

Nadav Rappoport
Senior Lecturer (Associate Professor)
Ben-Gurion University of the Negev, ISRAEL

PERSONAL DETAILS

Department of Software and Information Systems Engineering
Ben-Gurion University of the Negev
P.O.B. 653 Beer-Sheva
ISRAEL 8410501 E-mail: nadavrap@bgu.ac.il

POSITIONS AND EMPLOYMENTS

- *Webmaster* 2008 - 2011
Webmaster of School of Computer Science and Engineering.
The Hebrew University of Jerusalem, Israel
- *Computational tool mastering* 2010 - 2015
Maintenance, management and development of lab's web-tools and databases (e.g. [ProtoNet](#))
The Hebrew University of Jerusalem, Israel
- Post-doctoral fellowship at the **Bakar Computational Health Science Institute**, UCSF, USA 2015 - 2017
 - Host: Prof. Atul Butte
- Post-doctoral fellowship at the **Bakar Computational Health Science Institute**, UCSF, USA 2017 - 2019
 - Host: Prof. Noah Zaitlen
- Senior Lecturer, Department of Systems and Information Science Engineering, **Ben-Gurion University of the Negev**, ISRAEL 2019 - Current
Research fields:
 - Machine Learning
 - Big biomedical data
 - Medical Informatics

EDUCATION

- B.Sc. Computer Science and Computational Biology, **The Hebrew University of Jerusalem**, Jerusalem, Israel 2007 - 2009
 - Final Project Topic: "DNA Methylation Patterns in Mice Liver"
 - Advisor of final project: Prof. Nir Friedman
- Direct Track Ph.D. Computer Science **The Hebrew University of Jerusalem**, Jerusalem, Israel 2010 - 2015
 - Research Topic: "Gaining functional and quantitative knowledge on genes and molecular machines using a computational approach"
 - Advisor: Prof. Michal Linial

ACADEMIC ACTIVITY

- *Catalyst Awards Intern* 2017 - 2018
Internship in the Catalyst awards program in consulting and funding board for promising early-stage ideas for development of diagnostics, devices, therapeutics and digital health.
- Ad-hoc reviewer for a variety of journals, conferences and meetings 2011 - Current

AWARDS and SCHOLARSHIPS

- **Prize for Academic excellence** 2008
- **Sudarsky Travel Fellowship** 2010
- **ECCB12 Conference Fellowship** 2012
- **Noah Lichtenstein Prize**, The Hebrew University of Jerusalem 2013
- **Department selected monthly article (SMART) prize**
(Rappoport et al., 2013 *Nature Biotechnology*) 2013
- **Charles Clore Foundation Fellowship for Ph.D. students** 2014, 2015
- **ISCB Travel Fellowship** 2014
- **RECOMB Travel Fellowship** 2015

VOLUNTARY EXPERIENCE

- **Academic tutoring** 2000 - 2002
Academic aid with a high school pupil, helped him with homework he had difficulty in, and prepared him for exams.

TEACHING EXPERIENCE

- *Academic tutoring* 2000 - 2002
Academic aid with a high school pupil, helped him with homework he had difficulty in, and prepared him for exams.
- *Teaching assistant* 2009 - 2015
Teaching assistant in the courses: Introduction to Computer Science, Data Structures and Databases.
The Hebrew University of Jerusalem, Israel
- *Training graduate and undergraduate students* 2010 - 2015
The Hebrew University of Jerusalem, Israel
- *Teaching programming courses* 2012 - 2015
Teaching various programming courses including Java, C, C++ and Python.
The Hebrew University of Jerusalem, Israel
- *Teaching* 2019 - Current
Teaching: Machine Learning course, Clinical Data Science course.
Ben-Gurion University of Jerusalem, Israel
- *Teaching* 2019 - 2020
Teaching: Supervised Learning course.
Yandex School of Data Science, Israel

COMPUTER SKILLS**Languages:**

R, Python, Julia, Perl, SQL, C, C++, Java, Matlab, Unix shell scripts, PHP, HTML.

Data Science:

Experience efficiently managing large databases in SQL, Machine Learning and Extensive clustering analysis.

