Maria Emelianenko, PhD

Professor and Chair, Department of Mathematical Sciences
Associate Director, Quantum Science and Engineering Center
Institute for Digital InnovAtion (IDIA)

Education

PhD, Mathematics, The Pennsylvania State University

Key Interests

Mathematical Modeling | Cancer | Bioinformatics | Big Data | Pattern Recognition | Numerical Algorithms

CONTACT

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SELECT PUBLICATIONS

- C. DeMarino *et al.*, Differences in transcriptional dynamics between T-cells and macrophages as determined by a three-state mathematical model. *Nature Scientific Reports* 10, 2227 (2020).
- A. Baranova *et al.*, An efficient algorithm for systematic analysis of nucleotide strings suitable for siRNA design. *BMC Research Notes* 4(1):168 (2011)
- Q. Du *et al.*, Convergence properties of the Lloyd algorithm for computing the Centroidal Voronoi tessellations, *SIAM Journal on Numerical Analysis* 44, Issue 1, 102-119 (2006).

Research Focus

I am an interdisciplinary mathematician with research interests in the areas of scientific computing and modeling of complex systems. In relation to biological applications, my work has been focused on modeling cellular mechanisms in cancer and HIV systems and developing automated computational approaches for detecting patterns and anomalies in large-scale protein sequence databases. My group develops data-driven and physics-driven approaches to uncover spatiotemporal patterns to learn and control underlying mechanisms governing certain systems.

One of my long-standing research directions is the development of fast and accurate CVT-based numerical algorithms that can be linked to model and data reduction, classification, and clustering, as well as feature extraction. I use a variety of mathematical techniques, including ODE and PDE-based models, optimization, stochastic simulations, and network theory tools.

Current Projects

- One project, (joint with Mariaelena Pierobon and Lance Liotta), is aimed at studying adaptation mechanisms in cancer cells. We look at how the structure of the protein network affects the ability of the cells to adapt to stimuli, which potentially leads to drug resistance. Both dynamical and structural features of the systems are analyzed to identify critical nodes in each of the pathways.
- In joint work with Fatah Kashanchi, we develop mathematical models of HIV transcription, including response to different types of therapies.