

Itai Sharon – Curriculum Vitae

Email: itai@itaisharon.net

RESEARCH AND ACADEMIC EXPERIENCE

Principle Investigator, MIGAL – Galilee Research Institute, 08/2015 – present
Research focuses on the development of computational and other tools for microbial ecology

Senior Lecturer (Assistant Professor), Tel-Hai College, 10/2015 – present
Teaches basic and advanced courses at the Computer Science Department

Postdoctoral Researcher, University of California, Berkeley, 2010 – 2015
Research focus: dynamics and structure of microbial communities across different environments
Advisor: Prof. Jillian Banfield

Short postdoc, Technion, Israel Institute of Technology, 04 – 08/2010
Research focus: analysis of next generation sequencing
Affiliation: Laboratory of Dr. Itai Yanai

Algorithm developer, NDS Technologies, Haifa, Israel, 1998 – 2007
Developed algorithms and software for image analysis and understanding

EDUCATION

PhD, Technion – Israel Institute of Technology, Computer Science, 2010
Dissertation title: Computational methods for metagenomic analysis
Advisors: Prof. Oded Béjà and Prof. Ron Pinter

MSc, Technion – Israel Institute of Technology, Computer Science, 2005
Research focus: similarity detection for low complexity and remotely related proteins
Advisors: Dr. Golan Yona and Assoc. Prof. Ran El-Yaniv

BSc, Technion – Israel Institute of Technology, Computer Science, 1998
GPA: 89.6

REFEREED PUBLICATIONS

1. Suez, J., Zmora, N., Zilberman-Schapira, G., Mor, U., Dori-Bachash, M., Bashiardes, S., Zur, M., Regev-Lehavi, D., Ben-Zeev Brik, R., Federici, S., Horn, M., Cohen, Y., Moor, A.E., Zeevi, D., Korem, T., Kotler, E., Harmelin, A., Itzkovitz, S., Maharshak, N., Shibolet, O., Pevsner-Fischer, M., Shapiro, H., **Sharon, I.**, Halpern, Z., Segal, S. and Elinav, E. (2018). Post-antibiotic gut mucosal microbiome reconstitution is impaired by probiotics and improved by autologous FMT. *Cell*, 174, 1406-1423.
2. Zmora, N., Zilberman-Schapira, G., Suez, J., Mor, U., Dori-Bachash, M., Bashiardes, S., Kotler, E., Zur, M., Regev-Lehavi, D., Ben-Zeev Brik, R., Federici, S., Cohen, Y., Linevsky, R., Rothschild, D., Moor, A.E., Ben-Moshe, S., Harmelin, A., Itzkovitz, S., Maharshak, N., Shibolet, O., Shapiro, H., Pevsner-Fischer, M., **Sharon, I.**, Halpern, Z., Segal, E. and Elinav, E. (2018). Personalized gut mucosal colonization resistance to empiric probiotics is associated with unique host and microbiome features. *Cell*, 174, 1388-1405.
3. Pushkarev, A., Inoue, K., Larom, S., Flores-Uribe, J., Singh, M., Konno, M., Tomida, S., Ito, S., Nakamura, R., Tsunoda, S.P., Philosofo, A., **Sharon, I.**, Yutin, N., Koonin, E.V., Kandori, H. and Bèjà, O. (2018). A distinct abundant group of microbial rhodopsins discovered using functional metagenomics. *Nature*, 558, 595-599.
