

# Russell S Schwartz

## List of Publications by Year in descending order

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133  
papers

17,920  
citations

159585

30  
h-index

24982

109  
g-index

142  
all docs

142  
docs citations

142  
times ranked

19856  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Sequence of the Human Genome. <i>Science</i> , 2001, 291, 1304-1351.	12.6	12,623
2	Evolution of genes and genomes on the <i>Drosophila</i> phylogeny. <i>Nature</i> , 2007, 450, 203-218.	27.8	1,886
3	The evolution of tumour phylogenetics: principles and practice. <i>Nature Reviews Genetics</i> , 2017, 18, 213-229.	16.3	240
4	Molecular crowding shapes gene expression in synthetic cellular nanosystems. <i>Nature Nanotechnology</i> , 2013, 8, 602-608.	31.5	215
5	Whole Proteome pI Values Correlate with Subcellular Localizations of Proteins for Organisms within the Three Domains of Life. <i>Genome Research</i> , 2001, 11, 703-709.	5.5	189
6	Machine Learning Approaches for Predicting Radiation Therapy Outcomes: A Clinician's Perspective. <i>International Journal of Radiation Oncology Biology Physics</i> , 2015, 93, 1127-1135.	0.8	153
7	Local Rules Simulation of the Kinetics of Virus Capsid Self-Assembly. <i>Biophysical Journal</i> , 1998, 75, 2626-2636.	0.5	148
8	Optimal Haplotype Block-Free Selection of Tagging SNPs for Genome-Wide Association Studies. <i>Genome Research</i> , 2004, 14, 1633-1640.	5.5	113
9	Whole Proteome pI Values Correlate with Subcellular Localizations of Proteins for Organisms within the Three Domains of Life. <i>Genome Research</i> , 2001, 11, 703-709.	5.5	105
10	Single-Cell Genetic Analysis of Ductal Carcinoma in Situ and Invasive Breast Cancer Reveals Enormous Tumor Heterogeneity yet Conserved Genomic Imbalances and Gain of MYC during Progression. <i>American Journal of Pathology</i> , 2012, 181, 1807-1822.	3.8	104
11	Bioinformatics Curriculum Guidelines: Toward a Definition of Core Competencies. <i>PLoS Computational Biology</i> , 2014, 10, e1003496.	3.2	102
12	The development and application of bioinformatics core competencies to improve bioinformatics training and education. <i>PLoS Computational Biology</i> , 2018, 14, e1005772.	3.2	84
13	Frequencies of amino acid strings in globular protein sequences indicate suppression of blocks of consecutive hydrophobic residues. <i>Protein Science</i> , 2001, 10, 1023-1031.	7.6	83
14	Simulation Study of the Contribution of Oligomer/Oligomer Binding to Capsid Assembly Kinetics. <i>Biophysical Journal</i> , 2006, 90, 57-64.	0.5	67
15	Exploring the Parameter Space of Complex Self-Assembly through Virus Capsid Models. <i>Biophysical Journal</i> , 2008, 94, 772-783.	0.5	59
16	Robustness of Inference of Haplotype Block Structure. <i>Journal of Computational Biology</i> , 2003, 10, 13-19.	1.6	54
17	Applying unmixing to gene expression data for tumor phylogeny inference. <i>BMC Bioinformatics</i> , 2010, 11, 42.	2.6	54
18	Machine Learning and Radiogenomics: Lessons Learned and Future Directions. <i>Frontiers in Oncology</i> , 2018, 8, 228.	2.8	54

