PAVEL A. PEVZNER

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Education

Ph.D.   Moscow Institute of Physics and Technology   1988   Mathematics&Physics

Professional Experience

2002-present	Adjunct Professor of Mathematics
	University of California San Diego, CA
2000-present	Ronald R. Taylor Chair Professor of Computer Science
	University of California San Diego, CA
1995- 2000	Professor, Departments of Mathematics, Computer Science, and Molecular Biology
	University of Southern California, CA
1993-1995	Member, Institute for Molecular Evolutionary Genetics and Biotechnology Institute,
	The Pennsylvania State University, PA
1992-1995	Associate Professor, Department of Computer Science,
	The Pennsylvania State University, PA
1990-1992	Postdoctoral Research Associate (with M.Waterman) and Lecturer
	Department of Mathematics, University of Southern California,CA
1985-1990	Junior Scientist, Scientist, Senior Scientist,
	Laboratory of Mathematical Methods,
	National Center for Biotechnology NIIGENETIKA, Moscow, Russia
	(formerly Institute of Genetics of Microorganisms VNIIGENETIKA)
1986-1988	Ph.D. Trainee, Institute of Physics and Technology, Moscow, Russia

Professional Activities

Editorial Boards

- Executive Editor, *Journal of Computational Biology*

- Editorial Board, *Bioinformatics*

- Editorial Board, *Discrete Applied Mathematics*

- Editorial Board, *Journal of Computer and System Sciences*

- Editorial Board, *Journal of Bioinformatics and Computational Biology*

- Editorial Board, *Gene-COMBIS*, 1994-1997

- Co-editor (with S. Istrail amd M. Waterman). MIT Press *Computational Molecular Biology* book series.

Guest Editor

- Guest Editor of the special volume "Computer Genetics" of *Bio Systems*, **30**, issues 1-3, 1993

- Guest Editor of the special volume "Combinatorial Methods in DNA Mapping and Sequencing", *Journal of Computational Biology*, **2**, issue 2, 1995

- Guest Editor (with S.Istrail and R.Shamir) of the special series "Computational Molecular Biology", *Discrete Applied Mathematics.* First volume: **71**, 1996, second volume: **88**,1998, third volume **104**, 2000, fourth volume (in press).

- Guest Editor of the special RECOMB issues, *J. Comp. Biology.* First issue: **4**, 1997, second issue: **5**, 1998, third issue: **6**, 1999, fourth issue: **7**, 2000

- Guest Editor (with Ming Li and Ron Shamir) of the special issue *Journal of Computer and System Sciences*, 2002 (in press)

Professional Societies.

- Co-founder and Chair of Steering Committee, Annual International Computational Molecular Biology Conference (RECOMB), 1996-present

- Board of Directors, International Society for Computational Biology, 1998-2001.

Conference Organization

- Co-organizer, Mini-symposium *Combinatorial methods for genome rearrangements*, Los-Angeles, California, March,18, 1994

- Member of directorate and session organizer. *First World Congress on Computational Medicine and Biotechnology*, Austin, Texas, April,24-29, 1994

- Member of international organizing committee and session chair, *Third International conference on Bioinformatics and Supercomputing*, Tallahassee, Florida, June 1-4, 1994

- Co-chair, Program committee, DIMACS Computational Molecular Biology Year. Workshop *DNA mapping and sequencing*, New Brunswick, New Jersey, October 3-6, 1994

- Member, Program committee, DIMACS Computational Molecular Biology Year. Workshop *DNA sequence alignment*, Princeton, New Jersey, November 8-10, 1994

- Member, Program Committee, 6th Annual Symposium *Combinatorial Pattern Matching*, Helsinki, Finland, May, 1995

- Member, Advisory Committee, *4th DIMACS International Algorithm Implementation Challenge*, New Brunswick, New Jersey, September, 11-13, 1994

- Member, Program Committee, DIMACS Computational Molecular Biology Year. Workshop *Gene recognition*, Philadelphia, Pennsylvania, October, 1995

- Session Chair, Mathematics and Molecular Biology IV, Santa Fe, New Mexico, November, 1995

- Member, Program Committee, 2nd Sandia Workshop on Computational Molecular Biology, Albuquerque, New Mexico, March, 1996

- Member, Program Committee, Conference of Computational Molecular Biology to honor the 50th anniversary of ENIAC, Princeton, New Jersey, May, 1996

- Member, Program Committee, 4th Israeli Symposium on Theory of Computing and Systems, Jerusalem, Israel, June, 1996

- Member, Program Committee, 7th Annual Symposium *Combinatorial Pattern Matching*, Laguna Beach, California, June,1996

- Member, Program Committee, 3rd South American Workshop on String Processing, Recife, Brazil, August, 1996

- Member, Program Committee, 1st Annual International Computational Molecular Biology Conference (RECOMB 97), Santa Fe, NM, January, 1997

- American Mathematical Society meeting, Computational Biology Section, Corvalis, Oregon, April, 1997

- Member, Program Committee, Genome Informatics 1997, Tokyo, Japan, December 1997

- Chair, Program Committee, 2nd Annual International Computational Molecular Biology Conference (RECOMB 98), New York, New York, March, 1998

- Member, Program Committee, 3rd Annual International Computational Molecular Biology Conference (RECOMB 99), Lyon, France, April, 1999

- Member, Program Committee, Eleventh Annual ACM-SIAM Symposium on Discrete Algorithms (SODA 2000), San Francisco, California, January, 2000

- Member, Program Committee, 4th Annual International Computational Molecular Biology Conference (RECOMB 2000), Tokyo, Japan, April, 2000

- Member, Program Committee, The Thirty-Second Annual ACM Symposium on Theory of Computing (STOC 2000), Portland, Oregon, May 21-23, 2000.

