**Simon Kasif Key Work/Research Contributions Timeline**

**(both solo and group)**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Year  | Work | General AI/Biology/Medicine Topic  | With  | Color scheme of Innovation)AI (green)CS (red) Innovation Biology (blue) |
|  | \*Green: An early or pioneering contribution\*Considered a Textbook Result\*Transformative Community Work or Widely used Systems**Bold – highly cited or visible**  |  | **Red: Lab/Group Member**  **\***Blue: Collaborator |  |
| 1981 | Pyramid Linking Converges | Early Unsupervised Deep Learning (AI theory) |  A. Rosenfeld | XX |
| 1983 | First implemented Parallel AI Inference (Datalog) System on a distributed memory machine The system was using fork – join, an early and rudimentary implementation of Map – Reduce for parallel AI | Parallel Joins Coupled with Datalog (AI system)  | J. Minker et al | XX |
| 1983 | First Parallel Logic Programming AI System to be mapped and tested on a multiprocessor (ZMOB) | Parallel AI (system) | J. Minker et al | XX |
| 1985 | Founder, Johns Hopkins AI Laboratory | Initially Parallel AI, Scalability, Logical Inference, Networks)Later Machine Learning and Computational Biology  | S. Salzberg | X X X |
| 1985 | Arc Consistency / Discrete Relaxation is Inherently Sequential**FOUNDATIONAL THEORY AND HIGHLY CITED** | Parallel AI (AI theory) | Sole author | XX |
| 1985-1987  | Graph Separator based Parallel SAT Solving  | Parallel AI (AI theory) | J. Reif D. Sherlekar | XX |
| 1987 | Provably Optimal Parallel Term Matching and Anti-Unification | Parallel AI (AI theory) | Art Delcher  | XX |
| 1991 | An early introduction of Data Streaming into ML and Data MiningMostly theory. Upper, Lower Bounds for Data Streaming Application in Cognitive Science | Preceded by several years the early Data Streaming Results that popularized the area (AI Theory)  | D. Heath, R. Kosaraju, S. Salzberg | XX |
| 1990 | **223 moves to capture a piece and win** **\*Considered Texbook and seminal work in computer chess** **Follow up on Ken Thompson’s 51 moves to win** | Parallel AI System on the Connection Machine Revolutionized chess (AI system) | L. Stiller PhD Thesis | XX |
| 1993 | Introducing 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 | XX |
| 1993-  | **Bayes Networks and Biology** **HIGHLY CITED** | Early proposal for causal BNs in Biology | A. Delcher et al | X X X |
| 1993- | **Rudimentary generative AI in biology: a small but early step towards using AI in synthetic biology** | First of a kind Application of BN for Biology:  | A.Delcher et al | X X X |
| 1994 | **OC1 – Widely Used Open Access Decision Tree System** **HIGHLY CITED** | (Randomization, Scalability by Sorting on Attributes, Ensemble of DTs, AI system) | S. Murthy, S. Salzberg | XX |
| 1994 | Logarithmic Time Queries and Updates in Probabilistic NetworksFactorization Extending on Miller-Reif in Bayes Nets | Novel factorization and compilation of BNs enabling parallelism and dynamic updates Application to In-silico mutagenesis First application of graphical models to synthetic biology | J. PearlA. Grove, A. A. 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 Machine Learning from Toy Problems to Learning Complex Behaviors and Systems | S. RussellM. JordanD. KollerOver 100 scientists | XX |
| 1997 | **Human Centered Systems: Information, Interactivity and Intelligence** | Launched the Human Centered Intelligence Initiative at NSFEarly Warning about AI Safety and the problem of Control | J. Flannagan T. Huang P. Jones over 100 scientists | XX |
| 1998 | Computational Methods in Molecular Biology”, Elsevier Publ. Focus on AI and Biology including Bayes NetsSome textbook material – not all. | One of the earliest 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** **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 | X X |
| 1999-2001 | **Human Genome Project** **HIGHLY CITED** | **COMPUTATIONAL ANALYSIS TEAM** | Lander et al | XX X |
