ABIO 681 – Seminar in MCDN – Genome-scale Biology – Spring 2019

Meeting Time and Place: Tuesday at 9:00 am in LSRB 1010

<u>Course Description</u>: Seminar-style course for MCDN Master's and PhD students. Primary scientific literature will be read and discussed. The focus will genomics and systems biology, with an emphasis on advancements on techniques and approaches that have shaped modern genome biology. Students will participate in oral presentations and mock peer review sessions.

<u>Purpose</u>

The purpose of presenting a scientific manuscript to a journal club or class is to discuss how the work has conceptually advanced our understanding of a scientific problem or changed the way we are able to ask questions (especially for technology-based papers). This is the idea you should focus on as you read papers and as you prepare presentations.

Our goal is not to devote our mental energy to finding faults or describing shortcomings of the papers. There are absolutely issues with every paper and authors cannot do every experiment that a reviewer/reader might propose. Your job as a peer reviewer is to help the authors support their conclusions and not tear them down.

Your job as a student in this class is to read these papers with open eyes, to observe how the technology to interrogate the function of genomes has changed over the years, and to think about how these approaches and papers have altered our capabilities and views of biology.

Instructor:

Morgan Sammons LS 2078 masammons@albany.edu 518-442-4326 Office hours: Wed 11:00 am - 12:30 pm; Tues 12:00 - 1:30pm

Presentations

Students will be assigned 1 or more primary research articles (listed below) to present to the class. Presentations should include discussions of 1) the biological question being addressed by the authors, 2) the technological advances made in the paper, 3) the methods or discoveries that were instrumental in allowing the authors to make their own advance, 4) the advantages to using these approaches, 5) any disadvantages or limitations of the technology, 6) whether this approach or technology is still in use today (and what might be used now), and 7) how you might apply these technologies to your work.

Please limit your presentation length to about 15 uninterrupted minutes. We will be stopping and discussion/asking questions throughout the class session.

<u>Readings</u>

Students are expected to perform all of the readings assigned in the class and will be responsible for answering and proposing related questions in class and as assigned. Please see the presentation rubric listed above for the types of questions you should be thinking about as you read these manuscripts.

Grading:

This is a load-only course. The only possible grades are "L", "I", or "U". L is considered passing. "U" is unsatisfactory and is equivalent to a failing grade. The grade of "I", for "Incomplete" will not be assigned. Students may not have more than 2 absences from the course. *If a student is absent for more than 2 class sessions, a grade of "U" will be given.* If a student is absent on a day where they are scheduled to give a presentation, the student must contact Dr. Sammons as soon as is feasible and schedule another day to present. In order to earn a grade of "L", students must complete all assigned presentations.

<u>Academic Integrity</u>: Please note that failing grades "U" are given for plagiarism on an assignment. Students will be expected to adhere to University standards of academic integrity at all times, as outlined in the Graduate Bulletin of the University at Albany (https://www.albany.edu/graduatebulletin/requirements_degree.htm).

<u>Website</u>

PDF copies of all reading materials for the course can be found at http://thesammonslab.org/links/BIO681 Spring2019/

Class Schedule:

<u>Date</u> Tu 01/29	<u>Topic/Reading</u> Course Introduction Reading: (Casadevall and Fang, 2009)
Tu 02/05	Discussion of (Casadevall and Fang, 2009) Reading: (Fields and Song, 1989)
Tu 02/12	Discussion of (Fields and Song, 1989) Readings: (Wang and Reed, 1993; Wilson et al., 1991)
Tu 02/19	Discussion of (Wang and Reed, 1993; Wilson et al., 1991) by Group 1 Reading: (DeRisi, 1996)
Tu 02/26	Discussion of (DeRisi, 1996) Reading: (Burns et al., 1994; Giaever et al., 2002)
Tu 03/05	Discussion of (Burns et al., 1994; Giaever et al., 2002) Reading: (Krogan et al., 2006)
Tu 03/12	Discussion of (Krogan et al., 2006) Reading: (Bentley et al., 2008)
Tu 03/19	NO CLASS: Spring Break
Tu 03/26	Discussion of (Bentley et al., 2008) Reading: (Johnson et al., 2007; Ren et al., 2000)
Tu 04/02	Discussion of (Johnson et al., 2007; Ren et al., 2000) Reading: (Barski et al., 2007)
Tu 04/09	Discussion of (Barski et al., 2007) Reading: (Korthout et al., 2018)
Tu 04/16	Discussion of (Korthout et al., 2018) Reading: (Berg et al., 2016; Casadevall and Fang, 2014)
Tu 04/23	Discussion of Impact Factor and the Emergence of "Pre-prints" Reading: (Lee et al., 2018)
Tu 04/30	Discussion of (Lee et al., 2018)