4. Roitman, S., Hornung, E., Flores-Uribe, J., **Sharon, I.**, Feussner, I. and Bèjà, O. (2017). Cyanophage-encoded lipid desaturases: oceanic distribution, diversity and function. *ISME J*, 12, 343-455.
5. Fridman, S., Flores-Uribe, J., Larom, S., Alalouf, O., Liran, O., Yacoby, I., Salama, F., Bailleul, B., Rappaport, F., Ziv, T., **Sharon, I.**, Cornejo-Castillo, F.M., Philosofo, A., Dupont, C.L., Sanchez, P., Acinas, S.G., Rohwer, F., Lindell, D. and Bèjà, O. (2017). A myovirus encoding both photosystem-I and II proteins enhances cyclic electron flow in infected *Prochlorococcus* cells. *Nature Microbiol*, 2, 1350-1357.
6. Philosofo, A., Yutin, N., Flores-Uribe, J., **Sharon, I.**, Koonin, E.V., Bèjà, O. (2017). Novel abundant oceanic viruses of uncultured marine group II Euryarchaeota. *Curr Biol*, 27(9), 1362-1368.
7. Probst, A.J., Castelle, C.J., Singh, A., Brown, C.T., Anantharaman, K., **Sharon, I.**, Hug, L.A., Burstein, D., Emerson, J.B., Thomas, B.C., Banfield, J.F. (2017). Genomic resolution of a cold subsurface aquifer community provides metabolic insights for novel microbes adapted to high CO₂ concentrations. *Environ Microbiol*, 19(2), 459-474.
8. Raveh-Sadka, T., Firek, B., **Sharon, I.**, Baker, R., Brown, C.T., Thomas, B.C., Morowitz, M.J., Banfield, J.F. (2016). Evidence for persistent and shared bacterial strains against a background of largely unique gut colonization in hospitalized premature infants. *ISME J*, doi: 10.1038/ismej.2016.83.
9. Wrighton, K.C., Castelle, C.J., Varaljay, V.A., Satagopan, S., Brown, C.T., Wilkins, M.J., Thomas, B.C., **Sharon, I.**, Williams, K.H., Tabita, F.R., Banfield, J.F. (2016). RubisCO of a nucleoside pathway known from Archaea is found in diverse uncultivated phyla in bacteria. *ISME J*, doi: 10.1038/ismej.2016.53.
10. Probst, A.J., Castelle, C.J., Singh, A., Brown, C.T., Anantharaman, K., **Sharon, I.**, Hug, L.A., Burstein, D., Emerson, J.B., Thomas, B.C., Banfield, J.F. (2016). Genomic resolution of a cold subsurface aquifer community provides metabolic insights for novel microbes adapted to high CO₂ concentrations. *Environ Microbiol*, doi: 10.1111/1462-2920.13362
11. Burstein, D., Sun, C.L., Brown, C.T., **Sharon, I.**, Anantharaman, K., Probst, A.J., Thomas, B.C., Banfield, J.F. (2016). Major bacterial lineages are essentially devoid of CRISPR-Cas viral defence systems. *Nat Commun*, doi: 10.1038/ncomms10613
12. Hug, L.A., Thomas, B.C., **Sharon, I.**, Brown, C.T., Sharma, R., Hettich, R.L., Wilkins, M.J., Williams, K.H., Singh, A., Banfield, J.F. (2016). Critical biogeochemical functions in the subsurface are associated with bacteria from new phyla and little studied lineages. *Environ Microbiol*, 18(1), 159-173

