

10 Years of the International Conference on Research in Computational Molecular Biology (RECOMB)

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The RECOMB 10th Year Anniversary Committee

The tenth year of the annual International Conference on Research in Computational Biology (RECOMB) provides an opportunity to reflect on its history. RECOMB has been held across the world, including 6 different countries spanning 3 continents (Table 1). Over its 10 year history, RECOMB has published 373 papers and 170 individuals have served on its various committees. While there are many new faces in RECOMB each year, a significant number of researchers have participated over many years forming the core of the RECOMB community.

Over the past ten years, members of the RECOMB community were key players in many of the advances in Computational Biology during this period. These include the sequencing and assembly of the human genome, advances in sequence comparison, comparative genomics, genome rearrangements and the HapMap project among others.

Table 1. The locations and dates of each year of RECOMB. The program and conference chair are listed for each conference in the final two columns.

	Location	Dates	Program Chair	Conference Chair
1997	Santa Fe, USA	January 20-23	Michael Waterman	Sorin Istrail
1998	New York, USA	March 22-25	Pavel Pevzner	Gary Benson
1999	Lyon, France	April 11-14	Sorin Istrail	Mireille Régnier
2000	Tokyo, Japan	April 8-11	Ron Shamir	Satoru Miyano
2001	Montreal, Canada	April 22-25	Thomas Lengauer	David Sankoff
2002	Washington, USA	April 18-21	Eugene Myers	Sridhar Hannenhalli
2003	Berlin, Germany	April 10-13	Webb Miller	Martin Vingron
2004	San Diego, USA	March 27-31	Dan Gusfield	Philip Bourne
2005	Boston, USA	May 14-18	Satoru Miyano	Jill Mesirov, Simon Kasif
2006	Venice, Italy	April 2-5	Alberto Apostolico	Concettina Guerra

10 Years of RECOMB Papers

Over RECOMB's 10 year history, 731 authors have published a total of 373 papers in the conference proceedings. These papers span the diversity of research areas in

Computational Biology and present many new computational techniques for the analysis of biological data.

It should be noted that some authors have variances in how names appear throughout the years, including differing first names, initials, and middle names. While every effort was made to normalize the names, any such error could lead to the skewing of data and there may be small errors in the reporting of individual participation throughout the paper.

As a preliminary analysis, we consider the number of papers for each researcher that has appeared throughout the 10 years of RECOMB in the proceedings. In such a measure, Richard Karp who has authored 12 different papers in RECOMB throughout the 10 years would be the top participant.

Using the graph in Figure 1, we can identify the most collaborative members of the RECOMB community (hubs in a protein network). The most collaborative authors are the individuals that have the most number of co-authors. Ron Shamir is the most collaborative RECOMB author with 22 co-authors (Table 3).

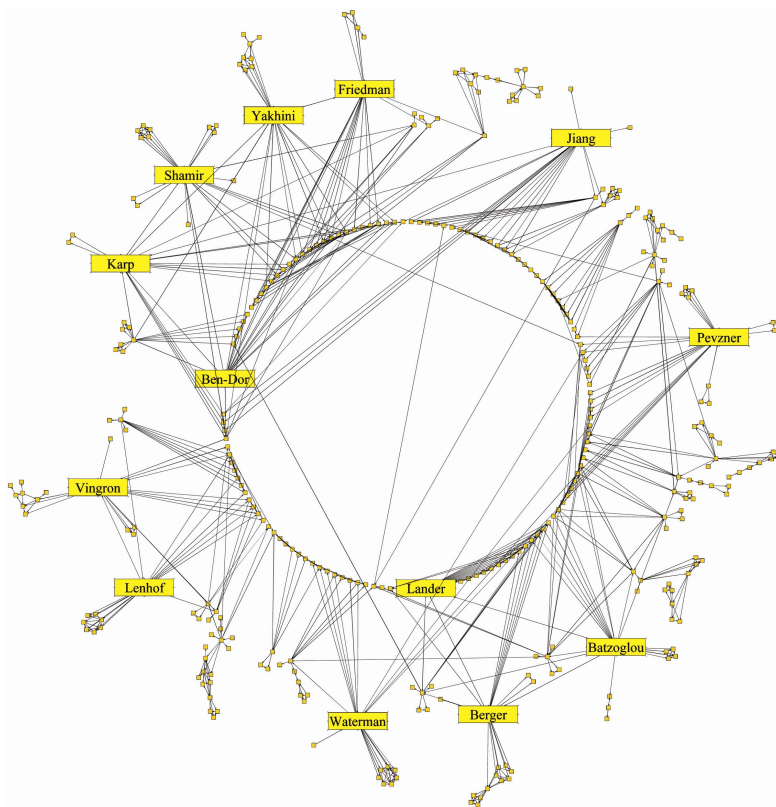


Fig. 1. Graphical view of interactions between RECOMB authors represented as a “protein interaction network” (giant component). Vertices of the graph represent authors while edges connect vertices corresponding to co-authors. Authors whose names are displayed are authors who have at least 16 coauthors.

Table 2. RECOMB's most prolific authors. The table identifies authors who have published at least 4 papers in RECOMB.