#	ARTICLE	IF	CITATIONS
19	Haplotypes and informative SNP selection algorithms. , 2003, , .		52
20	Mixed Integer Linear Programming for Maximum-Parsimony Phylogeny Inference. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 323-331.	3.0	50
21	Lattice Simulations of Aggregation Funnels for Protein Folding. Journal of Computational Biology, 1999, 6, 143-162.	1.6	48
22	Algorithms to Model Single Gene, Single Chromosome, and Whole Genome Copy Number Changes Jointly in Tumor Phylogenetics. PLoS Computational Biology, 2014, 10, e1003740.	3.2	46
23	“Local Rules” Theory Applied to Polyomavirus Polymorphic Capsid Assemblies. Virology, 2000, 268, 461-470.	2.4	44
24	Frequencies of hydrophobic and hydrophilic runs and alternations in proteins of known structure. Protein Science, 2006, 15, 102-112.	7.6	42
25	Phylogenetic analysis of multiprobe fluorescence in situ hybridization data from tumor cell populations. Bioinformatics, 2013, 29, i189-i198.	4.1	40
26	Deconvolution and phylogeny inference of structural variations in tumor genomic samples. Bioinformatics, 2018, 34, i357-i365.	4.1	40
27	Response of an actin filament network model under cyclic stretching through a coarse grained Monte Carlo approach. Journal of Theoretical Biology, 2011, 274, 109-119.	1.7	39
28	Comparative immunopeptidomics of humans and their pathogens. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 13268-13272.	7.1	38
29	Identification of novel mutations by exome sequencing in African American colorectal cancer patients. Cancer, 2015, 121, 34-42.	4.1	36
30	RECONSTRUCTING TUMOR PHYLOGENIES FROM HETEROGENEOUS SINGLE-CELL DATA. Journal of Bioinformatics and Computational Biology, 2007, 05, 407-427.	0.8	35
31	Classifying the Progression of Ductal Carcinoma from Single-Cell Sampled Data via Integer Linear Programming: A Case Study. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 643-655.	3.0	33
32	Surveying Capsid Assembly Pathways through Simulation-Based Data Fitting. Biophysical Journal, 2012, 103, 1545-1554.	0.5	31
33	Applying Molecular Crowding Models to Simulations of Virus Capsid Assembly In Vitro. Biophysical Journal, 2014, 106, 310-320.	0.5	31
34	HER2 expression as a potential marker for response to therapy targeted to the EGFR. British Journal of Cancer, 2006, 94, 1144-1153.	6.4	30
35	Single-Cell Genetic Analysis Reveals Insights into Clonal Development of Prostate Cancers and Indicates Loss of PTEN as a Marker of Poor Prognosis. American Journal of Pathology, 2014, 184, 2671-2686.	3.8	29
36	Queue-based method for efficient simulation of biological self-assembly systems. Journal of Computational Physics, 2005, 204, 100-120.	3.8	28

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37	Robust unmixing of tumor states in array comparative genomic hybridization data. <i>Bioinformatics</i> , 2010, 26, i106-i114.	4.1	28
38	Inferring models of multiscale copy number evolution for single-tumor phylogenetics. <i>Bioinformatics</i> , 2015, 31, i258-i267.	4.1	28
39	Aneuploidy, <i>TP53</i> mutation, and amplification of <i>MYC</i> correlate with increased intratumor heterogeneity and poor prognosis of breast cancer patients. <i>Genes Chromosomes and Cancer</i> , 2018, 57, 165-175.	2.8	27
40	A comparative genomics approach to identifying the plasticity transcriptome. <i>BMC Neuroscience</i> , 2007, 8, 20.	1.9	24
41	Applying, Evaluating and Refining Bioinformatics Core Competencies (An Update from the Curriculum) <i>Tj ETQq1 1 0.784314, igBT /Over</i>	3.2	24
42	Simulated De Novo Assembly of Golgi Compartments by Selective Cargo Capture during Vesicle Budding and Targeted Vesicle Fusion. <i>Biophysical Journal</i> , 2008, 95, 1674-1688.	0.5	23
43	Network-Based Inference of Cancer Progression from Microarray Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2009, 6, 200-212.	3.0	22
44	Algorithms for Efficient Near-Perfect Phylogenetic Tree Reconstruction in Theory and Practice. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2007, 4, 561-571.	3.0	20
45	Modeling Nuclear Blebs in a Nucleoskeleton of Independent Filament Networks. <i>Cellular and Molecular Bioengineering</i> , 2012, 5, 73-81.	2.1	20
46	The evolution of single cell-derived colorectal cancer cell lines is dominated by the continued selection of tumor-specific genomic imbalances, despite random chromosomal instability. <i>Carcinogenesis</i> , 2018, 39, 993-1005.	2.8	20
47	Pathway Complexity of Model Virus Capsid Assembly Systems. <i>Computational and Mathematical Methods in Medicine</i> , 2008, 9, 277-293.	1.3	18
48	Discrete, continuous, and stochastic models of protein sorting in the Golgi apparatus. <i>Physical Review E</i> , 2010, 81, 011914.	2.1	18
49	Stochastic off-lattice modeling of molecular self-assembly in crowded environments by Green's function reaction dynamics. <i>Physical Review E</i> , 2008, 78, 031911.	2.1	17
50	A Novel Subset of Human tumors that Simultaneously Overexpress Multiple E2F-responsive Genes Found in Breast, Ovarian, and Prostate Cancers. <i>Cancer Informatics</i> , 2014, 13s5, CIN.S14062.	1.9	17
51	A parameter estimation technique for stochastic self-assembly systems and its application to human papillomavirus self-assembly. <i>Physical Biology</i> , 2010, 7, 045005.	1.8	16
52	Stochastic steady state gain in a gene expression process with mRNA degradation control. <i>Journal of the Royal Society Interface</i> , 2012, 9, 1589-1598.	3.4	16
53	Phylogenetic analysis of multiple FISH markers in oral tongue squamous cell carcinoma suggests that a diverse distribution of copy number changes is associated with poor prognosis. <i>International Journal of Cancer</i> , 2016, 138, 98-109.	5.1	16
54	Epitope prediction algorithms for peptide-based vaccine design. <i>Proceedings</i> , 2003, 2, 17-26.	0.1	16