13. Brown, C.T., Hug, L.A., Thomas, B.C., **Sharon, I.**, Castelle, C.J., Singh, A., Wilkins, M.J., Wrighton, K.C., Williams, K.H. and Banfield, J.F. (2015). Unusual biology across a group comprising more than 15% of domain Bacteria. *Nature*, doi:10.1038/nature14486
14. Hug, L.A., Thomas, B.C., **Sharon, I.**, Brown, C.T., Sharma, R., Hettich, R.L., Wilkins, M.J., Williams, K.H., Singh, A., Banfield, J.F. (2015). Critical biogeochemical functions in the subsurface are associated with bacteria from new phyla and little studied lineages. *Environ Microbiol*, doi: 10.1111/1462-2920.12930
15. Paez-Espino, D., **Sharon, I.**, Morovic, W., Stahl, B., Thomas, B.C., Barrangou, R., Banfield, J.F. (2015). CRISPR immunity drives rapid phage genome evolution. *mBio*, 6(2), e00262-15
16. **Sharon, I.**, Kertesz, M., Hug, L.A., Pushkarev, D., Blauwkamp, T.A., Castelle, C.J., Amirebrahimi, M., Thomas, B.C., Burstein, D., Tringe, S.G., Williams, K.H., Banfield, J.F. (2015). Accurate, multi-kb reads resolve complex populations and detect rare microorganisms. *Genome Res*, 25, 534-543
17. Raveh-Sadka, T., Thomas, B.C., Singh, A., Firek, B., Brooks, B., Castelle, C.J., **Sharon, I.**, Baker, R., Good, M., Morowitz, M.J., Banfield, J.F. (2015). Gut bacteria are rarely shared by co-hospitalized premature infants, regardless of necrotizing enterocolitis development. *eLife*, 4, e05477
18. Wrighton, K.C., Castelle, C.J., Wilkins, M.J., Hug, L.A., **Sharon, I.**, Thomas, B.C., Handley, K.M., Mullin, S.W., Nicora, C.D., Singh, A., Lipton, M.S., Long, P.E., Williams, K.H., Banfield, J.F. (2014). Metabolic interdependencies between phylogenetically novel fermenters and respiratory organisms in an unconfined aquifer. *ISME J*, 8(7), 1452-1463
19. Brooks, B., Firek, B.A., Miller, C.S., **Sharon, I.**, Thomas, B.C., Baker, R., Morowitz, M.J., Banfield, J.F. (2014). Microbes in the neonatal intensive care unit resemble those found in the gut of premature infants. *Microbiome*, 2(1)
20. Di Rienzi, S.C.*, **Sharon, I.***, Wrighton, K.C., Koren, O., Hug, L.A., Thomas, B.C., Goodrich, J.K., Bell, J.T., Spector, T.D., Banfield, J.F., Ley, R.E. (2013). The human gut and groundwater harbor non-photosynthetic bacteria belonging to a new candidate phylum sibling to Cyanobacteria. *eLife*, 2, e01102
21. Brown, C.T., **Sharon, I.**, Thomas, B.C., Castelle, C.J., Morowitz, M.J., Banfield, J.F. (2013). Genome resolved analysis of a premature infant gut microbial community reveals a Varibaculum cambriense genome and a shift towards fermentation-based metabolism during the third week of life. *Microbiome*, 1(30)
22. Kantor, R.S., Wrighton, K.C., Handley, K.M., **Sharon, I.**, Hug, L.A., Castelle, C.J., Thomas, B.C., Banfield, J.F. (2013). Small genomes and sparse metabolisms of sediment-associated bacteria from four candidate phyla. *mBio*, 4(5), e00708-13
23. **Sharon, I.**, Morowitz, M.J., Thomas, B.C., Costello, E.K., Relman, D.A., Banfield, J.F. (2013). Time series community genomics analysis reveals rapid shifts in bacterial species, strains, and phage during infant gut colonization. *Genome Res*, 23(1), 111-120
24. Hug, L.A., Castelle, C.J., Wrighton, K.C., Thomas, B.C., **Sharon, I.**, Frischkorn, K.R., Williams, K.H., Tringe, S.G., Banfield, J.F. (2013). Community genomic analyses constrain the distribution of metabolic traits across the Chloroflexi phylum and indicate roles in sediment carbon cycling. *Microbiome*, 1(22)
25. Wrighton, K.C., Thomas, B.C., **Sharon, I.**, Miller, C.S., Castelle, C.J., VerBerkmoes, N.C., Wilkins, M.J., Hettich, R.J., Lipton, M.S., Williams, K.H., Long, P.E., Banfield, J.F. (2012). Fermentation, Hydrogen and Sulfur Metabolism in Multiple Uncultivated Bacterial Phyla. *Science*, 337(6102), 1661-1665
26. Avrani, S., Wurtzel, O., **Sharon, I.**, Sorek, R., Lindell, D. (2011). Genomic island variability facilitates Prochlorococcus-virus coexistence. *Nature*, 474, 604-608