- Member, Program Committee, 5th Annual International Computational Molecular Biology Conference (RECOMB 2001), Montreal, Canada, April, 2001

- Co-organizer (with E. Myers and M.S. Waterman), DNA Fragment Assembly, Los Angeles, California, May, 2001

- Member, Program Committee, 6th Annual International Computational Molecular Biology Conference (RECOMB 2002), Washington, DC, April, 2002

- Member, Program Committee, DNA Sequencing and Characterization, Palo Alto, California, May, 2002

- Co-organizer (with S. Tavare, S. Istrail, and B. Penner), Maps, Sequences, and Genomes. Special Conference devoted to the 60th birthday of Michael Waterman, Los Angeles. California, May, 2002

- Member, Program Committee, 13th Annual Symposium on Combinatorial Pattern Matching, (CPM 2002), Fukuoka, Japan, July 2002

- Member, Program Committee, 1st European Conference on Computational Biology, (ECCB 2002), Saarbruken, Germany, October 2002

- Member, Program Committee, 7th Annual International Computational Molecular Biology Conference (RECOMB 2003), Berlin, Germany April, 2003

- Member, Program Committee, Intelligent Systems in Molecular Biology (ISMB 2003), Brisbane, Australia, July, 2003

- Member, Organizing Committee, Bertinoro Computational Biology Meeting, Bertinoro, Italy, July 2003

- Member, Program Committee, The Second Asia Pacific Bioinformatics Conference, Dunedin, New Zealand, January, 2004

Review Panels

- Member, Review board of the Soviet Human Genome Program (Mathematics and Computer Science), 1989-1990
- Member, National Institute of Health Scientific Review Group, Houston, Texas, October 9-11, 1991
- Member, DOE Grant Review Panel, Washinghton, DC, October 6-9, 1992
- Member, National Institute of Health Scientific Review Group, Washinghton, DC, January 20-22, 1993
- Member, NSF HPCC Grant Review Panel, Washinghton, DC, April 26, 1993
- Member, Genome Study Section, National Institutes of Health, Bethesda, Maryland, February 24-26, 1994
- Member, DOE Informatics Panel, Washinghton, D.C., September, 12-14, 1994
- Member, NSF Theory of Computing Working Group, Las Vegas, Nevada, May 1-2, 1995
- Member, The Swedish Foundation for Strategic Research Advisory Committee, Stockholm, Sweden, September 24-26, 1998
- Member, DIMACS NSF Computational Molecular Biology Activities. Evaluation Committee. October, 1998
- Member, NSF Advisory Board on Computational Biology Activities, Washington, DC, May 1999
- Member, External Review Group, Computer Science Department at Duke University, March, 2003

Honors and Awards

- NSF Young Investigator Award, 1994

Consulting Service

- Hitachi, San Francisko, CA, 1991-1992
- Affymetrix, Santa Clara, CA, 1993-1998
- Millennium Pharmaceuticals, Boston, MA, 1996 - 2000.
- GeneData AG, Basel, Switzerland, 1997-2000 (Scientific Advisory Board)
- Anchorgen, Santa Monica, CA (co-founder), 1998-present.
- SurroMed, Palo Alto, 2000 - 2001
- X-Mine, Palo Alto, 2000 - present (Scientific Advisory Board)

Invited presentations at academic institutions

Convey's equation and paradoxes involving overlapping words
  Moscow State University, Moscow, USSR, March 1989
L-tuple sequence reconstruction
  Institute for Molecular Genetics, Belgrad, Yugoslavia,November 1989
Algorithms for DNA Sequencing by Hybridization
  European Molecular Biology Laboratory (EMBL), Heidelberg, Germany, December 1989.
L-tuple sequence reconstruction
  University of Southern California/Department of Mathematics,
  Los Angeles, California, June 1990
Multiple sequence alignment with guaranteed error bounds.
  University California, Davis/Computer Science Department
  Davis, California, December,1991
SBH and generalized sequencing chips.
  Pennsylvania State University, University Park, Pennsylvania, December,1991
Overlapping words paradox.
  San Diego State University/Department of Mathematics
  San Diego, California, April, 1992
Optimal sequencing chips.
  University California Berkeley/Computer Science Department
  Berkeley, California, May, 1992
Conway equation and DNA statistics
  Stanford University/Department of Mathematics
  Stanford, California, May, 1992
Recent advances in Sequencing By Hybridization.
  National Institutes of Health, Bethesda, Maryland, July, 1992
Towards DNA sequencing chips.
  Pennsylvania State University/Biology Department,
  University Park, Pennsylvania, April, 1993
Towards DNA sequencing chips.
  University of Washinghton/Department of Molecular Biotechnology
  Seattle, Washinghton, April,1993
Genome rearrangements and sorting by reversals.
  University of Southern California/Department of Mathematics
  Los Angeles, California, August, 1993
DNA statistics and the best bet for simpletons
  The Pennsylvania State University/Department of Statistics
  University Park, Pennsylvania, September, 1993
Genome Rearrangements, SBH and double digest problem
  Johns Hopkins University/Computer Science Department
  Baltimore, Maryland, October, 1993
Genome Rearrangements, SBH and double digest problem
  Carnegie Mellon University/Computer Science Department
  Pittsburgh, Pennsylvania, October, 1993
Recent advances in DNA Sequencing by Hybridization
  Baylor College of Medicine, Houston, Texas, November, 1993
Genome Rearrangements
  Stanford University/Department of Mathematics,
  Stanford, California, November, 1993
Genome Rearrangements, SBH and double digest problem
  Rutgers University/DIMACS
  New Brunswick, New Jersey, December, 1993
DNA statistics and the best bet for simpletons
  Mount Sinai Medical School, New York, New York, December, 1993
Genome Rearrangements, SBH and double digest problem

