumor cells to identify chemical inducers of mitochondrial apoptotic signaling. HT-DBP requires only 24 hours of ex vivo culture which enables the direct study of fresh primary tumor cells and minimizes adaptive changes that occur with prolonged ex vivo culture. Compounds identified by HT-DBP induce tumor regressions in genetically engineered and patient derived xenograft models of breast cancer. Using a genetically engineered mouse model of breast cancer that readily establishes cell lines, we showed that chemical vulnerabilities change as cancer cells are expanded ex vivo. We demonstrate that HT-DBP can be used to generate personalized apoptotic chemical vulnerabilities (which we refer to as pharmacotypes) for a set of colon cancer PDX models. We find that a PDX model derived from a primary site tumor and a metastatic lesion from the same patient have different pharmacotypes. Using annotations of small molecule targets, we can identify proteins and signaling pathways that represent apoptotic vulnerabilities in colon PDX models. Finally, we apply HT-DBP to primary human thyroid tumors and sarcomas to identify potential active therapies. In sum, HT-DBP can efficiently predict therapeutic sensitivity upon short-term ex vivo drug exposure and may empower functional precision medicine approaches in the clinic.
Number of hours per week: This position requires 6-20 hours depending on the academic term, and 40 hours per week during the summer. This is negotiable and depends on each student.
Requirements: None
If interested email: patrick_bhola@dfci.harvard.edu and anthony_letai@dfci.harvard.edu

Poster 50. Synergistic TLR7/8 and Mincle activation drives neonatal Th1 and CD8 immunity against Respiratory Syncytial Virus

Presenters: Simon van Haren, Ofer Levy
Principal Investigator: Ofer Levy, ofer.levy@childrens.harvard.edu
BCH, Division of Infectious Diseases HMS, Harvard Institutes of Medicine (HIM) 8th floor 4 Blackfan Circle Boston, MA 02115
http://www.childrenshospital.org/research/departments-divisions-programs/departments/pediatrics/precision-vaccines-program

Newborns and infants are highly susceptible to infection with intracellular pathogens, due in part to distinct cell-mediated immunity including impaired production of T-helper 1 (Th1)-polarizing cytokines, important for adaptive host defense against pathogens such as respiratory syncytial virus (RSV). We have previously demonstrated that dual stimulation with a Toll-like Receptor 7/8 agonist, R848, and an agonist of the C-type Lectin Receptor Mincle, trehalose-6,6-dibehenate (TDB), synergistically enables Th1 development in newborn cells in an age-specific manner. We explore innate immune mechanisms contributing to the action of novel vaccine components such as R848 and TDB in vitro and characterize their impact on immunogenicity in vivo. Our Phospho-proteomic analysis platform enables us to identify key signaling events leading to cell activation, as well as a newly developed human dendritic cell:T cell coculture platform. Our novel neonatal vaccine development platforms are a promising approach for development of early life vaccines against RSV and other intracellular pathogens.
Number of hours per week: negotiable
Requirements: none
If interested email: ofer.levy@childrens.harvard.edu

Poster 51. 3D Bioprinting of Melanoma-on-Chip Models for Immuno-Oncology

Presenters: Daniel Reynolds
Principal Investigator: Jennifer Lewis, jalewis@seas.harvard.edu
1. John A. Paulson School of Engineering and Applied Sciences 2. Wyss Institute for Biologically Inspired Engineering
52 Oxford St. Cambridge, MA 02138,
https://lewisgroup.seas.harvard.edu/

The Lewis Lab is at the cutting-edge of 3D printing and is principally involved in the printing of functional materials for soft robotics, structural

composites, and vascularized biological tissues for applications in both regenerative medicine and disease modeling. We are currently looking for a talented undergraduate researcher to join the Lewis Lab Bioteam. The undergraduate researcher will have the opportunity to work as part of an interdisciplinary team and assist in the 3D bioprinting of melanoma-on-chip models for the development of novel immuno-oncology therapies. The project is motivated by the fact that patient response to immunotherapies, such as checkpoint blockade or therapeutic vaccines, remains variable and poorly understood. To develop better immunotherapies, in vitro 3D melanoma models are needed. Towards this objective, we use 3D bioprinting to pattern multiple cell types alongside a fugitive ink that, upon removal, yields perfusable vessels. These printed features are then encapsulated in an extracellular matrix (ECM) to produce a 3D vascularized melanoma model. Our model, which contains multiple murine cell types (melanoma cells, immune cells, and stromal cells) and perfusable vasculature, enables longitudinal studies of its spatiotemporal evolution. In addition, while the current model involves murine cells, future work will incorporate human patient-derived cells through a collaboration with an oncologist at the Dana-Farber Cancer Institute. As an undergraduate researcher on the Lewis Lab Bioteam, you will gain experience in cell culture, 3D bioprinting, and biological assays (i.e., immunofluorescence, flow cytometry, and RNA sequencing). Prior research experience is not required, but candidates should demonstrate an eagerness to learn and be willing to dedicate ~10 hours per week.
Number of hours per week: Negotiable, but 10 hrs/week is preferable.
Requirements: None, but prior cell culture experience is preferred.
If interested email: dreynolds@seas.harvard.edu and jalewis@seas.harvard.edu

Poster 52. Neural coding of internal senses in the brainstem
Presenters: Chen Ran
Principal Investigator: Stephen Liberles
stephen_liberles@hms.harvard.edu
Department of Cell Biology, Harvard Medical School
240 Longwood Ave, Boston, MA 02115, https://liberles.hms.harvard.edu/

Our external senses of sight, smell, sound, touch, and taste enable us to perceive the external world. In addition, our internal sensory system monitors the physiological state of peripheral organs. The nucleus of the

solitary tract (NTS) is a brainstem nucleus that functions as the key gateway that transmits inputs from internal organs. The NTS receives sensory information from the cardiovascular, respiratory, and digestive systems via both vagal and spinal inputs, and then distributes this information to downstream brain regions to generate various internal senses, including hunger, satiety, air hunger, nausea, and visceral pain. Here, we use a combination of optical and genetic approaches to investigate how the NTS represents visceral signals. We developed an in vivo brainstem calcium imaging platform, which allows us to record the activities of thousands of NTS neurons that respond to internal stimuli. Using this platform, we uncover diverse neuronal responses to internal stimuli, while cell-types executing distinct functions are highly organized within the NTS. Using viral-genetic methods, we reveal unique projection patterns of NTS neurons. Ongoing work will connect the response profiles of NTS neurons to the connectivity to downstream target areas. Together, this work provides a roadmap for how the brain processes internal information from within the body may shed light on the treatment of viscerosensory and autonomic dysfunctions.
Number of hours per week: Working hour is negotiable during the academic term. Students are expected to work 40 hours per week during the summer.
Requirements: No prior research experience is required.
If interested email: chen_ran@hms.harvard.edu and stephen_liberles@hms.harvard.edu

Poster 53. Early Antiretroviral Therapy Reduces Latent Hiv-1 Reservoirs in Infants From Botswana

Presenters: Kevin Einkauf, Matt Osborn
Principal Investigator: Mathias Lichterfeld, mlichterfeld@mgh.harvard.edu
Ragon Institute of MGH, MIT and Harvard
400 Technology Sq, Cambridge, MA 02139,
http://www.ragoninstitute.org/portfolio-item/lichterfeld/

Background: Although antiretroviral therapy (ART) can effectively suppress HIV-1 replication and improve patient outcomes, treatment discontinuation typically results in viremic rebound due to the presence of latently-infected CD4 T cells. However, early treatment during acute infection appears to limit the establishment of this viral reservoir, possibly allowing for long-term remission. The Early Infant Treatment Study in

Botswana provides a unique opportunity to examine whether immediate initiation of ART can significantly decrease proviral reservoirs in HIV-1-infected infants, which may advance the search for a functional HIV-1 cure. Methods: Serial PBMC samples were collected from five infants with neonatal HIV-1 infection who started ART within 72 hours (n=4) or 31 days (n=1) after birth, and were followed for 84-96 weeks (w). Genomic DNA was subjected to near full-length amplification of single-genome HIV-1 templates. Resulting products were sequenced with Illumina MiSeq. Results: Intact full-genome proviral sequences represented an average of 41% of all detected sequences at baseline, compared to 21% of detected sequences after 84/96w of ART. This corresponded to an average frequency of 76 and 3 intact sequences per million PBMCs at baseline and after 84/96w of treatment, respectively, and is consistent with a half-life of 19 weeks for intact proviral sequences during the first two years of life. Discussion: ART initiated very early during neonatal HIV-1 infection leads to a profound decline of intact proviral sequences in infected infants, particularly after 84/96w of treatment. Monitoring of eligible patients during future analytic treatment interruption may indicate whether long-term remission is possible.
Number of hours per week: Negotiable
Requirements: None
If interested email: keinkauf@partners.org and mlichterfeld@mgh.harvard.edu

Poster 54. Connectomics of Inhibitory Neurons: Investigating the Role of Self Junctions

Presenters: Rachael Han
Principal Investigator: Jeff Lichtman, jeff@mcb.harvard.edu
Harvard University undergraduate
Northwest Building, Harvard University ,
https://lichtmanlab.fas.harvard.edu

Cortical processing in the brain is mostly comprised of two crucial, overarching classes of neurons. The glutamatergic excitatory neurons propagate action potentials over their relatively long axons and make up the majority of the neurons in the cortex (Kirkwood, 2015). On the contrary, GABAergic inhibitory neurons make up only 20% of the cortical neurons but can profoundly attenuate the magnitude and frequency of the firing by excitatory neurons (2015). The inability to maintain this excitation to inhibition ratio, also known as E/I balance, in the cortex has

shown implications in various cognitive, neuropsychiatric, and neurodegenerative diseases (Gao & Penzes, 2015). Connectomics, or the study of mapping neuronal connections, has shown implications in determining the underlying causes of many neurological disorders and diseases. For these illnesses of the nervous system, not only is there a lack of effective therapeutics, but also an absence of understanding the structural abnormality in the connections between neurons, or synapses, that occur. Due to this lack of information, neurological diseases have often been mischaracterized as mere abnormalities of behavior, thought, or pain and more importantly, inadequately treated (Morgan & Lichtman, 2013). Using a volume annotation and segmentation tool (VAST), reconstruction of several inhibitory neurons has been conducted from a human electron microscope dataset. In particular, the role of self-junctions, or instances of neuronal dendrites connecting to itself, has been detected and will be analyzed to elucidate a more detailed mechanism of inhibitory neurons in the cortex. Ultimately, obtaining a map of the different inhibitory neurons and its circuitry in the human cortex can help change our approaches to treatment of neurological diseases.
Number of hours per week: 15 hrs/week
Requirements: Recommended preparation with MATLAB VAST software training required
If interested email: rachael_han@college.harvard.edu and jeff@mcb.harvard.edu

Poster 55. Long-term rescue of retinal degeneration in Rho-P23H knockin mice via dual AAV-medicated allele-specific CRISPR-Cas9 gene editing

Presenters: Andrea D'Amico
Principal Investigator: Qin Liu, Qin_Liu@MEEI.HARVARD.EDU
Massachusetts Eye and Ear Harvard Medical School
243 Charles Street, Romm 520,
https://oculargenomics.meei.harvard.edu/labs/liu-lab/

Rhodopsin-P23H associated Retinitis Pigmentosa (RP) is the most common cause of autosomal dominant RP (adRP) in USA. This Rho-P23H mutant allele produces a misfolded rhodopsin protein that plays a dominant negative or gain-of-function role in photoreceptors, resulting in gradual rod degeneration followed by progressive visual loss. Our recent publication, revealed that gene editing with a CRISPR-Cas9 variant and

a truncated sgRNA could selectively inactive the Rho-P23H mutant allele, leading to a significant decrease of the P23H mutant transcript and protein, and preservation of photoreceptors in a Rho-P23H knock-in mouse model. In order to evaluate the long-term efficiency and allele-specificity of this method, we co-delivered the Cas9 nuclease and sgRNA via a dual-AAV approach. We utilized Anc80-pRK-SpCas9-VRQR and Anc80-pU6-sgRNA-pCMV-mCherry to deliver the CRISPR components into the retinas of Rho-P23H heterozygous mice at 14-18 days of age, and examined them 10 months post injection. Assessment of NHEJ-mediated editing efficiency by NGS analysis demonstrated that AAV-mediated Cas9/sgRNA gene editing in mouse retina could ablate the P23H mutant allele, with cleavage frequencies up to 26% in transduced cells. We observed that retinal morphology was significantly preserved in the treated regions of retinas, with two to five additional rows of outer nuclear layer (ONL) compared to retinas treated with sgRNA vector only or untreated retinas (in which only one row of cones remained after 10 months). Collectively, our results demonstrate that our CRISPR-Cas9 dual AAV approach executes effective editing in retinas in vivo, and suggests that long-term preservation of photoreceptor degeneration can be achieved.
Number of hours per week: It can be negotiable, and depends on arrangement with each individual student
Requirements: none
If interested email: andrea_damico@meei.harvard.edu and Qin_Liu@MEEI.HARVARD.EDU

Poster 56. Deep learning to assess health and disease from medical imaging

Presenters: Vineet Raghu, Michael Lu
Principal Investigator: Michael Lu, mlu@mgh.harvard.edu
Massachusetts General Hospital
165 Cambridge St, Suite 400 Boston, MA 02114,
https://www.massgeneral.org/heartcenter/research/researchlab.aspx?id=1023&display=overview

Our goal is to apply deep learning to assess health and predict disease from routine medical imaging (e.g. x-ray, CT scan and MRI). We work with high quality trial datasets of tens of thousands of patients with imaging and adjudicated outcomes. See our recent JAMA Open publication “Deep learning to assess long-term mortality from chest

radiographs”
https://jamanetwork.com/journals/jamanetworkopen/fullarticle/2738349
In this study, we developed a convolutional neural network to predict long-term mortality from 85,000 chest x-rays. In a held out testing dataset of ten thousand persons, persons considered at high risk by the model had a 12-year mortality rate of 53%, 18-fold higher than the low risk at 4%. Performance was maintained in a second external testing dataset of five thousand persons, and was independent of traditional risk factors like age, sex, and smoking. This demonstrates how deep learning can extract important information about health from everyday medical images. Persons at high risk may benefit from lifestyle, screening, and prevention interventions. Undergraduates in the lab will have the opportunity to assist in with data curation, model building, and publication of web/mobile applications. We are searching for students passionate about using deep learning to improve health. We expect students to be comfortable with Python and have a strong desire to learn applied deep learning techniques for clinical applications. We are located near the Charles/MGH Red Line station at 165 Cambridge St, Suite 400 Boston, MA 02114 https://goo.gl/maps/FKbGFWrb8wUi1pp6A Students will be mentored by Michael Lu, MD, MPH, Assistant Professor of Radiology and Director of Research, MGH Cardiovascular Imaging. Please send CVs to Dr. Lu at mlu@mgh.harvard.edu
Number of hours per week: Hours per week are flexible and depend on student's availability
Requirements: Some experience in Python Experience or strong desire to learn applied deep learning techniques for clinical applications
If interested email: mlu@mgh.harvard.edu

Poster 57. Probing the Functional Role of GSDMB in Asthma
Presenters: Ronald Panganiban
Principal Investigator: Quan Lu, qlu@hsph.harvard.edu
Harvard TH Chan School of Public Health
Rm 304, Bldg 1 Bldg 1 665 Huntington Ave,

Asthma is a complex airway disease caused by the interplay of poorly understood genetic and environmental factors. Nevertheless, genome-wide association studies (GWAS) have identified numerous genes that are significantly associated with asthma susceptibility but whose functional roles remain to be elucidated. Our group has previously shown that GSDMB, one of the long-suspected asthma genes, is highly

expressed in airway ciliated cells. We have also demonstrated that the GSDMB protein can be cleaved to yield an N-terminal fragment that triggers massive pyroptosis, a specific type of inflammatory cell death. Moreover, we have identified a GSDMB genetic variant associated with lower asthma risk and demonstrated that this variant abolishes GSDMB's pyroptotic activity, providing a mechanistic basis for the variant's decreased asthma association. Here, we show through in vitro cleavage assay that GSDMB is cleaved by caspase-1, but not by caspase-4, to yield the expected active GSDMB N-terminal fragment. Similarly, house dust mite (HDM) extracts, a known trigger of asthma, generates cleavage of the GSDMB protein. Treatment of bronchial airway epithelial cells with known asthma triggers show that rhinovirus A, but not mechanical compression or HDM, increases GSDMB expression by ~2-fold as measured by quantitative real-time PCR. This increase is associated with decreased level of ciliated cell marker, FOXJ1, suggesting that rhinovirus A causes reduction of airway ciliated cell number, possibly through increased pyroptotic activity. Collectively, our findings suggest that GSDMB is a bona-fide asthma gene. Future studies are aimed at investigating GSDMB cleavage in the lungs of animal models of asthma and identifying small-molecule inhibitors of cleaved GSDMB-mediated pyroptosis that could be developed as new asthma therapies.
If interested email: rpangan@hsph.harvard.edu and qlu@hsph.harvard.edu

Poster 58. Visualizing Ictal Networks with Granger Causality: Use with Stereotactic Electroencephalography (sEEG) to Enhance Intraoperative Decision-Making

Presenters: Eun-Hyoung Park, PhD, Hie Kim
Principal Investigator: Joseph Madsen,
Joseph.Madsen@childrens.harvard.edu
Department of Neurosurgery, BCH, HMS
The Neurodynamics Laboratory, BCH 1 Autumn Street, 4th floor (room 403) Boston, MA 02215, 1) PI site:
http://www.childrenshospital.org/directory/physicians/m/joseph-madsen
2) Publication site:
https://academic.oup.com/neurosurgery/article/82/1/99/3778239

