**Implicit Bias and Social Decision Making in Autism Spectrum Disorder**  
Caitlin Cooper  
*Mentors: Ralph Adolphs and Damian Alexander Stanley*

Trust is indispensable to forming relationships, and is influenced by implicit social biases of which we are often unaware, such as racial bias. Individuals with Autism Spectrum Disorder (ASD) are known to have atypical social processing, however, previous work from our lab shows that their implicit social biases remain intact. We investigated whether implicit social biases in ASD maintain their influence over social behavior. Data from 200 neurotypical participants was collected online using MTurk. Each participant completed two economic games, where they viewed faces of many different partners and made economic decisions that reflect trust and altruism, and a task in which they explicitly rated the trustworthiness of many faces. They then completed an implicit association test (IAT) and finally various questionnaires designed to measure traits associated with ASD as well as explicit race bias. Consistent with previous findings, we found individuals’ race disparity in trustworthiness ratings correlated with their implicit race bias. Interestingly this was not the case for the economic games. We are in the process of collecting data from ASD participants and matched controls as well as probing whether ASD traits in the general population account for variation in the association between trust and implicit race bias.

**A Neurocognitive Computational Approach to Understanding Theory of Mind**  
Isabelle A. Rosenthal  
*Mentors: Ralph Adolphs and Damian Stanley*

Inferring the beliefs and intentions of others (Theory of Mind; ToM) is critical for social cognition. Impaired ToM is a common characteristic of Autism Spectrum Disorder (ASD). While previous work has implicated certain brain structures as mediators of ToM processing, little is known about the specific computations they perform or what goes awry in ASD. We addressed this question using a novel task that permits computational modeling of ToM learning processes, while retaining the core features of traditional ToM tasks. Participants learned continuously about the intentions and beliefs of another person (the Agent) and integrated this information to make predictions about the Agent’s choices. Earlier work showed behavioral differences in control and ASD task performance. Here, we extend this research by adapting and testing the task to be viable for neuroimaging (MRI). By pairing MRI data and behavioral data with previously constructed computational models of learning, we hope to gain a better understanding of the neural correlates of ToM in both controls and ASD.

**Developing Mass Spectrometry Assays for Phosphorylation of CamKII**  
Maria Karelina  
*Mentors: Mary B. Kennedy, Dylan Bannon, and Leslie Schenker*

Phosphorylation plays a major role in cell signaling pathways. Due to the complexity of signaling pathways, a high throughput method to detect the phosphorylation states of cellular proteins would aid in the understanding of many biological processes such as Synaptic Plasticity. This study focused on developing assays to identify the phosphorylation state of CamKII phosphorylation sites with High Performance Liquid Chromatography (HPLC) and Multiple Reaction Monitoring Mass Spectrometry (MRM-MS). We used Filter Aided Sample Preparation (FASP) to produce tryptic peptides from hippocampal slices and neural cell cultures. From both types of preparations we were able to detect de-phosphorylated aCam286, bCamK1287, CamKII305 peptides using HPLC/MS-MRM. We found that the FASP derived from cell cultures had less noise in detection than the FASP derived from slices. The thin layer of culture is also more susceptible to pharmacological treatments than the thicker slices. This could mean that using cell cultures for studying the time-course of phosphorylation of proteins may be preferable to use of hippocampal slices. This can be used to verify these mass spectrometry methods by driving the phosphorylation above baseline in cultures and detecting a difference in phosphorylation levels between differently treated samples.

**The Gut Bacteria Lactobacillus brevis Influences Hyperactivity in Drosophila**  
Matthew D. Smalley  
*Mentors: Sarkis Mazmanian and Catherine Schretter*

It is well known that the microbiome holds a great deal of influence over its host organism. These gut bacteria can play important roles in metabolism, immunity, and social behavior. Axenic flies (with no gut bacteria) are hyperactive compared to regular flies. Normal locomotor activity is only restored when the bacteria *Lactobacillus brevis* is present in the fly gut. By measuring gene expression in brain and gut neurons and performing locomotion assays we examine the mechanism by which *L. brevis* is able to induce this change in fly behavior.
Investigating the Role of Cellulose in Morphogenesis of *Arabidopsis* Hypocotyls and Shoot Apical Meristem
Melina Theoni Gyparaki  
*Mentors: Elliot Meyerowitz and Arun Sampathkumar*

