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B.S. (1990), M.S. (1995) Ph.D. (2002) In Computer Science, Tel Aviv University, Israel
Postdoctoral Fellow, Molecular Genetics, Weizmann Institute of Science, Israel (2003)
Medical and Population Genetics, Broad Institute, Cambridge, MA (2006)

The Pe'er lab develops and applies computational tools for genomics and health analytics. Work in the lab involved understanding hidden relatedness among individuals (1-5) and other topics in population genomics, such as gene-gene interactions (6), imputation (7), replicability (8), pooled sequencing (9) and eQTLs (10-12). Current projects in the lab construct and infer temporal models for biological data across domains, from human population genetics (13) to microbiome dynamics (14) to fMRI scans (15).

Selected publications [\[full list\]](#)

1. S Carmi, ..., T Lencz, I Pe'er (2014) Sequencing an Ashkenazi reference panel supports population-targeted personal genomics & illuminates Jewish & European origins, *Nat Commun.* 5: 4835.
2. A Gusev, ..., I Pe'er (2009) Whole population, genome-wide mapping of hidden relatedness, *Genome research* 19 (2), 318-326
3. PF Palamara, T Lencz, A Darvasi, I Pe'er (2012) Length distributions of identity by descent reveal fine-scale demographic history, *Am J Hum Gen.* 91(5):809-22
4. A Gusev, EE Kenny, ..., I Pe'er (2011) DASH: a method for identical-by-descent haplotype mapping uncovers association with recent variation, *The American Journal of Human Genetics* 88 (6), 706-71
5. Y Erlich, T Shor, I Pe'er, S Carmi (2018) Identity inference of genomic data using long-range familial searches *Science* 362 (6415), 690-694
6. S Prabhu, I Pe'er Ultrafast genome-wide scan for SNP-SNP interactions in common complex disease *Genome research* 22 (11), 2230-2240
7. C Palmer, I Pe'er, Bias Characterization in Probabilistic Genotype Data and Improved Signal Detection with Multiple Imputation *PLoS genetics* 12 (6), e1006091
8. C Palmer, I Pe'er, Statistical correction of the Winner's Curse explains replication variability in quantitative trait genome-wide association studies, *PLoS genetics* 13 (7), e1006916
9. S Prabhu, I Pe'er. Overlapping pools for high-throughput targeted resequencing, *Genome research* 19 (7), 1254-126
10. A Kreimer, O Litvin, K Hao, C Molony, D Pe'er, I Pe'er (2012) Inference of modules associated to eQTLs *Nucleic acids research* 40 (13), e98
11. A Kreimer, I Pe'er (2013) Variants in exons and in transcription factors affect gene expression in trans, *Genome biology* 14 (7), R71
12. A Kreimer, I Pe'er (2014) Co-regulated transcripts associated to cooperating eSNPs define bi-fan motifs in human gene networks, *PLoS genetics* 10 (9), e1004587
13. TA Joseph, I Pe'er (2018) Inference of population structure from ancient DNA, *International Conference on Research in Computational Molecular Biology*, 90-104
14. R Zhong, T Joseph, JB Xavier, I Pe'er (2018) Latent Space Temporal Model of Microbial Abundance to Predict Domination and Bacteremia, *arXiv preprint arXiv:1808.10795*
15. A Moretti, A Stirn, G Marks, I Pe'er (2019) Autoencoding Topographic Factors, *Journal of Computational Biology* 26(0) 1-15