| 2000 | **DARPA SYSTEMS BIO AND SYNT. BIO SYMPOSIUM** | LANGUAGE MODELING FOR BIOLOGY  | Co-organizer with Bob Berwick et alOver 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 | **Network based Gene Function Prediction** **Wide impact on most popular GENE FUNCTION PREDICTION systems today HIGHLY CITED** | Introducing Network Propagation into Function PredictionEstablished DISCIPLINE | S. Letovsky | X X X |
| 2004 | **Hopfield Networks and Gene Function Prediction**  | Introducing Network propagation into Function Prediction | CM. DingT.M. MuraliC. Cantor | XXX |
| 2004-2020 | **Direct Involvement in Experimental Validation of Computational Predictions****(among the early pioneers of computational / experimental hybrid projects)****HIGHLY CITED** |  | R. RobertsC. CantorG. CooperM. SteffenR. JainB.BernsteinA. RegevR. KahnS. TsengME. PattiCombrex T. GardnerJ. Collins  | X |
| 2004 | Learning Hidden Matchings in Graphs from queries | New mini-area in graph theory  | N. AlonR. Beigel et al | XXX |
| 2004 | **Starting COMBREX CONSORTIUM****Academy Meeting** **(AI Driven Community Science)** | A Community Project using Active Learning for Recommending and Driving Experiments | Rich Roberts & > 50 scientists  | XXX |
| 2005 | Multi-nodes graphs and Multiplex PCR**MUPLEX System** | Multiplex PCR analysis and open access systemMotivated by non-invasive detection of fetal DNA in maternal blood (later liquid biopsy) | J. Rachlin CM. DingC. CantorN. Alon | XXX |
| 2006 | Biological Context Networks (BCN)-s  | Pioneered a mini new area of network science | V. Asodi J. Rachlin N. Alon | XXX |
| 2007- | Network Biology of Wellness (many talks given) | In progress  | R. KahnI. Kohane  | XXX |
| 2007 | **Inference of Regulatory Networks in Bacteria with Validation****HIGHLY CITED** | >1700 citations | J. FaithT. GardnerJ. Collins  | XXX |
| 2000 -  | **Popularizing Data Integration in Biological Science Using Networks**  | Large field now | With many independent contributions | XXX  |
| 2010-2014 | Using Machine Learning (AI) for Drug Monitoring in Social Medial (Twitter) |  | Clark FreifeldJ. Brownstein at al  |  |
| 2003- | Active Learning for BiologyTHE COMBREX PROJECT  |  | Rich Roberts et al | XXX |
| 2010-2017 | Director, Regional Bioinformatics and Systems Biology Core (the core contributed to many papers in Nature Medicine, Nature Cell, Cell Metabolism papers in major journals) | NIH Center |  | XXX |
| 2012 | Driving Citizen Science with AI  | NIH Common Fund Meeting  | L. Griffith MeyerS. Seung | XXX |
| 2013 | **The COMBREX REPORT** **First AI driven community science in Biology (by active learning) paper (2AI2BIO)\*** |  | COMBREX Consortium | XXX |
| 2014 | **Reprogramming Stem Cells driven by computational analysis and epigenomics****FOUNDATIONAL AND HIGHLY CITED** | Highly cited  | E. Rheinbay M. SuvaB. Bernsteinet al  | X |
| 2015 | The Biomed Collaboration Initiative  | Harvard Medical School |  | X X |
| 2010-2020 | The Provenance Initiative  | In progress | Rich Roberts et al | X X X |
| 2020- | AI and Biology Initiative  | In progress | Rich Roberts et al |  XXX |
| 2020- | Automating COVID Drug Discovery (small) | In progress  |  | XXX |
| 2020- | Use of Complexity Theory in Pooling COVID-19 TESTS (small) | Theory and system | R. Beigel | XX |
| 2018-  | AI based Genomic Inspectors  | System and Theory  | Brian HaasAviv Regev et al | XXX |
| 1996-2020 | Many advisory boards and steering/advisory committees at both local, single university or national or international level including Hopkins Mind/Brain Institute, BU, Harvard Med, CMU, Columbia, Alberta Innovation Academy, U. Chicago, NSF, Joslin Diabetes Center, start-ups, conferences, NIH, NSF, DARPA, industry and more) |  |  |  |
| 1985-2022 | Over 60 students/fellows mentored or co-mentored, many minorities, women<http://sites.bu.edu/phenogeno/people/> |  |  |  |
| 1985-2022 | Over 70 direct small group collaborators (in addition to consortium memberships and large papers)<http://sites.bu.edu/phenogeno/people/> |  |  |  |