Author	Number of Papers	Author	Number of Papers
Richard Karp	12	Serafim Batzoglou	6
Ron Shamir	11	Dan Gusfield	6
Pavel Pevzner	11	Webb Miller	5
Bonnie Berger	10	Fengzhu Sun	5
Amir Ben-Dor	10	Ralf Bundschuh	5
Nir Friedman	9	Jeremy Buhler	5
Eugene Myers	9	Jens Lagergren	5
Zohar Yakhini	9	Roded Sharan	4
Tao Jiang	9	Benno Schwikowski	4
Benny Chor	8	Nancy Amato	4
Michael Waterman	8	Eran Halperin	4
David Sankoff	8	Zheng Zhang	4
Martin Vingron	7	Martin Farach-Colton	4
Ting Chen	7	Sorin Istrail	4
Steven Skiena	7	Vlado Dancik	4
Eric Lander	7	Golan Yona	4
Hans-Peter Lenhof	6	Dannie Durand	4
John Kececiloglu	6	Mathieu Blanchette	4
Vineet Bafna	6	Adam Siepel	4
Bruce Donald	6	Tatsuya Akutsu	4
David Haussler	6	Eran Segal	4
Lior Pachter	6	Thomas Lengauer	4

Table 3. RECOMB contributors with more than 10 co-authors. For each author the number of individuals with whom they have coauthored papers is listed.

Author Name	Num of Coauthors	Author Name	Num of Coauthors
Ron Shamir	22	Hans-Peter Lenhof	16
Serafim Batzoglou	20	Vlado Dancik	14
Bonnie Berger	20	Steven Skiena	14
Pavel Pevzner	20	Benny Chor	14
Michael Waterman	19	Lydia Kavradi	13
Zohar Yakhini	19	Bruce Donald	13
Tao Jiang	18	Martin Farach-Colton	12
Richard Karp	18	Sorin Istrail	12
Eric Lander	18	Lior Pachter	12
Nir Friedman	18	Eugene Myers	11
Amir Ben-Dor	17	David Sankoff	11
Martin Vingron	17	Vineet Bafna	11

Similarly, we can identify which groups of authors have had the most success working together (complexes in protein networks). The team of Eric S. Lander, Bonnie Berger and Serafim Batzoglou have published 3 papers together and are the only group of three authors which have published more than two papers. The most prolific pair of authors is Amir Ben-Dor and Zohar Yakhini who have published 7 papers together. 21 pairs of authors have published at least 3 papers as shown in Table 4.

Relationships between individual authors can be established in other ways as well. In Figure 2 we analyze the relationships between the most prolific authors (Table 2). By examining the relationships between individuals as advisors in both PhD and postdoctoral positions, the connections between the most prolific authors can be seen as a phylogeny. In addition, the individuals are shown on a timeline indicating the times at which they first began publishing in the field of Computational Biology.

We manually classified each paper into one of 16 categories: Protein structure analysis, Molecular Evolution, Sequence Comparison, Motif Finding, Sequence analysis, Population genetics/SNP/Haplotyping, Physical and Genetic Mapping, Gene Expression, Systems Biology, RNA Analysis, Genome rearrangements, Computational

Table 4. Coauthor Pairs. All pairs of authors who have written 3 or more papers accepted by RECOMB throughout the 10 year history of the conference are listed in the table.

Author Names		Number of Papers
Amir Ben-Dor	Zohar Yakhini	7
Bonnie Berger	Eric Lander	4
Zheng Zhang	Webb Miller	4
Serafim Batzoglou	Bonnie Berger	3
Serafim Batzoglou	Eric Lander	3
Amir Ben-Dor	Benny Chor	3
Amir Ben-Dor	Richard Karp	3
Amir Ben-Dor	Benno Schwikowski	3
Benny Chor	Tamir Tuller	3
Tao Jiang	Richard Karp	3
Richard Karp	Ron Shamir	3
David Haussler	Adam Siepel	3
Eric Lander	Jill Mesirov	3
Fengzhu Sun	Ting Chen	3
Ralf Zimmer	Thomas Lengauer	3
Bruce Donald	Christopher Langmead	3
Bruce Donald	Ryan Lilien	3
Nir Friedman	Yoseph Barash	3
Michael Hallett	Jens Lagergren	3
Guang Song	Nancy Amato	3
Eran Segal	Daphne Koller	3

Proteomics, Recognition of Genes, Microarray design, DNA computing and Other. Using these classifications, we can observe which authors have written the most about a single topic and which authors have written about the most topics. Both Bonnie Berger and Benny Chor have contributed the most papers (6) on a single topic, Protein Structure Analysis and Molecular Evolution respectively. Table 5 shows the top contributors in a single area.

