

# Abhishek Sarkar

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**CONTACT INFORMATION** 235 Albany St., Room 3114A (919) 259-1733 — cell  
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**EDUCATION** **Massachusetts Institute of Technology**  
Ph.D. Computer Science (in progress)

**University of North Carolina, Chapel Hill**  
B.S. Computer Science, May 2011  
GPA: 3.930

**PROFESSIONAL EXPERIENCE** **Computational Genetics Research Group**, University of North Carolina, Chapel Hill  
*Undergraduate Research Assistant* **May 2008 – July 2011**

**Haplotype inference:** Collaborated on the implementation of a dynamic programming algorithm to solve the haplotype assignment problem for a single chromosome. Created extensions to this implementation to increase the accuracy of the results by exploring the space of parameters and to increase the throughput of the analysis by automating the process for many chromosomes across many animals. Provided haplotype assignments and rendered results to collaborators. Served as liaison to collaborators who used these analysis tools.

**Ancestry inference:** Collaborated on adapting the Lander–Green algorithm (which models recombination using a Hidden Markov Model) to exploit specific pedigree structures to improve the running time of analysis. Collaborated on the initial prototype implementation and implemented a publicly available version (<http://compgen.unc.edu/ancestry>).

**Expression Analysis, RTP**  
*Technical Student Intern* **May 2010 – August 2010**

Implemented algorithms for *digenysis*, a proprietary methodology for case-control genome-wide association studies. Implemented shell scripts to integrate these programs into the company's HPC infrastructure. Assisted in building and installing new software on the compute nodes.

**HONORS** National Science Foundation Graduate Research Fellow  
Honorable Mention, Computing Research Association Outstanding Undergraduate Researcher Awards 2011  
Member of Phi Beta Kappa honors fraternity  
UNC Dean's List (Fall 2007 – Spring 2011): maintained GPA above 3.5  
National Merit Scholarship

**PUBLICATIONS** David L. Aylor, William Valdar, Wendy Foulds-Mathes, Ryan J. Buus, Ricardo A. Verdugo, Ralph S. Baric, Martin T. Ferris, Jeffrey A. Frelinger, Mark Heise, Matt B. Frieman, Lisa E. Gralinski, Timothy A. Bell, John P. Didion, Kunjie Hua, Derrick L. Nehrenberg, Christine L. Powell, Jill Steigerwalt, Yuying Xie, Samir N.P. Kelada, Francis S. Collins, Ivana V. Yang, David A. Schwartz, Lisa A. Branstetter, Elissa J. Chesler, Darla R. Miller, Jason Spence, Eric Yi Liu, Leonard McMillan, **Abhishek Sarkar**, Jeremy Wang, Wei Wang, Qi Zhang, Karl W. Broman, Ron Korstanje, Caroline Durrant, Richard Mott, Fuad A. Iraqi, Daniel Pomp, David Threadgill, Fernando Pardo-Manuel de Villena, and Gary A. Churchill. "Genetic Analysis of Complex Traits in the Emerging Collaborative Cross." *Genome Research*. Published in advance 3/15/2011.

Zhang, Q., Liu, Y., **Sarkar, A.**, Wang, W. "Split-Order Distance for Clustering and Classification Hierarchies." *Proceedings of the 21st International Conference on Scientific and Statistical Database Management*, New Orleans, LA, USA. Springer-Verlag, 2009. 517–534.

**SKILLS** **Programming languages:** Python (advanced), Java (advanced), C/C++ (advanced), R (proficient)  
**Tools:** GNU Emacs, git, Subversion  
**Operating Systems:** Windows, Linux