Short Biosketch August 2019

Dan Gusfield, Distinguished Professor
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1 Education

Ph.D. 1980 University of California at Berkeley
- Engineering Science, thesis advisor: R.M. Karp
M.S. 1975 University of California at Los Angeles
- Computer Science
A.B. 1973 University of California at Berkeley
- Computer Science

2 Professional Experience

Distinguished Professor
Department of Computer Science
University of California, Davis. July 2016 - Present

Chair, Department of Computer Science
University of California, Davis, July 2000 - August 2004

Professor
Department of Computer Science
University of California, Davis. July 1992 - July 2016

Visiting Scientist
Simons Institute for Theoretical Computing
UC Berkeley
January 2014 - May 2014, January 2016 - May 2016

Associate Professor
Department of Computer Science
University of California, Davis. July 1986 - July 1992

On leave Fall 1994 at the DIMACS Center, Rutgers-Princeton,
Special Year on Mathematical Support for Molecular Biology.

Research Computer Scientist at the Human Genome Center,
Lawrence Berkeley Laboratory, University of California,
Berkeley, Summer 1988, 1989.

Assistant Professor, Department of Computer Science,
Yale University, July 1980 - June 1986

3   Fellow Elections

Elevated to Fellow of the IEEE 2015
Elevated to Fellow of the ISCB 2016
Elevated to Fellow of the ACM 2017

4   General and Research:

My background is in Combinatorial Optimization, and various applications
of Combinatorial Optimization. I have worked extensively on problems of
network flow, matroid optimization, statistical data security, stable mar-
riage and matching, string algorithms and sequence analysis, phylogenetic
tree inference, haplotype inference, inference of phylogenetic networks with
homoplasy and recombination, the multi-state perfect phylogeny problem,
using chordal graph theory and integer programming, and provably faster
algorithms for RNA folding, using the Four-Russians idea.

I received my Ph.D. in 1980 from UC Berkeley, working with Richard
Karp, and was an Assistant Professor at Yale University from 1980 to 1986.
My dissertation concerned problems of sensitivity analysis in graphs, network

flow and Matroid theory. My early publications mostly concern those topics, particularly network flow and its uses, for example in statistical data security. I moved to UC Davis in January 1987. In July 2016, I was promoted to the rank of Distinguished Professor.

My interest in the Stable Marriage Problem resulted in the publication of the book "The Stable Marriage Problem: Structure and Algorithms" (MIT press, 1988), co-authored with Rob Irving. Since then, I have mostly addressed problems in Computational Biology and Bioinformatics. I first addressed questions about building evolutionary trees, and then problems in molecular sequence analysis. I presently focus mostly on optimization problems related to population genetics and population-scale genomics. Three particular problems are haplotype inference, inferences about historical recombination, and the multi-state perfect phylogeny problem. Another area of research is the development of efficient algorithms for RNA folding, particularly developing methods based on the Four-Russians idea. Another general theme of my work is the development and use of integer linear programming to solve practical problem instances of problems in computational biology. I have written a book on this topic that was published by Cambridge University Press in August, 2019 – Integer Linear Programming in Computational and Systems Biology: An Entry Level Text and Course.

My main funding for computational biology and bioinformatics came initially from the Department of Energy Human Genome Project through the Lawrence Berkeley Labs Human Genome Center, then directly from DOE Human Genome Project, but since then, my work in computational biology has been funded by the NSF, in the IIS, ITR and CCF programs. In their spring semesters 2014 and 2016, I was an (invited, supported) visiting scientist at the Simons Institute for Theoretical Computing at UC Berkeley, and was previously a long-term (invited, supported) visitor at the DIMACS Center for Theoretical Computer Science at Rutgers/Princeton; and at the Isaac Newton Centre for Mathematics, Cambridge University. I have given over fifty invited (special), keynote, plenary, distinguished lectures, in addition to over one hundred competitive conference talks, and normal seminars at outside universities.