27. Handley, K.M., VerBerkmoes, N.C., Steefel, C.I., Williams, K.H., **Sharon, I.**, Miller, C.S., Frischkorn, K.R., Chourey, K., Thomas, B.C., Shah, M.B., Long, P.E., Hettich, R.L., Banfield, J.F. (2012). Biostimulation induces syntrophic interactions that impact C, S and N cycling in a sediment microbial community. *ISME J*, 7(4), 800-816
28. **Sharon, I.**, Battchikova, N., Aro, E.-M., Gligione, C., Meinel, T., Glaser, F., Pinter, R.Y., Breitbart, M., Rohwer, F., Béjà, O. (2011). Comparative metagenomics of microbial traits within oceanic viral communities. *ISME J*, 5(7), 1178-1190
29. Atamna-Ismaeel, N., Finkel, O.M., Glaser, F., **Sharon, I.**, Schneider, R., Post, A.F., Spudich, J.L., von Mering, C., Vorholt, J.A., Iluz, D., Béjà, O., Belkin, S. (2011). Microbial rhodopsins on leaf surfaces of terrestrial plants. *Environ Microbiol*, 14(1), 140-146
30. Alperovitch, A.*, **Sharon, I.***, Rohwer, F., Aro, E.M., Milo, R., Nelson, N., Béjà, O. (2011). Reconstructing a puzzle: Existence of cyanophages containing both photosystem-I & photosystem-II gene-suites inferred from oceanic metagenomic datasets. *Environ Microbiol*, 13, 24-32
31. **Sharon, I.***, Bercovici, S.*, Pinter, R., Shlomi, T. (2010). Pathway-based functional analysis of metagenomes. *J Comput Biol*, 18(3), 495-505 (RECOMB 2010 issue)
32. Bodaker, I.*, **Sharon, I.***, Suzuki, M.T., Feingersch, R., Shmoish, M., Andreishcheva, E., Sogin, M.L., Rosenberg, M., Maguire, M.E., Belkin, S., Oren, O., Béjà, O. (2010). Comparative community genomics in the Dead Sea, an increasingly extreme environment. *ISME J*, 4(3), 399-407
33. **Sharon, I.***, Alperovitch, A.*, Rohwer, F., Haynes, M., Glaser, F., Atamna-Ismaeel, N., Pinter, R.Y., Partensky, F., Koonin, E.V., Wolf, Y.I., Nelson, N., Béjà, O. (2009). Photosystem I gene cassettes are present in marine virus genomes. *Nature*, 461, 258-262
34. Feingersch, R., Suzuki, M.T., Shmoish, M., **Sharon, I.**, Sabehi, G., Partensky, F., Béjà, O. (2009). Microbial community genomics in eastern Mediterranean Sea surface waters. *ISME J*, 4(1), 78-87
35. **Sharon, I.**, Pati, A., Markowitz, V.M., Pinter, R.Y. (2009). A statistical framework for the functional analysis of metagenomes. *Proceedings of 13th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, LNCS, 5541:496-511
36. **Sharon, I.**, Davis, J.V. and Yona, G. (2009). Book chapter: Prediction of protein-protein Interactions: a study on the co-evolution model. *Methods Mol Biol: Computational Systems Biology*, 61-88, Springer-Verlag
37. Loy, A., Duller, S., Baranyi, C., Mußmann, M., Ott, J., **Sharon, I.**, Béjà, O., Le Paslier, D., Dahl, C., Wagner, M.(2008). Reverse dissimilatory sulfite reductase as phylogenetic marker for a subgroup of sulfur-oxidizing prokaryotes. *Environ Microbiol*, 11(2), 289-299
38. Atamna-Ismaeel, N., Sabehi, G., **Sharon, I.**, Witzel, K-P., Labrenz, M., Jurgens, K., Barkay, T., Stomp, M., Huisman, J., Béjà, O. (2008). Widespread distribution of proteorhodopsins in freshwater and brackish ecosystems. *ISME J*, 2(6), 656-662
39. Kagan, J., **Sharon, I.**, Béjà, O., Kuhn, J. (2008). The tryptophan pathway genes of the Sargasso Sea metagenome: new operon structure. *Genome Biol*, 9(1), R20
40. **Sharon, I.***, Tzahor, S.*, Williamson, S.*, Shmoish, M., Man-Aharonovich, D., Rusch, D.B., Yooseph, S., Zeidner, G., Golden, S.S., Mackey, S.R., Adir, N., Weingart, U., Horn, D., Venter, J.C., Mandel-Gutfreund, Y., Béjà, O. (2007). Viral photosynthetic reaction center genes and transcripts in the marine environment. *ISME J*, 1(6), 492-501
41. **Sharon, I.**, Birkland, A., Chang, K., El-Yaniv, R., Yona, G. (2005). Correcting BLAST e-values for low-complexity segments. *J Comput Biol*, 12(7), 978-1001

