

Curriculum Vitae – Gad Kimmel

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CONTACT INFORMATION

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EDUCATION

Tel Aviv University

2003 - 2006 **Ph.D. in Computer Science, with distinction.**

Subject of Dissertation: “Computational Problems in Modern Human Genetics”.

Advisor: Prof. Ron Shamir.

2002 - 2003 Completion of M.A. courses in Computer Science.

2001 - 2002 Completion of B.Sc. courses in Computer Science.

Technion - Israel Institute of Technology

1994 - 1998 **M.D. (Doctor of Medicine), Cum Laude.**

1990 - 1994 **B.Sc. in Medical Sciences, Cum Laude.**

RESEARCH EXPERIENCE

University of California, Berkeley

2006 - present **Postdoc in Computer Science** Division at University of California, Berkeley and the International Computer Science Institute.

Hosts: Prof. Michael Jordan and Prof. Richard Karp.

RESEARCH INTERESTS

- Computational biology (bioinformatics).
- Machine learning and statistical learning theory.
- Human genetics and genomic variation.

TEACHING EXPERIENCE

Guest Lecturer

Winter 2006 University of California, Berkeley, Computer Science Division.
Practical Machine Learning.

Teaching Instructor

2003 - 2005 (summer) Tel Aviv University, School of Computer Science.
Computational Models.

Teaching Assistant

2002 - 2006 Tel Aviv University, School of Computer Science.
Computational Models.

Winter 2002 Tel Aviv University, School of Computer Science.
Programming.

AWARDS AND SCHOLARSHIPS

- 2006 Rothschild fellowship for postdocs.
- 2005 Wolf Fund - award for outstanding Ph.D. students.
- 2004 Tel Aviv University, Faculty of Exact Sciences, School of Computer Science,
excellence award for distinction.
- 2001 Tel Aviv University, Faculty of Exact Sciences,
Dean's list of distinction.
- 1998 Technion, Israel Institute of Technology, Medical School,
MD thesis citation for excellence.
- 1993 Technion, Israel Institute of Technology, Medical School,
Dean's list of distinction.
- 1992 Technion, Israel Institute of Technology, Medical School,
Dean's list of distinction.
- 1991 Technion, Israel Institute of Technology, Medical School,
President's award for distinction.

PROGRAM COMMITTEE MEMBER

- ISMB / ECCB09.

REVIEWING ACTIVITIES

1. American Journal of Human Genetics.

2. Journal of the American Statistical Association (JASA).
3. Genome Research Journal.
4. Annual International Conference on Research in Computational Molecular Biology (RECOMB).
5. Annual International Conference on Intelligent Systems For Molecular Biology (ISMB).
6. Bioinformatics Journal.
7. Journal of Computational Biology (JCB).
8. BMC Bioinformatics Journal.
9. Pacific Symposium on Biocomputing Conference (PSB).
10. Computational Systems Bioinformatics Conference (CSB).
11. IEEE IEEE/ACM Transactions on Computational Biology and Bioinformatics Journal.

LIST OF PUBLICATIONS *

Selected

- Association mapping and significance estimation via the coalescent. Gad Kimmel, Richard M. Karp, Michael I. Jordan and Eran Halperin. **The American Journal of Human Genetics**, 2008.
- A randomization test for controlling population stratification in whole-genome association studies. Gad Kimmel, Michael I. Jordan, Eran Halperin, Ron Shamir and Richard M. Karp. **The American Journal of Human Genetics**, 2007.
- On the inference of ancestries in admixed populations. Sriram Sankararaman*, Gad Kimmel*, Eran Halperin and Michael I. Jordan (* Equal contribution). **Genome Research**, 2008.
- Estimating local ancestry in admixed populations. Sriram Sankararaman, Srinath Sridhar, Gad Kimmel and Eran Halperin. **The American Journal of Human Genetics**, 2008.
- A fast method for computing high significance disease association in large population-based studies. Gad Kimmel and Ron Shamir. **The American Journal of Human Genetics**, 2006. **Oral presentation, The Biology of Genomes** meeting, Cold Spring Harbor Laboratory, 2006.
- GERBIL: genotype resolution and block identification using likelihood. Gad Kimmel and Ron Shamir. Proceedings of the National Academy of Sciences of the United States of America (**PNAS**), 2005. **Oral presentation, Mutation Detection** conference, 2005.
- Tag SNP selection in genotype data for maximizing SNP prediction accuracy. Eran Halperin*, Gad Kimmel* and Ron Shamir (* Equal contribution). **Bioinformatics**, 2005. **Oral presentation**, The Annual Meeting of the International Society for Computational

* Available at <http://www.icsi.berkeley.edu/~kimmel/publications.html>

Biology (ISMB), 2005.