University of Pennsylvania/Computer Science Department

Philadelphia, Pennsylvania, December, 1993

Genome Rearrangements, SBH and double digest problem

Polytechnic University/Computer Science Department

Brooklyn, New York, December, 1993

Towards DNA Sequencing Chips

Massachusetts Institute of Technology/Whitehead Institute for Biomedical Research

Boston, Massachusetts, February, 1994

Genome Rearrangements

Massachusetts Institute of Technology/Computer Science Department

Boston, Massachusetts, February, 1994

Towards DNA Sequencing Chips

Boston University/Center for Advanced Biotechnology

Boston, Massachusetts, February, 1994

Genome Rearrangements

University of Maryland

College Park, Maryland, April 1994

Towards DNA Sequencing Chips

The Pennsylvania State University

University Park, Pennsylvania, June 1994

Transforming men into mice

University of Southern California

Los Angeles, California, June 1994

Seminar series: 1. Genome rearrangements, 2. DNA chips 3. Multiple alignment

German National Institute for Computer Science (GMD),

St. Augustin, Germany, August, 1994

Seminar series: 1. Towards DNA Sequencing Chips 2. Genomic sequence comparison

Weizmann Institute, Rehovot, Israel, January, 1995

Genome rearrangements

Tel Aviv University, Tel Aviv, Israel, January, 1995

Seminar series: 1. Towards DNA Sequencing Chips 2. Genomic sequence comparison

Washington University, St. Louis, May, 1995

Transforming Mice into Men

Steklov Mathematical Institute, Moscow, Russia, June, 1995

Towards DNA Sequencing Chips

Moscow State University, Moscow, Russia, July, 1995

Genome Rearrangements

INRIA, Paris, France, July, 1995

Genome Rearrangements

Universite de Paris-Sud, Centre d'Orsay, Orsay Cedex, France July, 1995

Towards DNA Sequencing Chips

Ohio State University, Columbus, Ohio, September, 1995

Transforming Mice into Men

Columbia University, New York, New York, September, 1995

A Spliced Alignment Problem: A New Approach to Gene Recognition

Princeton University, Princeton, New Jersey, October, 1995

Transforming Mice into Men

National Institutes of Health, Bethesda, Maryland, December 1995

A New Approach to Gene Recognition

Department of Biology, University of Southern California,

Los Angeles, California, February, 1996

Genome Rearrangements

Department of Computer Science, University of Washington,

Seattle, Washington, March, 1996

Gene Recognition via Spliced alignment
> Department of Molecular Biotechnology, University of Washington,
> Seattle, Washington, March, 1996

Transforming Mice into Men
> Tel Aviv University, Tel Aviv, Israel, May, 1996

New Approaches to Gene Recognition
> Pennsylvania State University, State College, PA, November, 1996

Transforming Mice into Men
> National Institute for Genetics, Mishima, Japan, December 1996

New Approaches to Gene Recognition
> RWCP (Real World Computing Partnership), Tokyo, Japan, December 1996

Genome Rearrangements
> Institute for Molecular Biology, Moscow, Russia, June,1997

Finding genes (children lecture)
> Canoga Park High School, Canoga Park, California, March, 1998

Computational proteomics
> Institute of Molecular Biology, Moscow, Russia, September 1998

Finding genes and breaking secret codes (children lecture)
> Nitanny Valley School, State College, Pennsylvania, December, 1998

Transforming Men into Mice
> SUNY at Albany, Albany, New York, December 1999 (Distinguished Lecture Series)

Transforming Men into Mice
> University of California San Diego, San Diego, California, February 2000

Transforming Men into Mice
> University of California at Los Angeles, Los Angeles, California, April, 2000

A New Approach to Sequence Alignment
> Institute for Molecular Biology, Moscow, Russia, October, 2000

Pattern Discovery in DNA
> University of Maryland, College Park, Maryland, November, 2000 (Distinguished Lecture Series)

Assembling Puzzles by Breaking them into Smaller Pieces
> Department of Genetics, Washington University, St. Louis, Missouri, May, 2001

Assembling Puzzles by Breaking them into Smaller Pieces
> San Diego Supercomputing Center, University of California at San Diego, La Jolla, California, May,

Assembling Puzzles by Breaking them into Smaller Pieces
> Human Genome Sequencing Center, Baylor College of Medicine, Houston, Texas, October, 2001

Assembling Puzzles by Breaking them into Smaller Pieces
> Genome Center, Columbia University, New York, New York, October, 2001

Reconstructing Gene Orders in the Ancestral Species
> National Cancer Institute, Frederick, Maryland, March, 2002

Finding Subtle Motifs in DNA sequences
> University of California at Irvine, Irvine, California, September, 2002 (distinguished lecture series)

Finding Subtle Motifs in DNA sequences
> University of California at Riverside, Riverside, California, March, 2003

Invited presentations at companies

Multiple filtration in fast database search
> Wagner, Inc., Sunnyville, California, April, 1992

Recent advances in DNA sequencing by Hybridization.
> Affymetrix, Inc., Santa Clara, California, August, 1993

A Spliced Alignment Problem: A New Approach to Gene Recognition
> Sequana, Inc., La Jolla, California, November, 1995

