



Position for a PhD student in investigating protein structure and dynamics of protein networks

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Laboratory research theme: Investigate protein structure and dynamics of protein networks to understand cell-fate decisions using cutting-edge technology and state-of-the-art bioinformatics approaches.

How do cells work? We can pose this question in two ways first, we could ask: what is the function of a gene and second, how do genes function as ensembles. In my lab, we want to be able to test hypotheses both about how genes function and how to study their interactions at a genome-wide scale. The sequencing of some 28,000 human genes has occupied a number of labs around the world and has motivated feverish activity among biomedical researchers to understand functions of genes. However, in the absence of simple methods to establish function, these activities have not advanced significantly. We have a situation analogous to having a complete list of telephone numbers for a city, but few easy ways of linking those numbers to their owners, let alone the relationships among them. One way to define the function of a newly identified gene is to study the interactions of its product (a proteins) with proteins for which we already know their function. We have developed experimental and theoretical methods that allow us to study how proteins form complexes with each other. Our methods allow us to determine how, when and where in the cell novel proteins interact with known proteins and what are resulting phenotypes specifically associated with a new gene. We also study how groups of proteins work as ensembles to regulate decision making by the cell. We have posed the hypothesis that cells use a limited number of molecular strategies to respond to environmental signals to make decisions to divide, to differentiate into new forms or to die. We are searching for these common mechanisms, which we call « logic motifs » at a genome-wide level. We have already discovered several logic motifs that are necessary to cell survival and for which their interruptions are implicated in several diseases including cancers and diseases of development and aging.

References :

- 1- Levy, E.D., Landry, C.R., and **Michnick, S.W.** (2010) Signaling through cooperation. *Science* 328, 983-984.
- 2- Malleshaiah, M.K., Shahrezaei, V., Swain, P.S., and **Michnick, S.W.** (2010) The scaffold protein Ste5 directly controls a switch-like mating decision in yeast. *Nature* 465, 101-105.
- 3- **Michnick, S. W.**, Ear, P. H. Landry, C. Malleshaiah, M. K. Messier, V.A. (2010) Toolkit of Protein-fragment Complementation Assays for studying and Dissecting Large-scale and Dynamic Protein-Protein Interactions in Living Cells. In Guide to Yeast Genetics: Functional Genomics, Proteomics and other Systems Analysis. Weissman, J., Guthrie, C., Fink, G. Eds. *Elsevier Press: New York, USA* Vol. 470, pp. 335-368.
- 4- Ear, P. O., & **Michnick, S. W.** (2009) A binary life or death selection strategy to re-engineer protein functions. *Nature Methods* 6, 813-816.
- 5- Landry, CR*, Levy ED*, **Michnick SW** (2009) Weak functional constraints on phosphoproteomes. *Trends in Genetics* 25(5):193-7.* Co-first author
- 6- Levy ED*, Landry CR*, **Michnick SW** (2009) How perfect can protein interactomes be? *Science Signaling* 3;2(60):pe11. * Co-first author

Disciplines/ Qualifications:

Candidates should have a formal training in biomedical sciences (biochemistry, chemistry, bio-informatics, molecular biology), have excellent organizational, interpersonal, and communication skills, and have a strong interest for cell biology, genomics and proteomics.

Contact:

Applicants should submit a resume, university records, a short statement of research interests, TOEFL results and two letters of recommendation to Dr. Stephen W. Michnik by email (stephen.michnick@umontreal.ca), if possible in one .pdf document.