Applications:

PostgreSQL, MySQL, L^AT_EX, SVN, Git.

Operating Systems:

Unix/Linux, OSX and Windows.

Miscellaneous:

High-level SQL database administration

Setting up large scale online bioinformatics frameworks and databases (e.g., [ProtoNet](#), [PAN-DORA](#))

Excellent troubleshooter.

Rich experience in teaching computer science courses to CS students and programming to non-CS students.

LANGUAGES

- Native Hebrew Speaker
- Native French Speaker
- Fluent English

PUBLICATIONS

Doctoral Dissertation

- [1] **N. Rappoport**, “Gaining functional and quantitative knowledge on genes and molecular machines using a computational approach”, Ph.D. dissertation (The Hebrew University of Jerusalem, 2015).

Book Chapters

- [2] D. Ofer, **N. Rappoport**, M. Linial, “The little known universe of short proteins in insects: a machine learning approach”, *Short views on insect genomics and proteomics* (Springer, 2015), pp. 177–202.

Journal Articles

- [0] D. Klinger, I. Blass, **N. Rappoport**, M. Linial, “Significantly improved covid-19 outcomes in countries with higher bcg vaccination coverage: a multivariable analysis”, *Vaccines (Basel)* **8**, 10.3390/vaccines8030378 (2020).
- [3] B. S. Glicksberg, B. Oskotsky, P. M. Thangaraj, N. Giangreco, M. A. Badgeley, K. W. Johnson, D. Datta, V. A. Rudrapatna, **N. Rappoport**, M. M. Shervey, R. Miotto, T. C. Goldstein, E. Rutenberg, R. Frazier, N. Lee, S. Israni, R. Larsen, B. Percha, L. Li, J. T. Dudley, N. P. Tatonetti, A. J. Butte, “PatientExploreR: an extensible application for dynamic visualization of patient clinical history from electronic health records in the OMOP common data model”, *Bioinformatics*, 10.1093/bioinformatics/btz409 (2019).
- [4] H. Paik, M. J. Kan, **N. Rappoport**, D. Hadley, M. Sirota, B. Chen, U. Manber, C. Mangurian, S. B. Cho, A. J. Butte, “Tracing diagnoses trajectories over millions of hospital discharges reveals association between schizophrenia and rhabdomyolysis”, Accepted on October 2019 to *Scientific Data* (2019).
- [5] N. Crawford, J. W. Oehlert, G. M. Shaw, D. K. Stevenson, **N. Rappoport**, M. Sirota, S. A. Tishkoff, N. Sondheim, “Divergent patterns of mitochondrial and nuclear ancestry are associated with the risk for preterm birth”, *The Journal of pediatrics* **194**, 40–46 (2018).
- [6] **N. Rappoport**, H. Paik, B. Oskotsky, R. Tor, E. Ziv, N. Zaitlen, A. J. Butte, “Comparing ethnicity-specific reference intervals for clinical laboratory tests from ehr data”, *The Journal of Applied Laboratory Medicine*, jalm–2018 (2018).
- [7] **N. Rappoport**, J. Toung, D. Hadley, R. J. Wong, K. Fujioka, J. Reuter, C. W. Abbott, S. Oh, D. Hu, C. Eng, “A genome-wide association study identifies only two ancestry specific variants associated with spontaneous preterm birth”, *Scientific reports* **8**, 226 (2018).
- [8] M. Linial, **N. Rappoport**, D. Ofer, “Overlooked short toxin-like proteins: a shortcut to drug design”, *Toxins* **9**, 350 (2017).