<u>References</u>

Barski, A., Cuddapah, S., Cui, K., Roh, T.-Y., Schones, D.E., Wang, Z., Wei, G., Chepelev, I., and Zhao, K. (2007). High-Resolution Profiling of Histone Methylations in the Human Genome. Cell *129*, 823–837.

Bentley, D.R., Balasubramanian, S., Swerdlow, H.P., Smith, G.P., Milton, J., Brown, C.G., Hall, K.P., Evers, D.J., Barnes, C.L., Bignell, H.R., et al. (2008). Accurate whole human genome sequencing using reversible terminator chemistry. Nature *456*, 53–59.

Berg, J.M., Bhalla, N., Bourne, P.E., Chalfie, M., Drubin, D.G., Fraser, J.S., Greider, C.W., Hendricks, M., Jones, C., Kiley, R., et al. (2016). Preprints for the life sciences. Science *352*, 899–901.

Burns, N., Grimwade, B., Ross-Macdonald, P.B., Choi, E.-Y., Finberg, K., Roeder, G.S., and Snyder, M. (1994). Large-scale analysis of gene expression, protein localization, and gene disrupuon in Saccharomyces cerevisiae. 20.

Casadevall, A., and Fang, F.C. (2009). Mechanistic Science. Infect. Immun. 77, 3517–3519.

Casadevall, A., and Fang, F.C. (2014). Causes for the Persistence of Impact Factor Mania. MBio 5, e00064-14.

DeRisi, J. (1996). Use of a cDNA microarray to analyse gene expression patterns in human cancer. Nat. Genet. 14, 457.

Fields, S., and Song, O. (1989). A novel genetic system to detect protein-protein interactions. Nature 340, 245–246.

Giaever, G., Chu, A.M., Ni, L., Connelly, C., Riles, L., Véronneau, S., Dow, S., Lucau-Danila, A., Anderson, K., André, B., et al. (2002). Functional profiling of the Saccharomyces cerevisiae genome. Nature *418*, 387–391.

Johnson, D.S., Mortazavi, A., Myers, R.M., and Wold, B. (2007). Genome-Wide Mapping of in Vivo Protein-DNA Interactions. Science *316*, 1497–1502.

Korthout, T., Poramba-Liyanage, D.W., van Kruijsbergen, I., Verzijlbergen, K.F., van Gemert, F.P.A., van Welsem, T., and van Leeuwen, F. (2018). Decoding the chromatin proteome of a single genomic locus by DNA sequencing. PLOS Biol. *16*, e2005542.

Krogan, N.J., Cagney, G., Yu, H., Zhong, G., Guo, X., Ignatchenko, A., Li, J., Pu, S., Datta, N., Tikuisis, A.P., et al. (2006). Global landscape of protein complexes in the yeast Saccharomyces cerevisiae. Nature 440, 637–643.

Lee, I., Razaghi, R., Gilpatrick, T., Sadowski, N., Sedlazeck, F., and Timp, W. (2018). Simultaneous profiling of chromatin accessibility and methylation on human cell lines with nanopore sequencing: Supplemental Figures and Tables. BioRxiv.

Ren, B., Robert, F., Wyrick, J.J., Aparicio, O., Jennings, E.G., Simon, I., Zeitlinger, J., Schreiber, J., Hannett, N., Kanin, E., et al. (2000). Genome-Wide Location and Function of DNA Binding Proteins. 290, 5.

Wang, M.M., and Reed, R.R. (1993). Molecular cloning of the olfactory neuronal transcription factor Olf-1 by genetic selection in yeast. Nature *364*, 121.

Wilson, T.E., Fahrner, T.J., Johnston, M., and Milbrandt, J. (1991). Identification of the DNA binding site for NGFI-B by genetic selection in yeast. Science 252, 1296–1300.