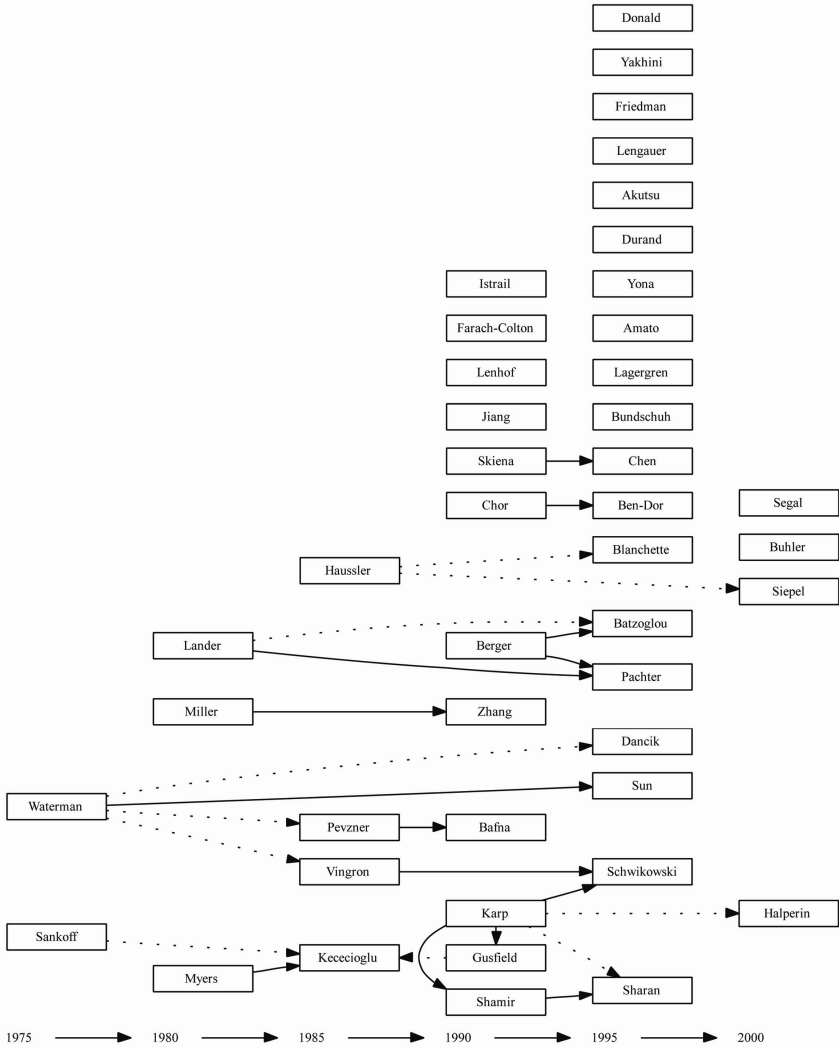


Fig. 2. Phylogeny of Authors. In this figure authors are organized across a timeline representing their earliest publications in the field of Computational Biology. Solid lines indicate PhD advisors, while dotted lines represent postdoctoral advisors. While we attempted to accurately link the timeline and RECOMB authors/genealogy, the figure represents only approximate time estimates and approximate topology of the RECOMB tree.

Table 5. Most consistent authors. For each author in the table, a subject is indicated for which he or she has written at least 3 papers. The number of papers in the 10 years of RECOMB by the author on the given subject is indicated.

Author Name	Author Name	Num of papers
Benny Chor	Molecular Evolution	6
Bonnie Berger	Protein structure analysis	6
David Sankoff	Genome rearrangements	5
Ralf Bundschuh	Sequence Comparison	5
Bruce Donald	Protein structure analysis	5
Nir Friedman	Gene Expression	5
Jens Lagergren	Molecular Evolution	5
Amir Ben-Dor	Gene Expression	4
Richard Karp	Physical and Genetic Mapping	4
Webb Miller	Sequence Comparison	4
David Haussler	Molecular Evolution	4
Zohar Yakhini	Gene Expression	4
Lior Pachter	Recognition of Genes	4
Dannie Durand	Molecular Evolution	4
Eugene Myers	Sequence Comparison	3
John Kececioglu	Sequence Comparison	3
Tao Jiang	Physical and Genetic Mapping	3
Ron Shamir	Sequence analysis	3
Michael Waterman	Physical and Genetic Mapping	3
Hans-Peter Lenhof	Protein structure analysis	3
Zheng Zhang	Sequence Comparison	3
Dan Gusfield	Population genetics/SNP/Haplotyping	3
Tandy Warnow	Molecular Evolution	3
Douglas Brutlag	Protein structure analysis	3
Jon Kleinberg	Protein structure analysis	3
Franco Preparata	Sequence analysis	3
Chris Bailey-Kellogg	Protein structure analysis	3
Michael Hallett	Molecular Evolution	3
Jonathan King	Protein structure analysis	3
Jeremy Buhler	Sequence Comparison	3
Kaizhong Zhang	RNA Analysis	3
Nancy Amato	Protein structure analysis	3
Eran Halperin	Population genetics/SNP/Haplotyping	3
Ryan Lilien	Protein structure analysis	3
Tamir Tuller	Molecular Evolution	3

Table 6. Most Diverse Authors. These are authors spanning the largest number of subjects. Authors are given who have papers in RECOMB in more than 4 subjects.