Objective: Stereoelectroencephalography (sEEG) recordings are an increasingly popular means of invasively localizing the seizure onsets in

patients with refractory focal epilepsy. Recently we have shown that Granger causality (GC) analysis has the potential to reveal seizure networks from interictal baseline data obtained from subdural grids. In this study, we produced “causal density” maps from interictal sEEG and again tested whether the regions of high GC would statistically resemble the topography of the seizure onset zone and resection. Methods: We analyzed interictal data from 20 consecutive patients. For each case, 10min of data was obtained immediately after all channels were connected. The “GC maps” were quantitatively compared to conventionally-constructed surgical plans and resections, by using non-parametric, rank-order statistics, as previously used in the evaluation of subdural recordings. Results: In 19 of 20 cases, the interictal GC rankings of the electrodes mapped to the seizure onset zone had higher causality than predicted by chance (range: $p<10^{-5}$ to 0.03). In 17 of 18 cases who had resection or ablation, causality in the resection zone was significantly increased (range: $p<10^{-5}$ to 0.03). The aggregate probability of such a match is very small ($p<10^{-38}$), suggesting that the networks highlighted in interictal GC maps correlate with surgically-relevant seizure networks. Conclusions: GC analysis applied to sEEG data has the potential to help localize ictal networks from interictal data. Since interictal data can be obtained in the operating room as the electrodes are being placed, it is possible that live GC analysis of sEEG could eventually aid surgical decision making, such as modification of the sEEG stereotactic plan to better sample highly causal regions and define the epileptogenic z
Number of hours per week: It is negotiable and it depends on arrangement with each student.
Requirements: Our projects have number of directions that students can contribute. No prior research experience is required but if they have computer programming skills and can use computer programming language such as MATLAB (matrix laboratory) those are desirable and helpful for the projects.
If interested email: Joseph.Madsen@childrens.harvard.edu

Poster 59. Deep Learning for Pathomics - Multimodal Diagnosis, Prognosis, and Therapeutic Response Prediction.
Presenters: Richard Chen, Max Lu
Principal Investigator: Faisal Mahmood,
faisalmahmood@bwh.harvard.edu
BWH, HMS and Dana-Farber Cancer Center

Hale Building for Transformative Medicine 60 Fenwood Rd (8002-B/K) Boston, MA 02115, www.mahmoodlab.org

Mahmood Lab aims to utilize machine learning, data fusion, and medical image analysis to develop streamlined workflows for cancer diagnosis, prognosis, and biomarker discovery. We are interested in developing automated and objective mechanisms for reducing interobserver and intraobserver variability in cancer diagnosis using artificial intelligence as an assistive tool for pathologists. The lab also focuses on the development of new algorithms and methods to identify clinically relevant morphologic phenotypes and biomarkers associated with response to specific therapeutic agents. We develop multimodal fusion algorithms for combining information from multiple imaging modalities, familial and patient histories and multi-omics data to make more precise diagnostic, prognostic and therapeutic determinations. In this poster, we present our recent work on fusing information from genomics and histopathology using multimodal deep learning, we also showcase our work on deep learning-based analysis of whole pathology slides.
Number of hours per week: Negotiable, and depends on the arrangement with each individual student
Requirements: Basic programming experience in python is required.
If interested email: faisalmahmood@bwh.harvard.edu

Poster 60. Discovery of novel human antibodies for targeted immunotherapy and CAR T cell development
Presenters: Matthew Chang, Quan Zhu
Principal Investigator: Wayne Marasco,
Wayne_Marasco@dfci.harvard.edu
Matthew Chang (Dana-Farber Cancer Institute), Quan Zhu (Dana-Farber Cancer Institute and Harvard Medical School), Wayne Marasco (Dana-Farber Cancer Institute and Harvard Medical School)
Dana-Farber Cancer Institute 450 Brookline Ave Boston, MA 02215 , https://marascolab.dana-farber.org/

Immunotherapy plays a greater role in modern medicine than ever before and nowhere is this more apparent than in immuno-oncology. Currently, there are a number of FDA approved immune checkpoint inhibitors and CAR T cells on the market, including pembrolizumab (Keytruda), nivolumab (Opdivo), axicabtagene ciloleucel (Yescarta), and tisagenlecleucel (Kymriah). While checkpoint molecules are critical in

protecting healthy tissues, cancerous cells also use them to create safe havens where the tumor is invisible to the immune system. Checkpoint inhibiting antibodies are able to disrupt the tumor's defense mechanisms, allowing the patient's immune system to recognize and attack the cancerous cells. As we continue to develop a greater understanding of the biology surrounding tumors and the means by which they evade the immune system, our focus will shift from simply blocking these checkpoint receptors to antibodies that can actively modulate the microenvironment surrounding the tumor. In addition to being a viable stand-alone therapy, these antibodies can serve as a powerful payload for genetically modified chimeric antigen receptor (CAR) T cells, allowing these engineered cells to create a favorable microenvironment that greatly increases the potency and efficacy of the host's immune system. To this end, our lab has focused on developing novel CAR T cells for the treatment of hematologic malignancies and solid tumors. Utilizing phage, yeast, and other display technologies, our lab seeks to discover new antibodies that can serve as a targeting moiety or novel immunomodulatory payload(s) for our CAR T cell factory programs. Students in the Marasco Lab will gain hands on experience in antibody discovery and CAR T cell engineering and will have a unique opportunity to contribute to projects headed towards clinical development.
Number of hours per week: We recommend 10-20 hours per week, but this is negotiable and accommodations can be made
Requirements: No prior research experience is required. Students are expected to commit to the agreed upon schedule, be well organized, have good time management skills, pay careful attention to experimental details, and have excellent communication skills. Students should also have a desire to learn and be self-motivated to carry out their projects. Completion of a general biology course is a plus.
If interested email: MatthewR_Chang@dfci.harvard.edu and Wayne_Marasco@dfci.harvard.edu

Poster 61. Research in the Mason Group: Manipulating Entropy and Porosity in Functional Materials

Presenters: Jae Hyeong Lee, Daniel Erdosy
Principal Investigator: Jarad Mason, mason@chemistry.harvard.edu
Harvard University Department of Chemistry and Chemical Biology
12 Oxford Street Cambridge, MA 02138,
https://www.mason.chemistry.harvard.edu/

The Mason Group applies the tools of synthetic chemistry and nanotechnology to the design of materials that address basic science challenges in energy and sustainable development. We are particularly interested in the development of chemical strategies to manipulate entropic effects, phase transitions, and porosity at different length scales in inorganic and organic materials. Project 1: Phase-Change Materials | Advanced materials that can store high capacities of thermal energy and deliver it on demand are critical to the more efficient and sustainable utilization of energy. Through the development of strategies to manipulate the thermodynamics and kinetics of order-disorder transitions, our laboratory synthesizes new phase-change materials for thermal energy storage and heat management. Project 2: Nanocrystal Frameworks | Owing to their size- and shape-dependent magnetic, electronic, catalytic, optical, and mechanical properties, colloidal nanocrystals are exceptionally powerful building blocks for the construction of tunable materials. Our laboratory investigates porous materials composed of inorganic nanocrystals bridged by rigid organic ligands. These materials will exhibit novel properties that are derived from individual nanocrystals and their collective interactions, along with functionalized organic ligands and guest species in well-defined pores. Project 3: Porous Liquids | Liquids present a new and unexplored prospect for porous materials, as liquids posses useful properties not found in solids. Our laboratory is interested in the development of both liquids with intrinsic porosity and nanocrystal-based porous liquids. These materials offer the opportunity to address long-standing challenges in adsorption as well as to develop new self-cooling and self-heating adsorbents and membranes for water purification.
Number of hours per week: Negotiable, but prefer students who can work at least 10-15 hours/week
Requirements: No prior experience required, but prefer students who have taken at least one lab course and have taken (or plan to take) CHEM 40
If interested email: mason@chemistry.harvard.edu

Poster 62. Neutrophil cross-talk with cells of the adaptive immune response

Presenters: Pei Liew, Tanya Mayadas
Principal Investigator: Tanya Mayadas, tmayadas@rics.bwh.harvard.edu
Brigham and Women's Hospital and Harvard Medical School
77 Avenue Louis Pasteur, NRB 752O,

The immune system has both an innate as well as an adaptive component that work together to maintain homeostasis and provide host defense. Neutrophils are considered part of the innate immune system. However, there is mounting evidence that they may collaborate with cells of the adaptive immune system to deliver a coordinated host response. Neutrophils are abundant in peripheral blood and are quiescent when they circulate. However, they are rapidly activated upon their recruitment to inflamed tissues, where they function to eliminate pathogens by generating cytotoxic molecules. Although this is critical for host defense it can also cause significant tissue damage in inflammatory diseases such as autoimmune disorders. The study of neutrophil behavior has been largely confined to inflamed peripheral organs. Neutrophils have been recently shown to accumulate in secondary lymphoid organs. Dr. Mayadas' lab is studying the behavior and function of neutrophils in these lymphoid organs during inflammation and cancer. For this, the laboratory uses state-of-art two-photon intravital microscopy of organs in living mice as well as live cell imaging of cells in culture in vitro. The student will be involved in the analysis of neutrophil behavior and interactions with other cell types in vivo and in vitro using cell culture and imaging techniques.
Number of hours per week: We agree with the recommended hours
Requirements: No prior research experience is required but the student needs to be highly motivated and hard working.
If interested email: tmayadas@rics.bwh.harvard.edu

Poster 63. Rapid, Large-Scale Molecular Profiling of Individual Synapses

Presenters: Marissa Sumathipala,
Principal Investigator: Steve McCarroll,
HMS Department of Genetics http://mccarrolllab.org/

How cells communicate in the brain at a chemical level remains a major unanswered question in neuroscience. Critical to this communication are synapses, the junctions between neurons. Though synapses are currently grouped in broad categories, such as excitatory/inhibitory or neurotransmitter type, synapses likely have underappreciated molecular diversity in their mRNA and protein content. Despite the crucial role of synapses in brain function and disease pathology, the exact molecular makeup of individual synapses remains unknown. Synapses can be

isolated from the rest of the neuron into membrane bound compartments, called synaptosomes, that form from the pre- and post-synaptic membranes. This study develops a new tool for high-throughput profiling of single synaptosomes by extending the single cell RNA sequencing technology, Drop-Seq. We isolated synaptosomes from adult mice via dissection and homogenization. We followed with ultracentrifugation to remove nuclei and cellular debris, and to separate synaptosomes from other material by density. Bulk RNA isolation and quantification confirmed high quality RNA was present. Immobilization on poly-lysine coated coverslips and immunofluorescence with synaptic markers revealed synaptosomes containing both pre- and post-synapse densities. Next, we adapted Drop-Seq for the isolated synaptosomes. Using microfluidics, we co-encapsulate synaptosomes and DNA-barcoded beads into droplets. Synaptosomal mRNAs bind to the bead, which are then reverse transcribed to cDNA, PCR amplified, and sequenced, yielding the first RNA sequence library of single synapse content. To identify what transcripts are enriched in synapses relative to nuclei, we are running Drop-Seq on nuclei separated during the synaptosome isolation. To simultaneously analyze RNA and proteins, we extend Drop-Seq by conjugating DNA barcodes to antibodies using cross-linking, for use in ongoing Drop-Seq experiments on synaptosomes. In parallel with synaptosomes, we have isolated extracellular vesicles and sequencing RNA and protein with Drop-Seq as a way to extend our method of sub-cellular profiling to another mechanism of cell communication.
Number of hours per week: negotiable

Poster 64. Visualizing clonal dynamics of HIV-1 in the female genital tract during systemic spread of HIV-1 infection
Presenters: Shariq Usmani
Principal Investigator: Thorsten Mempel, tmempel@mgh.harvard.edu
Massachusetts General Hospital
Building 149, 13th Street, Charlestown MA 02129,
https://www.massgeneral.org/ciid/research/researchlab.aspx?id=1331&display=overview

Male-to-female transmission of HIV-1 through sexual route accounts for nearly half of all newly aquired infections. It is currently believed that most new HIV-1 infections are caused by only one virus, the so called transmitted/founder (T/F) strain. While the basis for this rigorous

selection has remained unclear, one model posits that the mucosal epithelium imposes a barrier to infection and acts as a bottleneck, and that successful infections are rare stochastic transmission events, explaining the monoclonality of transmission. Here, we have put this hypothesis to test by intravital imaging of the genital mucosa. We intravaginally inoculated BLT humanized mice with a mixed virus inoculum consisting of viral strains that differed only by their expression of a unique fluorescent protein, which allowed us to track infected cells. We found productively infected cells in different parts of cervico-vaginal tract. However, by dynamic imaging we observed differences in infection spread and the motile behavior of infected cells within these distinct anatomical locations. All viral genotypes as well as co-infected cells were observed in vagina. The cervix and distal lymph nodes, on the other hand showed lesser viral diversity but infected cells had a robust migratory phenotype, compared to infected cells in the vagina. In summary, our studies suggest a new model whereby mucosal exposure to HIV-1 leads to multiple independent transmission events. Varying rates of infected cell motility in different anatomical sites correlate with the rate of local clonal expansion. Comparable early systemic propagation of all inoculated clones suggest that selection of a single T/F strain takes place later during the course of infection and may be shaped by advantageous traits that confer resistance to host factors exerting selection pressure.
Number of hours per week: Negotiable
Requirements: None
If interested email: smusmani@mgh.harvard.edu and tmempel@mgh.harvard.edu

Poster 65. Association Between Choroidal Indices and Visual Outcomes in Patients with Diabetic Macular Edema Treated with Anti-VEGF
Presenters: Raviv Katz
Principal Investigator: John Miller, john_miller@meei.harvard.edu
Massachusetts Eye and Ear Infirmary and Harvard Medical School
243 Charles Street Room 1209, retinaimaginglab.com

To evaluate the associations between anti-VEGF therapy and central choroidal thickness (CCT), choroidal vascular density (CVD) and choroidal vascular volume (CVV), in patients with Diabetic Macular Edema (DME) using Swept Source OCT (SS-OCT), and to correlate

these findings with treatment visual outcomes. Prospective longitudinal study, including consecutive patients with treatment-naive DME. BCVA and 3D horizontal volume macular SS-OCT scans were obtained before 1st injection (M0), 1 month after loading dose (M3), and at 6 (M6) and 12 months (M12) after 1st injection. Treatment visual outcome was defined as BCVA improvement after M3 and categorized into 2 groups: Good Responders(≥5 letters) and Poor Responders(<5 letters). Twenty-three naïve DME eyes were included. After the loading dose of IVT ranibizumab (M3), 17 eyes (73.9%) were good responders and 7 (30.4%) poor responders. At baseline, good responders showed a thicker choroid compared with poor responders (p=0.134). Macular CVD and CVV were also significantly higher in good responders (CVD=0.26±0.06 vs 0.21±0.03; CVV=1.73±0.95 vs 1.28±0.48;p=0.151). After treatment, two distinct behaviors were observed: a significant decrease of CCT in good responders (-11.3%;p=0.014) and an increase in poor responders that did not reach statistical significance (+8.5%;p=0.576). CVD and CVV showed analogous changes with statistically significant reductions in good responders and increases in poor responders (+16.2%;p=0.006 and +34.1%;p=0.134,respectively). Reduced CVD at baseline identified well the good responders to anti-VEGF treatment (ROC AUC=0.74;p=0.030). Choroidal indices such as CVD and CVV, measured at baseline, seems to discriminate the good and poor responders to anti-VEGF therapy in DME patients, and may be robust predictors of treatment response.
Number of hours per week: 10-15 hours per week
Requirements: None
If interested email: Raviv_katz@meei.harvard.edu and john_miller@meei.harvard.edu

Poster 66. Role of T Cells in the Autoimmune Disease Systemic Lupus Erythematosus
Presenters: Melissa Carr-Reynolds, Jesus Lopez
Principal Investigator: Vaishali Moulton, vmoulton@bidmc.harvard.edu
Beth Israel Deaconess Medical Center, Harvard Medical School
3 Blackfan Circle, CLS-928 Boston, MA 02115 Longwood Medical Area
https://connects.catalyst.harvard.edu/Profiles/display/Person/70234

Autoimmune diseases occur when the immune system fails to recognize “self”, becomes overactive and attacks the body’s healthy tissues. Systemic Lupus Erythematosus (SLE) or lupus, is a debilitating chronic

multi-system autoimmune disease with no cure. Lupus disproportionately affects women over men, and is among the leading causes of mortality in young women. Most patients suffer from painful joints and skin lesions while complications can lead to kidney failure. Genetics, environmental factors and hormones are implicated as causes of lupus. Abnormally functioning hyperactive T cells contribute to lupus pathogenesis. Our goal is to understand the cellular/molecular defects, which cause T cell dysfunction in lupus. Our research has identified a new protein serine arginine-rich splicing factor 1 (SRSF1), which normally controls genes important for T cell function. SRSF1 is aberrantly low in several lupus patients especially in those with severe disease. We have generated new mice, which lack Srsf1 in T cells, and interestingly these mice develop lupus-like disease. Ongoing research in the lab is focused on understanding the role and regulation of SRSF1 in T cells and autoimmune disease. Projects with human studies include the investigation of the role of the female hormone estrogen and the role of microRNAs in the control of SRSF1 in human T cells. Other projects include animal studies in Srsf1-knockout and lupus-prone mice to understand how SRSF1 controls T cell function and its role in autoimmune disease. In summary, our lab conducts basic and translational biomedical research utilizing cellular immunology, cell biology, biochemistry and molecular biology approaches, to better understand the underlying pathogenesis of a complex debilitating disease to pave the path to identify better drug targets and biomarkers.
Number of hours per week: Freshmen & Sophomores 6-10hours/week. Juniors & Seniors 15-20 hours/week.
If interested email: vmoulton@bidmc.harvard.edu

Poster 67. Blue light activates pulvinar nuclei in congenital idiopathic photophobia: A case report.