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55	Efficiently Finding the Most Parsimonious Phylogenetic Tree Via Linear Programming. , 2007, , 37-48.		15
56	Local rule mechanism for selecting icosahedral shell geometry. Discrete Applied Mathematics, 2000, 104, 97-111.	0.9	14
57	Fixed Parameter Tractability of Binary Near-Perfect Phylogenetic Tree Reconstruction. Lecture Notes in Computer Science, 2006, , 667-678.	1.3	14
58	Direct maximum parsimony phylogeny reconstruction from genotype data. BMC Bioinformatics, 2007, 8, 472.	2.6	13
59	Quantitative computational models of molecular self-assembly in systems biology. Physical Biology, 2017, 14, 035003.	1.8	13
60	FISHtrees 3.0: Tumor Phylogenetics Using a Ploidy Probe. PLoS ONE, 2016, 11, e0158569.	2.5	13
61	Computational models of molecular self-organization in cellular environments. Cell Biochemistry and Biophysics, 2007, 48, 16-31.	1.8	12
62	Inference of Tumor Phylogenies from Genomic Assays on Heterogeneous Samples. Journal of Biomedicine and Biotechnology, 2012, 2012, 1-16.	3.0	12
63	Biological colloid engineering: Self-assembly of dipolar ferromagnetic chains in a functionalized biogenic ferrofluid. Applied Physics Letters, 2012, 101, 063701.	3.3	12
64	A simplicial complex-based approach to unmixing tumor progression data. BMC Bioinformatics, 2015, 16, 254.	2.6	11
65	A Report of the Curriculum Task Force of the ISCB Education Committee. PLoS Computational Biology, 2012, 8, e1002570.	3.2	10
66	Phenotypic Signatures Arising from Unbalanced Bacterial Growth. PLoS Computational Biology, 2014, 10, e1003751.	3.2	10
67	Structurally Governed Cell Mechanotransduction through Multiscale Modeling. Scientific Reports, 2015, 5, 8622.	3.3	10
68	Reference-free inference of tumor phylogenies from single-cell sequencing data. BMC Genomics, 2015, 16, S7.	2.8	10
69	Tumor Copy Number Deconvolution Integrating Bulk and Single-Cell Sequencing Data. Journal of Computational Biology, 2020, 27, 565-598.	1.6	10
70	A mixed integer linear programming model to reconstruct phylogenies from single nucleotide polymorphism haplotypes under the maximum parsimony criterion. Algorithms for Molecular Biology, 2013, 8, 3.	1.2	9
71	Network and Pathway Analysis of Cancer Susceptibility (A). Cancer Informatics, 2014, 13s5, CIN.S24095.	1.9	9
72	Simple Reconstruction of Binary Near-Perfect Phylogenetic Trees. Lecture Notes in Computer Science, 2006, , 799-806.	1.3	9

