Asaf Peer, PhD

Computational Biologist

Current Position

Apr. 2018 and on	Associate computational scientist at The Jackson Laboratory. In this position I execute the computational aspects of several projects related to mouse genomics and the microbiome.

Higher Education

Oct. 2003-Sep. 2006	•BSc degree in computer science and computational biology from the School of Computer Science and Engineering at the Hebrew University.
Oct. 2006 – Sep. 2008	•MSc degree in computer science and computational biology from the School of Computer Science and Engineering at the Hebrew University. Supervisor: Prof. Hanah Margalit. Worked on predicting bacterial sRNA-mRNA interactions.
Oct. 2008 – Jan. 2014	•PhD degree at the Faculty of Medicine of the Hebrew University. Direct track to PhD. Supervisor: Prof. Hanah Margalit. During my doctoral studies I developed methods for studying evolution of bacterial sRNA-mRNA interactions, structural and functional properties of sRNAs and more.

Work Experiences

Aug. 2004 – Oct. 2006	•Research Assistant in the Bioinformatics lab of Prof. Hanah Margalit, The Hebrew University

2007 – 2008	•Article writing in the fields of Biology and Medicine for the online magazine www.thefutureofthings.com
2009 – 2014	•Teaching Assistant in the course "Bioinformatics – computerized analysis of biological sequences", The Hebrew University
2014-2015	•Research Associate (started as a postdoctoral fellow) at the Hebrew University with Prof. Hanah Margalit. Worked in close collaboration with the experimental lab on developing NGS based methods for detecting bacterial RNA-RNA interactions, RNA structure and sRNA targets *in-vivo*. Was in charge of the computational analysis of RNA-Sequencing in these projects. The project was sponsored by the European Research Council.
2015-2016	•Lecturer at "Campus Strauss", a branch of Hadassah College. Taught the course "Bioinformatics tools"
Dec. 2015-Mar. 2017	•Computational Genomics scientist and algorithms developer at Evogene Ltd. This position includes developing and maintaining computational pipelines for analyzing NGS and other experiments, executing the various pipelines and supporting the researchers with designing and interpreting the results of experiments. I was handling mainly bacterial and metagenomics data.
Apr. 2017-Mar. 2018	•Computational platform development leader at Evogene Ltd. In this position I characterized, designed and lead the development of computational tools to support the company's Ag-Biologicals efforts.

Skills

Programming Languages (linux environment)	•Python •Matlab •R/bioconductor •Perl

•JAVA

•c++

•SQL

NGS data analysis

•Custom scripts and algorithms for handling and processing NGS data (e.g. the RILseq package)

•Processing tools like Fastqc, cutadapt

•Experienced with mapping algorithms such as: Bowtie, Tophat, bwa, STAR, Rockhopper

•Differential expression with DESeq2, cufflinks

•RIP-seq analysis

•De-novo assembly tools for metagenomics data e.g. megahit, SPAdes, idba_ud and more

Teaching experience – Online resources

•UCSC genome browser and the ENCODE database

•Galaxy

•EMBOSS package

•NCBI resources

•NCBI BLAST

•Tuxedo suite for RNA-seq analysis

•MEME and MAST

Military and Civil Service

Jul. 2000 – Aug. 2003

•Military service in the Armored Corps, serving most of the time as a tank commander.

•Received an Appreciation Award while serving as a tank commander in the Gaza Strip.

2004 – 2014

•Reserve service.