Principal Investigator: Eric Moulton, eric.moulton@childrens.harvard.edu
Boston Children's Hospital
1 Autumn Street, 3rd floor Boston, MA 02215,
https://painandthebrain.org

To address clinical issues in ophthalmology, our lab uses patient-centric neuroscience imaging methods including functional magnetic resonance imaging and in vivo corneal microscopy. The overall mission of the lab is to understand the neural mechanisms underlying ocular pain and discomfort in order to develop more efficacious treatments. Numerous

pathologies can contribute to photophobia, a common and debilitating symptom that describes painful sensitivity to light. When considering light transduction alone, photophobia may be triggered through melanopsin pathways (non-image forming), rod and cone pathways (image-forming), or some combination of the two. We evaluated a 39 year old female patient with congenital idiopathic photophobia that was exacerbated by blue light, and tested her by presenting visual stimuli in an event-related fMRI experiment. Analysis showed significantly greater activation in bilateral pulvinar nuclei, associated with the melanopsin intrinsically photosensitive retinal ganglion cell (ipRGC) visual pathway, and their activation is consistent with the patient's report that blue light differentially evoked photophobia. This appears to be the first demonstration of functional activation of the ipRGC pathway during photophobia in a patient.
Number of hours per week: Summer: 40 hours/week Academic term for Freshmen and Sophomores: 6-10 hours/week Academic term for Juniors and Seniors: 15-20 hours/week
Requirements: No prior research experience is required
If interested email: eric.moulton@childrens.harvard.edu

Poster 68. Mechanics of Total Drum Replacement Tympanoplasty Measured with Wideband Acoustic Immittance
Presenters: Kristine Eberhard, Heidi Nakajima
Principal Investigator: Heidi Nakajima,
heidi_nakajima@meei.harvard.edu
Eaton-Peabody Laboratories, Department of Otolaryngology, HMS
243 Charles Street Boston MA 02114

Tympanic membrane (TM) perforations are commonly treated with surgical total eardrum replacement using temporalis fascia. How reconstructed TM compares mechanically to normal, native TMs is unknown. Here we measure TM mechanics with wideband acoustic immittance (WAI). Ears having undergone type 1 tympanoplasty using total eardrum replacement technique with temporalis fascia only were identified. Inclusion criteria included healed drum graft without perforation and no evidence of ossicular pathology. Exclusion criteria included previous middle ear surgery. WAI was measured in ears that had tympanoplasties and compared to a cohort of normal hearing ears with normal, native TMs. Eight ears from eight different patients were included in the tympanoplasty group. Four were male, four were female

and age at surgery ranged from 28-62 years, median 47 years. Time from surgery to WAI measurements ranged from 2-122 months, median 53 months. The native TM group included 56 ears from 29 different patients, 13 males and 16 females with age ranging from 22-64 years, median 33 years. Generally, WAI measurements in the tympanoplasty group had lower absorbance from 1-4 kHz compared to ears in the native TM group. At low frequencies (< 1 kHz), WAI absorbance was similar between ears of the tympanoplasty and native TM groups. Our data show that the mechanics of the TM with total eardrum replacement using fascia differed from the normal native TM. In general, at low frequencies (< 1 kHz) the absorbance in ears with fascia graft is comparable to absorbance in ears with native TM. However, at high frequencies, the fascia graft is mechanically different indicated by a decrease in absorbance from 1-4 kHz.
Number of hours per week: Negotiable
Requirements: MATLAB experience preferred.
If interested email: heidi_nakajima@meei.harvard.edu

Poster 69. Oncolytic viral immunotherapy for cancer treatment
Presenters: Hiroshi Nakashima, Shilka Saini
Principal Investigator: Hiroshi Nakashima,
hnakashima@bwh.harvard.edu
Brigham and Women's Hospital
60 Fenwood Rd (RM 8012), Boston MA

Our research has focused on the oncolytic HSV-based immunotherapy for patients with glioblastoma, an aggressive form of brain tumors. Oncolytic viruses can infect tumor and amplify own copies to spread like other viruses. These viruses are usually engineered from the wild type to restrict toxicity and infectivity to the tumors. They can also stimulate host immunity to fight back to cancer. Currently, postdocs in our laboratory are exploring the fields of cancer immunology relating to the glioma and oHSV treatment. These include T-cell immunity, tumor-secreting micro-vesicles, and animal models to design novel therapeutics. You will have various opportunities in our lab to learn the techniques and knowledge about the viral-based immunotherapy in cancer and contribute scientific discovery and translation of our research outcomes to the bedside. In the poster session, we will introduce you to one of our research to understand how our bench research can interact with clinical trial

research and vice versa.
https://www.ncbi.nlm.nih.gov/myncbi/14kIYzFDerq/bibliography/public/
Number of hours per week: during the academic term (Sept-May) Freshmen and Sophomores work 6-10 hours/week, Juniors and Seniors 15-20 hours/week. During the summer all students can work up to 40 hours per week. However, we are flexible to discuss with you about actual day and time.
Requirements: none
If interested email: hnakashima@bwh.harvard.edu

Poster 70. Urinary Inflammatory Proteome of Progressive Diabetic Kidney Disease

Presenters: Salina Moon, Monika Niewczas
Principal Investigator: Monika Niewczas,
monika.niewczas@joslin.harvard.edu
Research Division, Joslin Diabetes Center
Joslin Diabetes Center One Joslin Place, r466 Boston, MA 02215 ,

High-throughput technologies allow us to examine comprehensive profiles of inflammatory proteins. Identified proteins could potentially be used as targets for therapeutics to treat progressive DKD. Therefore we conducted a case-control study nested within the Joslin Kidney Study comprised of two panels; T1D (Discovery; n= 60) or T2D (Validation; n= 52). Cases were defined as an eGFR loss >40% within 5 years. We used aptamer proteomics (SOMAScan) to measure an array of inflammatory proteins in baseline urine. We identified a signature of 26 proteins associated with progressive DKD. Complement (n=12) and chemokines (n=6) were the most represented protein classes of our signature. All 26 proteins were associated with progressive DKD in the univariable logistic regression model and after adjustment by HbA1c, eGFR. The top signature protein was chemokine CCL21 (6Ckine) with odds ratio for progressive DKD: OR 3.9 (95% CI, 2.2, 6.7), and p-value: 1.6E-06. The top complement protein was C5a with odds ratio for progressive DKD: OR 3.5 (95% CI, 2.0, 5.9) and p-value: 4.9E-06. We identified an inflammatory protein signature enriched in the complement system, suggesting that the complement is linked to the progression of DKD. Interestingly, there are a number of complement inhibitors considered for the treatment of other kidney diseases.
Number of hours per week: negotiable

Requirements: programming skills (R, SAS) are welcome, but not necessary
If interested email: harry.spaulding@joslin.harvard.edu and monika.niewczas@joslin.harvard.edu

Poster 71. Chemical Synthesis and Biological Evaluation of Nanoparticles for Imaging Immune Function

Presenters: Hushan Yuan
Principal Investigator: Marc D. Normandin, normandin@mgh.harvard.edu
Massachusetts General Hospital
149 13th Street, Charlestown, MA 02129,
http://gordon.mgh.harvard.edu/gc/

Molecular imaging plays important roles for accurate diagnoses of human diseases and prognostic evaluation of related treatments. It is widely involved in basic research studies, drug discovery, and clinical settings. Molecular imaging features as a field of interdisciplinary. We focus on the development of novel chemical methods to create multifunctional materials for multimodal molecular imaging. Currently we are repurposing a clinical nanoparticle (NP) drug (Feraheme, FH) from its current uses of iron anemia treatment (approved) and MR contrast agent (off-label) to a Positron Emission Tomography (PET) agent, allowing experience with a well-established drug to suggest the safety, pharmacokinetics and clinical applications of our new modified NPs. The chemistry we recruit is Heat Induced Radiolabeling (HIR) method recently developed in our lab, which differs from other conventional methods in its (i) radiocation flexibility by using multiple cations widely employed in clinical imaging (e.g. 89Zr4+ or 64Cu2+ for PET and 111In3+ for SPECT), (ii) procedural simplicity: bonding radiocations to a NP drug with heat without the complication of chelation chemistry, (iii) leaving the physical and biological properties of the NP drug unchanged, save for the presence of trace amounts of radiocation and, (iv) ability to generate multivalency of surface targeting groups. When injected, HIR FH NPs can be internalized by circulating monocytes that traffic to normal lymph nodes and abnormal sites of inflammation. Therefore they are potentially translatable for the imaging of inflammation disease in clinical settings. The project will involve chemistry, molecular biology, molecular imaging, and animal studies.
Number of hours per week: Negotiable

Requirements: none / previous experiences of chemistry and biology are plus
If interested email: hyuan@mgh.harvard.edu and normandin@mgh.harvard.edu

Poster 72. Evolutionary patterns of body fusion in early arthropods throughout the Paleozoic

Presenters: Sarah Losso
Principal Investigator: Javier Ortega-Hernández, jortegahernandez@fas.harvard.edu
Harvard University, 2nd floor, Museum of Comparative Zoology Laboratories, 26 Oxford Street, Cambridge, MA 02138, https://ortega-hernandezlab.oeb.harvard.edu/

Trilobites are the dominant group of arthropods (living representatives include insects, crustaceans, and spiders) throughout the Paleozoic (541-251 million years ago) with over 20,000 described species known from all the continents and a variety of environments. Their prominence in the fossil record is in part due to their robust biomineralized exoskeleton and allows for large scale studies of evolutionary patterns. Arthropod exoskeletons are composed of segments which can fuse together to create functional units such as the cephalon and the pygidium or remain articulated as in the thorax which allows trilobites to either partially or fully enroll for defense. The total numbers of segments and amount of the body that can articulate are important for coping with low oxygen environments and how well the animal could protection itself, yet we see great variation in body plans. Qualitative studies report a general trend of younger species having proportionally larger pygidia and a lower amount of morphological variation, but this has yet to be statistically shown or relative to other factors. We seek to understand the pattern of body fusion in these important early arthropods by quantitatively describing the how segments are allocated to these units and if there is correlation with environment, biogeographic region, age or phylogenetic position. To this end, we are collecting a comprehensive data set on articulated specimens to investigate patterns of fusion within trilobites and other early arthropods. Students will collect data by imaging specimens housed in the MCZ collections and through literature reviews and use statistical methods to analyze the dataset.
Number of hours per week: During the semester: Freshmen and Sophomores work 6-10 hours/week, Juniors and Seniors 15-20

hours/week. During the summer: up to 40 hours. Hours per week are negotiable.
Requirements: None
If interested email: sarahlosso@g.harvard.edu and jortegahernandez@fas.harvard.edu

Poster 73. CMOS-based Nano-electrode Arrays for High-Throughput Electrophysiology
Presenters: Jeffrey Abbott, Tianyang Ye
Principal Investigator: Hongkun Park, hpark@g.harvard.edu
Chemistry and Chemical Biology
12 Oxford St, https://hongkunparklab.com/

The parallelization of intracellular recording can greatly benefit the study of complex neuronal networks, but it has proven difficult to achieve. In this work, we combine the intracellular recording capabilities of nano-scale electrodes with the massive parallelism of complementary metal-oxide-semiconductor (CMOS) circuits to build the CMOS-based nanoelectrode array (CNEA). Our experiments demonstrate the device's ability for sensitive intracellular recording of hundreds to thousands of cardiomyocytes and neurons within cardiac tissues and neuronal networks
Number of hours per week: 10
If interested email: hpark@g.harvard.edu

Poster 74. Optical Devices and New Light-Matter Interactions in Atomically Thin Semiconductors
Presenters: Ryan Gelly, Giovanni Scuri
Principal Investigator: Hongkun Park, hpark@g.harvard.edu
Department of Chemistry & Chemical Biology and Department of Physics
Conant Lab, 12 Oxford St, Cambridge, MA 02138,
https://hongkunparklab.com/

Atomically thin materials, graphene being the most famous example, have revolutionized the research landscape in physics, chemistry, and materials science in the last decade. Our lab researches a class of atomically thin semiconductors: the transition metal dichalcogenides (TMD). TMDs, despite being only 0.6 nm thick, interact strongly with light. For example, our group demonstrated that a TMD monolayer can act as a mirror, reflecting over 85% of the light incident upon it. We

continue to research both the fundamental optical properties of these materials, as well as how to control their optical properties for use in new optoelectronic and quantum optical devices. We will share how a combination of electrostatic doping, electric fields, and strain can modify the emission properties of these TMDs. Additionally, we discuss how we can integrate these materials with nanopatterned substrates to generate quantum sources of light: single photon emitters. Finally, we explore how you can achieve radically different optical properties when you go from a single layer of these ultra-thin materials to a bilayer.
Number of hours per week: To be arranged with Prof. Park
Requirements: Seeking students both with and without prior research experience. All experience levels welcome!
If interested email: hpark@g.harvard.edu

Poster 75. Validation of Ambulatory EEG and Mobile Cognitive Tasks as Predictors of Impulsive Behaviors During Psychiatric Treatment

Presenters: Andrew Peckham
Principal Investigator: Andrew Peckham
adpeckham@mclean.harvard.edu
McLean Hospital and Harvard Medical School
115 Mill Street, Mail Stop 113, Belmont, MA 02478,
https://cbeard2.wixsite.com/carelab

Impulsive behaviors, particularly those that are triggered by strong emotion, are a robust transdiagnostic feature of many types of mental illness. Deficits in cognitive control—in particular, deficits in prepotent response inhibition—may be a common mechanism underlying impulsivity during strong emotion. However, links between trait deficits in inhibition and trait impulsivity do not help to predict the specific occurrence of impulsive actions within individuals. In this study, adults receiving treatment for acute symptoms of psychiatric disorders will complete twice-daily assessments of two aspects of inhibitory control: behavioral performance on a tablet-based inhibition task, and brain response to inhibition as measured with an ambulatory electroencephalography (EEG) headband. Participants will also report engagement in impulsive behaviors twice per day, in order to test whether cognitive measures from the previous timepoint can predict future impulsive behavior. Finally, we will collect clinical assessments of emotion and affective motivations for impulsive behavior, so that we can

test the interaction of cognition, brain response, and state emotions in predicting impulsivity. This study has the potential to elucidate brain mechanisms underlying impulsive behavior, moving from broad trait-like relationships to a matter of hours.
Number of hours per week: Minimum of 8-16 hours per week (1-2 days). Specific days/times are negotiable. Data collection in the clinical research program takes place between 8:30am and 4pm on weekdays; the program is not open on weekends.
Requirements: Requirements for this position include excellent interpersonal skills, the ability to work independently, professional behavior appropriate for a clinical setting and interacting with psychiatric patients, and an interest in clinical research. Minimum GPA 3.5.
If interested email: adpeckham@mclean.harvard.edu

Poster 76. Center for Depression, Anxiety, and Stress Research
Presenters: Amelia Moser
Principal Investigator: Diego Pizzagalli, dap@mclean.harvard.edu
McLean Hospital, Harvard Medical School
115 Mill St, Belmont, MA 02478, https://cdasr.mclean.harvard.edu/

The Center for Depression, Anxiety and Stress Research (CDASR; Director: Diego A. Pizzagalli, Ph.D.) was launched in 2010 at McLean Hospital - the largest psychiatric facility of Harvard Medical School. Using an interdisciplinary approach, CDASR investigators are working to identify the biological, environmental, and psychological factors that contribute to depression and anxiety. The ultimate goal of this research is to develop better prevention and treatment strategies for these prevalent disorders. The Center is located in the deMarneffe Building at McLean Hospital. Combining outstanding research facilities with world-class clinical care, McLean and CDASR provide a unique mix of cutting-edge research focused on depression and anxiety.
Number of hours per week: 8+ (negotiable)
Requirements: Prior research experience is preferred, but not required.
If interested email: djcrowley@mclean.harvard.edu and dap@mclean.harvard.edu

Poster 77. Functional magnetic resonance imaging of the human brain at ultra-high resolution
Presenters: Olivia Viessmann, Avery Berman
Principal Investigator: Jonathan Polimeni, jrp@nmr.mgh.harvard.edu

HMS, MGH, HST, A. Martinos Center For Biomedical Imaging 149 13th street, Charlestown, https://www.nmr.mgh.harvard.edu/lab/mr-pig

Functional Magnetic Resonance Imaging (fMRI) is used to study neuronal activity in the human brain non-invasively. FMRI techniques are continuously refined and pushed to higher resolution and faster sampling rates. The hope is to improve the ability of fMRI to more accurately measure neuronal function. Our lab works on the forefront of implementing, evaluating and improving fMRI measurement techniques and data analysis. A substantial aspect of fMRI is post-acquisition data processing. This involves multiple steps, such as subject motion correction, registrations, filtering and inhomogeneity corrections. The order and combination of these steps changes the “effective” resolution and can make or break our ability to fully harness the information in high-resolution data. We are looking for a student who is curious to learn about signal processing and pipeline implementation. The student will investigate image processing steps and their effect on fMRI data quality with the goal of determining an optimal pipeline. Another research focus is the better understanding of fMRI signals through modelling. FMRI signals are driven by changes in the brain’s vasculature that supply oxygenated blood to meet the metabolic demand during neuronal activity. We are looking for students eager to model these fMRI signals with us from first Principals. Traditional modelling is based on simplistic models of blood vessel (e.g. a set of cylinders). We are improving these approaches by using realistic reconstructions of the brain’s vasculature generated from optical microscopy. Using these models, we can then simulate the fMRI signals. This will allow us to more accurately interpret the fMRI signals that we measure and guide the next generation of fMRI acquisitions and analyses.
Number of hours per week: negotiable
Requirements: familiarity with UNIX/LINUX, some experience using Matlab or another programming language; a strong interest for signal analysis, statistics and/or modelling; curiosity to lean more about human brain function and physiology
If interested email: oviessmann@mgh.harvard.edu and jrp@nmr.mgh.harvard.edu