# of Subjects	Author Name	# of Subjects	Author Name
8	Pavel A. Pevzner	5	Fengzhu Sun
7	Steven S. Skiena	5	Ting Chen
7	Richard M. Karp	4	Tatsuya Akutsu
7	Ron Shamir	4	Bonnie Berger
6	Amir Ben-Dor	4	Hans-Peter Lenhof
6	Tao Jiang	4	Benno Schwikowski
6	Martin Vingron	4	Dan Gusfield
6	Eric S. Lander	4	Thomas Lengauer
6	Zohar Yakhini	4	Vineet Bafna
5	Serafim Batzoglou	4	Nir Friedman
5	Eugene W. Myers	4	Eran Segal
5	Michael S. Waterman	4	Roded Sharan

On the opposite end of the spectrum are the authors who contributed papers on different topics (Table 6).

For each author we create a topic profile which is a 16 dimensional vector containing the number of papers of each topic that an individual has published in RECOMB normalized by dividing by the total number of papers published. Intuitively, an author's topic profile represents the areas of research in which the author works on. Not surprisingly, co-authors tend to work on the same topics. The average pairwise Euclidean distance between any two authors topic profile is 1.19 while the average distance between co-authors is only 0.61. Similarly, papers written by the same author tend to be on the same topic. The chances that any two papers are on the same topic are 0.09 while the chance that two papers that share one author is on the same topic is 0.21.

Trends in RECOMB Authors over Time

The number of authors contributing to the conferences has fluctuated with the largest number in 2006 at 134. 1998 represents the year in which the fewest number of authors submitted multiple papers, that is, most authors had a single paper that was accepted to the conference (Table 7)

2006 had the lowest proportion of single-authored papers with only one of the 40 accepted papers showing a single author (Table 8 and Figure 3).

It appears that over the years there is a trend in an increase in the number of authors per paper with a slight decrease in papers per author. This indicates that while there are more authors on any one single paper, authors are less likely to have multiple papers in any given year.

Table 7. “Authors per paper” and “papers per author” statistics

Year	Papers	Authors	Averages	
			Author per Paper	Paper per Author
1997	42	101	2.8	1.2
1998	38	96	2.6	1.0
1999	35	106	3.3	1.0
2000	36	122	3.8	1.1
2001	35	92	2.8	1.1
2002	35	87	2.7	1.1
2003	35	88	2.8	1.1
2004	38	111	3.1	1.1
2005	39	121	3.4	1.1
2006	40	134	3.4	1.1

Table 8. Author Numbers in Papers. The table shows the percent of papers in each that had the given number of authors determined by counting the number of papers with the indicated number of authors and dividing it by the total number of papers in RECOMB in that year.

Year	Percent of papers with given number of authors										
	1	2	3	4	5	6	7	8	9	10	11
1997	19.0	42.9	14.3	9.5	9.5	0.0	0.0	2.4	0.0	0.0	2.4
1998	18.4	31.6	28.9	15.8	5.3	0.0	0.0	0.0	0.0	0.0	0.0
1999	8.6	37.1	22.9	8.6	11.4	5.7	5.7	0.0	0.0	0.0	0.0
2000	2.8	30.6	19.4	22.2	13.9	5.6	0.0	0.0	0.0	0.0	5.6
2001	17.1	31.4	28.6	8.6	8.6	2.9	2.9	0.0	0.0	0.0	0.0
2002	14.3	34.3	25.7	17.1	8.6	0.0	0.0	0.0	0.0	0.0	0.0
2003	8.6	42.9	25.7	5.7	17.1	0.0	0.0	0.0	0.0	0.0	0.0
2004	7.9	39.5	21.1	13.2	10.5	2.6	2.6	2.6	0.0	0.0	0.0
2005	2.6	28.2	28.2	25.6	7.7	2.6	2.6	2.6	0.0	0.0	0.0
2006	2.5	30.0	32.5	12.5	12.5	5.0	2.5	0.0	2.5	0.0	0.0

There are multiple ways to gauge the participation of individuals in the conference. One such measure might be to determine the span of years over which individuals have papers appearing in the proceedings. This was measured by determining the years of the first followed by the most recent papers of individual authors, and determining the span of years over which they had participated. Using such a measure, ten authors have papers published over a span of all ten years of the conference listed in the table. These authors are Benny Chor, Bonnie Berger, Sampath Kannan, John Kececioglu, Martin Vingron, David Haussler, Pavel Pevzner, Serafim Batzoglou, Dan Gusfield and Tao Jiang.