My book, "Algorithms on Strings, Trees and Sequences: Computer Science and Computational Biology" (Cambridge Press, 1997) has helped to define the intersection of computer science and computational biology. I have also authored the book "ReCombinatorics: The Algorithmics of Ancestral Recombination Graphs and Explicit Phylogenetic Networks", which

was published by MIT Press in July 2014. My latest book "Integer Linear Programming in Computational and Systems Biology: An entry-level text", was published by Cambridge University Press in August, 2019.

5 Major Professional Service and Recognition:

I wrote the scientific section of the proposal to create the IEEE/ACM Transaction on Computational Biology and Bioinformatics (www.computer.org/tcbb/), and served as the journal's founding Editor-in-Chief for five years. I was later chair the Steering Committee for the journal. I serve on the editorial board of the Journal of Computational Biology, and served on the editorial board of the SIAM J. on Computing. I have served on many NSF and DOE research-proposal panels on computer science, bioinformatics and computational biology, and on numerous conference program committees. I co-chaired the program committee for the 1994 conference on Combinatorial Pattern Matching; I co-organized the 1995 Dagstuhl Conference on Bioinformatics at the Dagstuhl Center in Germany; I co-chaired the program committee of the 2002 Workshop on Algorithms for Bioinformatics (WABI) held in Rome; I was the Program Chair of the 2004 RECOMB (Research on Computational Molecular Biology) conference in San Diego; and was the Proceedings Chair of the ISMB (Intelligent Systems in Molecular Biology) 2009 Conference in Stockholm. In fall 2014 I served on the Committee of Visitors for the four-year review of the CISE directorate of the NSF.

In 2015 I was elevated to the rank of Fellow of the IEEE (Institute for Electrical and Electronics Engineers) with the citation: For contributions to combinatorial optimization and computational biology. In 2015 I won the College of Engineering Deans award for the Outstanding Senior Faculty Member. In 2016 I was made Fellow of ISCB (International Society of Computational Biology) with the citation: For his notable contributions to computational biology, particularly his algorithmic work on building evolutionary trees, molecular sequence analysis, optimization problems in population genetics, RNA folding, and integer programming in biology. In 2017 I was elevated to the rank of Fellow of the ACM.

6 Major UC Davis Service:

At UC Davis I was chair of the Computer Science Department for four years. I wrote the bioinformatics section (one of three) of the Genomics/Bioinformatics initiative proposal that resulted in the creation of the UCD Genomics Center (which hired 17 new faculty), and I served on the steering committee of the Genome Center, and committees for center faculty hiring in bioinformatics. I was co-chair of the UCD campus initiative on "Computational Characterization and Exploitation of Biological Networks", which hired seven new faculty in seven different departments. I was the College of Engineering faculty chair for one year, and served on the College of Engineering Faculty Personnel Committee. I also served for more than three years on Committee on Academic Personnel (CAP) for the Davis campus, which reviews and makes recommendations on all tenure and promotion actions, and all faculty hires other than a lowest-step assistant professor. In a campus the size and diversity of UC Davis, that was a huge service contribution.

7 Major Educational Efforts:

I developed and taught an undergraduate course on the Theory and Practice of Bioinformatics taught mostly to biology students, and a graduate course on Sequence Analysis and Computational Biology, taught mostly to computer science and mathematics students. I have videos of about 30 hours of my lectures on topics in bioinformatics, posted on my website. These have been edited for distribution on ItunesUniversity, and should appear there shortly.

In the area of computer science theory, I teach both the undergraduate and graduate courses on Algorithms, and have recorded and edited more than 70 hours of videos of my lectures on undergraduate and graduate courses on Design and Analysis of Algorithms, and another 24 hours of lectures on Theory of Computation. I recently made and posted two video lectures, and a write-up, on Godel's (first) incompleteness theorem. The lectures present a streamlined, yet rigorous, proof of the theorem requiring minimal background (you don't have to speak German or ponder the meaning of "truth" to understand the proof). I gave those lectures in my first classes in the undergraduate course on Theory of Computation in fall 2014. More recently, I made and posted four hours of lectures on the Fast Fourier Transform, the most important algorithm that computer science students don't regularly

learn. I am now editing videos for a course on Combinatorial Optimization, and another course on advanced Graph Theory, which will be posted on ItuneU. Most of the videos are also available through my website, and some are posted on Youtube. These have been viewed over a half-million times.