Poster 78. Modeling human musculo-skeletal development with pluripotent stem cells
Presenters: Margarete Diaz Cuadros,

Principal Investigator: Olivier Pourquie,
pourquie@genetics.med.harvard.edu
HMS Dept. of Genetics, BWH Dept. of Pathology
60 Fenwood Rd. Boston MA 02115,

During development, a specialized type of mesoderm called the paraxial mesoderm gives rise to the body's skeletal muscle, axial skeleton (vertebral column, ribs), and, brown fat as well as the connective tissue in the back. In the Pourquie lab, we study this mesoderm using a variety of tools including the chicken embryo, mouse genetics, and directed differentiation from human pluripotent stem cells. We have developed protocols for the generation of paraxial mesoderm progenitors as well as mature skeletal muscle from pluripotent stem cells. We also study the molecular mechanisms that pattern paraxial mesoderm into the characteristic repeating structure of the vertebral column and ribs, and the tissue mechanical properties that make this patterning possible. If you are interested in stem cells, developmental biology and interdisciplinary science, our lab is a good match! We have projects available for students from all years and levels of experience, particularly for work with human pluripotent stem cells.
Number of hours per week: Negotiable
Requirements: No previous research experience required
If interested email: mdiazcuadros@g.harvard.edu and
pourquie@genetics.med.harvard.edu

Poster 79. The Biomechanics of Hearing
Presenters: Caitlin O'Connell-Rodwell
Principal Investigator: Sunil Puria, Sunil_Puria@meei.harvard.edu
MEEI
Eaton Peabody Lab Mass Eye & Ear 243 Charles St. Boston, MA 20114,
https://projects.iq.harvard.edu/otobiomechanics

We study the biomechanics of the ear—one of the world’s most extraordinary biological sensors. Research into the auditory system brings together fields as diverse as engineering, computational modeling, signal processing, medicine, audiology, physiology, psychoacoustics, neuroscience, and imaging. As a result of this breadth, students can become proficient in a variety of distinct disciplines, techniques, and research approaches, while also developing interdisciplinary problem-solving skills. Our current projects involve the scientific, engineering, and

clinical aspects of cochlear and middle-ear biomechanics, hearing-loss prevention in high-noise environments, devices that deliver sound through the bone-conduction pathway, and the commercial development of novel hearing aids that directly actuate the middle ear. These studies incorporate physiological experiments for determining structure–function relationships within the ear; imaging studies for obtaining the 3-D anatomy of the tiny structures within the middle ears and cochleae of multiple species including human, gerbil, mice, and elephants; and the development of computational models that incorporate the imaging results, can be validated against the physiological results, and can be used to test hypotheses related to clinical and technological improvements for the treatment and prevention of hearing loss. For more information, see https://projects.iq.harvard.edu/otobiomechanics. [Work supported by NIH grants R01 DC 07910 and R01 DC 05960.]
Number of hours per week: 10 hours/week during the semester and 40 hours/week during the summer
Requirements: passionate about hearing sciences!
If interested email: Caitlin_Oconnell@meei.harvard.edu and Sunil_Puria@meei.harvard.edu

Poster 80. A new mechanism of neuronal communication and protein homeostasis in the nervous system
Principal Investigator: Kapil Ramachandran,
kapil_ramachandran@fas.harvard.edu
Department of Molecular and Cellular Biology, Harvard Society of Fellows
16 Divinity Ave, Biolabs 1102/4, Cambridge MA, ramachandranlab.org

The bulk of our understanding of the mammalian brain is predicated upon studies of canonical neurotransmission (eg. glutamate, GABA, etc) as well as genetically-encoded peptide modulation (eg. dynorphin, enkephalin, ghrelin, etc). In the past few years, I discovered a novel modality of neuromodulation through a diverse class of 4-18aa peptides generated by a unique neuronal-specific plasma membrane bound proteasome complex. This neuroproteasome contains a minimal subunit composition necessary to carry out degradation and lacks the subunits necessary to recognize and unfold a ubiquitinated substrate. Instead, neuroproteasomes turnover a particular fraction (~250) of substrates as nascent chains on an actively translating ribosome. Specific inhibition of this complex and the resulting peptides leads to a dysregulation of

neuronal synchrony as well as a deficit in tested memory paradigms. Conversely, the peptides themselves stimulate a variety of specific and localized patterns of calcium activity in both neurons and glial cells. Our future work will elucidate 1. the molecular mechanisms that underlie neuroproteasome-mediated signaling and 2. how this form of peptide neuromodulation is coded and decoded in the mammalian brain. Overall, this work reveals a Principal of protein homeostasis in neurons which is subverted into a new modality of peptide neuromodulation.
Number of hours per week: 15 hrs/wk
Requirements: Curiosity, dependability, rigor, hard work ethic. Laboratory experience with cell culture or cloning is a big plus.
If interested email: kapil_ramachandran@fas.harvard.edu

Poster 81. Risk Factors Predictive of Papillary Thyroid Carcinoma Nodal Recurrence

Presenters: Rachel Weitzman, Natalie Justicz
Principal Investigator: Gregory Randolph,
Gregory_Randolph@meei.harvard.edu
Harvard Medical School, Massachusetts Eye and Ear
Department of Otolaryngology – Head & Neck Surgery Harvard Medical School, Massachusetts Eye and Ear 243 Charles Street Boston, MA 02114, https://researchers.masseyeandear.org/details/166 , https://connects.catalyst.harvard.edu/profiles/display/Person/40855

Objectives: Papillary thyroid carcinoma (PTC) accounts for the majority of thyroid malignancies; it has been demonstrated that risk of PTC recurrence over a 30-year period is approximately 30%, of which 70% occur as nodal metastases. Certain clinical and histopathological factors have been speculated to increase risk of disease recurrence, but the majority of these studies do not consider risk factors for nodal recurrence. We aim to determine variables predictive of nodal recurrence of PTC in order to inform clinical decision making. Methods: Retrospective chart review at a tertiary academic medical institution identified 41 patients who experienced nodal recurrence of PTC and 284 who did not experience recurrence following thyroid surgery from 2000 to 2015. Patients who recurred were compared to non-recurrent patients with regards to maximum tumor size, extrathyroidal extension, extranodal extension, history of lymph node dissection, number of metastatic lymph nodes, and lymph node ratio (LNR). Results: Results demonstrated that right and left lateral lymph node dissection have

significantly negative correlation with nodal recurrence of PTC. Results remain in process for the remainder of the variables. Lymph node ratio (LNR) has been shown to be an important prognostic factor for PTC recurrence and to strongly correlate with thyroglobulin levels; we anticipate that LNR and thyroglobulin levels will have high weights, compared to other variables. Conclusions: This study will demonstrate risk factors, as well as develop a “recurrence calculator,” incorporating the relative weight of each variable to identify each patient’s risk of nodal recurrence of PTC.
Number of hours per week: Negotiable, depends on arrangement with each individual student.
Requirements: No prior research experience is required.
If interested email: Dipti_Kamani@meei.harvard.edu and Gregory_Randolph@meei.harvard.edu

Poster 82. Enteric neurobiology in digestive health and disease
Presenters: Amy Shepherd, Aleks Prochera
Principal Investigator: Meenakshi Rao,
Meenakshi.Rao@childrens.harvard.edu
Boston Children's Hospital Harvard Medical School
300 Longwood Avenue, Enders Research Building,
https://raolab.hms.harvard.edu/

The gastrointestinal (GI) tract is by far the largest interface between the mammalian body and the external environment. It is also unique among other organs because it contains its own intrinsic, enteric nervous system (ENS) embedded within its walls. The ENS is large, complex, and an important component of the gut-brain axis. Remarkably, the ENS can orchestrate many behaviors independently of the CNS because it contains local microcircuits with both afferent (sensory) and efferent (motor) neurons located within the gut. Understanding how sensory information about nutrients and microbes is transduced by these ENS circuits and used to drive behaviors, ranging from gut motility to immune responses, is an important frontier in biology. The overarching goal of our lab is to determine how the cells of the ENS detect and integrate information to modulate autonomic behaviors, including gastrointestinal motility, intestinal epithelial specification, innate immune responses, and nutrient handling. We aim to learn fundamental Principals about how the nervous, immune and endocrine systems interact with each to regulate organ function. In order to investigate the molecular mechanisms by

which enteric neurons, glia and specialized sensory epithelial cells in the gut transduce information and communicate with each other to modulate behaviors, we use mouse genetic models, imaging of live and fixed tissues, as well as a variety of in vivo and in vitro assays. Prospective students excited by the prospect of working in a field at the interface of GI biology and neuroscience to investigate how molecular interactions between cell types impact health and disease are invited to come chat with us at our poster.
Number of hours per week: We are looking for students who can work up to 10 hours a week during the semester (minimum commitment of two semesters), with potential for 40 hours a week in the summer.
Requirements: Prior research experience is preferred but not required.
If interested email: Meenakshi.Rao@childrens.harvard.edu

Poster 83. Development of precision therapeutics to tackle challenges in cancer immunology and autoimmune disease
Presenters: Taha Rakhshandehroo, Omar Abousaway
Principal Investigator: Mohammad Rashidian,
mohammad_rashidian@dfci.harvard.edu
Dana-Farber Cancer Institute, Harvard Medical School
Dana-Farber Cancer Institute, Mayer 652 440 Brookline Avenue Boston, MA 02215, https://rashidianlab.dana-farber.org/

Our lab studies cancer immunology and autoimmune disease using expertise in molecular biology, immunology and chemical biology. We are focused in understanding the underlying mechanisms of how the tumor microenvironment is shaped, and continuously changed in response to cancer immunotherapies. Furthermore, we are exploring the mechanisms triggering initiation of an autoimmune disease. Additionally, we aim to develop new and improved diagnostic, prognostic, and therapeutic tools to detect, diagnose, characterize, treat, and prevent autoimmune diseases and cancer. Our research aims are fivefold: (1) to develop methods for non-invasive monitoring of immune responses; (2) to design and engineer novel CAR T cells; (3) to investigate changes in the tumor microenvironment (TME) in response to treatment; (4) to explore how to reshape the TME to a more pronounced anti-tumor status and develop tools to realize this possibility; and (5) to develop precision therapeutics for cancer and autoimmune diseases. In the long term, our goals are to help better understand dynamics of immune responses, to investigate what is behind the heterogeneous response to cancer

immunotherapy and to understand how an autoimmune disease is triggered. These are essential for developing more effective therapies, more effective methods for early detection of cancer, and new prognostic modalities.
Number of hours per week: negotiable, and depends on arrangement with each individual student
Requirements: none
If interested email: mohammad_rashidian@dfci.harvard.edu

Poster 84. In vivo Magnetic Resonance Spectroscopy and Perfusion Imaging of Brain Tumors
Presenters: Eva-Maria Ratai, Michael Wenke
Principal Investigator: Eva-Maria Ratai, eratai@mgh.harvard.edu
Department of Radiology, MGH Martinos Center for Biomedical Imaging
Building 149, 13th Street, Charlestown, MA 02129
https://www.nmr.mgh.harvard.edu/lab/ratailab

We are looking for Harvard undergraduate students in Life Sciences who are interested in conducting research related to Neuroimaging. Glioblastomas (GBM) are challenging cancers to treat, and positive clinical outcome in patients with recurrent glioblastoma continues to be low. One of the most informative imaging tools to monitor treatment response or treatment failure in brain tumors such as GBM is magnetic resonance imaging (MRI). MRI is a non-invasive technique primarily used in medical settings to produce high quality images of the inside of the human body. In addition, magnetic resonance spectroscopy (MRS) is a promising imaging technique that enables investigators to determine the presence and amount of specific metabolites. Thus, MRS provides information about the metabolic activity of tumors, and may give physicians critical insight into tumor activity.
Number of hours per week: Negotiable
Requirements: No prior research experience is required
If interested email: eratai@mgh.harvard.edu

Poster 85. Natural Killer (NK) cells display an immature phenotype with impaired function after haploidentical ('half matched') allogeneic hematopoietic stem cell transplantation.
Presenters: Benedetta Rambaldi, MD,
Principal Investigator: Rizwan Romee, MD,
rizwan_romee@dfci.harvard.edu

Dana Farber Cancer Institute, Harvard Medical School
M531, 5th Floor, Mayer Building, Dana Farber, 440 Brookline Ave, Boston, MA 02215, https://www.dfhcc.harvard.edu/insider/member-detail/member/rizwan-romee-md/

Haploidentical stem cell transplantation (haplo-SCT) with post-transplant cyclophosphamide (PTCy) as graft versus host disease (GVHD) prophylaxis is frequently used for patients who do not have HLA-identical donors. Despite a high incidence of early viral infections, the effect of PTCy on NK cell reconstitution has not been studied extensively. We quantified immune reconstitution in 60 patients after haplo-SCT with PTCy, mofetil mycophenolate and tacrolimus (TAC) and compared results to 34 patients with 8/8 HLA matched related or unrelated donors (MD) receiving TAC and methotrexate for GVHD prophylaxis. Samples were prospectively collected at fixed time points after transplant and analyzed using multi-color flow cytometry. Haplo NK cells were then characterize phenotypically at 1 month using a CyTOF panel and functional NK activity was tested in vitro at 2 months. Absolute NK cells were lower at 1 month after PTCy, due to reduced numbers of CD56dimCD16+ NK cells, that remained significantly lower in the PTCy group until 3 months after HCT. In contrast, recovery of immature CD56brightCD16- NK cells was increased in the PTCy cohort at 2, 3 and 6 months after HCT. CyTOF analysis performed 1 month after haplo-HCT showed that NK cells expressed higher level of activating receptor NKp46, CD95, granzyme-B and inhibitory receptor NKG2A and lower expression of CD57 compared to HD. Functional assays showed that PTCy NK cells displayed reduced degranulation and release of IFNγ after activation compared to HD. These functions were rescued after priming with low dose IL-15 in vitro. Impairment of NK recovery early after PTCy-based HST underscores the need to adopt novel strategies to overcome immune defects induced by this platform. We are currently exploring cytokine based approaches to overcome NK cell impairment after HCT.
Number of hours per week: Negotiable
Requirements: No prior research experience required. Goal is to expose students to the cutting edge research in Natural Killer based immunotherapy approaches being developed for patients with advanced tumors.
If interested email: rizwan_romee@dfci.harvard.edu

Poster 86. BMP signaling in bone

Presenters: David Maridas,
Principal Investigator: Vicky Rosen,
Department of Developmental Biology – Harvard School of Dental Medicine 188 Longwood Avenue, 5th floor, Boston, MA 02115,
https://hsdm.harvard.edu/people/vicki-rosen

The Rosen laboratory studies Bone Morphogenetic Proteins (BMP) signaling in the skeleton. We know that BMP signaling is required for formation of the embryonic skeleton, for the subsequent growth of the skeleton after birth, and for regeneration of skeletal tissues after injury. These functions are supported by many different BMPs, BMP receptors and BMP antagonists that must work in an orchestrated manner to achieve the right amount of BMP signaling at the correct location. Using genetic modifications in mice, our laboratory aims to define the mechanisms by which BMPs carry out these diverse functions. We are currently focusing on the following projects:

1. The role of BMP2 in bone: Our Bmp2 conditional knockout mice have skinny bones that spontaneously fracture and do not heal. We are using these mice to investigate the role of BMP signaling in skeletal stem cell differentiation and the maintenance of the skeletal stem cell niche.
2. The functional BMP ligand and receptor pairings that maintain bone mass. To understand how the ligand environment is interpreted by bone cells, our laboratory is characterizing the phenotypes of mice carrying deletions of individual BMPs and BMP receptors in skeletal stem cells and in mature bone forming cells.
3. The role of BMP signaling in osteoblasts: To clarify which functions of the bone-forming cells are regulated by BMP signaling, we are trying to delete the intracellular mediators of BMP signaling in osteoblasts in mice.