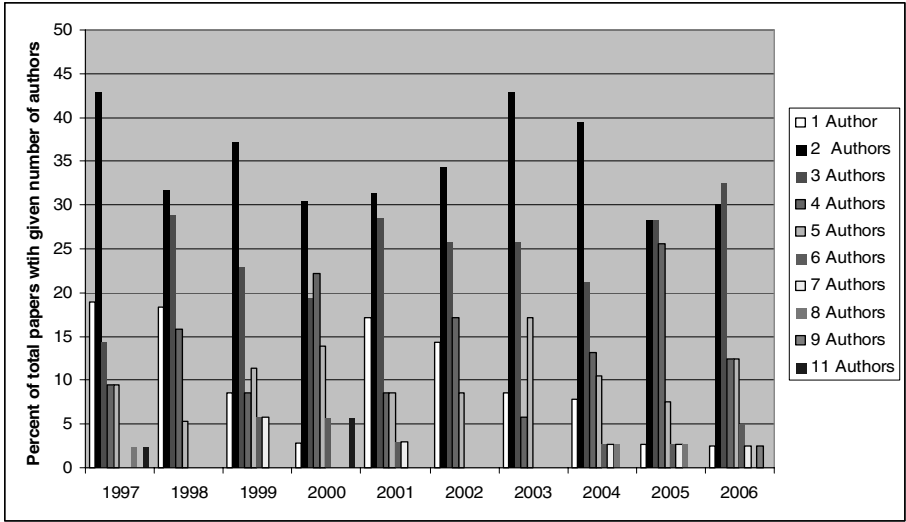


Fig. 3. Distribution of papers with given number of authors over the 10 years of RECOMB

Table 9. Authors with RECOMB papers in most number of years

Author Name	Num of Years	Author Name	Num of Years
Bonnie Berger	9	Tao Jiang	5
Pavel Pevzner	9	Benno Schwikowski	4
Ron Shamir	8	Nancy Amato	4
Amir Ben-Dor	8	Eran Halperin	4
Richard Karp	8	Vineet Bafna	4
Benny Chor	7	Sorin Istrail	4
Zohar Yakhini	7	Webb Miller	4
David Sankoff	7	Vlado Dancík	4
Eugene Myers	6	David Haussler	4
Bruce Donald	6	Mathieu Blanchette	4
Lior Pachter	6	Fengzhu Sun	4
Hans-Peter Lenhof	5	Adam Siepel	4
John Kececioglu	5	Serafim Batzoglou	4
Nir Friedman	5	Dan Gusfield	4
Martin Vingron	5	Jens Lagergren	4
Ting Chen	5	Steven Skiena	4
Ralf Bundschuh	5	Eric Lander	4
Jeremy Buhler	5	Thomas Lengauer	4
Michael Waterman	5		

However, such a measure may not be completely representative of a researcher's participation in the conference. Over the 10 years of RECOMB, no author has contributed to every year of the conference (Table 9).

Trends in RECOMB Paper Topics

As bioinformatics has grown and changed over the 10 years since RECOMB's inception, so have the subjects which comprise the papers accepted at each conference (Table 10). Some subjects, such as Protein Structure Analysis has remained a stronghold in the papers throughout the 10 years of RECOMB. Not only is it the most represented subject over the course of time, at 72 total papers in this field, with a steady portion of the total papers in each year in this field, it entails nearly 30 percent of the accepted papers in 2006.

Table 10. Distribution of topics of RECOMB papers. "Other" category includes more specific subjects such as drug design, DNA denaturation, etc.

Subject	Total	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006
Protein structure analysis	72	16.7	18.4	25.7	27.8	17.1	17.1	11.4	15.8	12.8	30.0
Molecular Evolution	52	4.8	15.8	14.3	13.9	11.4	8.6	11.4	13.2	20.5	25.0
Sequence Comparison	40	28.6	21.1	2.9	8.3	5.7	8.6	2.9	7.9	7.7	10.0
Motif Finding	32	0.0	15.8	5.7	8.3	14.3	8.6	11.4	15.8	7.7	0.0
Sequence analysis	22	0.0	0.0	5.7	5.6	22.9	11.4	8.6	5.3	0.0	2.5
Population genetics/ SNP/ Haplotyping	21	2.4	2.6	0.0	0.0	0.0	11.4	20.0	7.9	7.7	5.0
Physical and Genetic Mapping	20	23.8	7.9	8.6	5.6	0.0	0.0	2.9	0.0	2.6	0.0
Gene Expression	20	0.0	0.0	8.6	11.1	8.6	17.1	5.7	2.6	2.6	0.0
Systems Biology	20	0.0	0.0	5.7	2.8	2.9	2.9	11.4	5.3	12.8	10.0
RNA Analysis	18	0.0	2.6	2.9	2.8	2.9	5.7	2.9	10.5	7.7	10.0
Genome rearrangements	15	9.5	5.3	2.9	2.8	0.0	2.9	5.7	2.6	5.1	2.5
Computational Proteomics	14	0.0	0.0	2.9	2.8	8.6	0.0	2.9	5.3	10.3	5.0
Recognition of Genes	10	7.1	0.0	2.9	2.8	5.7	0.0	0.0	5.3	2.6	0.0
Other	10	0.0	10.5	11.4	2.8	0.0	0.0	0.0	2.6	0.0	0.0
Microarray design	5	2.4	0.0	0.0	2.8	0.0	5.7	2.9	0.0	0.0	0.0
DNA computing	2	4.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0

While protein structure remained a consistent part of the RECOMB content, other subjects have fluctuated, disappeared, or gained strength over time. Sequence comparison, which composed well over 25 percent of all papers in the first year of RECOMB, fell to 10 percent of the total content of the 2006 conference. Similarly, Physical and Genetic Mapping which exceeded protein structure analysis in 1997 has completely disappeared in 2006. RNA analysis and Systems Biology have also been

growing in popularity since the first papers were accepted in the subjects in 1998 and 1999 respectively.

