

[REDACTED]; Tel: [REDACTED]

## Education

### **Princeton University, Princeton, USA**

2005-2009

- Ph.D. in Biological Dynamics  
*Dissertation: Quantitative Approaches to Influenza Virus Surveillance*
- M.A. in Biological Dynamics

### **Morgan State University, Baltimore, USA**

1999-2003

- Bachelor of Science in Biology (Magna Cum Laude)

### **Towson University, Towson, USA**

2001-2002

- Independent studies in biology

## Research experience

### **Postdoctoral researcher, Department of Immunology, Weizmann Institute of Science**

2009-2012

Developed computational methods for reducing substantially the experimental effort required to collect high-quality serological data measuring antibody-pathogen reactivities, by modeling the individual data points as “compressed” sensors of the underlying reactivities (5). Also, co-led the development of new experimental and theoretical methods for quantitative, high-throughput sequencing and analysis of T-cell receptor (TCR) repertoires (4). Subsequent applications of these methods uncovered: A physical organizing principle that governs gene rearrangement at the TCR beta-chain locus, in both mice and humans (4); a threshold mathematical condition that explains extensive sharing of certain TCRs among individuals, in terms of the rates at which those TCRs are produced during gene rearrangement (4); TCR signatures for murine splenic T cells with specificity for brain-restricted antigens, which overlap significantly with signatures for T cells actually found in the murine brain (3); and TCR signatures for T cells involved in the pathogenesis of a murine model for multiple sclerosis (1).

### **Doctoral researcher & Burroughs-Wellcome Training Fellow, Program in Biological Dynamics, Princeton University**

2005-2009

Co-led research that discovered a physical organizing principle that governs evasion by influenza A/H3N2 virus of B cell responses, leading to a novel proposal for the design of an improved influenza vaccine (7; reviewed in ref. 6). Also, initiated and led research that: Developed a biophysical model that provided a new insight into the mechanistic basis of the standard serological assay that is used for influenza surveillance (Supplementary information of ref. 5); demonstrated that this new insight is consistent with empirical data (8); used an experimentally consistent biochemical model of *Escherichia coli* metabolism to elucidate factors influencing the accessibility of adaptive phenotypes in fitness landscapes

induced by growing *E. coli* with different carbon sources (11); used a previously developed computational approach (14) to elucidate factors influencing the accessibility of RNA structures in RNA folding energy landscapes (10); and developed a new statistical mechanics-inspired technique for predicting RNA folding rates (12).

**Research assistant, Departments of Biology and Mathematics, Morgan State University**

2003-2005

Developed and applied models of RNA folding kinetics (13-15); HIV immunodynamics (9); and DNA microsatellite sequences (16-18).

**Undergraduate researcher, Department of Biology, Morgan State University**

2001-2002

Performed laboratory experiments that identified three protein biomarkers of an environmental pollutant called 2,4-D in certain rivers found in Baltimore city, USA, using 2-dimensional sodium dodecyl sulfate polyacrylamide gel electrophoresis and protein densitometry.

**Awards**

- Postdoctoral fellowship, Weizmann Institute of Science, 2009-2012
- Burroughs-Wellcome Training Fellowship in Biological Dynamics, Princeton University, 2006-2008
- Graduate fellowship, Princeton University, 2005
- Board of Regents' Honors Scholarship, Morgan State University, 1999-2003
- Baltimore Collaborative for Environmental Biology Honors Scholar, Towson University, 2002
- Travel award from the Kavli Institute for Theoretical Physics, Santa Barbara, USA, for "Evolution of Molecular Networks" workshop, 2007
- Travel award from the Institute for Pure and Applied Mathematics, Los Angeles, USA, for "Conference for African American Researchers in the Mathematical Sciences", 2005
- Travel award from the Mathematical Sciences Research Institute, Berkeley, USA, for "Conference for African American Researchers in the Mathematical Sciences", 2004

**Refereed publications, and manuscripts**

(\* First author; † Corresponding author)