Journals

1. Association mapping and significance estimation via the coalescent.
Gad Kimmel, Richard M. Karp, Michael I. Jordan and Eran Halperin.
The American Journal of Human Genetics 83: 675-683, 2008.
2. Increasing association power via prediction-based tag-SNP Selection.
Ofir Davidovich*, Gad Kimmel*, Eran Halperin and Ron Shamir (* Equal contribution).
Submitted for publication.
3. On the inference of ancestries in admixed populations.
Sriram Sankararaman*, Gad Kimmel*, Eran Halperin and Michael I. Jordan (* Equal contribution).
Genome Research 18: 668-675, 2008.
4. Estimating local ancestry in admixed populations.
Sriram Sankararaman, Srinath Sridhar, Gad Kimmel and Eran Halperin.
The American Journal of Human Genetics 82: 290-303, 2008.
5. A randomization test for controlling population stratification in whole-genome association studies.
Gad Kimmel, Michael I. Jordan, Eran Halperin, Ron Shamir and Richard M. Karp.
The American Journal of Human Genetics 81: 895-905, 2007.
6. Lack of association of the 3'-UTR polymorphism in the NFKBIA gene with Crohn's disease in an Israeli cohort.
Esther Leshinsky-Silver, Amir Karban, Sarit Cohen, M. Fridlander, Ofir Davidowich, Gad Kimmel, Ron Shamir, and Arie Levine.
International Journal of Colorectal Disease, 2007.
7. GEVALT: An integrated software tool for genotype analysis.
Ofir Davidovich, Gad Kimmel and Ron Shamir.
BMC Bioinformatics 8: 36, 2007.
8. Risk factors for Perianal Crohn's disease: The role of genotype, phenotype and ethnicity.
Amir Karban, Maza Itay, Ofir Davidovich, Esther Leshinsky, Gad Kimmel, Herma Fidler, Ron Shamir, Matti Waterman, Rami Eliakim and Arie Levine.
American Journal of Gastroenterology 102: 1702-1708, 2007.
9. A fast method for computing high significance disease association in large population-based studies.
Gad Kimmel and Ron Shamir.
The American Journal of Human Genetics 79: 481-492, 2006.
10. ATM haplotypes and breast cancer risk in Jewish high risk women.
Marie Koren, Gad Kimmel, Edna Ben-Asher, Inbar Gal, Moshe Z. Papa, Jacques S. Beckmann, Doron Lancet, Ron Shamir and Eitan Friedman.

- British Journal of Cancer**, 94: 1537-1543, 2006.
11. A specific RAD51 haplotype increases breast cancer risk in Jewish non-Ashkenazi high-risk women.
Inbar Gal, Gad Kimmel, Ruth Gershoni-Baruch, Moshe Z. Papa, Efrat Dagan, Ron Shamir, and Eitan Friedman.
European Journal of Cancer, Volume 42(8): 1129-1134, 2006.
 12. A block-free hidden markov model for genotypes and its application to disease association.
Gad Kimmel and Ron Shamir.
Journal of Computational Biology (JCB) 12(10): 1243-1260, 2005.
 13. Tag SNP selection in genotype data for maximizing SNP prediction accuracy.
Eran Halperin*, Gad Kimmel* and Ron Shamir (* Equal contribution).
Bioinformatics 21(1): 195-203, 2005.
 14. GERBIL: genotype resolution and block identification using likelihood.
Gad Kimmel and Ron Shamir.
Proceedings of the National Academy of Sciences of the United States of America (PNAS) 102: 158-162, 2005.
 15. The incomplete perfect phylogeny haplotype problem.
Gad Kimmel and Ron Shamir.
Journal of Bioinformatics and Computational Biology (JBCB) 3(2): 359-384, 2005.
 16. Computational problems in noisy SNP and haplotype analysis: block scores, block identification and population stratification.
Gad Kimmel, Roded Sharan and Ron Shamir.
INFORMS Journal on Computing, 16(4): 360-370, 2004.

