Interview with Leah Edelstein-Keshet, Professor at the University of British Columbia in the Department of Mathematics, and recipient of the 2021 Arthur T. Winfree Prize for her outstanding contributions to many areas of biology.

Web: https://pwias.ubc.ca/profile/leah-edelstein-keshet

Your scientific research focuses on mathematical biology. Could you tell us about your research background and contributions, how you arrived in your current position and what attracted you to this field?

I was attracted to what was then called "Biomathematics" by an advertisement posted on a bulletin board at my Alma Mater – they were looking to recruit MSc students to this new program. At the time, I was already attuned to mathematics and biology from my parents' areas of work, but I was unaware that the two disciplines could be combined. This poster drew my attention, I applied, and was accepted. This chance event led me to an MSc with Professor Robert Rosen, then at Dalhousie University. In that first encounter with mathematical biology, I had entered an abstract and philosophical path. That experience was unique, since in my later PhD studies at the Weizmann Institute with Prof Lee A Segel, the focus was on modeling, on applied mathematics, and a more direct connection with biological data. Many years later, I was hired as a faculty member at the University of British Columbia, and we moved to Vancouver, BC, in Canada. My young family and I settled in this beautiful west-coast city. I started working on problems in cell biology in the late 1980's and early 1990's and have combined that with occasional research on swarming and aggregation ever since.

What is something exciting that you are currently working on?

I'm excited about my recent "adventures" with computing cell shapes and cell-cell interactions in development. I am delighted to be a user of Morpheus [1], one of the new open-source computational platforms (developed by a team in TU Dresden). Morpheus makes it easy to experiment and learn new things without having to reinvent all the wheel. I continue to explore the link between intracellular signaling, the actin cytoskeleton, and the dynamics of cell shape and motility. I am also writing a book on modeling in cell and molecular biology, for which simulations prove handy, both as an educational tool and as a way to demonstrate ideas.

What do you foresee as the biggest challenges in mathematical biology research and education?

I believe that it is important to train more young people at the interface – mathematicians should be exposed to modern biology, but biology students also need a much stronger training in quantitative methods, modeling, and computational methods. While the opportunities for such training have increased greatly over the past decades, there is still more to be done.

Have you ever found the complexity of biological systems daunting?

All the time! But I got used to the fact that we are not trying to represent or capture the full complexity (or even a fraction of it), and that our models are merely tools to probe one or another aspect and gain some limited insights.

What is your favourite research paper that you have written?

It's hard to pick, but I really enjoyed the paper [2] with former PhD student Ryan Lukeman. It came about serendipitously from noticing the flocks of funny ducks at the waterfront in downtown Vancouver. This was not exactly a pre-planned direction of research – it just happened. Ryan was able to capture time sequences and reverse-engineer what the birds were doing to maintain their spatial arrangements. It turned out to be among the first examples of this kind of inference, followed closely by many fascinating tracking papers from much more experienced groups of researchers.

How have you found working with experimentalists?

It is both fascinating and scary. Experimentalists ask great questions and have a true appreciation of the real biological systems. Sometimes the pace of experiments and theory are out of synch, and sometimes the experimental data is just not amenable to modeling – either too many missing pieces, or not enough quantitative measurement. But in many cases, it leads to the most satisfying interdisciplinary results.

What advice would you give to a junior mathematical biologist?

It is easy these days to learn about biological systems from online seminars as well as review papers. My advice is to look for the questions that biologists are asking, rather than just settling on tried-and-true mathematical biology directions. At the same time, we also see many opportunities to apply "classical" modeling methods (e.g., dynamics of diseases) to emergent world problems, as evident in the recent Covid-19 pandemic. Young people can contribute to such fundamental challenges while they build up their research along various other directions.

Where is the best place you have travelled for work? And why?

I greatly enjoyed a trip to Gold Coast in Australia for an Australia and New Zealand Industrial and Applied Mathematics (ANZIAM) conference a few years ago, followed by a visit to Queensland University of Technology (QUT) in Brisbane. The talks were great, and the setting and hospitality were first-class. I am hoping to revisit Australia, if/when this pandemic ever ends.

What do you do in your spare time?

In my spare time, I like gardening. Because winter is long and drab in Vancouver, part of the garden comes indoors, so we can continue to enjoy some fresh greens between seasons.

[1] Starruß J, De Back W, Brusch L, Deutsch A. Morpheus: a user-friendly modeling environment for multiscale and multicellular systems biology. Bioinformatics. 2014 May 1;30(9):1331-2.

[2] Lukeman R, Li YX, Edelstein-Keshet L. Inferring individual rules from collective behavior. Proceedings of the National Academy of Sciences. 2010 Jul 13;107(28):12576-80.