Gene Recognition via Spliced alignment
　　　　Amgen, Inc., Thousand Oaks, California, April, 1996
Gene Recognition via Spliced alignment
　　　　Millenium Pharmaceutical, Inc., Boston, Massachussets, May, 1996
New Approaches to Gene Recognition
　　　　Novartis, Basel, Switzerland, May 1997
Gene hunting without genomic sequencing: the twenty questions game with genes
　　　　SmithKline Beecham, King of Prussia, Pennsylvania, August, 1997
Gene hunting without genomic sequencing: the twenty questions game with genes
　　　　Millenium Pharmaceuticals, Boston, Massachussets, October, 1997
Transforming Mice into Men
　　　　IBM, Yorktown Heights, NY, December 1997
Gene hunting without genomic sequencing: the twenty questions game with genes
　　　　Human Genome Sciences, Rockville, Maryland, March 1998
Gene prediction: merging computational and experimental approaches
　　　　Ceres, Inc., Malibu, California, September 1998
Finding post-translational modifications in proteins
　　　　Sequenom, La Jolla, California, January, 2000
Proteomics in the postgenomic era: finding postranslational modifications in proteins
　　　　Celera Genomics, Rockville, Maryland, March, 2000
A New Approach to Sequence Alignment
　　　　Paracel, Pasadena, California, July, 2000
Assembling Puzzles by Breaking them into Smaller Pieces
　　　　Integrative Genomics, Chicago, Illinois, October, 2000
Finding post-translational modifications in proteins
　　　　SurroMed, Palo Alto, California, June, 2001
Finding post-translational modifications in proteins
　　　　Syngenta, La Jolla, California, October, 2001
Assembling Puzzles by Breaking them into Smaller Pieces
　　　　Omnigon, Carsbad, California, November, 2001
Human and mouse genomic Sequence reveal evidence against random breakage model of chromosome evolution
　　　　Celera Genomics, Rockville, MD, November, 2003
Human and mouse genomic Sequence reveal evidence against random breakage model of chromosome evolution
　　　　The Center for Genomic Research, Rockville, MD, November, 2003

Invited presentations at professional meetings

Combinatorial methods for SBH
　　　　Sequencing by Hybridization, Washinghton,DC, May 1991
Nucleotide sequences versus Markov chains.
　　　　Open Problems in Computational Molecular Biology 1991,
　　　　Telluride, Colorado, June 1991
Multiple alignment and communication cost
　　　　3rd Annual Symposium 'Combinatorial Pattern Matching 1992,
　　　　Tucson, Arizona, April,1992
Generalized sequence alignment.
　　　　3rd Annual Symposium 'Combinatorial Pattern Matching 1992,
　　　　Tucson, Arizona, April,1992
Sequencing by hybridization
　　　　Computational biology - cutting edge'
　　　　Irvine, California, May, 1992
Overlapping word paradox and DNA statistics.

Supercomputing and Complex Genome Analysis 1992,
St. Petersburg Florida, June, 1992

Multiple sequence alignment with guaranteed error bounds.
Algorithms for DNA Sequence Comparison,
Albuquerque, New Mexico, November 1992

Nucleotide sequences versus Markov models.
Mathematics and Molecular Biology III. Santa Fe, New Mexico, November 1992

A fast filtration algorithm for the substring matching problem.
4th Annual Symposium "Combinatorial Pattern Matching 93",
Padova, Italy, June,1993

Multiple sequence comparison and n-dimensional image recognition.
4th Annual Symposium "Combinatorial Pattern Matching 93",
Padova, Italy, June,1993

Towards DNA sequencing chips.
Open Problems in Computational Molecular Biology 1993
Telluride, Colorado, July, 1993

DNA inhomogeneity and overlapping words paradox
DNA sequence analysis, Stanford, California, August, 1993

How to combine SBH with additional biochemical experiments
Second International SBH Workshop, Houston, Texas, October, 1993

Sorting by reversals
Combinatorial Methods for Genome Rearrangements,
Los Angeles, California, March 1994

Towards DNA sequencing chips
1st World Congress on Computational Medicine, Public Health and Biotechnology,
Austin, Texas, April 1994

Towards computational theory of genome rearrangements
Bioinformatics and Complex Genome Analysis 1994,
Tallahassee, Florida, June, 1994

Genome rearrangements
Computational Molecular Biology, Albuquerque, New Mexico, June, 1994

Rearrangement of maps, sequences and genomes
IMA Summer Program in Molecular Biology, University of Minnesota,
Minneapolis, Minnesota, July, 1994

Towards DNA sequencing chips
19th International symposium on Mathematical Foundations in Computer Science
Kosice, Slovakia, August, 1994

Rearrangement of maps, sequences and genomes
Combinatorial Methods in DNA Mapping and Sequencing, DIMACS, Rutgers University
New Brunswick, New Jersey, October, 1994

Towards DNA sequencing chips
Combinatorial Structures in Molecular Biology, DIMACS, Rutgers University
New Brunswick, New Jersey, November, 1994

Genomic sequence comparison
DNA Sequence Alignment,
Princeton, New Jersey, November, 1994

Open Problems in Computational Molecular Biology
3rd Israel Symposium on Theory of Computing and Systems
Tel Aviv, January, 1995 (one of five invited speakers)

Transforming Mice into Men
Evolutionary Molecular Biology, Canadian Research Council
Montreal, Canada, August, 1995

