

Simon Kasif Work Timeline

Year	Work	General AI/Biology/Medicine Topic	With	Bayes X Bio CS Innovation Biology Innovation
	<p>*Green: Early or pioneering contribution</p> <p>*Considered Textbook</p> <p>*Transformative Community Work or Widely used Systems</p> <p>Bold – highly cited or visible</p>		<p>Red : Lab Member</p> <p>*Blue: Major Researcher</p>	
1981	Pyramid Linking Converges	Early Unsupervised Deep Learning (AI theory)	A. Rosenfeld	X
1983	<p>One of the earliest (if not first) implemented Parallel Logic Programming System on a distributed memory machine (ZMOB)</p> <p>A very early implementation of fork-join in parallel AI systems</p> <p>Fork-join is an evolutionary ancestor of MAP-REDUCE</p>	Parallel AI system	J. Minker et al	X
1985	<p>Arc Consistency / Discrete Relaxation is Inherently Sequential</p> <p>HIGHLY CITED</p>	Parallel AI (AI theory)	Sole author	X
1985-1987	Graph Separator based Parallel SAT Solving (similar proposals were made by others at that time)	Parallel AI (AI theory)	J. Reif D. Sherlekar	X
1987	Provably Optimal Parallel Term Matching and Anti-Unification	Parallel AI (AI theory)	Art Delcher	X
1991	<p>Early introduction of Data Streaming into ML and Data Mining</p> <p>Proving Upper, Lower Bounds for a new Streaming Model (several years ahead of the field)</p>	Preceded by several years the early Data Streaming Results that popularized the area (AI Theory)	D. Heath, R. Kosaraju, S. Salzberg	X
1990	<p>223 moves to capture a piece and win</p> <p>*Considered Textbook and seminal work in computer chess</p> <p>Follow up on Ken Thompson's 51 moves to win</p>	Parallel AI System on the Connection Machine Revolutionized chess (AI system)	L. Stiller PhD Thesis	X

1993	Early introduction of Randomization in Decision Tree (DT) Induction Prior to Random Forests HIGHLY CITED	Randomization in DTs, Random Projections (system)	D. Heath, S. Murthy, R. Beigel, S. Salzberg	X
1993-	Bayes Networks and Biology HIGHLY CITED	Early proposal for causal BNs in Biology	A. Delcher	X X X
1994	OC1 – Widely Used Open Access Decision Tree System HIGHLY CITED	(Randomization, Scalability by Sorting on Attributes, Ensemble of DTs, early open access ML system)	S. Murthy, S. Salzberg	X
1994	Logarithmic Time Queries and Updates in Probabilistic Networks Factorization Extending on Miller-Reif in Bayes Nets This method enables parallelism, space limited and dynamic data structures for incremental computation in Bayes Networks	Novel factorization and compilation of BNs enabling parallelism and dynamic updates Application to In-silico mutagenesis First application of graphical models to synthetic biology	Judea. Pearl Adam. Grove, Art Delcher	X X X
1994-1996	First of a kind Bayes Nets Kernels (very early and perhaps the first of a kind EMPIRICAL work but lacks mathematical rigor found in the follow-up papers)	Producing a BN Kernel, integrating BN-s with k-NN, Testing on ML Benchmarks (system and theory)	J. Rachlin, D. Waltz S. Salzberg	X X X
1996	AAAI Symposium Learning Complex Behaviors	Moving ML from Toy Problems to Learning Complex Behaviors and Systems	S. Russell M. Jordan D. Koller Over 100 scientists	X
1997	Human Centered Systems: Information, Interactivity and Intelligence	Launched the Human Centered Intelligence Initiative at NSF Early Warning about AI Safety and the problem of Control	J. Flannagan T. Huang P. Jones over 100 scientists	X

1998	Computational Methods in Molecular Biology”, Elsevier Publ. Focus on AI and Biology including Bayes Nets Some textbook material – not all.	One of the first books in Computational Molecular Biology	S. Salzberg D. Searls	X X X
1998	GLIMMER: widely Used Open Access AI System for Microbial Annotation First variable length models in Bio HIGHLY CITED	Millions of new enzymes identified with massive impact on science and biotechnology (open access system)	A. Delcher S. Salzberg O. White	X X X
1999	MUMMER: widely used and early system for whole genome comparison (bacteria) First open access whole genome bacterial analysis (extended to other organisms in follow-ups) HIGHLY CITED	Wide use in clinical and biological research with exceptional impact on biology and disease (open access system)	A. Delcher S. Salzberg	X X
1999	Multiplex PCR for Gap Closing in Genomes	Bridge between Complex Combinatorics and Genomics (theory and experimental implementation)	S. Salzberg H. Tettelin (with significant contributions by Noga Alon)	
1999-2001	Human Genome Project HIGHLY CITED	COMPUTATIONAL ANALYSIS TEAM	Lander et al	X X X
2000	DARPA SYSTEMS BIO AND SYNT. BIO SYMPOSIUM	LANGUAGE MODELING FOR BIOLOGY	Co-organizer Over 100 scientists attended	X X X
2000	Bayes Nets and Genomic Integration		V. Pavlovic	X X X
2002	Center for Advanced Genomic Technology (at BU)		Charles Delisi	
2003-2005	Early Network Based Gene Function Prediction	Introducing Network Propagation into Function Prediction (large field now)	S. Letovsky	X X X