Number of hours per week: Completely negotiable, preferable between 6 to 20hrs/week
Requirements: no requirements
If interested email: David_maridas@hsdm.harvard.edu

Poster 87. Blockade of synaptic release promotes retinal ganglion cell survival and axon regeneration after optic nerve injury

Presenters: Elena Sergeeva,
Principal Investigator: Paul Rosenberg,
Paul.Rosenberg@childrens.harvard.edu

BCH Neurology, HMS, Center for Life Sciences F.M. Kirby Neurobiology Center, 13 floor 3 Blackfan Cir Boston, MA 02115, https://www.hms.harvard.edu/dms/neuroscience/fac/Rosenberg.php

Retinal ganglion cells, the neurons that convey visual information from the eye to brain, cannot regenerate their axons once the optic nerve has been injured and soon begin to die, leaving patients with glaucoma and optic nerve trauma irreversibly blind. Increases in mobile zinc have been implicated in CNS neurodegeneration, and in a mouse model of optic nerve injury, we have evidence suggesting an elevation in mobile zinc over the first 24 hours in synaptic vesicles in the inhibitory synapses formed by amacrine cells onto retinal ganglion cell dendrites. The apparent increase in mobile zinc diminishes to near normal by day 3. Injection of a chelator of zinc improved retinal ganglion cell survival and optic nerve regeneration (Li et al., PNAS, 2017). Tetanus neurotoxin selectively targets inhibitory neurons and, via cleavage of the SNARE protein synaptobrevin, inhibits exocytosis of synaptic vesicles. When tetanus neurotoxin was injected immediately after optic nerve crush, the putative zinc signal remained elevated at day 3, suggesting that tetanus neurotoxin prevented exocytotic release of the zinc that was initially elevated after optic nerve injury. Blockage of exocytosis by the toxin nearly doubled retinal ganglion cell survival and quadrupled levels of axon regeneration post nerve injury compared to vehicle-treated controls. These data suggest that the exocytosis of vesicular zinc from amacrine cell terminals suppresses retinal ganglion cell survival and axon regeneration and that these events can be partially reversed with tetanus neurotoxin. Additional studies will determine whether the effects of tetanus neurotoxin on cell survival and axon regeneration are mediated by inhibiting the release of zinc, or inhibitory neurotransmitter, or both zinc and neurotransmitter.
Number of hours per week: Negotiable, depends on arrangement with each individual student
Requirements: No prior research experience is required
If interested email: Paul.Rosenberg@childrens.harvard.edu

Poster 88. Mindfulness meditation and mental health
Presenters: Matthew Sacchet
Principal Investigator: Matthew Sacchet, msacchet@mclean.harvard.edu
McLean Hospital / Harvard Medical School

Center for Depression, Anxiety, and Stress Research, McLean Hospital, 115 Mill St., Belmont, MA, 02478,
mcleanhospital.org/biography/matthew-sacchet;
stanford.edu/~msacchet; cdasr.mclean.harvard.edu

Mindfulness meditation is a contemplative practice that targets the development of present-centered awareness and acceptance of psychological phenomena. Mindfulness is widespread in clinical psychology, the workplace, and general wellness and is associated with myriad health-related benefits. Mindfulness meditation-based therapies have been shown to be helpful for reducing depression and anxiety, in both community and psychiatric samples. To date little is understood regarding the psychological and biological mechanisms of action of mindfulness meditation for depression and anxiety. Understanding the mechanisms of action of mindfulness promises to provide a foundation for improved treatments. The objective of the current study is to advance our understanding of mindfulness meditation for depression and anxiety by investigating cognitive, affective, behavioral, neural, and psychoneuroimmunological (including epigenetic) effects of mindfulness practice. The project includes acquisition of magnetic resonance imaging (MRI) and electroencephalography (EEG) data from depressed and anxious patients before and after they have completed a mindfulness-based intervention or one of several control interventions. The project promises to provide new insights into the psychological and biological mechanisms of action of mindfulness meditation for depression and anxiety that will contribute to improved mindfulness-based treatments and thus better outcomes and reduced suffering for individuals with mental illness.
Number of hours per week: Volunteers are expected to contribute 10 to 15 hours per week for at least two semesters. Students will receive considerable training, so preference will be made for applicants who can contribute for two or more semesters. McLean Hospital is the primary psychiatric teaching hospital of Harvard Medical School and is recognized as the #1 Best Psychiatric Hospital in the country by U.S. News and World Report. Traveling to and from McLean Hospital may take an additional 35 minutes via public transportation from Cambridge, so students should consider whether this can fit in their schedule. Interested students may become involved in this study in a number of ways across all phases of research, including but not limited to supporting aspects of protocol development, participant recruitment, and

data acquisition (e.g., collecting EEG, blood samples, questionnaires, interviews from study participants, behavioral and cognitive tests). Thus students will gain experience with laboratory and research skills including within the domains of study design, data analysis, presentation, and scientific writing. Depending on the interests, goals, and skills of prospective students and the duration of involvement it may be possible for students to take on additional opportunities including data analysis, software programming, paper writing, and increasingly self-directed projects. Such projects may be based on the current study dataset or datasets previously collected. Students will work directly and continuously with Dr. Sacchet. If of interest to the participating student, the Dr. Sacchet is prepared to provide mentorship toward application to graduate programs, including in research and/or clinical fields. Students will be encouraged to attend general center and laboratory meetings as well. Students may apply for course credit (e.g., PSY 910r or Neuorbio 98r) and to a variety of Harvard resources for supplemental financial support (e.g., Harvard fellowships: https://lifesciences.fas.harvard.edu/research-opportunities).
Requirements: Candidates must be highly motivated and reliable. Experience conducting laboratory research in any discipline is preferred while not required. Our research focuses on humans with clinical mental health concerns, so experience working with human subjects in a research or therapeutic setting is also preferred while not required. Students will receive in-depth training in all necessary skills to contribute to the research project.
If interested email: msacchet@mclean.harvard.edu

Poster 89. Pharmacological Induction of PGC1-A For the Treatment of Degenerative and Angiogenic Ocular Pathologies

Presenters: Ilakya Senthilkumar, Scott Frank
Principal Investigator: Magali Saint-Geniez,
Magali_Saintgeniez@MEEI.HARVARD.EDU
Schepens Eye Research Institute Mass Eye and Ear
20 Staniford Street, Boston MA 02114

INTRODUCTION: Retinal Pigment Epithelium (RPE) degeneration and choroidal neovascularization are two key events in the development and progression of age-related macular degeneration (AMD). Our group has previously shown that the transcriptional co-activator PGC-1α promotes RPE oxidative metabolism and protects cells from AMD-associated

metabolic dysfunction. Here we evaluated the anti-oxidant and anti-angiogenic effects of ZLN005, a small molecule activator of PGC-1α, as a new approach for the treatment of advanced AMD. RESULTS: Gene expression analysis of human RPE cell line treated with ZLN005 shows upregulation of PGC-1α and its associated transcription factors and enzymes. ZLN005 efficiently protects cells from cytosolic and mitochondrial pro-oxidants. ZLN005 cytoprotective effect is negated in PGC1α-silenced cells. ZLN005 inhibits cell migration and proliferation in primary human retinal endothelial cells. Using an ex-vivo choroidal explant model, we show that ZLN005 blocks choroidal angiogenesis. CONCLUSION: This study shows that ZLN005 efficiently protects RPE cells from oxidative damage through selective induction of PGC-1α. ZLN005 also blocks angiogenesis and choroidal sprouting. All together these findings identify ZLN005 as a new pharmacological treatment for advanced AMD through its ability to protect RPE from oxidative stress and inhibit angiogenesis. Further evaluation of ZLN005 as a therapeutic agent in AMD models is on going.
Number of hours per week: Hours are negotiable, and depends on arrangement with each individual student.
Requirements: Prior research experience is not required as long as student is highly motivated and willing to learn.
If interested email: Magali_Saintgeniez@MEEI.HARVARD.EDU

Poster 90. Electrographic Seizures in Children with Epilepsy
Presenters: Dhwani Bharvad, Melissa DiBacco
Principal Investigator: Arnold Sansevere,
Arnold.sansevere@childrens.harvard.edu
Boston Children's Hospital Harvard Medical School
Dr. Arnold Sansevere Department of Neurology Division of Epilepsy 333 Longwood Ave, 4th Floor Boston, MA 02115,
http://www.childrenshospital.org/research/researchers/s/arnold-sansevere

Rationale Epilepsy is a serious illness that impacts between 0.5% and 1.0% of the US population. A diagnosis warrants an individual to undergo two unprovoked seizures occurring more than twenty-four hours apart. Continuous EEG monitoring (cEEG) is a tool used to detect seizures in children with neurological conditions who are susceptible to these events. The aim of this study is to investigate the prevalence of seizures in epilepsy patients and analyze factors which might contribute to high

seizure burdens. Methods Prospective study of patients from >44 weeks gestational age to 19 years, who underwent a clinically indicated cEEG in the pediatric ICU from June 2016 to June 2019 at Boston Children's Hospital. cEEG was defined as greater than three hours of uninterrupted EEG. Electrographic seizures included both electro-clinical and electrographic-only seizures. Results Thirty five patients with a prior diagnosis of epilepsy were admitted to the ICU and underwent an EEG. The mean age was 6.4 yr, with 65.7% (23/35) male. Eighteen patients (51.4%) contained a genetic predisposition, and sixteen (45.7%) had a structural brain abnormality. The admission diagnosis was a seizure in the majority of cases, and respiratory distress the next most common. Epileptiform discharges occurred in 57.1% (20/35), and asymmetry in 11.4% (4/35). The average seizure burden was 0.3 hr, with the highest of 3.5 hr. The gender of the patient with seizure burden, and death with seizure burden were not significant. Mortality during the hospitalization occurred in one child, 2.9%. Conclusions Children with genetic predispositions are at a high risk for epilepsy and disruptions in neurological development. Additional analysis to follow for developmental outcome in relation to seizure burden.
Number of hours per week: Typically, student interns complete about 8-10 hours per week (during the school year), however we can always work with students to develop a schedule that fits with their academic commitments.
Requirements: Our lab accepts interns at all levels of study. We will train our interns on the specific projects. Role primarily includes medical record abstraction Includes screening for the appropriate targeted patient Provides the experience of building a database and assisting with data entry using the RedCap database No prior research experience required Experience with REDCap is a plus
If interested email: Melissa.dibacco@childrens.harvard.edu and Arnold.sansevere@childrens.harvard.edu

Poster 91. Neurogenomics Lab: A unique place to study the precision medicine of neurological diseases

Presenters: Xianjun Dong
Principal Investigator: Clemens Scherzer,
cscherzer@rics.bwh.harvard.edu
Harvard Medical School, Brigham and Women's Hospital
60 Fenwood Road, Boston, MA, https://scherzerlaboratory.org

The Neurogenomics Laboratory uses big data to reinvent health care for Parkinson's and brain diseases. The interdisciplinary lab includes computer scientists, biologists, and clinicians. In analogy to how a search engine targets advertisements to a user, the lab's goal are to match drugs and tests to a patient based on a search of his entire disease biology (Science Translational Medicine, 2010; Science, 2017). This research is powered by the Harvard Biomarkers Study, today with more than 3,000 participants one of the largest longitudinal biobanks for Parkinson's in the world (Lancet Neurology, 2017). To understand how the human genome encodes human brain cells in health and disease, the BRAINcode project (http://www.humanbraincode.org) led by Dr. Scherzer and Dr. Dong in the lab uses the laser-captured total RNAseq and single-cell RNAseq methods to profile the transcriptome of human brain cells in high resolution (Nature Neuroscience, 2018). These work are funded by the National Institutes of Health and the Department of Defense. The Principal Investigator, Clemens Scherzer, M.D. is a Professor of Neurology at Harvard Medical School and Director of the Precision Neurology Program of Brigham & Women's Hospital. He is the Founding Director of the Advanced Center for Parkinson's Disease Research of the American Parkinson Disease Association, Brigham & Women's Hospital and Harvard. In his clinical practice, Dr. Scherzer is a specialist for movement disorders and co-leads the Harvard Biomarkers Study, which he co-founded in 2007.
Number of hours per week: We generally recommend that during the academic term (Sept-May) Freshmen and Sophomores work 6-10 hours/week, Juniors and Seniors 15-20 hours/week. During the summer all students can work up to 40 hours per week. But this is negotiable and depends on the arrangement with each individual student.
Requirements: No requirement. If you want to work on the computational biology team, it would be a plus to know some programming skills.
If interested email: cscherzer@rics.bwh.harvard.edu

Poster 92. eSyM– Integration and Implementation of patient reported outcomes for Symptom Management for improving the patient experience after surgery and after cancer chemotherapy
Presenters: Deb Schrag
Principal Investigator: Deb Schrag, deb_schrag@dfci.harvard.edu
HMS and DFCI, 450 Brookline Avenue Boston MA 02215-Dana Building Lab is Dana 1114

The eSyM project collaboration is a research initiative comprised of 6 hospital systems across the country including New England, Appalachia and the Mississippi Delta in partnership with Epic, a leading electronic health records vendor to design and implement a new digital health electronic symptom management tool (eSyM). Each site brings a unique perspective with a focus on improving symptom management in rural and community care settings. eSyM is embedded directly in the medical record and is available to patients through their portal. eSyM enables patients to regularly report symptoms and receive tailored self-management education. In addition, patients who report a severe symptom are alerted to contact their care team. On the clinical side, eSyM allows care teams to efficiently track and react to symptoms through panel reports and severe symptom alerts. To promote harmonization and acceptance across all sites, stakeholders have been engaged at all phases, including design, development, and testing. eSyM is currently being deployed through a stepped-wedge cluster randomized trial with a minimum of 6048 patients expected to participate. This project is looking to evaluate whether eSyM improves health outcomes, care delivery, and patient satisfaction. Specifically, the primary study outcome is evaluating 30-day emergency department and hospital readmission rates after initiating a new chemotherapy treatment plan or undergoing a surgery. This digital health project is funded by the National Cancer Institute in association with the Beau Biden Cancer Moonshot Initiative aims to make healthcare more efficient. Number of hours per week: We have an exciting set of projects focused on the emerging fields of digital health and mobile health and are eager to partner with undergrads seeking part time or full time works and/or thesis projects. We have many related projects in the field of Data Science/Public Health/Implementation Science/Health Care Policy related to cancer. If interested email: deb_schrag@dfci.harvard.edu

Poster 93. Functional genetics of tissue factor in bleeding and thrombotic risk

Presenters: Sol Schulman,
Principal Investigator: Sol Schulman, sschulm1@bidmc.harvard.edu
Beth Israel Deaconess Medical Center and Harvard Medical School
3 Blackfan Circle, https://hemostasis.bidmc.org/people/sol-schulman-md-phd/

Tissue factor (TF) binds blood coagulation factor VII/VIIa to initiate blood coagulation in humans. Inappropriate TF procoagulant activity underlies substantial human suffering, including that due to myocardial infarction, venous thromboembolism, cancer-associated thrombosis, and stroke. TF expression and activity must therefore be carefully regulated in vascular tissues to enable hemostasis following injury but prevent pathologic thrombosis. Despite decades of close investigation, the mechanisms by which TF expression and procoagulant activity are regulated on the vascular cell surface remain incompletely understood. We combine functional genomics, human and rodent genetics, cell biology, and protein biochemistry to dissect the TF-dependent initiation of blood coagulation. Because the contribution of cellular TF is not captured by clinical coagulation testing, these critical modifiers of human bleeding and thrombotic risk remain undetected in human populations. Our human genetic and functional genomic approaches have identified several new mechanisms that regulate coagulation initiation, with several well validated discoveries awaiting a motivated student to take ownership of a project. Opportunities are available primarily for wet lab but also computational investigations.
Number of hours per week: Hours are negotiable, but the hope is that students are able to make a regular commitment during the academic term (6-10 hours/week for Freshmen/Sophomores, 15-20 hours/week for Juniors/Seniors doing thesis research) and a 40 hour/week commitment over summers.
Requirements: No prior research experience is required. Additional projects may be available to students with computer programming experience.
If interested email: sschulm1@bidmc.harvard.edu

Poster 94. Microbiota-derived molecules ameliorate pro-inflammatory cytokines profile in gut organoids-derived monolayers from healthy and celiac patients after gliadin exposure
Presenters: Stefania Senger
Principal Investigator: Stefania Senger, ssenger@mgh.harvard.edu
Mucosal Immunology and Biology Research Center, Massachusetts General Hospital for Children and Harvard Medical School
114, 16th St, Charlestown Navy Yard,)2129, Boston, MA,

Our research focuses on dissecting the biological processes that modulate differentiation and function of intestinal epithelium in

relationship of environmental stimuli, including pathogens, food antigens, microbiota and derived bioproducts. To carry out our studies we have developed a repository of intestinal epithelium primary cultures (organoids) derived from donors. In our recent study we have used the organoids technology to study the response to intestinal epithelia derived from celiac subjects to gluten. Celiac disease (CeD) is an immune mediated enteropathy triggered by gluten in genetically predisposed subjects. Recently, intestinal dysbiosis has been associated with CeD onset. While the involvement of the adaptive immune response to CeD has been extensively studied, little is known regard the contribution of the epithelium and the role of microbiota-derived molecules in modulating the epithelium response to gliadin (gluten's protein). We developed intestinal epithelial organoids from celiac and non-celiac duodenal biopsies. Organoids RNA sequencing revealed significantly altered expression of genes associated with barrier, innate immune, and stem cell functions. Functionally, CeD epithelia exposed to gliadin showed increased permeability and released significantly more proinflammatory cytokines. Microbiota-derived butyrate, lactate and PSA from B. fragilis improved barrier function and reduced gliadin-induced cytokine secretion. We concluded that: the epithelium of patients with CeD actively contribute to the disease; genetic or epigenetic differences might reflect on expressional and functional differences observed; microbiota-derived bioproducts are promising factors to modulate the immune response to gluten. Finally we validate the use of patient-derived organoids for the study and treatment of CeD.
Number of hours per week: 20
Requirements: No previous research experience required
If interested email: ssenger@mgh.harvard.edu

Poster 95. Novel Bioactive Specialized Pro-Resolving Mediators in Resolution of Inflammation

Presenters: Charlotte Jouvene, Stephania Libreros
Principal Investigator: Charles Serhan, cserhan@bwh.harvard.edu
Brigham and Women's Hospital, Harvard Medical School
Center for Experimental Therapeutics and Reperfusion Injury Serhan Laboratory Hale of Building of Transformative Medicine, Room 3016 60 Fenwood Road Boston, MA 02115, http://serhanlab.bwh.harvard.edu