Towards DNA chips
Microfabrication Technology, Cambridge Healthtech Institute

San Francisko, California, September, 1995
Genome Rearrangements
      4th DIMACS Implementation Challenge, DIMACS, Rutgers University
      New Brunswick, New Jersey, September, 1995
A Spliced Alignment Problem: A New Approach to Gene Recognition
      DIMACS Gene Recognition Workshop
      Philadelphia, Pennsylvania, October, 1995
Genome Rearrangements
      Mathematics and Molecular Biology IV
      Santa Fe, New Mexico, November, 1995
Gene Recognition: Combinatorics versus Statistics
      2nd Sandia Workshop on Computational Molecular Biology
      Albuquerque, New Mexico, March, 1996
Genome Rearrangements
      Conference on Computational Molecular Biology to honor 50th anniversary of ENIAC
      Princeton, New Jersey, May, 1996
Gene Recognition
      Israeli Computational Molecular Biology Conference
      Nasholim, Israel, June, 1996
Transforming Mice into Men
      Workshop on String Processing
      Recife, Brazil, August, 1996 (one of four invited speakers)
Transforming Mice into Men
      Genome Informatics 1996, Tokyo, Japan, December 1996 (one of four invited speakers)
Las Vegas Algorithms for Gene Recognition
      1st International Conference on Computational Molecular Biology,
      Santa Fe, New Mexico, January, 1997
Transforming Mice into Men
      Invited Address at the American Mathematical Society meeting,
      Corvalis, Oregon, April, 1997
Transforming Mice into Men
      Computational Biology Workshop, Zurich, Switzerland, May, 1997
Gene hunting without genomic sequencing: the twenty questions game with genes
      German Conference on Bioinformatics,
      Kloster Irsee, Germany, September, 1997 (one of five invited speakers)
Gene hunting without genomic sequencing: the twenty questions game with genes
      Gene prediction in silico, Atlanta, GA November, 1997
Gene hunting without genomic sequencing: the twenty questions game with genes
      Functional Gene Analysis, Cambridge Healthtech Institute,
      San Francisko, California, February, 1998
Gene hunting without genomic sequencing: the twenty questions game with genes
      Understanding the Genome: technological and mathematical aspects,
      Berkeley, California, May 1998
Computational challenges in gene hunting
      Computational Biology School, Udine, Italy, June 1998
De novo protein sequencing by mass-spectrometry
      The 46th ASMS Conference on Mass-Spectrometry, Orlando, Florida, June 1998
Transforming Mice into Men
      DIMACS 10th Anniversary Celebration, Piscataway, New Jersey, October, 1998
      (one of six principal presentations)
De novo protein sequencing by mass-spectrometry
      Computational Genomics, The Institute for Genomic Research,
      Rockville, Maryland, November, 1998
Genome rearrangements

Lipari Computational Biology School, Lipari, Italy. June, 1999

De novo protein sequencing
Symposium on String Processing and Information Retrieval (SPIRE 99),
Cancun, Mexico, September 99 (one of four invited lectures)

Transforming Men into Mice
Canadian Mathematical Society Winter Meeting, Montreal, Canada, December 99
(one of six plenary lectures)

Finding Post-Translational Protein Modifications
Bioinformatics 2000, Elsinor, Denmark, May, 2000

Finding Post-Translational Protein Modifications
Cambridge Healthtech Institute Conference on Bioinformatics, San Francisko, California, June, 2000

Finding Post-Translational Protein Modifications
Beyond the Genome, Berkeley, California, June, 2000

Edgar Allan Poe and Computational Molecular Biology
Genome Research Perspectives for Helmholtz Association, Munich, Germany, November, 2000

Assembling Puzzles by Breaking them into Smaller Pieces
Genome Sequencing and Biology, Cold Spring Harbor, New York, May, 2001

Assembling Puzzles by Breaking them into Smaller Pieces
Beyond Genome, Cambridge Healthtech Institute Conference, San Francisko, California, June, 2001

Assembling Puzzles by Breaking them into Smaller Pieces
Post-genomic Bioinformatics, Madrid, Spain, April, 2002

Assembling Puzzles by Breaking them into Smaller Pieces
Maps, Sequences, and Genomes, Los Angeles, CA, May, 2002

Assembling Puzzles by Breaking them into Smaller Pieces
SIAM Conference on Discrete Mathematics, San Diego, CA, August, 2002 (one of seven plenary spe

Publications

Selected from over 100 articles, patents and software manuals.

Pevzner P.A., M. Yu. Borodovsky and A.A. Mironov (1989) Linguistics of Nucleotide Sequences I: the significance of deviations from mean statistical characteristics and prediction of the frequencies of occurrence of words. *J. Biom. Str. & Dyn.*, **6**, 1013-1026

Pevzner P.A., M. Yu. Borodovsky and A.A. Mironov (1989) Linguistics of Nucleotide Sequences II: stationary words in genetic texts and the zonal structure of DNA. *J. Biom. Str. & Dyn.*, **6**, 1027-1040

Pevzner P.A., V.P. Veiko (1989) Cycles in graphs and oligonucleotide linkers. *Molek. Biol.*, **4**, 1075-1079

Pevzner P.A. (1989) *L*-tuple DNA sequencing: computer analysis. *J. Biomol. Str. & Dyn.*, **7**, 63-74

Borodovsky M.A., Pevzner P.A. (1990) Statistical analysis of genetics texts. *Computer Analysis of Genetics Texts*, Chapter 2, Ed. M.D. Frank-Kamenetzkii, Nauka, Moscow, 36-80 (In Russian)

Pevzner P.A. (1990) DNA physical mapping. *Computer Analysis of Genetic Texts*, Chapter 5, Ed. M.D. Frank-Kamenetzkii, Nauka, Moscow, 154-188 (In Russian)

Pevzner P.A. (1990) Methods of filtration and database search. *Biopolymers & Cell,* **6**,7-13.

Kozhukhin C.G.,Pevzner P.A. (1991) Genome inhomogeneity is determined mainly by WW and SS dinucleotides. *Comp. Appl. in Biosci.*, **7**, 39-49.

Pevzner P.A., Y. Lysov, K. Khrapko, V., Belyavsky A.V., Florentév and A. Mirzabekov (1991) Improved matrices for Sequencing by Hybridization., *J. Biomol. Struct. and Dynamics*, **9**, 399-410.