	Wide impact on most popular gene function prediction systems today HIGHLY CITED			
2004	Hopfield Networks and Gene Function Prediction	Introducing Network propagation into Function Prediction	CM. Ding T.M. Murali C. Cantor	X X
2004-2020	Direct Involvement in Experimental Validation of Computational Predictions HIGHLY CITED Key discoveries: <ul style="list-style-type: none"> • RimO (Anton et al) • Lazy Genes (Tullai/Schaffer et al) • Inflammation precedes Metabolic Disregulation in Diabetic mouse models • Networks associated with Insulin Resistance (Liu et al) • ZNF complex associated with differentiation (Ramirez et al) • Reprogramming Cancer Stem Cells (Suva/Bernstein) • Functional characterization of multiple bacterial proteins • Bacterial Regulons (Faith et al) • Multiple Metabolic Prediction in both Muscle Cells and Adipocytes 		R. Roberts C. Cantor G. Cooper M. Steffen R. Jain B. Bernstein A. Regev R. Kahn S. Tseng ME. Patti Combrex T. Gardner J. Collins and many students and fellows	X
2004	Learning Hidden Matchings in Graphs from queries	New mini-area in graph theory	N. Alon R. Beigel	X X
2004	Starting the COMBREX CONSORTIUM Academy of Microbiology Meeting	A Community Project using Active Learning (AI) for Recommending Experiments	Rich Roberts & > 50 scientists	X X X
2005	Multi-nodes graphs and Multiplex PCR MUPLEX System	Multiplex PCR analysis and open access system Motivated by non-invasive detection of fetal DNA in maternal blood	J. Rachlin CM. Ding C. Cantor N. Alon	X X

2006	Biological Context Networks (BCN)-s Considered a textbook formalism	Pioneered a mini new area of network science	V. Asodi J. Rachlin N. Alon	X X
2007-	Network Biology of Wellness (many talks given)	In progress	R. Kahn I. Kohane	X X X
2007	Inference of Regulatory Networks in Bacteria with Validation HIGHLY CITED	1500+ citations	J. Faith T. Gardner J. Collins	X X X
2000-2020	Popularizing Multi-Omic Data Integration in Biological Science Using Networks	Large field now	With many independent contributions	X X X
2003-2020	Active Learning for Biology THE COMBREX PROJECT		Rich Roberts, Martin Steffen et al	X X
2010-2017	Regional Bioinformatics and Systems Biology Core	NIH Center		
2012	Driving Citizen Science with AI	NIH Common Fund Meeting	L. Griffith Meyer S. Seung	X X
2013	The COMBREX REPORT First community driven by active learning paper		COMBREX Consortium	X X X
2014	Reprogramming Stem Cells driven by computational analysis and epigenomics HIGHLY CITED	Highly cited	E. Rheinbay M. Suva B. Bernstein	X
2015	The Biomed Collaboration Initiative	Harvard Medical School		X X
2010-2020	The Provenance Initiative		Rich Roberts et al	X X X
2019-	AI and Biology Initiative	In progress		X X
2020	Automating COVID Drug Discovery	In progress	Murali et al	X X
2020	Use of Complexity Theory in Pooling COVID-19 TESTS	Theory and system	R. Beigel	X X
1996-2020	Many advisory boards and steering committees at both local, single university or national or international level including Johns Hopkins, BU, Harvard Med, CMU, Columbia, Alberta Innovation Academy, U. Chicago, NSF,			

	Joslin Diabetes Center, Flybase (Harvard Med), start-ups, conferences, industry and more)			
1985-2020	Over 60 students/fellows mentored or co-mentored, many minorities, women http://sites.bu.edu/phenogeno/people/			
1985-2020	Over 70 direct small group collaborators (in addition to consortium memberships and large papers) http://sites.bu.edu/phenogeno/people/			