

# Shreepriya Das

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CONTACT INFORMATION	4709 Harmon Ave Apt # 503 Austin, TX 78751 USA	<i>Phone:</i> (512) 788-1877 <i>E-mail:</i> shreedas@utexas.edu <i>WWW:</i> <a href="http://www.cerc.utexas.edu/~shree/main.html">www.cerc.utexas.edu/~shree/main.html</a>
RESEARCH INTERESTS	<i>Computational Biology/Bioinformatics</i> <i>Machine Learning</i> <i>Optimization</i> <i>Statistical Signal Processing</i>	
EDUCATION	<b>The University of Texas at Austin</b> , Austin, Texas USA Ph.D. Candidate, Electrical and Computer Engineering (expected graduation date: July 2015) <ul style="list-style-type: none"><li>• Dissertation Topic: “Algorithms for Next Generation Sequencing Data”</li><li>• Advisor: Dr. Haris Vikalo</li></ul> M.S., Electrical and Computer Engineering, May 2012  <b>Indian Institute of Technology</b> , Kharagpur, INDIA B.Tech., Electronics and Electrical Communication Engineering, May, 2007	
HONORS AND AWARDS	<b>Microelectronics and Computer Development Fellowship</b> awarded by University of Texas at Austin 2007- 2009  <b>Bidhan Chandra Roy Memorial Gold Medal</b> awarded by IIT Kharagpur to the Best Outgoing Allrounder 2007  <b>Jagadis Bose National Science Talent Search Scholar</b> 2003 -2007 Ranked 115 in the All India IIT Joint Entrance Examination, 2003	
INTERNSHIP	<b>The University of Washington at Seattle</b> , Seattle, Washington USA Summer 2006 Advisor: Prof David Allstot Worked on Sigma-Delta Modulators	
ACADEMIC EXPERIENCE	<b>The University of Texas at Austin</b> , Austin, Texas USA <i>Graduate Research Assistant</i> <b>Fall, 2009 - present</b> Includes current Ph.D. research, Ph.D. and Masters level coursework and research projects.  <i>Teaching Assistant</i> <b>Fall, 2009 - Spring 2010</b> Duties at various times have included office hours and leading weekly lab exercises.  <i>Guest Lecturer</i> <b>Spring, 2014</b> Guest Lecturer for the course “Genomic Signal Processing”	
BOOK CHAPTERS	<ul style="list-style-type: none"><li>• S. Das, H. Vikalo, and A. Hassibi, Affinity-Based Biosensors: Stochastic Modeling and Figures of Merit, in CMOS Biomicrosystems: Where Electronics Meet Biology, Wiley, 2011.</li></ul>	
PUBLICATIONS	J5 S. Das and H. Vikalo, Single Individual haplotype assembly for next generation sequencing platforms - Sphere decoding solutions, Submitted (Transactions of Signal Processing).	

Preliminary version in [C5] S. Das and H. Vikalo, Optimal Haplotype Assembly with Statistical Pruning, IEEE International Workshop on Genomic Signal Processing and Statistics (GENSIPS), Atlanta,GA, December 2014.

- J4 S. Das and H. Vikalo, SDhaP: Low-rank SDP Solutions for Single Individual Haplotyping from High-Throughput Sequencing Data, Accepted (BMC Genomics).

Preliminary version in [C4] S. Das and H. Vikalo, Single Individual Haplotyping with Low Rank Semidefinite Programming, NIPS Workshop on Machine Learning and Computational Biology, Montreal, Canada, December 2014.

- J3 S. Das and H. Vikalo, Base calling for high-throughput short-read sequencing: Dynamic programming solutions, BMC Bioinformatics, vol 14:129, 2013. doi:10.1186/1471-2105-14-129

Preliminary version in [C3] S. Das and H. Vikalo, Base-calling for Illumina’s next-generation sequencing via Viterbi algorithm, 49th Annual Allerton Conference on Communication, Control, and Computing, Monticello, IL, September 2011, pp. 1733-1736 (invited).

- J2 S. Das and H. Vikalo, OnlineCall: Fast online parameter estimation and base calling for Illumina’s next generation sequencing, Bioinformatics, vol. 28, no. 13, pp. 1677-1683, 2012.

Preliminary version in [C2] S. Das and H. Vikalo, Model-based sequential base calling for Illumina sequencing, IEEE International Workshop on Genomic Signal Processing and Statistics (GENSIPS), Cold Spring Harbor, NY, November 2010.

- J1 S. Das, H. Vikalo, and A. Hassibi, On scaling laws of biosensors: a stochastic approach, Journal of Applied Physics, vol. 105, no. 10, May 2009, pp. 102021-7.

Preliminary version in [C1] S. Das, H. Vikalo, and A. Hassibi, Stochastic modeling of reaction kinetics in biosensors using the Fokker-Planck equation, in IEEE International Workshop on Genomic Signal Processing and Statistics (GENSIPS), Minneapolis, MN, 2009.

#### IN PREPARATION

- S. Das and H. Vikalo, Fast and accurate joint genotyping-haplotyping for diploid/polyploid species with known/unknown ploidy, In preparation.
- S. Das and H. Vikalo, TurboCall: Exchanging Soft Information to Leverage Error Rates for Illumina’s Next-Generation Sequencing, In preparation.
- S. Das and H. Vikalo, Fast MAXCUT and MAX-K-CUT for large sparse graphs, In preparation.

#### PROFESSIONAL ACTIVITIES

Reviewer: Bioinformatics, GlobalSIP

#### NATIONALITY

Indian

#### EMPLOYMENT STATUS

F1 status

## REFERENCES

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