M.Gelfand, C.Kozhukhin, Pevzner P.A. (1992) Extendable words in nucleotide sequences *Comp. Appl. in Biosci.*, **8**, 129-135

Pevzner P.A. (1992) Statistical distance between texts and filtration methods in rapid similarity search algorithm. *Comp. Appl. in Biosci.*,**8**,121-127

Pevzner P.A. (1992) Nucleotide sequences versus Markov models. *Computers and Chemistry*, **16**, 103-106,

Pevzner P.A. (1992) DNA physical mapping, flows in networks and minimum cycles mean in graphs. *DIMACS Series in Discrete Mathematics and Theoretical Computer Science*, **8**, 99-112

Pevzner P.A. (1992) Multiple alignment, communication cost, and graph matchings. *SIAM J. Appl. Math.*, **52**, 1763-1779

P.A. Pevzner, M.Waterman (1992) Generalized longest common subsequence problem and Hilbert basis. A.Apostolico, M.Crochermore, Z.Galil, U.Manber (eds.) Combinatorial Pattern Matching 1992. *Lecture Notes in Computer Science*, **644**, 79-89

Pevzner P.A. (1992) Multiple sequence alignment and communication cost. A. Apostolico, M. Crochermore, Z. Galil, U. Manber (eds.) Combinatorial Pattern Matching 1992. *Lecture Notes in Computer Science*, **644**, Springer-Verlag, 1992, 205-213

Pevzner P.A., M.Waterman (1993) Generalized sequence alignment and duality. *Adv. in Appl. Math.*, **14**, 139-171.

Pevzner P.A., M.Waterman (1993) A fast filtration algorithm for the substring matching problem. A.Apostolico, M.Crochermore, Z.Galil, U.Manber (eds.) Combinatorial Pattern Matching 1993. *Lecture Notes in Computer Science*, **684**, 197-214 (appeared in *Algorithmica*, **13** (1995), 135-154)

M.Vingron, Pevzner P.A. (1993) Multiple sequence alignment and n-dimensional image reconstruction. A.Apostolico, M.Crochermore, Z.Galil, U.Manber (eds.) Combinatorial Pattern Matching 1993. *Lect. Notes in Comp. Sci.*, **684**, 243-253 (appeared in *Advances in Applied Mathematics*, **16** (1995), 1-22)

Pevzner P.A. (1993) Overlapping word paradox and Conway equation. In C. Cantor, J. Fickett, R. Robbins and H. Lim (eds.) *Supercomputing, Bioinformatics and Complex Genome Analysis*, World Scientific, 71-78

M. Gelfand, P.A. Pevzner (1993) Editor's Foreword. *Bio Systems*, **30**, 1-4

Pevzner P.A. (1994) 3-non-crossed families and multicommodity flows. In A.K. Kelmans (ed.) *Selected Topics in Discrete Mathematics*, **158**, American Mathematical Society, 201-206

Pevzner P.A. (1994) Packing branchings in weighted graphs. In A.K. Kelmans (ed.) *Selected Topics in Discrete Mathematics*, **158**, American Mathematical Society, 1994, 185-200

Feldman W., Pevzner P.A. (1994) Gray Code Masks for DNA Sequencing by Hybridization *Genomics*, **23**, 233-235

Pevzner P.A. (1994) Combinatorial methods for DNA physical mapping. *IEEE Computers in Medicine and Biology* **13**, 146-150

V.Bafna, E.Lawler, Pevzner P.A. (1994) Approximation algorithms for multiple alignment. M. Crochermore and D.Gusfield (eds.) *Combinatorial Pattern Matching 1994, Lecture Notes in Computer Science*, **807**, 43-53

X.Huang, Pevzner P.A., W.Miller (1994) Parametric recomputing in alignment graphs. M. Crochermore and D.Gusfield (eds.) *Combinatorial Pattern Matching 1994, Lecture Notes in Computer Science*, **807**, 87-101

Pevzner P.A., Lipshutz R. (1994) Towards DNA Sequencing Chips. *19th Symposium on Mathematical Foundations of Computer Science, Kosice, Slovakia, Lecture Notes in Computer Science*, **841**, 143-158

Pevzner P.A. (1994) Rearrangements of DNA sequences and SBH. *Computers and Chemistry*, **18**, 221 - 223

Pevzner P.A. (1995) DNA physical mapping and alternating Eulerian paths in colored graphs. *Algorithmica*, **13**, 77-105

Pevzner P.A., Waterman M.S. (1995) Open combinatorial problems in computational molecular biology. *Proc. of the Third Israel Symposium on Theory of Computing and Systems, January, 1995, Tel Aviv, Israel*, IEEE Computer Society Press, 158-173

Pevzner P.A. (1995) Editor's Foreword. *J. of Computational Biology*, **2**, 153-158

Hannenhalli S., C. Chappey, Koonin E., Pevzner P.A. (1995) Genome rearrangements and evolution of herpes viruses. *Proc. of 3rd International Conference on Bionformatics and Complex Genome Analysis*, World Scientific, 91-106

Hannenhalli S., C. Chappey, Koonin E., Pevzner P.A. (1995) Genome sequence comparison and scenarios for gene rearrangements: a test case. *Genomics*, **30**, 299-311

Mironov A.A., Alexandrov N.N., Bogodarova N.Y, Grigoriev A., Lebedev V., Lunovskaya-Gurova, Grigoriev A., Lebedev V.Truchan M., Pevzner P.A. (1995) DNASUN: a software package for the biotechnology laboratory, *Computer Applications in Biological Sciences*, **11**, 331-335

Bafna V. and Pevzner P.A. (1995) Sorting by reversals: genome rearrangements in plant organelles and evolutionary history of X chromosome. *Molecular Biology and Evolution*, **12**, 239-246