Research in the Serhan Laboratory focuses on structural elucidation of bioactive molecules that activate the resolution of inflammation. Our

overall mission is “To identify novel mediators, pathways, and their cellular receptors and targets critical in promoting resolution of inflammation and reperfusion tissue injury and establish their relation to human disease.” Dr. Serhan demonstrated the assembly and activation of anti-inflammatory, pro-resolving lipid mediator circuits activated during the resolution phase of acute inflammation. These include the discovery, structural elucidation, and temporal-spatial distinct actions of novel molecules (the lipoxins, resolvins, protectins, and maresins) and pathways that serve as pro-resolving and/or endogenous anti-inflammatory chemical signals. Each of these families of mediators is biosynthesized within the resolution phase to promote the return of the host tissues to homeostasis. These molecules play important roles including stimulation of resolution of inflammatory responses, reduction of pain, clearance of bacteria and stimulation of tissue regeneration. We’ve designed novel therapeutic approaches using these structures as biotemplates by state-of-the-art technologies. New therapeutic approaches built with the knowledge of these signaling pathways could be more potent, selective and better tolerated since they are based on structures naturally evolved in these processes. Several of these new designer pro-resolving therapeutics have already been shown effective in humans. Serhan Lab’s research provides new avenues to control inflammation and its natural resolution pathways with precision. These ongoing studies now open the new field of resolution pharmacology and its potential uses in human disease.
Number of hours per week: Summer students: 40 hours per week
Juniors and Seniors: 15-20 hours/week
Requirements: None
If interested email: cjouvene@bwh.harvard.edu and cserhan@bwh.harvard.edu

Poster 96. Engineered Cell based Therapies for Cancer
Presenters: Kok Siong Chen, Nobu Kanaya
Principal Investigator: Khalid Shah, kshah@bwh.harvard.edu
Brigham and Womens Hospital, Harvard Medical School
60 Fenwood Road, csti.bwh.harvard.edu

Cell-based therapies are emerging as a promising strategy to tackle cancer. We have developed tumor cell surface receptor targeted T cells and adult stem cells expressing novel bi-functional pro-apoptotic and immunomodulatory proteins and oncolytic viruses . We have engineered

different cell surface receptor targeted adult stem cells types to release (i) pro-apoptotic proteins to specifically induce apoptosis in tumor cells; (ii) anti-proliferative nanobodies (ENb) to inhibit tumor cell proliferation; (iii) immunomodulatory proteins to enhance T cell function; and (iv) oncolytic viruses to induce viral oncolysis; and demonstrated the therapeutic efficacy of these engineered stem cells both in vitro and in vivo. Recently, we have reverse engineered cancer cells using CRISPR/Cas9 technology and demonstrated self-tumor tropism and therapeutic potential of receptor self-targeted engineered cancer cells. These studies demonstrate the strength of employing engineered cells and real-time imaging of multiple events in preclinical-therapeutic tumor models and form the basis for developing novel cell based therapies for cancer.
If interested email: kshah@bwh.harvard.edu

Poster 97. Genetic analysis of oncogenic histone mutations
Presenters: Alan Jiao
Principal Investigator: Yang Shi, yang_shi@hms.harvard.edu
Boston Children's Hospital and Harvard Medical School
300 Longwood Ave, Boston, MA 02115, https://www.harvardshilab.org/

The aim of this project is to investigate cancer-associated histone mutations in a genetically tractable animal model of development and epigenetic inheritance. Histones are core components of chromatin, and are heavily decorated by post-translational modifications to ensure proper gene regulation. A conserved histone modification is the methylation of H3 on lysine 27 (H3K27me) by the Polycomb Repressive Complex (PRC2), which marks repressive chromatin domains and regulates cell differentiation in diverse species ranging from Caenorhabditis elegans (C. elegans) to humans. Mutation of H3K27 to methionine (H3K27M) was recently discovered to be the major genetic driver of a deadly childhood brain tumor known as diffuse intrinsic pontine glioma (DIPG), and represents the first histone mutation to be implicated in any human disease. H3K27M mutations cause global epigenetic changes in DIPG tumors which are thought to promote tumor growth. Re-normalization of the epigenome in H3K27M cells is a major goal in current therapeutic strategies, but methods to achieve this remain elusive, with no platform for large-scale testing. We have designed such a platform in C. elegans, where we not only discovered that H3K27M mutations recapitulate the major molecular phenotypes observed in

human cells, but also uncovered, through genetic screening, additional mutations that can reverse these phenotypes. Current projects include dissecting the molecular mechanisms of H3K27M suppression in C. elegans and in human cells, testing transgenerational epigenetic inheritance in histone mutants, and genetically engineering additional histone mutant models. This work will significantly increase our molecular understanding of histone mutations, which represent a new and rapidly growing class of epigenetic drivers of human diseases.
Number of hours per week: Freshmen and Sophomores are recommended to work 6-10hrs/week. Juniors and Seniors are recommended to work 15-20hrs/week. During the summer all students are expected to work 40hrs/week, but hours can be negotiable on an individual basis.
Requirements: No prior research experience is required.
If interested email: alan.jiao@childrens.harvard.edu and yang_shi@hms.harvard.edu

Poster 98. Layer 1 Cortical Circuits for Auditory Plasticity and Learning

Presenters: Lucas Vattino, Maryse Thomas
Principal Investigator: Anne Takesian, anne_takesian@meei.harvard.edu
Harvard Medical School, Mass Eye and Ear
Mass Eye and Ear, 243 Charles Street, Boston,
https://takesian.hms.harvard.edu/people/anne-e-takesian

Our understanding of the world is based on sensory experiences, such as hearing, which allow us to adapt to and learn about our surroundings. A major question in neuroscience research is how such experiences can lead to long-lasting changes in the brain. In the auditory system, recent research by our group has identified layer 1 of the primary auditory cortex as a brain area that receives both sensory inputs and behaviorally-relevant information, making it a powerful hub for initiating plastic changes based on experience. This layer is made up primarily of inhibitory interneurons, which contribute to auditory processing and plasticity by modulating the activity of other neurons. In our laboratory, we combine state-of-the-art techniques to investigate the role of these layer 1 interneurons in the mouse brain. By using anatomical tracing and immunohistochemical strategies we are able to identify projections both arising from and contacting these cells. We also perform in vitro fluorescence-guided electrophysiological recordings paired with

optogenetic manipulations to map the circuits in which they are involved. Finally, by monitoring cellular activity in behaving mice using 2-photon imaging we can assess their responses to sound and how that might change with learning. Through this work, we will gain knowledge about how layer 1 interneurons help us understand and interact with the world around us. Our hope is that understanding these circuits will lead to new therapeutic strategies to improve auditory learning and promote recovery from hearing loss.
Number of hours per week: 10-20 hours/week
Requirements: none
If interested email: lucas_vattino@meei.harvard.edu and anne_takesian@meei.harvard.edu

Poster 99. Therapeutic and Diagnostic Strategies for Pediatric and Adult Brain Cancer

Presenters: Jian Teng, Markus Schweiger
Principal Investigator: Bakhos Tannous,
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MGH, HMS, Neuroscience Center at Massachusetts General Hospital
Massachusetts General Hospital – East Building 149, 13th Street
Charlestown, MA, www.tannouslab.com

Despite extensive treatment, long-term survival for pediatric and adult primary gliomas and brain metastases remains uncommon. Our work focuses on developing novel diagnostics and treatment strategies against tumors in the brain using three different strategies: (1) High Throughput Screening: We have developed a high-throughput drug screening pipeline that allows for the evaluation of thousands of different compounds against pediatric and adult glioblastomas and are testing a handful of promising drugs in patient-derived pre-clinical models. Further, by repurposing old drugs, we could show that Hydroxyurea, used to treat sickle cell disease, improves survival of mice with glioblastomas and we are currently testing this therapy in a clinical trial. (2) Gene and Cell Therapy: We develop novel gene/cell therapeutic approaches using different viral vectors, platelets or stem cells to delivery anti-cancer therapeutics and test the novel role of olfactory cells for anti-glioma therapy through intra-nasal injection, their natural route to CNS. (3) Diagnostics: Our work elucidates the role of extracellular vesicles and tumor-educated platelets in brain tumor metastasis/progression and therapeutic resistance. In addition, we utilize the power of platelets to

develop a novel diagnostic platform and to deliver therapeutic agents against brain tumors.
Number of hours per week: negotiable, depending on arrangement with each individual student
Requirements: no prior research experience required
If interested email: bakhos_tannous@hms.harvard.edu

Poster 100. Incidence and Cognitive Correlates of Strangulation in Intimate-Partner Violence

Presenters: Annie-Lori Joseph, Nathalia Quiroz
Principal Investigator: Eve Valera, eve_valera@hms.harvard.edu
HMS - Psychiatry; MGH - Psychiatry, 149 13th Street Charlestown, MA 02129, https://www.nmr.mgh.harvard.edu/lab/valera

Globally, intimate partner violence (IPV) is experienced by approximately 1 in 3 women and represents the number one cause of homicide and violence against women. Within IPV, up to 80-90% of injuries reported are to the neck and higher, and includes lethal and non-lethal strangulation. Strangulation can represent a form of acquired brain injury if an alteration in consciousness (AIC) is associated with the event. As such, cognitive sequelae might be expected, but such sequelae of nonfatal strangulation in IPV has not been evaluated in a systematic manner. Here we used several neuropsychological measures and the Brain Injury Severity Assessment (BISA) interview to examine the association between strangulation-induced AICs and several measures of cognitive functioning. Results indicated that 25% of the sample sustained at least one AIC from strangulation with nearly half of the women reporting more than one. Additionally, number of strangulation-induced AICs were associated with a woman's ability to learn a list of words that were read to her five times. This association was not accounted for by other brain injuries the woman may have sustained via her abuse. This is the first report to assess strangulation in this manner and demonstrate a link to cognitive functioning. These data contribute to our knowledge of strangulation and its effects in women who have experienced IPV.
Number of hours per week: Negotiable.
Requirements: None.
If interested email: eve_valera@hms.harvard.edu

Poster 101. Non-coding RNAs, RNPs & Translation in Cancer

Presenters: Syed Irfan Bukhari, Samuel Truesdell
Principal Investigator: Shobha Vasudevan,
vasudevan.shobha@mgh.harvard.edu
MGH Cancer Center, HMS, MGH Center for Regenerative Medicine, Harvard Stem Cell Institute HMS Initiative for RNA Medicine
185 Cambridge St, CPZN 4202, Boston MA 02114 MGH Cancer Center, https://www.massgeneral.org/cancerresearch/research/researchlab.aspx?id=1275

Syed I.A. Bukhari, Samuel S. Truesdell, Sooncheol Lee, Chandreyee Datta, Brianna Buchanan, Ramzi Elased, and Shobha Vasudevan
Vasudevan Lab Department of Medicine, Harvard Medical School, MGH Cancer Center, MGH Center for Regenerative Medicine & Harvard Stem Cell Institute MGH, Main Campus, Simches Research Bldg, 185 Cambridge St, CPZN 4100/4202, Boston, MA 02114 Ph: 617-643-3143
vasudevan.shobha@mgh.harvard.edu
https://hsci.harvard.edu/people/shobha-vasudevan-phd
http://dms.hms.harvard.edu/BBS/fac/Vasudevan.php Quiescent (G0) cancer cells are dormant, reversibly-arrested cells, including stem cells, which resist clinical therapy that eliminates proliferating cancer cells. Upon chemotherapy removal, G0 cells sense the loss of their proliferating neighbors and restart cell division, restoring the cancer as recurrence. G0 shows a switch to a distinct gene expression program where RNA regulation enables persistence of this critical state. mRNA control elements and regulatory RNAs such as non-coding RNAs and microRNAs, interact with RNA binding proteins to form RNA-protein complexes (RNPs) and direct expression of clinically relevant genes; their deregulation leads to a range of clinical effects such as tumor resistance, immune and developmental disorders. The primary goal of our research program is to investigate non-coding RNA- and RNA binding protein-controlled expression of critical genes in tumors, which lead to resistance and tumor expansion. A second focus is to characterize the mechanisms of expression or translation of critical genes in G0 states in cancers, stem cells and germ cells. A third aim is to develop therapeutic approaches to modulate RNA-controlled expression in tumor resistance. These investigations will provide insights and novel therapeutics on non-coding RNAs in tumor resistance. Number of hours per week: Negotiable, arranged according to student's needs.

Requirements: Prior experience is not needed, a passion to learn & persistence are.
If interested email: vasudevan.shobha@mgh.harvard.edu

Poster 102. Computational Drug Discovery Platform based on Structure-Based Virtual Screenings

Presenters: Christoph Gorgulla,
Principal Investigator: Gerhard Wagner
gerhard_wagner@hms.harvard.edu
Harvard Medical School, Department of Biological Chemistry and Molecular Pharmacology 240 Longwood Ave Boston, MA 02115, https://gwagner.hms.harvard.edu/

In most diseases, biological macromolecules like proteins play a central role. Often these diseases can be treated, cured, or prevented by small molecules that bind to a specific site of a certain protein. In the human body there at least 20,000 different proteins, and finding a suitable small molecule for a certain target is a great challenge. On average, an approved drug today costs $2-3 billion and takes over 10 years to develop. To a large extent, this is due to expensive and time-consuming wet-lab experiments and poor initial hit and lead compounds. Computer-aided drug design has the potential to mitigate these problems dramatically. We are developing a new open-source virtual screening platform with many exciting features, which allows preparing and screen ligand libraries on scales not possible before. For this purpose, our platform is capable of running on the world's largest supercomputers and cloud computing platforms (like the GCP, AWS or Azure). The project offers the opportunity to obtain first-hand experience in an open-source project at the scientific frontier of computer-aided drug design. We are looking for students with experience in software development who are interested in extending our drug discovery platform with new exciting features. Experience with Linux and Bash are required. Experience with GPU programming, Python and/or Linux clusters are favorable, but not essential. The work can be done partially offsite from the HMS campus.
Number of hours per week: Negotiable, depends on arrangement with each individual student.
Requirements: Experience with software development, Linux and Bash are required.
If interested email: christoph_gorgulla@hms.harvard.edu and gerhard_wagner@hms.harvard.edu

Poster 103. Nuclear Magnetic Resonance spectroscopy of magnetic dipoles in Chiral molecules using quantum defects in diamond
Presenters: Oren Ben Dor
Principal Investigator: Ronald Walsworth, rwalsworth@cfa.harvard.edu
Smithsonian-Harvard Astrophysical Observatory Harvard Physics
60 Garden St, Cambridge, http://walsworth.physics.harvard.edu/

Chiral molecules, namely molecules that cannot be superimposed on their own mirror image, are highly abundant in nature, yet, our understanding of the role and cause of homochirality - chiral molecules are found in nature in a single form - remains enigmatic. Interestingly, chiral molecules show self-induced magnetic fields once they're adsorbed on ferromagnetic substrates. This extraordinary behavior is explained by an interaction between the electric and magnetic dipoles within the molecules. To date, the various methods used to study this phenomenon, both experimentally and theoretically, could only do so indirectly/partially, therefore providing insufficient insight into the underlined mechanisms at play. Nonetheless, in recent years, nitrogen-vacancy (NV) centers in diamond have become a benchmark for atomic-sized quantum magnetometers, characterized by long coherence times, while allowing room temperature and low magnetic fields functionality. In this configuration, adsorption of chiral molecules on top of the diamond surface enables nuclear magnetic resonance (NMR) spectroscopy of proton signals stemming from ~1200 chiral molecules, while taking advantage of the NVs several nanometers proximity to the molecules. This state-of-the-art technique has the potential to directly probe the chiral molecules' unique magnetic dipoles. NV-NMR has the potential to further probe homochirality and could, therefore, shed new light on the origins of life to which the homochiral mystery is inherent.
Number of hours per week: 8 hrs/week Sophomores 15 hrs/week Junior and Seniors If during summer then let's discuss specifically
Requirements: Programming capabilities (Matlab, Python, Mathematica) Experience in optics (not obligatory) Good hands for clean room/machine shop etc.
Interested email: orenbendor@gmail.com & rwalsworth@cfa.harvard.edu

Poster 104. Unraveling novel molecular mechanisms in osteocyte differentiation and function
Presenters: Marc Wein
Principal Investigator: Marc Wein, mnwein@mgh.harvard.edu

Endocrine Unit, MGH, Broad Institute of MIT and Harvard, HMS
Thier Research Building, Room 1101 MGH Endocrine Unit 50 Blossom Street Boston, MA 02114, https://scholar.harvard.edu/wein/home

Osteoporosis is a major public health problem in our aging society. Skeletal fragility is caused by an imbalance between bone formation by osteoblasts and bone resorption by osteoclasts. Osteocytes, cells buried deep within mineralized bone matrix, orchestrate bone remodeling by cells on bone surfaces. The Wein laboratory is interested in the molecular processes that govern osteocyte function. Work currently focuses on three major questions in osteocyte biology: 1. How do osteocytes respond to parathyroid hormone to regulate bone homeostasis in response to changing calcium levels? 2. How do osteocytes respond to mechanical cues to regulate bone remodeling in response to exercise and skeletal unloading? 3. How do osteoblasts trans-differentiate into osteocytes? We use cutting edge molecular cell biology and genetic approaches to pursue investigation into these major unanswered questions in skeletal biology. Work is focused on defining new molecular mechanisms and then pursuing the therapeutic potential of novel discoveries for patients with osteoporosis.
Number of hours per week: negotiable
Requirements: none
If interested email: mnwein@mgh.harvard.edu and mnwein@mgh.harvard.edu