***Lymphocyte repertoires, infectious diseases***

1. Shifrut et al. CD4+ TCR $\beta$  repertoire diversity is compromised in the spleen but not in the bone-marrow of aged mice due to private and sporadic clonal expansion, in preparation.
2. Asaf M, et al. T-cell receptor repertoires of mice of different MHC haplotypes include shared, public CDR3 sequences that are abundant, rich in convergent recombination, and associated with self-related immunity, in preparation for submission to *Science*.
3. Ndifon W, et al. Regulatory vs. helper CD4+ T cell ratios and the development of AIDS, in preparation for submission to *JAIDS*.
4. Ndifon\* W, Gal\* H, Shifrut\* E, Aharoni R, Friedman N, Arnon† R. T-cell receptor signatures of experimental autoimmune

- encephalomyelitis and therapeutic intervention identified by high-throughput sequencing, in preparation for submission to *J Immunol*.
5. Thomas N, Heather J, Ndifon W, Shawe-Taylor J, Chain<sup>†</sup> B. Decombinator: A tool for fast, efficient gene assignment in T cell receptor sequences using a finite state machine. *Bioinformatics* 2013; 29:542-550.
  6. Baruch<sup>\*</sup> K, Ron-Harel<sup>\*</sup> N, Gal<sup>\*</sup> H, Shifrut E, Ndifon W, Deckowska A, Mirlas-Neisberg N, Cardon M, Vaknin I, Cahalon L, Berkutzki T, Mattson MP, Gomez-Pinilla F, Friedman N, Schwartz<sup>†</sup> M. CNS-specific immunity at the choroid plexus shifts towards destructive Th2-inflammation in brain aging. *Proceedings of the National Academy of Sciences USA* 2013; 110:2264-2269.
  7. Ndifon<sup>\*</sup> W, Gal<sup>\*</sup> H, Shifrut E, Aharoni R, Waysbort N, Yissachar N, Reich-Zeliger S, Arnon R, Friedman<sup>†</sup> N. Chromatin conformation governs T-cell receptor J $\beta$  gene segment usage. *Proceedings of the National Academy of Sciences USA* 2012; 109:15865-15870.
  8. Ndifon W. New methods for analyzing serological data with applications to influenza surveillance. *Influenza and Other Respiratory Viruses* 2011; 5:206-212. For supplementary information, see <http://arxiv.org/abs/1109.2209>.
  9. Nara PL, Tobin GJ, Chaudhuri AJ, Trujillo JD, Lin G, Cho MW, Levin<sup>†</sup> SA, Ndifon W, Wingreen NS. How can vaccines against influenza and other viral diseases be made more effective? *PLoS Biology* 2010; 8:e1000571.
  10. Ndifon<sup>†</sup> W, Wingreen<sup>†</sup> NS, Levin<sup>†</sup> SA. Differential neutralization efficiency of hemagglutinin epitopes, antibody interference, and the design of influenza vaccines. *Proceedings of the National Academy of Sciences USA* 2009; 106:8701-8706.
  11. Ndifon<sup>†</sup> W, Dushoff J, Levin SA. On the use of hemagglutination-inhibition for influenza surveillance: Surveillance data are predictive of influenza vaccine effectiveness. *Vaccine* 2009; 27:2447-2452.
  12. Ndifon W. A NetLogo-based agent-oriented simulation of HIV immunodynamics. In Yilmaz L (ed.), *Proceedings of the Agent-Directed Simulation Symposium*. SCS Press, USA, ISBN: 1-56555-291-1, 2005, pp. 193-197.