Hannenhalli S., Pevzner P.A. (1995) Transforming cabbage into turnip (polynomial algorithm for sorting signed permutations by reversals). *Proc. of the 27th Annual Symposium on the Theory of Computing (STOC 95)*, 178-189 Las Vegas, Nevada

Hannenhalli S., Pevzner P.A. (1995) Transforming mice into men (polynomial algorithm for genomic distance problem). *Proc. of the 36 Annual Symposium on Foundations of Computer Science (FOCS 95)*, Milwaukee, Wisconsin, 581-592

Hannenhalli S., Pevzner P.A. (1995) Towards Computational Theory of Genome Rearrangements. In J. van Leeuwen, (ed.) *Computer Science Today: Recent Trends and Developments.* Lecture Notes in Computer Science, **1000**, 184-202 (invited paper in a jubilee volume)

Hannenhalli S., Pevzner P.A. (1996) To cut... or not to cut: applications of comparative physical maps in molecular evolution. *Proc. of the Seventh Annual ACM-SIAM Symposium on Discrete Algorithms (SODA 96)*, Atlanta, Georgia, 304-313

V.Bafna, Pevzner P.A. (1996) Genome rearrangements and sorting by reversals. *SIAM J. Computing*, **25**, 272-289. (preliminary version appeared in Proc. of 34th IEEE Symposium on Foundations of Computer Science (FOCS 93), November 3-5, 1993, Palo Alto, CA, 148-157)

Hannenhalli S., W. Feldman, H. Lewis, S.Skiena, Pevzner P.A. (1996) Positional Sequencing by Hybridization. *Computer Appl. in Biol. Sciences* **12**, 19-24

M. Gelfand, A. Mironov, P.A. Pevzner (1996) Spliced Alignment Problem: A New Approach to Gene Recognition. *Combinatorial Pattern Matching 1996, Lecture Notes in Computer Science*, **1075**, 141-158

M.Gelfand, A. Mironov, P.Pevzner (1996) Gene Recognition via Spliced Alignment *Proc. National Academy of Sciences USA*, **93**, 9061-9066

S.H. Sze, P.A. Pevzner (1997) Las Vegas Algorithms for Gene Recognition. *Proc. of the 1st Annual International Conference on Computational Molecular Biology*, Santa Fe, New Mexico, January, 1997, 300-309

Belyi I., Pevzner P.A. (1997) Software for DNA sequencing by hybridization. *Computer Applications in Biological Sciences*, **13**, 205-210

A.V. Aho, D.S. Johnson, R.M. Karp, S.R. Kosaraju, C.C. McGeoch, C.H. Papadimitriou, P.A. Pevzner (1997) Emerging Opportunities for Theoretical Computer Science, *SIGACT News*, **28**, 65-74

V.Bafna, E.Lawler, Pevzner P.A. (1997) Approximation algorithms for multiple alignment. *Theoretical Computer Science*, **182**, 233-244

S.H. Sze, P.A. Pevzner (1997) Las Vegas Algorithms for Gene Recognition: Suboptimal and Error-Tolerant Spliced Alignment. *J. Comp. Biol.*, **4**, 297-310

G.Xu, S.H. Sze, C.P.Lin, P.A. Pevzner, N. Arnheim. (1998) Gene Hunting without Sequencing Genomic Clones: Finding Exon Boundaries in cDNAs. *Genomics*, **47**, 171-179

Sze S.-H., Roytberg M.A., Gelfand M.S., Mironov A.A., Astakhova T.V. and Pevzner P.A. (1998) Algorithms and software for support of gene identification experiments. *Bioinformatics*, **14**, 14-19

A. Mironov, M. Roytberg, P.A. Pevzner, M.Gelfand, (1998) Performance Guarantee Algorithms for Gene Recognition. *Genomics* **51**, 332-339

Bafna V., Pevzner P.A. (1998) Sorting by transpositions. *SIAM J. Discrete Math.*, **11**, 224-240 (preliminary version appeared in *Proceedings of the Sixth Annual Symposium on Discrete Algorithms (SODA 95)*, San Francisco, CA, 614-623)

L. A. Goldberg, P. W. Goldberg, M. S. Paterson, P. A. Pevzner, S. Cenk Sahinalp, and E. Sweedyk: (1999) Complexity of Gene Placement. *Tenth Annual ACM-SIAM Symposium on Discrete Algorithms*, January 17-19, 1999 Baltimore, Maryland.

V.Dancik, T.Addona, K.Clauser, J.Vath, P.Pevzner (1999) *De novo* protein sequencing via tandem mass-spectrometry. *J. Comp. Biol.*, **6**, 327-341

E. Hubbell, P. A. Pevzner (1999) Fidelity probes for oligonucleotide arrays. Seventh International Conference on Intelligent Systems for Molecular Biology (ISMB 99), Heidelberg, Germany, August, 1999, 113-116

A. Mironov, P.A. Pevzner (1999) SST versus EST in gene recognition. *Microbial and Comparative Genomics*, **4**, 254-260

S. Hannenhalli, P.A. Pevzner (1999) Transforming cabbage into turnip: a polynomial algorithm for sorting signed permutations by reversals. *Journal of ACM*, **46**, 1-27

P.A. Pevzner, V.Dancik, C. Tang (2000) Mutation- and modification-tolerant protein identification via tandem mass-spectrometry. *J. Comp. Biology*, **7**, 777-787 (conference version appeared in the Fourth International Conference on Computational Molecular Biology RECOMB 2000, Tokyo, Japan, April 2000, 231-236)

V. Bafna, D. Beaver, M. Furer, P.A. Pevzner. Circular permutations and genome shuffling. In Comparative Genomics - Empirical and Analytical Approaches to Gene Order Dynamics, Map Alignment and the Evolution of Gene Families. (eds. D. Sankoff and J. Nadeau), Kluwer, 2000.