Poster 105. Alterations in the gut microbiota in progressive and relapsing remitting MS are associated with quality of life measurements

Presenters: Laura Cox
Principal Investigator: Howard L. Weiner hweiner@rics.bwh.harvard.edu
Ann Romney Center for Neurologic Diseases, Brigham & Women's Hospital, Harvard Medical School
60 Fenwood Road, 10032, Boston, MA 02115,
http://weinerlab.bwh.harvard.edu

The intestinal microbiota can shape the immune system, influence the brain, and is hypothesized to play a role in the neurologic disease multiple sclerosis (MS). While alterations have been detected in patients with relapsing-remitting MS, little is known about microbiota differences in progressive MS patients, and how the microbiota is related to clinical

parameters. We investigated the gut microbiota samples from 41 healthy controls, 202 relapsing remitting MS patients, and 42 progressive MS patients by sequencing the V4 region of the microbial 16S rRNA and measured clinical outcomes including expanded disability status scale (EDSS) and quality of life measurements. In the microbiome, we found that the overall community structure in both RRMS and progressive MS patients differed from healthy controls, based on principal coordinate analysis of unweighted UniFrac distances and the permanova test for clustering. There was no global difference between RRMS and progressive MS patients. At the compositional level, we found several members of the microbiota that were altered in both RRMS and progressive, with enhanced changes in progressive patients compared to RRMS. Furthermore, we identified bacteria that significantly correlated with expanded disability status scale (EDSS) and quality of life. Altogether, these data provide evidence that while RRMS and progressive patients share many alterations in their microbiota, we observe enhanced changes in progressive patients, and which we link for the first time to clinical outcomes.
Number of hours per week: Academic Term 15-20 hours/week. Summer 40 hours/week
Requirements: Interest in neurology, microbiology, immunology, or bioinformatic analysis. Previous research experience preferred.
If interested email: lcox@bwh.harvard.edu and hweiner@rics.bwh.harvard.edu

Poster 106. Current Research at McLean Hospital's Alcohol and Drug Abuse Clinical Research Program

Presenters: Elizabeth Kneeland, Blake Hilton
Principal Investigator: Roger Weiss, rweiss@mclean.harvard.edu
McLean Hospital/Harvard Medical School
McLean Hospital, 115 Mill Street, Belmont, MA 02478,

The Alcohol and Drug Abuse clinical research program at McLean Hospital is an ongoing, multidisciplinary, prolific research program focused on improving outcomes for individuals with substance use disorders (SUDs). Investigator disciplines include psychiatry, psychology, sociology, and social work. Roger Weiss, MD, is director of the research program, and also a Principal Investigator (PI) of the New England node of the National Drug Abuse Treatment Clinical Trials Network, a nationwide collaborative project testing the effectiveness of behavioral

and pharmacotherapeutic interventions for SUD. Highlights of publications include finding that a 12-week medication treatment was more successful than a briefer treatment for OUD, initial buprenorphine response can be predicted 2 weeks into treatment, and chronic pain is an important predictor of continued opioid use. Further, a long-term series of exploratory studies (N>1500) collects data on the inpatient detoxification unit to identify risk factors associated with clinical severity among individuals seeking intensive SUD treatment. Interesting findings among OUD patients include low levels of grit, high prevalence of overdose along a continuum of suicidal intent, and common misuse of benzodiazepines. The ADATP research program includes the Stress, Anxiety and Substance Use Laboratory (PI: Kathryn McHugh, PhD); current studies include a clinical trial testing a new behavioral intervention for opioid use disorder. Additional ongoing studies include an experiment on the association between perceived control over physical pain and stress and alcohol use (PI: Elizabeth Kneeland, PhD) and a feasibility study of adopting a ketogenic diet during opioid withdrawal in patients with opioid use disorder (PI: Blake Hilton, PsyD).
Number of hours per week: 8-16 hours per week
Requirements: Prior lab experience preferred.
If interested email: ekneeland@partners.org and rweiss@mclean.harvard.edu

Poster 107. Investigating neural functions of imprinted, non-coding RNAs

Presenters: Udbhav Chitta
Principal Investigator: Amanda Whipple
amanda_whipple@fas.harvard.edu
Harvard University Department of Molecular and Cellular Biology
16 Divinity Avenue, #4004, https://www.whipplelab.com/

Genomic imprinting is an epigenetic phenomenon that establishes monoallelic, parent-of-origin gene expression. Imprinted gene expression is enriched is the brain, and disrupted in several neurodevelopmental disorders. Small nucleolar RNAs (snoRNAs) are non-coding RNAs that direct chemical modifications to specific RNA target sites. Canonical C/D box snoRNAs guide the Fibrillarin (FBL) methyltransferase complex to deposit 2'-O-methylation on complementary ribosomal RNA (rRNA) transcripts. Interestingly, several neuron-specific C/D box snoRNAs are imprinted but have no known targets. This suggests parental genomes

may utilize an RNA modification pathway in the brain, but the effects of this process are unknown. To study the activity of imprinted snoRNAs, we established an in vitro system that permits quantification of allelic expression in neurons. Hybrid embryonic stem cells (ESCs) from an M.m.musculus x M.m.castaneous cross were differentiated to induced neurons by Neurogenin-2. Induced neurons maintain proper expression of imprinted genes and are electrophysiologically active. We are now using this system to identify the function of imprinted snoRNAs. The Rian cluster of snoRNAs is expressed in a maternal-specific manner and is up-regulated upon neuron differentiation. We determined that these snoRNAs are bound to FBL, suggesting they direct 2'-O-methylation on complementary RNA transcripts. We aim to identify the direct targets of Rian snoRNAs, thereby providing insight into a novel mechanism by which parental genomes affect neuronal gene expression in offspring.
Number of hours per week: 15+
Requirements: Strong background in biology required. Previous laboratory experience strongly encouraged, must be proficient at micropipetting. Strong interpersonal skills are required, as is the ability to work both independently and as part of a team. Must be self-motivated and well-organized with attention to detail.
If interested email: amanda_whipple@fas.harvard.edu

Poster 108. Robots composed of and powered by materials that are sustainable, nonhazardous, biodegradable, and edible
Presenters: Jeff Rawson,
Principal Investigator: George Whitesides,
gwhitesides@gmwgroup.harvard.edu
Chemistry and Chemical Biology
Mallinckrodt 238 12 Oxford St., Cambridge,
https://gmwgroup.harvard.edu/

Many applications for robotics, including environmental monitoring, agriculture, and medicine, require autonomous devices that are disposable, nonhazardous to people and the environment, and produced sustainably. We address these needs by developing naturally-derived and bioinspired substances for soft robotics, where elastic materials and compliant structures replace rigid components and electric motors. We show how gelatin compositions that were inspired by food technology can be used to replace silicone elastomers. We also demonstrate a

simple approach to powering single-use devices using baking soda and vinegar.
Number of hours per week: Negotiable, but the more you work, the more you get from the experience.
Requirements: Enthusiasm for visualizing, observing, investigating, and making.
If interested email: jrawson@gmwgroup.harvard.edu and gwhitesides@gmwgroup.harvard.edu

Poster 109. The Impact of Future Volcanic Eruptions on Stratospheric Ozone

Presenters: Eric Klobas, David Wilmouth
Principal Investigator: David M. Wilmouth, wilmouth@huarp.harvard.edu
SEAS/EPS/CCB
12 Oxford Street, Mallinckrodt-Link, https://www.arp.harvard.edu/

The ozone layer is essential for surface life on Earth; small reductions in its thickness produce significant impacts on human health. Due to the Montreal Protocol, stratospheric ozone is now on a slow trajectory toward recovery as halocarbons in the atmosphere decay. In the future, the most significant perturbations to Earth's ozone layer may be caused by volcanic eruptions. Large, explosive volcanic eruptions have the capability to significantly alter spatiotemporal profiles of column ozone via changes in trace gas composition/aerosol loading of the stratosphere. The extent to which stratospheric ozone will be perturbed by a future volcanic eruption is dependent on several factors: (a) the physicochemical state of the stratosphere – e.g., greenhouse gas loading, lapse rate, and background halocarbon inventories; (b) the physicochemical state of the eruption column – e.g., initial volcanic gas composition and halogen speciation, intracolumn volcanic gas-aerosol partitioning, total volcanic mass and mass ejection rate; and (c) meteorological and geographical effects – e.g., environmental air masses entrained within the eruption column, height of the tropopause, radiative-dynamical impacts on circulation. Understanding the weight of the variables that control the response of stratospheric ozone to volcanic injection is of high importance. The primary objectives of this project are threefold: (1) characterize column ozone sensitivity to contemporary and future explosive volcanic eruptions as a function of volcanic latitude and season; (2) determine ozone column sensitivity to the direct stratospheric co-injection of inorganic chlorine, bromine, and iodine along

with sulfur dioxide from volcanic eruption; and (3) quantify future bromine and iodine alpha factors in a variety of greenhouse gas emission scenarios.
Number of hours per week: flexible: 10 - 20 hours/week
Requirements: This is a computer modeling project using a state-of-the-art chemistry-climate-aerosol model on the Harvard Odyssey supercomputer. While no prior research experience is expected or required, a basic familiarity with (or desire to learn) the linux operating system, fortran, bash, python, and julia are helpful.
If interested email: klobas@huarp.harvard.edu and wilmouth@huarp.harvard.edu

Poster 110. Synthetic gene circuits for cancer immunotherapy: Turning cancer cells against themselves
Presenters: Ming-Ru Wu,
Principal Investigator: Ming-Ru Wu, ming-ru_wu@dfci.harvard.edu
Dana-Farber Cancer Institute and Harvard Medical School
1 Jimmy Fund Way, Boston, MA 02115, https://syntheticimmunity.net

Cancer immunotherapy has demonstrated robust efficacy in clinical trials, but challenges such as the lack of ideal targetable tumor antigens, severe toxicity, and tumor-mediated immunosuppression still limit its success. To overcome these challenges, I have designed a synthetic cancer-targeting gene circuit platform that enables a localized and robust combinatorial immunotherapy from within cancer cells: a Trojan horse-like approach. Once the circuits are introduced into cells, they will sense cancer-specific transcription factor activities, and trigger an effective combinatorial immunotherapy selectively from within cancer cells, while keeping normal cells unharmed. The circuit cured disseminated ovarian cancer in vivo in a mouse model. This platform can be adjusted to treat multiple cancer types and can potentially trigger any genetically-encodable immunomodulators as therapeutic outputs. Moreover, this gene circuit platform can be adapted to treat additional diseases exhibiting aberrant transcription factor activities, such as chronic metabolic diseases and autoimmune disorders.
Number of hours per week: It is negotiable and depends on arrangement with each individual student
Requirements: none
If interested email: ming-ru_wu@dfci.harvard.edu

Poster 111. Design and Development of Deep Learning and Advanced Mathematics Techniques in Brain Imaging Research and Clinical Applications

Presenters: Min Zhang, Geoffrey Young
Principal Investigator: Xiaoyin Xu, xxu@bwh.harvard.edu
Department of Radiology BWH, HMS
75 Francis Street Boston, MA 02115,

Computer-aided detection and diagnosis and image quantification play an important role in facilitate brain-related research and clinical practice. We focus on designing and developing deep learning-based and advanced mathematics techniques such as partial differential equations, differential geometry and conformal mapping for modeling and analyzing brain images acquired by magnetic resonance imaging, computed tomography, and angiography. Our overarching goal is to improve the quantification capability of existing techniques, automatically and semi-automatically detect abnormalities in both structural and functional brain imaging, and predict patients' responses to novel therapies. We develop deep learning algorithms and other computational techniques to address clinical questions. In this process, we deal with a diverse topics in applied mathematics, computer science, electrical engineering, and other quantitative science fields to address clinical research challenges in cancer, neurodegenerative conditions like Alzheimer's disease, cognitive deficits, and brain blood vessel deformation. We collaborate with researchers with diverse backgrounds in radiology, neurosurgery, neurology, oncology, physics, mathematics, computer science, computer and electrical engineering, and neuropsychiatry.
Number of hours per week: Negotiable
Requirements: None
If interested email: xxu@bwh.harvard.edu

Poster 112. Mapping the wiring of the human brain with diffusion MRI

Presenters: Chiara Maffei
Principal Investigator: Anastasia Yendiki, ayendiki@mgh.harvard.edu
Martinos Center for Biomedical Imaging, MGH, HMS
149 Thirteenth Street, Rm 2301, Charlestown, MA 02129,
https://proxy.qualtrics.com/proxy/?url=https%3A%2F%2Fscholar.harvard.edu%2Fa-

y&token=vpAPQnSGr%2Bst%2BG1m4uzMGnngPrpPqToPx6m41G%2B3yYo%3D

Our group works on mapping the white matter connections of the human brain. We use very high-resolution diffusion magnetica resonance imaging (dMRI) and optical imaging techniques that are only feasible ex vivo to create accurate models of brain pathways from post mortem human brains. We then use these models to train algorithms that can automatically reconstruct the same connections from the much lower resolution MRI brain scans that can be performed on living subjects in clinical settings. Our goal is to develop computational tools that allow clinicians and researchers to study how the brain is wired in healthy subjects as well as patients with psychiatric and neurological disorders. Here we show our efforts to map different both well known and more challenging connections of the human brain. We use unique high quality data from the Human Connectome Project to suggest optimal macroanatomical landmarks for the virtual dissection of these pathways, and show how we can train tractography on such data and improve the accuracy of tractography in more widely available routine quality diffusion data.
Number of hours per week: Negotiable depending on project
Requirements: Some of our projects require prior experience in computer programming. However there are also projects available that do not require prior experience.
If interested email: ayendiki@mgh.harvard.edu

Poster 113. Exploring mammalian systems at single-cell resolution
Presenters: Shengbao Suo, Ruben Dries
Principal Investigator: Guo-Cheng Yuan, gcyuan@jimmy.harvard.edu
Department of Pediatric Oncology, DFCI and HMS
Room 1060, Longwood Center Street Address: 360 Longwood Ave, Boston. MA 02215. , http://bcb.dfci.harvard.edu/~gcyuan/index.html

The cell is considered the fundamental unit in biology. For centuries, biologists have known that multicellular organisms are characterized by a plethora of distinct cell types, which need to work together to form a functional tissue and organ, such as the brain or lung. In the lab of Dr. Guo-Cheng Yuan we develop state-of-the-art algorithms and tools to discover the true diversity of cell types and how they communicate or interact. Recently, the lab has made a number of contributions to the

international effort of the human cell atlas consortium. First, we helped building a mouse cell atlas using single cell RNA sequencing data. In total, we analyzed more than 700,000 single cells covering 14 major mouse organs and subsequently revealed aging related regulatory networks and pathways by systemically profiling the whole life span of a mouse. Second, our collaborators have recently developed powerful technologies to map single-cell transcriptomes with highly-resolved spatial information. We created a novel open-source pipeline that integrates both analysis and visualization of this type of data which allowed us to dissect a previously invisible layer of spatial information. For example, we could identify how different cell types in the brain cortex use different ligand-receptor signaling pathways to directly interact or communicate with each other. Furthermore, by using a novel browser-based visualization tool user can both explore their spatial data and generate new hypotheses in an intuitive and interactive manner. In sum, our lab develops cutting-edge methods to analyze and interpret how mammalian systems operate at the single-cell level.
Number of hours per week: 10 hours/week
Requirements: Need to write code to solve biological problem.
If interested email: gcyuan@jimmy.harvard.edu

Poster 114. Engineering Biomimetic Living Systems through Biofabrication

Presenters: Sushila Maharjan, Nan Jiang
Principal Investigator: Yu Shrike Zhang, yszhang@bwh.harvard.edu
Brigham and Women's Hospital, Harvard Medical School
65 landsdowne street, Cambridge MA 02139,
https://www.shrikezhang.com/

The poster will discuss our recent efforts on developing a series of bioprinting strategies including sacrificial bioprinting, microfluidic bioprinting, and multi-material bioprinting, along with various cytocompatible bioink formulations, for the fabrication of biomimetic 3D tissue models. These platform technologies, when combined with microfluidic bioreactors and bioanalysis, will likely provide new opportunities in constructing functional microtissues with a potential of achieving precision therapy by overcoming certain limitations associated with conventional models based on planar cell cultures and animals.
Number of hours per week: 8 hours/week for Freshmen and Sophomores

Requirements:
If interested email: ruma_sushila@hotmail.com and yszhang@bwh.harvard.edu

Poster 115. Cortical surface registration using unsupervised learning

Presenters: Jieyu Cheng
Principal Investigator: Lilla Zollei, lzollei@nmr.mgh.harvard.edu
Laboratory of Computational Neuroimaging, AA Martinos Center, MGH
149 13th St, Charlestown MA 02129,
https://www.nmr.mgh.harvard.edu/lab/lcn

Non-rigid cortical registration is a challenging task due to the intricate geometric complexity of the human cortex and high inter-subject variability. A conventional solution is to use a spherical representation of surface properties and perform registration by aligning cortical folding patterns in that space. This strategy produces accurate spatial alignment, however, the computational cost is often high. Convolutional neural networks (CNNs) have demonstrated the potential to speed up registration tasks. However, due to distortions introduced by projecting a sphere to a 2D plane, a direct application of recent learning-based methods, yields poor results. We propose a diffeomorphic registration framework for cortical surfaces using deep networks to address these issues. We construct a weighted graph that produces a stationary velocity field and a weighted log-likelihood framework to eliminate distortion introduced by the projection. We demonstrate the proposed method on both a brain parcellation task and the alignment of functional activations. Our experiments show that the proposed framework is capable of modeling the geometric registration problem using Euclidean image registration as well as demonstrate superior registration accuracy and computational efficiency.
Number of hours per week: 10-20hrs / week (This is negotiable)
Requirements: Coding / scripting background is very useful, knowledge of neuroanatomy is a plus
If interested email: lzollei@nmr.mgh.harvard.edu