- [9] Y. Jiang, R. T. Oron, T. W. Clark, R. A. Bankapur, D. D'Andrea, R. Lepore, S. C. Funk, I. Kahanda, M. K. Verspoor, A. Ben-Hur, E. D. C. Koo, D. Penfold-Brown, D. Shasha, N. Youngs, R. Bonneau, A. Lin, E. S. M. Sahraeian, L. P. Martelli, G. Profiti, R. Casadio, R. Cao, Z. Zhong, J. Cheng, A. Altenhoff, N. Skunca, C. Dessimoz, T. Dogan, K. Hakala, S. Kaewphan, F. Mehryary, T. Salakoski, F. Ginter, H. Fang, B. Smithers, M. Oates, J. Gough, P. Törönen, P. Koskinen, L. Holm, C.-T. Chen, W.-L. Hsu, K. Bryson, D. Cozzetto, F. Minneci, T. D. Jones, S. Chapman, D. BKC, K. I. Khan, D. Kihara, D. Ofer, **N. Rappoport**, A. Stern, E. Cibrian-Uhalte, P. Denny, E. R. Foulger, R. Hieta, D. Legge, C. R. Lovering, M. Magrane, N. A. Melidoni, P. Mutowo-Meullenet, K. Pichler, A. Shypitsyna, B. Li, P. Zakeri, S. ElShal, L. Tranchevent, S. Das, L. N. Dawson, D. Lee, G. J. Lees, I. Sillitoe, P. Bhat, T. Nepusz, E. A. Romero, R. Sasidharan, H. Yang, A. Paccanaro, J. Gillis, E. A. Sedeño-Cortés, P. Pavlidis, S. Feng, M. J. Cejuela, T. Goldberg, T. Hamp, L. Richter, A. Salamov, T. Gabaldon, M. Marcet-Houben, F. Supek, Q. Gong, W. Ning, Y. Zhou, W. Tian, M. Falda, P. Fontana, E. Lavezzo, S. Toppo, C. Ferrari, M. Giollo, D. Piovesan, C. S. Tosatto, A. Pozo, M. J. Fernández, P. Maietta, A. Valencia, L. M. Tress, A. Benso, S. Di Carlo, G. Politano, A. Savino, U. H. Rehman, M. Re, M. Mesiti, G. Valentini, W. J. Bargsten, J. A. D. Dijk, B. Gemovic, S. Glisic, V. Perovic, V. Veljkovic, N. Veljkovic, C. D. Almeida-e-Silva, N. R. Z. Vencio, M. Sharan, J. Vogel, L. Kansakar, S. Zhang, S. Vucetic, Z. Wang, E. M. J. Sternberg, N. M. Wass, P. R. Huntley, J. M. Martin, C. O'Donovan, N. P. Robinson, Y. Moreau, A. Tramontano, C. P. Babbitt, E. S. Brenner, M. Linial, A. C. Orengo, B. Rost, S. C. Greene, D. S. Mooney, I. Friedberg, P. Radivojac, "An expanded evaluation of protein function prediction methods shows an improvement in accuracy", *Genome Biology* **17**, 1–19 (2016).
- [10] **N. Rappoport**, M. Linial, "Protobug: functional families from the complete proteomes of insects", *Database (Oxford)* **2015**, bau122 (2015).
- [11] **N. Rappoport**, M. Linial, "Trends in genome dynamics among major orders of insects revealed through variations in protein families", *BMC Genomics* **16**, 583 (2015).
- [12] S. Karsenty, **N. Rappoport**, D. Ofer, A. Zair, M. Linial, "Neuropid: a classifier of neuropeptide precursors", *Nucleic Acids Res* **42**, W182–6 (2014).
- [13] **N. Rappoport**, A. Stern, N. Linial, M. Linial, "Entropy-driven partitioning of the hierarchical protein space", *Bioinformatics* **30**, i624–30 (2014).
- [14] **N. Rappoport**, M. Linial, "Functional inference by protonet family tree: the uncharacterized proteome of daphnia pulex", *BMC Bioinformatics* **14 Suppl 3**, S11 (2013).
- [15] **N. Rappoport**, N. Linial, M. Linial, "Protonet: charting the expanding universe of protein sequences", *Nat Biotechnol* **31**, 290–2 (2013).
- [16] **N. Rappoport**, S. Karsenty, A. Stern, N. Linial, M. Linial, "Protonet 6.0: organizing 10 million protein sequences in a compact hierarchical family tree", *Nucleic Acids Res* **40**, D313–20 (2012).
- [17] **N. Rappoport**, M. Linial, "Viral proteins acquired from a host converge to simplified domain architectures", *PLoS Comput Biol* **8**, e1002364 (2012).