Conference Proceedings

1. On the inference of ancestries in admixed populations.
Sriram Sankararaman*, Gad Kimmel*, Eran Halperin and Michael I. Jordan (* Equal contribution).
The 12th Annual International Conference on Research in Computational Molecular Biology (**RECOMB**), 2008.
2. Maximum likelihood resolution of multi-block genotypes.
Gad Kimmel and Ron Shamir.
In proceedings of the Eighth Annual International Conference on Research in Computational Molecular Biology (**RECOMB**), pp. 2-9. The Association for Computing Machinery, 2004.
3. The incomplete perfect phylogeny haplotype problem.
Gad Kimmel and Ron Shamir.
In Proceedings of the Second **RECOMB** Satellite Workshop on Computational Methods

for SNPs and Haplotypes, pp. 59-70, 2004.

4. Identifying blocks and sub-populations in noisy SNP data.

Gad Kimmel, Roded Sharan and Ron Shamir.

In Proceedings of the Workshop on Algorithms in Bioinformatics (**WABI**), pp. 303-319, 2003.

PRESENTATIONS

1. A randomization test for controlling population stratification in whole-genome association studies. Invited oral presentation, Computer Science Department, Stanford University, California, USA, October 29, 2007.
2. A randomization test for controlling population stratification in whole-genome association studies. Invited oral presentation, Celera, Alameda, California, USA, August 30, 2007.
3. A randomization test for controlling population stratification in whole-genome association studies. Invited oral talk, Cornell University, Ithaca, New York, USA, May 14, 2007.
4. A randomization test for controlling population stratification in whole-genome association studies. Invited oral talk, Workshop in Biostatistics, Stanford University, Stanford, California, USA, May 3, 2007.
5. Evaluating disease significance in genome wide association studies. Invited oral talk, Montgomery Slatkin's group seminar, University of California Berkeley, Berkeley, California, USA, March 2, 2007.
6. Evaluating disease significance in genome wide association studies. Invited oral talk, University of California Davis, Davis, California, USA, February 8, 2007.
7. Evaluating disease significance in genome wide association studies. Invited oral talk, BioEECS group lunch talk, University of California Berkeley, Berkeley, California, USA, February 2, 2007.
8. Evaluating disease significance in genome wide association studies. Invited oral presentation, Third RECOMB Satellite Workshop on: Computational Methods for SNPs and Haplotypes, University of Southern California, Los Angeles, California, USA, January 27-28, 2007.
9. Evaluating disease significance in genome wide association studies. Invited oral presentation, University of Southern California, Los Angeles, California, USA, October 26, 2006.
10. Evaluating disease significance in genome wide association studies. Invited oral presentation, Perlegen Sciences, Inc., Mountain View, California, USA, October 20, 2006.
11. Rapid and accurate significance evaluation in disease association tests of SNPs and haplotypes. Oral presentation, The Biology of Genomes, Cold Spring Harbor Laboratory, New York, USA, May 10-14, 2006.
12. Tag SNP selection in genotype data for maximizing SNP prediction accuracy. Oral pre-

sentation, The Annual Meeting of the International Society for Computational Biology (ISMB), Detroit, Michigan, USA, June 25-29, 2005.

13. Introduction to the computational problems of SNPs and haplotypes. Invited speaker, International School of Advanced BioMedicine and BioInformatics, Pantelleria, Italy, June 18-25, 2005.
14. Improved algorithms and models for large-scale genotype phasing, block partition, and tag SNP selection: GERBIL, STAMPA and HINT. Invited speaker, International School of Advanced BioMedicine and BioInformatics, Pantelleria, Italy, June 18-25, 2005.
15. Improved algorithms for large-scale genotype phasing, block partition, and tag SNP selection. Oral presentation, Mutation Detection conference, Santorini, Greece, May 31 - June 4, 2005.