* equal contribution

REVIEWS

42. **Sharon, I.**, Banfield, J.F. (2013). Genomes from metagenomics. *Science*, 342(6162), 1057-1058

ACADEMIC ACTIVITY

- Session chair, ISM 2017
- Program committee, ISMB/ECCB 2013
- Co-organizer of the international Tel-Hai Next Generation Sequencing Data Analysis workshop, 2017 and 2018
- Reviewer for *Nature Biotechnology*, *Genome Research*, *PLoS Genetics*, *ISME J*, *Applied and Environmental Microbiology*, *Proceedings of the Royal Society B*, *BMC Evolutionary Biology*, *Bioinformatics*, *PLOS ONE*, *BMC Bioinformatics*, *Nature Scientific Reports*, the Israel Science Foundation (ISF)
- Reviews for the 9th, 12th, and 14th RECOMB conferences, and the Genome Informatics Workshop (GIW) 2009

SELECTED AWARDS AND FELLOWSHIPS

2017	Excellent Lecturer, Computer Science Department, Tel-Hai College Awarded based on student surveys
2012	InnoCentive \$10k prize for the challenge “Microbial Strain Identification from a Mixture of Genetic Material” Single winner out of 139 solvers
2010-2012	The European Molecular Biology Organization (EMBO) Long Term Postdoctoral Fellowship Acceptance rate: 13%
2010	Mark of Distinction in Teaching, Faculty of Computer Science, Technion Awarded to top 10% of lecturers based on student surveys
2010	Technion Graduate School Award for Excellent Journal Publication Awarded annually to 3 publications at the Technion
2008, 2010	Excellence Fellowship, Faculty of Computer Science, Technion
2009	Jacobs Fellowship, Jacobs Graduate School, Technion Awarded annually, one of two recipients at the Faculty of Computer Science
2006	Excellent Teaching Assistant Award, Faculty of Computer Science, Technion Awarded to top 10% of teaching assistants based on student surveys

TEACHING EXPERIENCE

- | | |
|-------------------------------|---|
| Senior Lecturer (Tel Hai) | i. Introduction to Systems Programming (2 semester) |
| | ii. Big Data (2 semester) |
| | iii. Algorithms I (1 semester) |
| | iv. Introduction to programming in Python (1 semester) |
| Lecturer (Technion) | i. Introduction to Computers (CS234112, 1 semester) |
| | ii. Introduction to Computer Science (CS234114, 2 semesters) |
| | iii. Introduction to Systems Programming (CS234122, 1 semester) |
| Teaching Assistant (Technion) | i. Topics in Microarray Data Analysis, (CS236632, 1 semester) |
| | ii. Algorithms in Computational Biology (CS236522, 1 semester) |
| | iii. Introduction to Computer Science (CS234114, 2 semesters) |
| | iv. Object Oriented Programming (CS236703, 5 semesters) |

SELECTED INVITED AND CONFERENCE TALKS

- 2017 **The 116th International Titisee Conference**
“Computational challenges and opportunities in human microbiome research”. **Invited.**
- 2017 **Israeli Society for Bioinformatics General Meeting (IBS 2017)**
“Uncovering Earth microbiome, thousands of genomes at a time”. **Invited.**
- 2016 **Israeli Society for Microbiology General Meeting (ISM 2016)**
“Strain variation in microbial communities”. **Invited.**
- 2015 **Neve Ya’ar**
“Strain variation in microbial populations and its impact on community resilience”.
Invited.
- 2015 **Illumina**
“Accurate, multi-kb Illumina Truseq synthetic reads resolve complex microbial populations and detect rare microorganisms”. **Invited.**
- 2014 **Joint Genome Institute (JGI) User meeting**
“Multi-kb Illumina reads reveal significant strain variation and rare organisms in aquifer sediment microbial communities”. **Contributed.**
- 2014 **Joint Genome Institute (JGI) MGM Workshop**
“Metagenomic binning”. **Invited.**
- 2012 **UC Berkeley**
“Reconstructing complete genomes from metagenomic data and the way to community genomics”. **Invited.**
- 2012 **American Society for Microbiology General Meeting (ASM 2012)**
“Microbial species and strain variations during infant gut colonization”. **Invited.**
- 2011 **University of Haifa**
“Metagenomics based study of microbial genes in phages”. **Invited.**
- 2010 **Research in Computational Molecular Biology (RECOMB 2010)**
“Pathway-based functional analysis of metagenomes”. **Contributed.**
- 2009 **Research in Computational Molecular Biology (RECOMB 2009)**
“A statistical framework for the functional analysis of metagenomes”. **Contributed.**
- 2009 **Israeli Society for Microbiology General Meeting (ISM 2009)**
“Studying genes and gene organizations from metagenomic data”. **Invited.**