Computational Proteomics and Population Genetics each represented five percent of the total number of accepted papers. While neither was very abundant in the first four years of the conference, they seem to be gaining momentum over time. Genome rearrangement has maintained a consistent presence throughout the 10 years of RECOMB. Most notably, however, is the area of molecular evolution which has evolved from a small presence of 4.8 percent of all accepted papers in 1997 to 25 percent of the total accepted papers in 2006.

Table 11. Paper Acceptance Rates. The table gives the paper acceptance rates based on the number of papers submitted and accepted over the 10 years of RECOMB.

Year	Number Submitted	Number Accepted	Rate
1997	117	43	37%
1998	123	38	31%
1999	147	35	24%
2000	110	36	33%
2001	128	35	27%
2002	118	35	30%
2003	175	35	20%
2004	215	38	18%
2005	217	38	18%
2006	215	40	19%

Table 12. Proportion of USA/Non-USA RECOMB papers

Year	USA	Non-USA
1997	67%	33%
1998	66%	34%
1999	66%	34%
2000	54%	46%
2001	69%	31%
2002	86%	14%
2003	71%	29%
2004	74%	26%
2005	54%	46%
2006	65%	35%

RECOMB has grown more competitive over time, with an increase in submissions to over 200 in the last three years (Table 11). The number of submissions in 2006 has nearly doubled over the first year of the conference.

Origins of RECOMB Papers

The first authors of the papers have spanned the globe, representing 25 countries. While US first authors regularly contributed over 60 percent of the papers accepted to the conference, in 2000 and 2005, held in Tokyo and Boston respectively, the split neared 50 percent (Table 12). Most strikingly, over 85 percent of the papers the 2002 conference held in Washington, DC had first authors from US institutions.

Israel, Germany and Canada had first authors contributing papers to nearly every conference (Figure 4). Israel became the second most represented country during 5 years, including 2003 when the conference was held in Germany where 80 percent of non-US authors were from Israel. Canada, Germany and Italy represented the runner-up position during 2 years each. Italy contributed the largest proportion of first authored papers during 2002 when 40% of non-USA first authors were from Italian institutions, which is the second largest percentage in any year.

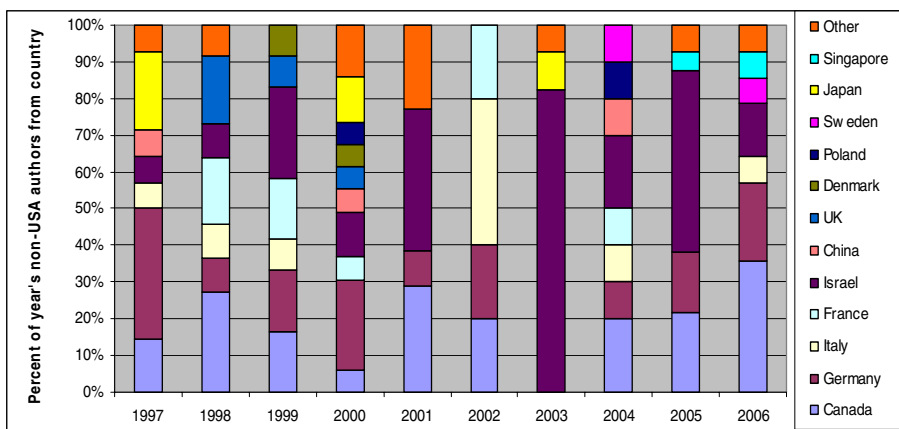


Fig. 4. Distribution of countries of origin of non-US first authors¹

Throughout RECOMB's history, over 90% of the first authors were involved in the public sector with the exception of a brief interruption in 2001 when just over 11% of first authors were from Industry. In 2002, the conference was hosted by Celera, during which nearly 9% of first authors were involved in the private sector, the second largest amount during the conference's history. However, the contributions from industry have steadily declined since 2002.

¹ Category Other includes Chile, Belgium, Australia, Spain, Netherlands, Finland, Switzerland, New Zealand, Austria, and Taiwan.

RECOMB's Most Cited Papers

Several of the papers published in RECOMB have had a significant influence on research in Computational Biology and have been widely cited. Table 13 contains a list of the most cited RECOMB papers as of January 2006 according to Google Scholar. A difficulty in obtaining this list is that many of the RECOMB papers are later published in journals and the citations are split between the original RECOMB version and the journal version which may lead to some inaccuracies in calculating the number of citations.

Table 13. RECOMB's most cited papers. The number of citations given in the final column is based on the journal in which they were published, and are accurate as of January 1, 2006 when the citations were last confirmed.