P. A. Pevzner, S. H. Sze (2000) Combinatorial algorithm for finding subtle signals in DNA sequences. Eighth International Conference on Intelligent Systems for Molecular Biology (ISMB 2000), San Diego, California, August 2000, 269-278

P.A. Pevzner, H. Tang (2001) Fragment assembly with double-barreled data. *Bioinformatics*, (Proceedings of ISMB 2001) Suppl 1:S225-33.

A.N. Arslan, O. Egecioglu, P.A. Pevzner. (2001) A new approach to sequence comparison: normalized sequence alignment. *Bioinformatics* **17**, 327-337 (conference version appeared in the Fifth International Conference on Computational Molecular Biology RECOMB 2001, Montreal, Canada, April 2001)

P.A. Pevzner, Z. Mulyukov, V. Dancik, C.L. Tang (2001) Efficiency of database search for identification of mutated and modified proteins via mass spectrometry. *Genome Res.* **11**, 290-299.

L. A. Goldberg, P. W. Goldberg, M. Paterson, P. Pevzner, S. C. Sahinalp, E. Sweedyk. (2001) The Complexity of Gene Placement *Journal of Algorithms*, **41**, 225-243

P.A. Pevzner (2001) Assembling puzzles from preassembled pieces. *Genome Res.*, **11**, 1461-1462

P.A. Pevzner, H. Tang, M.S. Waterman (2001) An Eulerian path approach to DNA fragment assembly *Proceedings of the National Academy of Sciences*, **98**, 9748-9753 (extended abstract appeared in the Fifth International Conference on Computational Molecular Biology RECOMB 2001, Montreal, Canada, April 2001)

Z. Muluykov and P.A. Pevzner (2002) EULER-PCR: finishing experiments for repeat resolution in DNA sequencing. Pacific Symposium on Biocomputing (PSB 2002), Kauai, Havaii, 199-210

S.H. Sze, M.S. Gelfand, and P.A. Pevzner (2002) Finding subtle motifs in DNA sequences. Pacific Symposium on Biocomputing (PSB 2002), Kauai, Havaii, 235-246

G. Bourque and P.A. Pevzner (2002) Genome-scale evolution: reconstructing gene orders in the ancestral species. *Genome Research*, **12**, 26-36.

S. Heber, M. Alekseyev, S.H. Sze, H. Tang and P.A. Pevzner Splicing Graphs and EST Assembly Problem. (2002) *Bioinformatics*, **18**, S181-188 (Proceedings of ISMB 2002)

E. Eskin and P.A. Pevzner. (2002) Finding composite regulatory patterns in DNA sequences. Bioinformatics, **18**, S354-363 (Proceedings of ISMB 2002)

U. Keich and Pavel A. Pevzner. (2002) Finding motifs in the twilight zone. *Bioinformatics*, **18**, 1374-1381 (extended abstract appeared in the Sixth International Conference on Computational Molecular Biology RECOMB 2002, Washington, DC, April 2002)

U. Keich and Pavel A. Pevzner. (2002) Subtle motifs: defining the limits of motif finding algorithms. *Bioinformatics*, **18**, 1382-1390

A. B. Kahng, I. I. Mandoiu, P. A. Pevzner, S. Reda, A. Z. Zelikovsky. (2002) Border Length Minimization in DNA Array Design. *Workshop on Algorithms in Bioinformatics (WABI 2002)*, Lecture Notes in Computer Science Series **2452**, 435-448

V. Lunyak, R. Burgess, G. Prefontaine, C. Nelson, S.H. Sze, J. Chenoweth, P. Schwartz, P.A. Pevzner, C. Glass, G. Mandel, and M. G. Rosenfeld. (2002) Corepressor depending silencing of chromosomal regions encoding neuronal genes. *Science*,**298**, 1747-1752

R. Waterston, ..., P.A. Pevzner. G. Tesler, ..., E. Lander. (2002) Initial sequencing and analysis of the mouse genome. *Nature*, **420**, 520-562

E. Eskin, U. Keich, M.S. Gelfand, P.A. Pevzner. (2003) Genome-wide analysis of bacterial promoter regions. Pacific Symp. Biocomput, Hawaii, 29-40.

P.A. Pevzner and G. Tesler (2003) Genome rearrangements in mammalian genomes: Lessons from human and mouse genomic sequences. *Genome Research*, **13**, 37-45

P.A. Pevzner and G. Tesler (2003) Transforming men into mice: the Nadeau-Taylor chromosomal breakage model revisited. Sixth International Conference on Computational Molecular Biology RECOMB 2003, Berlin, Germany, April 2003

A. B. Kahng, I. I. Mandoiu, P. A. Pevzner, S. Reda and A. Z. Zelikovsky. Engineering a scalable placement heuristic for DNA probe arrays. Sixth International Conference on Computational Molecular Biology RECOMB 2003, Berlin, Germany, April 2003

Books and Book Chapters

A. Alexandrov, N. Alexandrov, M. Borodovsky, Y. Kalambet, A. Kister, A. Mironov, P.A. Pevzner, V. Shepelev. *Computer Analysis of Genetic Texts*, Nauka, Moscow, 1990.

P.A. Pevzner. *Computational Molecular Biology: An Algorithmic Approach*, The MIT Press, Cambridge, MA 2000

S. Hannenhalli, E. Hubbell, R. Lipshutz, P.A. Pevzner: Combinatorial Algorithms for Design of DNA Arrays. In *Chip Technology*, (editor: J. Hoheisel), Springer-Verlag, 2002, pp. 1-19.

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