2014 and on

•Member of Etzion-Yehuda Search and Rescue Team

Publications

see my Google scholar page as well

Jan. 2018	•Melamed S*, Faigenbaum-Romm R*, **Peer A***, Reiss N, Shechter O, Bar A, Altuvia Y, Argaman L, and Margalit H (2018) "RIL-seq: An experimental-computational methodology for mapping the small RNA interactome in bacteria" Nature Protocols 13(1):1-33
Sep. 2016	•Melamed S*, **Peer A***, Faigenbaum-Romm R*, Gatt YE, Reiss N, Bar A, Altuvia Y, Argaman L, and Margalit H (2016) "Global mapping of small RNA-target interactions in bacteria" Molecular Cell 63(5):884-897
Jan. 2015	•Nitzan M, Fechter P, **Peer A**, Altuvia Y, Bronesky D, Vandenesch F, Romby P, Biham O and Margalit H (2014) "A Defense-offense multi-layered regulatory switch in a pathogenic bacterium" NAR 43(3):1357-69
May. 2014	•**Peer A** and Margalit H (2014) "Evolutionary patterns of *Escherichia coli* small RNAs and their regulatory interactions" RNA 20(7):994-1003
Nov. 2011	•Babu M, Díaz-Mejía1 JJ, Phanse S, Vlasblom J, Gagarinova A, Graham C, Ding H, Hu P, Yousif F, Nazarians-Armavil A, Pogoutse O, Ali M, **Peer A**, Wodak SJ, Moreno-Hagelsieb G, Greenblatt JF, and Emili A (2011) "Genetic Interaction Maps in Escherichia coli Reveal Functional Crosstalk among Cell Envelope Biogenesis Pathways" PloS Genet 7(11):e1002377
Apr. 2011	•**Peer A** and Margalit H (2011) "Accessibility and Evolutionary Conservation Mark Bacterial Small RNA Target-binding Regions" J. Bacteriol. 193(7):1690-701
Nov. 2009	•Belotserkovsky, I, Baruch, M, **Peer A**, Dov E, Ravins M, Mishalian I, Persky M, Smith Y, and Hanski E (2009) "Functional analysis of the quorum-sensing streptococcal invasion locus *sil* "

PLoS Pathog 5(11): e1000651. doi:10.1371/journal.ppat.1000651

Conferences and Meetings

Jun. 15-19, 2015	•CSAMA 2015 (course): Statistics and Computing in Genome Data Science, Italy. **Lecture:** "Transcriptome-wide mapping of small RNA-target interactions in bacteria"
Jun. 8-10, 2015	•Broad-Israel Symposium, Jerusalem. Poster: "Transcriptome-wide mapping of small RNA-target interactions in bacteria"
May 26, 2015	•Israel Bioinformatics Symposium (IBS), Tel Aviv. Poster: "Transcriptome-wide mapping of small RNA-target interactions in bacteria". **Best poster award**
Jun. 25-27, 2014	•Broad-Israel Symposium, Cambridge, MA. Poster: "Evolutionary patterns of small RNAs and their targets"
Feb. 10-13, 2014	•ILANIT/FISEB 7th meeting, Eilat, Israel. **Lecture:** "Evolutionary patterns of small RNAs and their targets"
Jun. 4-8, 2013	•"Regulating with RNA in Bacteria", Würzburg, Germany. **Lecture:** "Evolutionary patterns of small RNAs and their targets"
Feb. 7-10, 2011	•ILANIT/FISEB 6th meeting, Eilat, Israel. Poster: "Accessibility and Evolutionary Conservation Mark Bacterial Small RNA Target-binding Regions"
Sep. 1-3, 2010	•The Regulatory Role of Small RNA, Weizmann institute, Israel. Poster: "Accessibility and Evolutionary Conservation Mark Bacterial Small RNA Target-binding Regions"
Jun. 20-22, 2010	•Institute for Medical Research Israel-Canada meeting, Eilat, Israel. Poster: "Physical Characterization of Bacterial Promoter Strength"
Sep. 15-16, 2008	•BACRNAs European consortium meeting, Strasbourg, France. **Lecture:** "Predicting sRNA-mRNA Interactions".
Jan. 16, 2008	•BACRNAs European consortium meeting, Ein-Gedi, Israel. **Lecture:** "Modeling the Recognition Pattern of RNase III"
Oct. 7-11, 2007	•Signal Transduction in Host Bacterial Interactions, Jerusalem, Israel. Poster: "Computational Prediction of *Staphylococcus aureus* RNAIII Targets Mediated by RNase III"