Paper Title	RECOMB Year	Journal	# Citations
Nir Friedman, Michal Linial, Iftach Nachman, Dana Pe'er. "Using Bayesian networks to analyze expression data"	2000	J Comp Biol 2000:7	506
Manolis Kamnitsis, Nick Patterson, Bruce Birren, Bonnie Berger, Eric S. Lander. "Whole-genome comparative annotation and regulatory motif discovery in multiple yeast species"	2003	Nature 2003: 423	385
Amir Ben-Dor, Zohar Yakhini. "Clustering gene expression patterns"	1999	J Comp Biol 1999:6	355
Harmen J. Bussemaker, Hao Li, Eric D. Siggia. "Regulatory element detection using correlation with expression (abstract only)"	2001	Nat Genet 2001:27	265
Amir Ben-Dor, Laurakay Bruhn, Nir Friedman, Iftach Nachman, Michèl Schummer, Zohar Yakhini. "Tissue classification with gene expression profiles"	2000	J Comp Biol 2000:7	245
Serafim Batzoglou, Lior Pachter, Jill P. Mesirov, Bonnie Berger, Eric S. Lander. "Human and mouse gene structure: comparative analysis and application to exon prediction"	2000	Genome Res 2000:10	190
Isidore Rigoutsos, Aris Floratos. "Motif discovery without alignment or enumeration"	1998	Bioinformatics 2000:14	150
Jeremy Buhler, Martin Tompa. "Finding motifs using random projections"	2001	J Comp Biol 2002:9	138
Martin G. Reese, Frank H. Eeckman, David Kulp, David Haussler. "Improved splice site detection in Genie"	1997	J Comp Biol 1997:4	131
Haim Kaplan, Ron Shamir, Robert E. Tarjan. "Faster and simpler algorithm for sorting signed permutations by reversals"	1997	SIAM J Comput 1999:29	127

Table 13. (Continue)

Alberto Caprara. "Sorting by reversals is difficult"	1997	RECOMB 1997	111
Vlado Dancík, Theresa A. Addona, Karl R. Clauser, James E. Vath, Pavel A. Pevzner. "De Novo Peptide Sequencing via Tandem Mass Spectrometry"	1999	J Comp Biol 1999:6	109
Pierluigi Crescenzi, Deborah Goldman, Christos Papadimitriou, Antonio Piccolboni, Mihalis Yannakakis. "On the complexity of protein folding"	1998	J Comp Biol 1998:5	104
Bonnie Berger, Tom Leighton. "Protein folding in the hydrophobic-hydrophilic (HP) is NP-complete"	1998	J Comp Biol 1998:5	89
Donna K. Slonim, Pablo Tamayo, Jill P. Mesirov, Todd R. Golub, Eric S. Lander. "Class prediction and discovery using gene expression data"	2000	RECOMB 2000	87
Mathieu Blanchette. "Algorithms for phylogenetic footprinting"	2001	J Comp Biol 2002:9	84
David Sankoff, Mathieu Blanchette. "Multiple genome rearrangements"	1998	J Comp Biol 1998:5	84
Donna K. Slonim, Leonid Kruglyak, Lincoln Stein, Eric S. Lander. "Building human genome maps with radiation hybrids"	1997	J Comp Biol 1997:4	81

Table 14. Invited speakers over the 10 years of RECOMB

Year	Speaker names
1997	David Botstein, Sam Karlin, Martin Karplus, Eric Lander, Robert Lipshutz, Jonathan King, Rich Roberts, Temple Smith, Terry Speed
1998	Ruben Abagyan, Charles Cantor, David Cox, Ron Davis, Klaus Gubernator, Joshua Lederberg, Michael Levitt, David Schwartz, John Yates
1999	Peer Bork, Cyrus Chothia, Gene Myers, John Moulton, Pitor Slonimsky, Ed Southern, Peter Willett, John Wooley
2000	Eric Davidson, Walter Gilbert, Takashi Gojobori, Leroy Hood, Minoru Kanehisa, Hans Lehrach, Yvonne Martin, Yusuke Nakamura, Svante Paabo
2001	Mark Adams, Roger Brent, George Church, Franz Lang, Klaus Lindpaintner, Yvonne Martin, Mark Ptashne, Philip Sharp, Matthias Wilm
2002	Ruben Abagyan, Ali Brivanlou, Evan Eichler, Harold Garner, David Ho, Gerry Rubin, Craig Venter, Marc Vidal
2003	Edward Trifonov, Christiane Nüsslein-Volhard, Árpád Furka, Andrew Clark, David Haussler, Arthur Lesk, Dieter Oesterhelt, Terry Speed, Kari Stefansson
2004	Carlos Bustamante, Russell Doolittle, Andrew Fire, Richard Karp, William McGinnis, Deborah Nickerson, Martin Nowak, Christine Orengo, Elizabeth Winzeler
2005	David Altshuler, Wolfgang Baumeister, James Collins, Charles DeLisi, Jonathan King, Eric Lander, Michael Levine, Susan Lindquist
2006	Anne-Claude Gavin, David Haussler, Ajay Royyuru, David Sankoff, Michael Waterman, Carl Zimmer, Roman Zubarev

RECOMB Keynote Speaker Series

The conference has been honored to have many excellent speakers throughout the 10 years of the conference. Every year between 7 and 9 distinguished individuals were invited to deliver lectures at the conference in a variety of fields (Table 14).