Poster 116. Biology of Hematopoiesis and Cancer

Presenters: Meredith Stanhope, Georgia Stirtz
Principal Investigator: Leonard Zon,
leonard.zon@enders.tch.harvard.edu

Stem Cell Program and Division of Hematology/Oncology BCH, DFCI, Howard Hughes Medical Institute, HMS, Harvard Stem Cell Institute, Sherman Fairchild Biochemistry Building Ground Floor 7 Divinity Ave Cambridge, MA 02138, zonlab.org

The Zon Laboratory focuses on the developmental biology of hematopoiesis and cancer in zebrafish and mouse systems, as well as human cell lines. We have collected well over 30 mutants affecting the hematopoietic system. Some of the mutants represent excellent animal models of human disease. Recently, we identified several chromatin factors with essential roles at various stages of hematopoiesis. We have developed suppressor screening genetic methods and found that transcriptional elongation regulates blood cell fate. We also have performed chemical genetic screens to identify components implicated in blood development and have found that prostaglandins increase the number of blood stem cells. This has led to a clinical trial to improve engraftment for patients receiving cord blood transplants; phase I trials were just successfully completed. The laboratory has also developed zebrafish models of cancer. Using transgenics, we have generated a melanoma model in the zebrafish system. Transgenic fish get nevi, and when combined with a p53 mutant, fish develop melanomas. We recently found a histone methyltransferase that can accelerate melanoma, and discovered a small molecule that blocks transcription elongation and suppresses melanoma growth.
Number of hours per week: Negotiable: depends on arrangement.
Requirements: Prior lab experience is recommended but not required.
If interested email: meredith_stanhope@fas.harvard.edu and leonard.zon@enders.tch.harvard.edu

Poster 117. Beam monitoring device for real-time verification of radiation treatment for cancer
Presenters: Davide Brivio, Yulia Lyatskaya
Principal Investigator: Piotr Zygmanski, pzygmanski@bwh.harvard.edu
Medical Physics and Biophysics Division Department of Radiation Oncology BWH, DFCI and HMS
75 Francis st, Boston 02115, http://mesoscopic.bwh.harvard.edu/

There are more than 14 million new cancer cases diagnosed worldwide each year. Radiation therapy (RT) can cure about 3.5 million out of these cases and provide palliative relief for additional 3.5 million people. RT

uses high energy particle accelerators loaded with sophisticated equipment to dynamically shape the treatment beams (x-rays, electrons, protons, heavy ions) and treat cancer patients. Assuring accurate, safe and nondisruptive operation of RT equipment and delivery of radiation is challenging. A beam monitoring device is a sensor that measures distribution and magnitude of radiation in real time during operation of the treatment machine (linac). Present devices are not well suited for high throughput, continual operation and supply of comprehensive data. We are developing beam monitoring devices for medical linacs for treatment of cancer with radiation. The problems involved for the design and the fabrication of such device include material science, physics of signal formation and ionizing radiation science. Opportunities are in simulation of the physics of sensor response, nanofabrication and/or 3D printing fabrication as well as experiments with medical radiation sources.
Number of hours per week: Sep-May 15-20h Summer 40h
Requirements: Some exposure to physics and math is desirable
If interested email: dbrivio@bwh.harvard.edu and pzygmanski@bwh.harvard.edu

Poster 118. Form, function and evolution of "invisible" parasitic flowering plants
Presenters: Luiza Teixeira-Costa
Harvard University Herbaria
22 Divinity Avenue Cambridge, MA 02138,

Parasitic flowering plants have evolved at least 12 times, comprising ca. 1% of all extant Angiosperms. These plants show a wide variety of habits, host ranges and geographical distribution. Among such diversity, over five different plant families include species that, during most of their life cycle, remain "invisible" to the naked eye. Parasites such as the Rafflesiaceae are restricted to a few parenchyma cells inside their host's bark and wood for years, until blooming the largest flowers in the world. My current research focus on analyzing how these peculiar and reduced plants are able to connect to their hosts. Investigating the structure of the haustorium, i.e., the organ responsible for host attachment and connection, can shed light on how these parasitic plants could have evolved from non-parasitic ancestors. In addition, I'm interested in the class of substances exchanged between host and parasite via the haustorium. This provides information about the effects caused by one

plant on the other. Finally, my work also targets the understanding of how parasitic plants can shift from one host species to another - a crucial information in the context of global climate change.
Number of hours per week: Number of hours per week is negotiable, depending on arrangements made with each individual student.
Requirements: None.
If interested email: lteixeiracosta@fas.harvard.edu

Informational Tables

Table 1. Life Sciences Concentration Advising & Undergraduate Research Advising

Life Science Concentration Advising
Biomedical Engineering: Lindsey Moyer, lmoyer@seas.harvard.edu, 206C Pierce Hall
Chemical and Physical Biology: Dominic Mao, dominicmao@fas.harvard.edu, Sherman Fairchild Room 195
Chemistry: Gregory Tucci, tucci@fas.harvard.edu, Science Center, Room 114
Cognitive Neuroscience and Evolutionary Psychology, a track in the **Psychology concentration:** Katherine Powers, kpowers@fas.harvard.edu, William James Hall, Room 218
Human Developmental and Regenerative Biology: Bill Anderson, wanders@fas.harvard.edu, Bauer Laboratory Room 204
Human Evolutionary Biology: Carole Hooven, hooven@fas.harvard.edu**,** Peabody 52F; Dr. Neil Roach ntroach@fas.harvard.edu Peabody Museum 47, Dr. Daniel Green drgreen@fas.harvard.edu, Peabody Museum 53B
Integrative Biology: Andrew Berry, berry@oeb.harvard.edu, BioLabs Room 1082B
Molecular and Cellular Biology: Dominic Mao, dominicmao@fas.harvard.edu, Sherman Fairchild Room 195
Neurobiology: Ryan Draft, draft@fas.harvard.edu, Biolabs Room 1082A; Laura Magnotti, magnotti@fas.harvard.edu, BioLabs Room 1082D

Undergraduate Science Research Advising
Many Harvard undergraduates participate in science research at one of Harvard's campuses. If you are interested in research, the Undergraduate Science Research Advisor, Anna Babakhanyan, can help you navigate the process of finding a research group. She can help you: define your research interests, navigate research group websites, create and edit a science resume and cover letter, identify and contact research groups, interviews, apply for fellowships and funding, integrate effectively into your research group and make the most of your research experiences.

Contact: Dr. Anna Babakhanyan, ababakhanyan@fas.harvard.edu
http://lifesciences.fas.harvard.edu/research

Table 2. Harvard T.H. Chan School of Public Health Summer Internship Programs

The School offers summer programs for current undergraduates and recent post-baccalaureate students from underrepresented groups interested in public health. Both the Summer Program in Biostatistics & Computational Biology and Summer Program in Epidemiology expose students to quantitative methods through coursework, lectures, and research projects. Additionally, the Summer Internship in Biological Sciences in Public Health focuses on laboratory-based biological research and is only open to undergraduate students.

Contact: Kerri Noonan, pthareja@hsph.harvard.edu,
https://www.hsph.harvard.edu/admissions/degree-programs/summer-programs/
158 Longwood Avenue, Boston, MA

Table 3. Summer Program in Biostatistics and Computational Biology

The Summer Program is an intensive 6-week program, during which qualified participants receive an introduction to biostatistics, epidemiology, and public health research. This program is designed to expose undergraduates to the use of quantitative methods for biological, environmental, and medical research.

Contact: Priti Thareja, pthareja@hsph.harvard.edu,
https://www.hsph.harvard.edu/biostatistics/
655 Huntington Avenue Building 2, 4th Floor Boston, MA 02115

Table 4. Mind Brain Behavior Undergraduate Program

As an interfaculty initiative, Mind Brain Behavior (MBB) does not have its own faculty and research programs as departments do. Instead, MBB serves as a clearinghouse for research opportunities for undergraduates. These opportunities are usually based in FAS or the Medical School and are available to any student with an interest in MBB topics. In addition,

Mary Gordon Roberts MBB Summer Research Fellowships are available to help fund the thesis research of rising seniors in an MBB track or the MBB secondary field. For further information, visit https://mbb.harvard.edu/pages/undergraduate-research.
Contact: Shawn Harriman, shawn_harriman@harvard.edu, https://mbb.harvard.edu/pages/undergraduate-research (included in write-up)
1384 William James Hall, 33 Kirkland Street

Table 5. Office of Undergraduate Research and Fellowships (URAF)

The Office for Undergraduate Research & Fellowships (URAF) helps Harvard College students navigate the broad array of institutional, domestic, and international research opportunities that are available to them. The office further aims to develop connections among stakeholders in the academic research landscape (schools, academic departments and affiliated research enterprises, the housing communities, and student organizations).

URAF holds walk-in advising hours Monday through Friday from 2:00pm to 4:00pm at 77 Dunster Street, and at other times by appointment (telephone: 617-495-5095). Information about conducting research as an undergraduate—including how to get started, your responsibilities as a researcher, and links to research opportunities and funding at Harvard and beyond—may be found at the URAF website: https://uraf.harvard.edu/.

For students interested in research in the sciences, URAF offers the Program for Research in Science and Engineering (PRISE), the Harvard-Amgen Scholars Program, the Herchel Smith-Harvard Undergraduate Science Research Program, and the Harvard College Research Program (HCRP). Below you can read more about each of these programs.

PRISE is a ten-week summer program that aims to build community and stimulate creativity among Harvard undergraduate researchers in the life, physical/natural, engineering, and applied sciences. To participate in PRISE, you must find a research position on your own, and apply to PRISE separately. Selected fellows work on projects with Harvard-affiliated researchers and get to live in the Harvard Summer Undergraduate Research Village (HSURV) with other fellows in the

PRISE, BLISS, PRIMO, SHARP, and SURGH research programs. These fellows live in one of the Harvard College houses and participate in extensive evening and weekend programming that includes both social and academic activities. In addition to receiving lodging and being members of a diverse, vibrant intellectual and social community, fellows also receive a nominal stipend, partial board, and (for those students on financial aid) full coverage of the required summer savings obligation.

Harvard-Amgen Scholars Program is a ten-week residential summer research program for undergraduates in biotechnology. Following an interview selection process, participants in the Harvard-Amgen Scholars Program will be paired with faculty mentors and a direct supervisor (postdoctoral fellow or graduate student) in the laboratory. In addition to research, Amgen Scholars will participate in a number of intellectual, preprofessional development, and social activities throughout the program.

Harvard-Amgen Scholars live in one of Harvard's historic houses as active members of the Harvard Summer Undergraduate Research Village community. The cohort will comprise both Harvard students and students from other US institutions. Harvard-Amgen Scholars also receive a generous stipend, roundtrip travel to the Amgen Scholars Symposium in Los Angeles, CA, and (for those students on financial aid) full coverage of summer saving obligation.

Applicants must meet the following criteria: US citizenship or US permanent residency status; enrolled in good standing as a current sophomore, junior, or non-graduating senior; and a cumulative GPA of 3.2 or above.

Herchel Smith is a competitive and generous award supporting high potential undergraduates who are conducting promising summer research projects in mathematics; engineering; and life, physical, natural, or computer sciences. The program experience is designed specifically to prepare students in good standing for competitive postgraduate fellowships (such as NSF), graduate/doctoral study domestically and internationally (such as at Cambridge University), and postbaccalaureate research positions in the private sector. The project can be based anywhere in the world, but must be affiliated with a university, lab, or research enterprise and be highly substantive: at least ten weeks in

duration, full-time in commitment, and exhibiting some degree of autonomy and input by the applicant in its design and execution.

HCRP provides funding in support of student-initiated, independent scholarly research or creative endeavors undertaken with guidance of Harvard-affiliated faculty mentors. HCRP grants advance academic experiences outside the classroom and expand opportunities for students to work closely with faculty members. In contrast to a research assistantship, HCRP recipients demonstrate autonomy in the development, direction, and preparation of the overall research project. Awards are available for fall and spring terms of the academic year, as well as for the summer. Undergraduate students from all concentrations are encouraged to apply.

Suggestions for Other Sources of Research Funding:
1. Visit CARAT (Centralized Application for Research and Travel) to identify funding sources to which you can apply for term-time or summer: https://carat.fas.harvard.edu/.

2. Check with your academic department to inquire whether there are any funds to support students conducting research. Some departments may have funds to help a student present a paper at a conference or conduct senior thesis research.

3. Visit the Student Employment Office (SEO) Jobs Database to look for posted research assistant positions: https://seo.harvard.edu/.

4. Talk with your faculty advisor to see if they would be willing to apply for the Faculty Aide Program (FAP). FAP encourages professors to hire undergraduate research assistants by subsidizing students' pay. Potential faculty hosts are encouraged to post these research assistantships through the SEO's jobs database. Note: while faculty members apply for this award, students are encouraged to inform their faculty mentors about FAP. Knowing that FAP can subsidize students' pay often increases the ability/willingness of faculty to hire student researchers on their projects. For more information visit https://seo.harvard.edu/faculty-aide-program.

Contact: Pamela Gaddi, pjgaddi@fas.harvard.edu, uraf.harvard.edu 77 Dunster Street, Cambridge, MA 02138

Table 6. MGHC Digestive Disease Summer Research Program

The MGHfC Digestive Disease Summer Research Program offers short-term NIH support for 10 students matched with research mentors to perform independent research focused on digestive diseases over a 10-week period during the summer. In addition to presenting their research at a summer's end symposium, students will also participate in a peer-driven presentation-based biomedical course and a panel discussion on biomedical careers. Currently 22 MGH independent investigators with interest in digestive diseases serve as mentors spanning a wide range of topics and technical training. Research topics include obesity, food allergy, microbial pathogenesis, gut-brain axis, probiotics, intestinal development and maintenance, cystic fibrosis, celiac disease, inflammation, intestinal parasites, and adaptive immunity. Techniques applied to research projects include, advanced imaging, microfluidics, molecular biology, computational biology, stem cell biology, immune cell isolation, in vivo modeling, and patient-based clinical research. The MGHfC Digestive Disease Summer Research Program provides an excellent opportunity for science, math, and engineering students interested in biomedical research.

Contact: Bryan Hurley, bphurley@mgh.harvard.edu, https://www.massgeneral.org/mucosal-immunology/Education/summer-research-program.aspx
MIBRC-Pediatrics Massachusetts General Hospital 55 Fruit Street, Jackson 1402 Boston, MA 02114

Table 7. Harvard College Undergraduate Research Association (HCURA)

The Harvard College Undergraduate Research Association (HCURA) was founded in 2007 with the mission of building an interdisciplinary research community among undergraduate students, and promoting undergraduate research. Our goal to increase the scope and visibility of Harvard undergraduate research is the focus of our many on-campus initiatives, including the Faculty Dinner Program, the Visitas Undergraduate Research Symposium, which showcases Harvard undergraduate research to prefrosh (150 attendees), and new projects such as The Labs Database, a resource for undergraduates looking for research opportunities that catalogues over 100 Harvard labs, and Brevia, a publication for short research articles that presents a

nontechnical treatment of cutting-edge research. Every January, we host the National Collegiate Research Conference (NCRC) at Harvard as a continuation of our vision to provide the best platform for undergraduates from across the nation to share their research. NCRC features distinguished speakers, panelists, and student presenters. Student participants have the opportunity to present their research through poster and plenary sessions.

Contact: Gabriela Pelayo, gpelayo@college.harvard.edu,
https://www.hcura.org/
32 Mill St. Cambridge, MA 02138

Table 8. Harvard Stem Cell Institute Internship Program (HIP)

The Harvard Stem Cell Institute (HSCI) Internship Program (HIP) provides undergraduate students with a focused and challenging summer research experience in a cutting-edge stem cell science laboratory. Interns are exposed to different professional options within the scientific arena through a stem cell seminar series, a career pathways presentation, and a weekly stem cell companion course. Students present their summer research findings, both orally and in poster format, at the HIP Symposium—a requirement of all program participants.

Contact: Maureen Herrmann, maureen_herrmann@harvard.edu,
www.hsci.harvard.edu/internship
7 Divinity Avenue, Bauer Building Room G02A, Cambridge, MA 02138

Table 9. MGH Center for Diversity and Inclusion Summer Research Trainee Program

The Massachusetts General Hospital (MGH) Center for Diversity and Inclusion runs the Summer Research Trainee Program (SRTP). Founded in 1992, SRTP attracts college and medical students from around the nation to MGH. The goal of this program is to inspire students who are underrepresented in medicine (URM)* to consider careers in academic medicine by immersing them in cutting-edge research opportunities. Twenty students, selected from a nationwide competition, join SRTP each summer. Each student is assigned to a specific MGH laboratory,

clinical site, health policy, or health services research area where they undertake an original research project under the mentorship and guidance of an MGH investigator. Assignments are carefully considered and are made with the student's research and career interests in mind. In addition to this unique research experience, students participate in weekly didactic seminars, and career mentoring sessions and have opportunities for clinical shadowing at MGH. Once accepted, SRTP provides free housing, living stipend, travel grants, meals, research mentorship, career coaching, social and career networking. 2020 SRTP applications will open on Monday, November 18th, 2019.

Contact: Sandra Ordonez, sordonezpena@mgh.harvard.edu, massgeneral.org/cdi
55 Fruit Street, Boston, Ma 02114 BUL 123

Acknowledgments

HUROS Organizers

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HARVARD
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