Cellulose is synthesized at the plasma membrane by rosette-like cellulose synthase complexes (CESA). Primary cell wall formation requires CESA1, 3 and either CESA2, 5, 6 or 9, while secondary wall formation requires CESA4, 7 and 8. The deposition and guidance of the CESA complexes are mediated by the microtubule cytoskeleton. The Meyerowitz lab has shown that mechanical stress acts as an instructing signal to regulate cell wall synthesis at subcellular and tissue scales via the microtubule cytoskeleton network. However, the molecular aspects of CESA gene regulation have not been fully described with regards to mechanical forces in different tissues and cell types. Cytokinin is a hormone involved in shoot apical meristem formation among other processes. The aim of this project was to investigate the interactions between the CESA genes, the microtubule network and cytokinin and how they are all related to cellulose synthesis as well as hypocotyl and meristem development. A variety of techniques was used including In-Fusion cloning of *CESA1* and *CESA3* genes, next-generation *in situ* hybridization, imaging of cytokinin markers in hypocotyls as well as mechanical perturbation coupled with confocal microscopy. Our results demonstrate a putative interaction between cytokinin signalling, microtubules and cellulose synthase gene regulation.

DNA-Based Competitive Fuel Implementation of the Winner-Take-All Function
Siyuan Stella Wang  
*Mentors: Lulu Qian, Kevin Cherry, and Robert Johnson*

Since its discovery, DNA has been proven to be not only the source of genetic information but also an effective building material in programmable nanodevices and soluble circuits for applications in targeted medical delivery and control of cell systems. DNA motifs for the linear threshold model of the neuron can be used to compose tunable neural networks capable of pattern-recognition and completion. These circuits can be simplified using the winner-take-all (WTA) function. My project seeks to develop and experimentally test a WTA implementation with desirable qualities such as constant number of toeholds, linear increase in system size, and complexes of no more than two strands. Competition imposed by a limited shared fuel helps to achieve the linear size, and use of a previously developed seesaw DNA motif allows for a constant number of toeholds with two-stranded complexes while using a reliable motif. The project consists of understanding published theoretical, developing a new system with desirable properties using that understanding, simulating its behavior, and testing its behavior experimentally. Through this investigation, we can learn how effective fuel-driven competition is at minimizing circuit size and possibly develop a WTA motif unit for more complex computation.

Investigation of Neuronal Populations Controlling Thirst
Jisoo Mok  
*Mentors: Yuki Oka, Vineet Augustine, and Nikki Cruz*

The fluid homeostasis is the set of processes that regulate the salt and fluid balance of the body. When this balance shifts, several regions in the circumventricular organs (CVO) of the hypothalamus are activated, and the stimulation of specific brain regions can lead to changes in drinking behavior. The Oka Lab is currently investigating the subfornical organ (SFO) and the organum vasculosum of lamina terminalis (OVLT) to discover a molecular and genetic mechanism behind this brain-body interaction that controls the fluid homeostasis and hence influences that drinking behavior. Although the Oka lab has recently demonstrated that the two regions mentioned above govern the balancing of the fluid homeostasis, it is still unclear which neuronal population is involved. The lab has been utilizing the optogenetics and immunohistochemistry to find the neurons that trigger or sense the changes in the fluid homeostasis and to understand the genetic background. One of the neuronal markers, ER81, which could be tied with the fluid homeostasis, has been identified with the immunohistochemistry technique. Further investigation of the SFO and the OVLT and search for new neuronal markers will offer better understanding of how the mouse brain governs the drinking behavior and the fluid homeostasis.

Engineering Conditional CRISPR Interference
Andrew Hou  
*Mentors: Niles Pierce and Mikhail Hanewich-Hollatz*

CRISPR/Cas9 is a novel gene editing tool which has been repurposed for regulation of gene expression, via a guide RNA which confers sequence-specificity and a catalytically dead Cas9 endonuclease (dCas9, for short). Termed CRISPR interference (CRISPI), dCas9 and the guide RNA form a complex which binds to and blocks transcription
of a specific target gene. Using RNA design principles, we sought to re-engineer guide RNAs such that CRISPRi can be conditionally activated or inactivated by synthetic or endogenous inputs in *E. coli*. To this end, we demonstrated that guide RNAs can be inactivated either by binding a separately expressed antisense strand, or by self-complementarity. However, as is, the guide RNA sequence is heavily constrained. In order to obtain the programmability required for conditionality, we added extra nucleotides to the loop region found in the secondary structure of the guide RNA. We hypothesize that: (1) a guide RNA with an extended loop could be conditionally inactivated by an input strand which is antisense to the loop, and (2) a guide RNA with self-complementarity to the extended loop would be natively inactivated, and that it could be conditionally activated via toehold-mediated strand displacement.