**Dr. Serdar Bozdag and Ziynet Nesibe Kesimoglu (Mathematics, Statistics and Computer Science) for their project, “Inferring disease-specific competing endogenous RNA (ceRNA) interactions.”**

**Introduction:** MicroRNAs (miRNAs) are one of the non-coding RNA types that regulate RNA expression by binding to them. There is a regulation multiplicity between miRNAs and RNAs, meaning that a miRNA could have multiple RNA targets, and an RNA could be targeted by multiple miRNAs. Furthermore, recently it has been discovered that RNAs targeted by common miRNAs could "compete" for these miRNAs and thereby regulate each other indirectly (Salmena, Poliseno, Tay, Kats, & Pandolfi, 2011). Such RNAs are called competing endogenous RNAs (ceRNAs). It has been shown that ceRNA interactions have key roles in several disease conditions including cancer (Peng et al., 2015).

Giving the enormous number of RNAs in the genomes, it is cost and labor prohibitive to identify ceRNA interactions experimentally. Thus, several computational studies have been developed to infer ceRNA interactions from biological datasets. One of these tools is Cancerin (Do & Bozdag, 2018), a tool developed in our lab. Cancerin integrates multiple types of biological datasets to infer cancer-associated ceRNA interactions. In this proposed study, we aim to extend Cancerin to address some of its drawbacks. Based on the premise that several ceRNAs could work together to sequester miRNA(s) targeting one or more key ceRNAs, we will extend Cancerin to infer group-wise interactions among ceRNAs besides pairwise ceRNA interactions. In the current computational studies, including ours, a miRNA could be assigned to "mediate" thousands of ceRNA interactions without considering if the miRNA has sufficient abundance. We will extend Cancerin to address this issue, too. Furthermore, we will integrate time series expression datasets to infer directional ceRNA interactions.

**Significance:** Approximately four fifth of the human genome is transcribed to RNA. While only less than 2% of the human genome is responsible for coding proteins, the remaining part has many regulatory elements, most of which are not demystified. Current experimental methods cannot identify genome-wide ceRNA interactions. Our computational tool will help identify putative ceRNA interactions genome-wide, which would shed light on the underlying complex regulatory circuitry in disease conditions. Our tool would enable researchers to find potential disease drivers and key regulatory interactions.

**Innovation/Forward Thinking:** This study will utilize various biological data types to infer ceRNA interactions. We will identify group-wise ceRNA interactions, which could not be possible to detect using pairwise-based methods only. Most studies cannot infer the directionality of the ceRNA interactions. We will identify directed ceRNA interactions, which will help us identify potential key ceRNAs associated with diseases.

**Dr. Henry Medeiros and Philipe Ambrozio Dias (Electrical and Computer Engineering) for their project, “Region growing refinement of semantic segmentations masks.”**

**Introduction:** The combination of deep learning models known as convolutional neural networks (CNN) and

increasingly larger public datasets has led to substantial improvements in image classification. For classification at pixel-level, however, conventional CNNs provide segmentation masks that only coarsely adhere to object boundaries. Moreover, abundant and reliable data are crucial for development of deep learning models, but high-quality annotation of image segmentation datasets usually requires a huge number of hours. We have been developing the Region Growing Refinement (RGR) algorithm, which has the potential to address both issues. RGR is a unsupervised method that employs region growing to aggregate pixels with low confidence levels to its neighboring areas with high confidence scores and similar appearance. The efficacy of RGR for segmentation refinement culminate in the corresponding paper (Dias & Medeiros, 2018).

**Significance:** For applications such as action and activity recognition, fine-grained segmentation is crucial as the interaction between different objects has to be identified. Interactions are characterized by the proximity, contact between agent and object, such that detections with poor adherence to object boundaries can lead to incorrect interpretations of the scene. As for the annotation of image segmentation datasets, manual labeling of large datasets is challenging and timeconsuming. For example, the annotation of the COCO dataset required 55k worker hours for instance segmentation, which makes such processes often prohibitively expensive.

**Innovation/Forward Thinking:** In addition to better theoretical modeling and further improvements of RGR, we have been also developing FreeLabel (Dias, Tabb, & Medeiros, 2018), an intuitive open-source web interface based on RGR that allows users to obtain high-quality segmentation masks with just a few freehand scribbles, in a matter of seconds. To benefit the computer vision community, we design FreeLabel such that it can be used for both crowdsourced or private annotation, with a modular structure that can be easily adapted for any image dataset. **Henry Medeiros,**

**Dr. Henry Medeiros and Reza Jalil Mozhdehi (Electrical and Computer Engineering) for their project, “Visual tracking: deep convolutional iterative particle filter with multiple correlation models.”**

**Introduction:** Visual Tracking refers to automatically following a specific target even under challenging scenarios such as fast target motion, occlusion and deformation in a video. Recently, machine learning methods have been successfully employed in tracking algorithms to improve their performance. Thus, we have focused on different methods of machine learning in the context of visual tracking.

**Significance:** Recent breakthroughs in machine learning is resulting dramatic technological shifts in many areas. Most of the new deep learning methods that are being applied in these fields were originally developed by computer vision researchers, and hence the state of the art in this area is still being pushed by researchers. Visual Tracking is one of most important fields of computer vision. It has significant applications in many fields such as robotics, surveillance, autonomous driving, automation, medicine, and Unmanned Aerial Vehicles. However, there is no tracker to be successful in all challenging scenarios such as occlusion, deformation and out of view. So, it is an interesting area for all computer vision researchers to propose new trackers.

**Innovation/Forward Thinking:** In this project, we are going to improve our previous visual trackers. Our first tracker (DCPF) integrates a deep convolutional neural network (CNN) with a particle filter and a correlation filter [3]. After extracting target features for each particle from the CNN, they are compared with the correlation model to estimate target positions. Our second tracker (DCPF2) extends the particle filter to estimate target size and generates several correlation models based on all high-likelihood particles to account for potential errors in the model generation [4]. In our new tracker (DCPF3), we use an iterative particle filter, which helps particles to correct themselves and converge to the true target position so that the most relevant particles are reused. Also, our new tracker generates many more correlation models to improve the accuracy in the correlation filter. Another contribution of our new tracker is to define a confidence score for each frame. According to these confidence scores, three different tracker states are considered: target-found, partially-lost and fully-lost. For each state, different strategies are then applied to generate the correlation models. In the next step, we will work on dynamically extracting the target features from different CNN layers and automatically tuning the thresholds of our algorithm. Finally, we will test DCPF3 on some famous benchmarks such as OTB100 and VOT2016.