RESEARCH OPPORTUNITY PROGRAM
299Y/399Y PROJECT DESCRIPTIONS 2019-2020
FALL/WINTER

Name and Title: Tony Harris, Professor
Department: Cell and Systems Biology

TITLE OF RESEARCH PROJECT: Analyses of Computer Simulations of Cytoskeletal Networks of the Drosophila Embryo

Number of 299Y Spots: 1

OBJECTIVES AND METHODOLOGY:
Under the surface membrane of a cell, cytoskeletal networks give the cell its particular shape. Cell shape is linked closely to cell activity (e.g. cell division, cell migration, cell-cell interaction, etc.), and is based on the molecular polymers and accessory proteins that form the cytoskeleton. These cytoskeletal networks can be observed by advanced microscopy, and the basic role of an individual component can be determined by removing it through genetic approaches. However, by microscopy and genetics alone we are unable to fully examine the physical properties of the cytoskeletal networks. To increase our understanding of the networks, we are generating mathematical models of the networks run as computer simulations using MATLAB software. These simulated networks are structured locally as nodes and edges and organized globally based on patterns we observe in embryos by microscopy. Our current wet-lab data provide only limited insight into the local structure and activity of the networks as the form, grow and impact cell shape. Our goal is to probe such parameters in our mathematical model to determine which values produce the most robust mimic of the whole-network behavior observed in the embryo (for both the normal embryo and a number of specific mutants in which network abnormalities arise). Using our model, we are pursuing network properties that explain network behaviors important for controlling cell shape in the embryo.

DESCRIPTION OF STUDENT PARTICIPATION:
Working under the direct supervision of a PhD student in the lab, the 299Y student will formulate new versions of the model or quantitative computational tools to evaluate how changes to parameters affect model output. The project will be computer-based and theoretical. Students with a solid background in computer programming and physics, and with a strong interest in applying this background to molecular and cellular biology are encouraged to apply.

MARKING SCHEME (assignments with weight and due date):
Progress Report (10%) Due Jan 6
Journal/lab book (10%) Due Jan 6
Final Report (50%) Due April 3
(includes literature review, results, discussion, figures, tables, references)
Progress meetings (15%)
Lab work and interactions (15%)
RESEARCH OPPORTUNITY PROGRAM
299Y/399Y PROJECT DESCRIPTIONS 2019-2020
FALL/WINTER

Name and Title: Nicholas Provart, Professor
Department: Cell and Systems Biology

TITLE OF RESEARCH PROJECT: Bioinformatic Tools for Understanding Plant Biology

Number of 299Y Spots: 1

OBJECTIVES AND METHODOLOGY:
One of the foci of the Provart laboratory is the Bio-Analytic Resource, available online at http://bar.utoronto.ca. The BAR is used about 60,000 a month by plant researchers around the world. The "electronic fluorescent pictograph" or "eFP" Browser is the most popular of these tools - it allows researchers to quickly ascertain where their gene of interest is being expressed in the plant. This tool has been incorporated into our recently published “ePlant” (see http://bar.utoronto.ca/eplant; Waese et al. 2017, http://dx.doi.org/10.1105/tpc.17.00073), which offers not only viewing of gene expression data at the centimetre scale but also natural variation data at the kilometre scale, all the way down to the gene product’s protein structure at the nanometre scale, with several other kinds of data viewable for hypothesis generation in between those levels. The idea is to provide a seamless environment for exploring biological data from plants. Aspects that we would like to add to ePlant include metabolic pathway data, GWAS information, etc.

DESCRIPTION OF STUDENT PARTICIPATION:
The CSB299Y student would be involved in several aspects of the above described project, which is ongoing in my laboratory, depending on the state of progress at the time of starting, and would thus acquire skills in programming, dynamic image generation, web-based interfaces and database design and query. The student would preferably have some experience in programming for the web using Python and/or Javascript/CSS/HTML5/jQuery.