- [18] **N. Rappoport**, M. Fromer, R. Schweiger, M. Linial, “Pandora: analysis of protein and peptide sets through the hierarchical integration of annotations”, *Nucleic Acids Res* **38**, W84–9 (2010).

Submitted

- [19] B. Sheppard, **N. Rappoport**, P.-R. Loh, S. Sanders, A. Dahl, N. Zaitlen, “Coordinated interaction: a model and test for synergist and antagonistic epistasis in complex phenotypes”, Submitted on November 2019 to *Science Translational Medicine*, 2019.
- [20] M. Subramaniam, R. K. Perez, M. C. Kim, M. G. Gordon, G. Hartoularos, C. Lanata, **N. Rappoport**, S. Targ, Y. Sun, L. Maliskova, S. Kwek, T. Li, M. Mouw, M. Calvo, L. Trupin, M. Slyper, J. Waldman, O. Dionne, L. Fong, M. Dall’era, A. Regev, J. Yazdany, L. A. Criswell, N. Zaitlen, C. J. Ye, “Multiplexed rna-sequencing of 1m immune cells reveals the cellular, molecular, and genetic correlates of systemic lupus erythematosus”, Submitted on October 2019 to *Nature*, 2019.

CONFERENCE PRESENTATION

- ECCB 2010, Gent, Belgium
Poster: Functional Inference for Experimental Proteomics: The PANDORA (Annotations graph) and ProtoNet (Family Tree) Resources
- ISMB / ECCB 2011, Vienna, Austria
Poster: Viral proteins acquired from a host converge to simplified domain architectures
- AFP / CAFA Satellite, ISMB / ECCB 2011, Vienna, Austria
Poster: The Daphnia Uncharacterized Proteome of Short Sequences Is Revealed via the ProtoNet Classification Tree
- ECCB 2012, Basel, Switzerland
Highlight presentation: Viral-host coevolution: Playing ‘seek and hide’
Poster: 18 Insects whole proteomes tree construction identify proteins families specialized in different Insects branches
- ISMB 2012, Long Beach, CA USA
Highlight presentation: Viral-host coevolution: Playing ‘seek and hide’
Poster: A tree construction of all 18 insects complete proteomes reveals extensive expansion and shrinking of proteins families
- IBS 2012, Jerusalem, Israel

Poster: Functional Inference by ProtoNet Family Tree: The Uncharacterized proteome of *Daphnia pulex*

- ISMB/ECCB 2013, Berlin, Germany

Poster: Representation of Protein Complexes as Multilayer Graphs

- RECOMB 2013, Beijing, China

Poster: Representation of Protein Complexes as Multilayer Graphs

- ISMB 2014, Boston, MA US

Poster: ProtoBug: Automatic Classification of Insects? Complete Proteomes

- ECCB 2014, Strasbourg, France

Lecture: Entropy driven partitioning of the hierarchical protein space

Poster: Comparative Analysis of Insects' Complete Proteomes

- ISMB/ECCB 2015, Dublin, Ireland

Poster: Entropy-driven partitioning of the hierarchical protein space

- RECOMB 2015, Warsaw, Poland

Poster: Entropy-driven partitioning of the hierarchical protein space

- RECOMB 2016, Los Angeles, California

Poster: Predict demographic features from lab tests

- Transatlantic Data Science Workshop 2016, NIH, Bethesda, MD

- Pediatric academic societies meeting 2017, San Francisco, California

Poster: Genome-wide Association Study Identifies Ancestry Specific Variants Associated with Spontaneous Preterm Birth

- Health Disparities Research Symposium, 2017, San Francisco, California

Lecture: Creating ethnicity-specific reference intervals for diagnostic tests from EHR data

- Biomedical big data science conference, 2018, Israel

Poster: Creating ethnicity-specific reference intervals for lab tests from EHR data

- Israeli Human Population Genetics Meeting, 2019, Israel

Lecture: Leveraging electronic health records to define ethnicity-specific reference ranges for common lab tests

- Frontiers in Computational Healthcare, 2019, Israel

Lecture: A system for prediction of bleeding volumes during surgery from medical records