RECOMB includes a distinguished lecture series which consists of the Stanislaw Ulam Memorial Computational Biology lecture, the Distinguished Biology lecture, and New Technologies lectures delivered by a different set of individuals every year (Table 15) with the exception of 1999 and 2005. In 1999 There was no Biology lecture, while in 2005 no distinguished lectures were delivered on new technologies. 2004 included an additional address in which Richard Karp delivered the lecture awarded the Fred Howes Distinguished Service Award.

Table 15. Distinguished lecture series in Computational Biology, Biology, and New Technologies

Year	Stanislaw Ulam Memorial Computational Biology Lecture	Distinguished Biology Lecture	Distinguished New Technologies Lecture
1997	Eric Lander	Rich Roberts	Robert Lipshutz
1998	Joshua Lederberg	Ron Davis	David Cox
1999	Pitor Slonimsky		Ed Southern
2000	Minoru Kanehisa	Walter Gilbert	Leroy Hood
2001	George Church	Philip Sharp	Mark Adams
2002	Craig Venter	David Ho	Harold Garner
2003	Edward Trifonov	Christiane Nüsslein-Volhard	Árpád Furka
2004	Russell Doolittle	Andrew Fire	Carlos Bustamante
2005	Charles DeLisi	Jonathan King	
2006	Michael Waterman	Anne-Claude Gavin	Roman Zubarev

The RECOMB Organizers

Since its inception in 1997, many scientists have participated in the conference in many fashions. While the committees have enjoyed the membership of over 170 different individuals between 1997 and 2006, many have participated over multiple years. The Steering Committee had consistent presence of 5 scientists between 1997 and 2005, including Michael Waterman, Pavel Pevzner, Ron Shamir, Sorin Istrail and Thomas Lengauer. The steering committee included 6 members throughout the first 8 years of the conference, with Richard Karp rounding out the group through 2003, and passing the position on to Terry Speed in 2004. In 2005 Michal Linial joined the Steering Committee to increase its size to 7.

Table 16. RECOMB Committee Membership. Each year shows the number of members in each committee.

Year	Number of Members		
	Steering	Organizing	Program
1997	6	5	23
1998	6	4	21
1999	6	6	29
2000	6	8	27
2001	6	9	23
2002	6	11	28
2003	6	5	31
2004	6	9	42
2005	7	17	43
2006	7	9	38

Table 17. RECOMB Program Committee Membership

Name	Years
Michael Waterman	10
Pavel Pevzner	10
Ron Shamir	10
Thomas Lengauer	10
Sorin Istrail	10
Martin Vingron	9
Richard Karp	9
Terry Speed	7
David Sankoff	6
Satoru Miyano	6
Gene Myers	5
Tandy Warnow	5
Dan Gusfield	5
Gordon Crippen	5
Sridhar Hannenhalli	5

The organizing committee has had a far more variable composition. Between 1997 and 2006, a total of 81 individuals have comprised the committee. The program committee has grown in size throughout the years of the conference (Table 16). While the size of the organizing and program committees do not correlate perfectly, the trend toward an increasing number of members per year has been exhibited in both. Numerous individuals have served on program committees in multiple years (Table 17).

RECOMB Funding

RECOMB has received support from a variety of sources. The US Department of Energy, US National Science Foundation and the SLOAN Foundation have been 3 major sponsors over the 10 years. Many other sponsors have significantly contributed to the conference, including IBM, International Society for Computational Biology (ISCB), SmithKline Beecham, Apple, Applied Biosystems, Celera, Compaq, Compugen, CRC Press, Glaxo-SmithKline, Hewlett-Packard, The MIT Press and the Broad Institute, Accelerlys, Affymetrix, Agilent Technologies, Aventis, Berlin Center for Genome Based Bioinformatics-BCB, Biogen, Boston University's Center for Advanced Genomic Technology, Centre de recherche en calcul applique (CERCA), CNRS, Conseil Regional Rhone-Alpes, Eurogentec-Seraing, Geneart GmbH, Genome Therapeutics, IMGT, INRA, LION Bioscience, LIPHA, Mairie de Lyon, Mathworks, Millennium Pharmaceuticals, Max Planck Institute for Molecular Genetics, Microsoft Research, NetApp, Novartis, Paracel, Partek Incorporated, Pfizer, Rosetta Biosoftware, Schering AG, Sun Microsystems, Technologiestiftung Berlin, The European Commission, High-level Scientific Conferences, The German Federal Ministry for Education and Research, The San Diego Supercomputer Center, The University of California-San Diego, Timelogic, Wyeth, Universitat degli Studi di Padova, Italy, DEI and AICA.

Conclusion

The approach of the 10th RECOMB conference held in Venice Italy provides us an opportunity to reflect on RECOMB's history. The landscape of computational biology has changed drastically since the first RECOMB Conference was held in Santa Fe, New Mexico. Today's conference contains papers covering research topics that did not exist 10 years ago. Over this period, many individuals have made significant research contributions through published papers. Many of the original founders of the RECOMB conference are still active, and many new faces are becoming active in the community each year.