The ROP student will interact on a one-on-one basis with Provart Lab research team (Prof. Provart, graduate students, post-docs and/or technicians) for training and assistance in carrying out experiments. The student will communicate his or her findings as decided upon signing the ROP project contract. Typically, there is a mixture of a literature review, lab book note keeping, a poster presentation during the ROP fair, and a final report (with weightings decided at the start of the year). The student might also present in lab meetings, and in the past some students have actually published their results as part of a larger publication from the Provart Lab.

MARKING SCHEME (assignments with weight and due date):
Project proposal / literature review 20 Oct 2019 20%
Poster/undergrad research forum Mar 2020 20%
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<tr>
<th>Activity</th>
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<tbody>
<tr>
<td>Final write-up</td>
<td>4 Apr 2020</td>
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<tr>
<td>Lab book/participation</td>
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RESEARCH OPPORTUNITY PROGRAM
299Y/399Y PROJECT DESCRIPTIONS 2019-2020
FALL/WINTER

Name and Title: Nicholas Provart, Professor
Department: Cell and Systems Biology

TITLE OF RESEARCH PROJECT: Molecular and Bioinformatic Characterization of Novel Environmental Stress-Associated Genes from Plants

Number of 299Y Spots: 1 Number of 399Y Spots: 1

OBJECTIVES AND METHODOLOGY:
On the molecular side: using the INTACT and TRAP systems for isolating mRNA populations from specific cell types (guard cells), we have identified several novel stress-associated genes (NSAGs) in Arabidopsis thaliana, the model system for plant research. Preliminary analysis of knock-out mutants of these genes indicates their necessity in response to drought. We have little knowledge about the precise molecular function of the gene products. To this end, we are applying several molecular and biochemical techniques, such as creating promoter::NSAG::GFP fusions to study tissue-specific and subcellular expression patterns via confocal microscopy. Other possible venues for exploration include the overexpression of these genes in heterologous systems such as yeast or E. coli or identifying gene regulatory networks using the yeast one hybrid system in the case of NSAGs that are transcription factors, or “Arabidopsizing” yeast to study new pathways.

On the bioinformatic side: one of the foci of the Provart laboratory is the Bio-Analytic Resource, available online at http://bar.utoronto.ca. The BAR is used about 60,000 a month by plant researchers around the world. The "electronic fluorescent pictograph" or "eFP" Browser is the most popular of these tools - it allows researchers to quickly ascertain where their gene of interest is being expressed in the plant. This tool has been incorporated into our recently published “ePlant” (see http://bar.utoronto.ca/eplant; Waese et al. 2017, http://dx.doi.org/10.1105/tpc.17.00073), which offers not only viewing of gene expression data at the centimetre scale but also natural variation data at the kilometre scale, all the way down to the gene product’s protein structure at the nanometre scale, with several other kinds of data viewable for hypothesis generation in between those levels. The idea is to provide a seamless environment for exploring biological data from plants. For the NSAGs described above, we would like to add new views to ePlant to include metabolic pathway data, GWAS information, etc. to be able to characterize these genes better.

DESCRIPTION OF STUDENT PARTICIPATION:
The CSB299Y/CSB399Y students would be involved in several aspects of the above described projects, which are ongoing in my laboratory, depending on the state of progress at the time of starting, and would thus potentially acquire skills in confocal microscopy, genotyping, phenotyping, image analysis and other molecular methods (while...
working in the wet lab) or acquire skills in programming, dynamic image generation, web-based interfaces and database design and query (for the bioinformatic component). For the bioinformatic component the student would preferably have some experience in programming for the web using Python and/or Javascript/CSS/HTML5/jQuery.

The ROP students will interact on a one-on-one basis with Provart Lab research team (graduate students, post-docs and/or technicians) for training and assistance in carrying out experiments. The student will communicate his or her findings as decided upon signing the ROP project contract. Typically, there is a mixture of a literature review, lab book note keeping, a poster presentation during the ROP fair, and a final report (with weightings decided at the start of the year). The student might also present in lab meetings, and in the past some students have actually published their results as part of a larger publication from the Provart Lab.

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- Final write-up 4 Apr 2020 50%
- Lab book/participation 10%