### **RNA folding, evolution**

13. Ndifon<sup>†</sup> W, Dushoff J. Finding attractors on a folding energy landscape. In Liu LA, Wei D, Li Y (eds.) *Handbook of Research on Computational and Systems Biology*. Igi-Global, USA, 2011.
14. Ndifon<sup>†</sup> W, Plotkin JB, Dushoff J. On the accessibility of adaptive phenotypes of a bacterial metabolic network. *PLoS Computational Biology* 2009; 5:e1000472.
15. Nkwanta A, Ndifon<sup>†</sup> W. A contact-waiting-time metric and RNA folding rates. *FEBS Letters* 2009; 583:2392-2394.
16. Ndifon<sup>†</sup> W, Nkwanta A. An RNA foldability metric; implications for the design of rapidly foldable RNA sequences. *Biophysical Chemistry* 2006; 120:237-239.
17. Ndifon W. A complex adaptive systems approach to the kinetic folding of RNA. *Biosystems* 2005; 82:257-265.
18. Ndifon<sup>†</sup> W, Nkwanta A. An agent-oriented simulation of RNA folding

and its application to the analysis of RNA conformational spaces. In Yilmaz L (ed.), *Proceedings of the Agent-Directed Simulation Symposium*. SCS Press, USA, ISBN: 1-56555-291-1, 2005, pp. 198-204.

### **DNA microsatellites**

19. Hill<sup>†</sup> D, Ndifon W, Nkwanta A. Differential enrichment of simple sequence repeats in selected Alzheimer-associated genes. *Cellular and Molecular Biology (Noisy-le-grand)* 2007; 53:23-31.
20. Ndifon<sup>†</sup> W, Nkwanta A, Hill D. Some probabilistic results on the non-randomness of simple sequence repeats in DNA sequences. *Bulletin of Mathematical Biology* 2006; 68:1747-1759.
21. Ndifon W, Nkwanta<sup>†</sup> A, Hill D. Identifying nonrandom occurrences of simple sequence repeats in genomic DNA sequences. *Ethnicity and Disease* 2005; 15:S567-S570.

### **Books**

1. Ndifon W. Quantitative Approaches to Influenza Virus Surveillance, ProQuest LLC, Ann Arbor, Michigan, USA 2009 (182 pages).
2. Ndifon W. CourseMate User's Manual, Lulu.com, 2004 (144 pages).

### **Invention**

Ndifon W, Wingreen NS, Levin SA, Dushoff J. Approaches to Influenza Vaccine Design and Vaccine Strain Selection, ProQuest LLC, Ann Arbor, Michigan, USA 2009 (182 pages).

### **Selected talks**

1. Immunosignatures of health and autoimmune disease: Insights from mouse models, Division of Infection & Immunity, University College London, UK, January 2012.
2. A biophysical mechanism for influenza viral escape from antibodies, Center for Systems Biology, Institute for Advanced Study, Princeton, USA, November 2008.
3. Empirical support for some theoretical insights into the nature of influenza surveillance data, Lewis-Sigler Institute for Integrative Genomics, Princeton University, October 2008.
4. Towards a thermo-kinetic view of the RNA genotype-phenotype map, Laboratory of Prof. Devarajan Thirumalai, University of Maryland, USA, February 2006.
5. Evolution of DNA and RNA, Princeton-Penn-Rutgers Graduate Student Retreat, University of Pennsylvania, USA, April 2006.
6. Some approaches to RNA secondary structure prediction, Mathematical Modeling graduate course, Morgan State University, April 2005.
7. A novel combinatorial method for quantifying SSR-dependent nonrandomness in genomic DNA, International Conference for Mathematics in Biology and Medicine, University of Michigan, USA, July 2004.

### **Service to scientific community**

1. Advised undergraduate and graduate students, including Eric Shifrut, currently a Ph.D. student in Immunology at the Weizmann Institute of Science; Helene Nguewou, currently a Ph.D. student at Johns Hopkins University, USA; and Raaj Mehta, currently a medical student at Harvard Medical School, USA.

2. Served on the technical program committee of the International Conference for Computational and Systems Immunology, Shanghai, China
3. Served as a reviewer for Biology Letters, Cellular and Molecular Biology, Virology Journal, Journal of Molecular Evolution.