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73	OPTIMAL IMPERFECT PHYLOGENY RECONSTRUCTION AND HAPLOTYPING (IPPH). , 2006, , .		9
74	Evaluating Spatial Constraints in Cellular Assembly Processes Using a Monte Carlo Approach. Cell Biochemistry and Biophysics, 2006, 45, 195-202.	1.8	8
75	Automated deconvolution of structured mixtures from heterogeneous tumor genomic data. PLoS Computational Biology, 2017, 13, e1005815.	3.2	8
76	Efficient stochastic sampling of first-passage times with applications to self-assembly simulations. Journal of Chemical Physics, 2008, 129, 204109.	3.0	7
77	Unified regression model of binding equilibria in crowded environments. Scientific Reports, 2011, 1, 97.	3.3	7
78	Generalized Buneman Pruning for Inferring the Most Parsimonious Multi-State Phylogeny. Journal of Computational Biology, 2011, 18, 445-457.	1.6	7
79	Modeling Effects of RNA on Capsid Assembly Pathways via Coarse-Grained Stochastic Simulation. PLoS ONE, 2016, 11, e0156547.	2.5	7
80	Robust and accurate deconvolution of tumor populations uncovers evolutionary mechanisms of breast cancer metastasis. Bioinformatics, 2020, 36, i407-i416.	4.1	7
81	Modeling molecular interactions to understand spatial crowding effects on heterodimer formations. Physical Review E, 2007, 76, 041904.	2.1	6
82	Investigating Scaling Effects on Virus Capsid-Like Self-Assembly Using Discrete Event Simulations. IEEE Transactions on Nanobioscience, 2007, 6, 235-241.	3.3	6
83	Editorial. Bioinformatics, 2014, 30, i1-i2.	4.1	6
84	3D Collagen Vascular Tumor-on-a-Chip Mimetics for Dynamic Combinatorial Drug Screening. Molecular Cancer Therapeutics, 2021, 20, 1210-1219.	4.1	6
85	A Consensus Tree Approach for Reconstructing Human Evolutionary History and Detecting Population Substructure. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 918-928.	3.0	5
86	A method for efficient Bayesian optimization of self-assembly systems from scattering data. BMC Systems Biology, 2018, 12, 65.	3.0	5
87	Tumor heterogeneity assessed by sequencing and fluorescence <i>in situ</i> hybridization (FISH) data. Bioinformatics, 2021, 37, 4704-4711.	4.1	5
88	Understanding actin organization in cell structure through lattice based Monte Carlo simulations. Mcb Mechanics and Chemistry of Biosystems, 2004, 1, 123-31.	0.3	5
89	Implementation of a Discrete Event Simulator For Biological Self-Assembly Systems. , 0, , .		4
90	Parameter effects on binding chemistry in crowded media using a two-dimensional stochastic off-lattice model. Physical Review E, 2009, 80, 041918.	2.1	4

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91	Medoidshift clustering applied to genomic bulk tumor data. BMC Genomics, 2016, 17, 6.	2.8	4
92	Tumor Copy Number Deconvolution Integrating Bulk and Single-Cell Sequencing Data. Lecture Notes in Computer Science, 2019, , 174-189.	1.3	3
93	Computational Models for Cancer Phylogenetics. Computational Biology, 2019, , 243-275.	0.2	3
94	Neural Network Deconvolution Method for Resolving Pathway-Level Progression of Tumor Clonal Expression Programs With Application to Breast Cancer Brain Metastases. Frontiers in Physiology, 2020, 11, 1055.	2.8	3
95	Inferring Piecewise Ancestral History from Haploid Sequences. Lecture Notes in Computer Science, 2004, , 62-73.	1.3	3
96	Three-Dimensional Stochastic Off-Lattice Model of Binding Chemistry in Crowded Environments. PLoS ONE, 2012, 7, e30131.	2.5	3
97	Phylogenies Derived from Matched Transcriptome Reveal the Evolution of Cell Populations and Temporal Order of Perturbed Pathways in Breast Cancer Brain Metastases. Lecture Notes in Computer Science, 2019, , 3-28.	1.3	3
98	Optimal imperfect phylogeny reconstruction and haplotyping (IPPH). Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference, 2006, , 199-210.	0.4	3
99	Inference of tumor phylogenies from genomic assays on heterogeneous samples. , 2011, , .		2
100	Novel Multisample Scheme for Inferring Phylogenetic Markers from Whole Genome Tumor Profiles. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1422-1431.	3.0	2
101	Assessing the contribution of tumor mutational phenotypes to cancer progression risk. PLoS Computational Biology, 2021, 17, e1008777.	3.2	2
102	Joint Clustering of Single-Cell Sequencing and Fluorescence In Situ Hybridization Data for Reconstructing Clonal Heterogeneity in Cancers. Journal of Computational Biology, 2021, 28, 1035-1051.	1.6	2
103	ConTreeDP: A consensus method of tumor trees based on maximum directed partition support problem. , 2021, , .		2
104	Reconstructing tumor clonal lineage trees incorporating single-nucleotide variants, copy number alterations and structural variations. Bioinformatics, 2022, 38, i125-i133.	4.1	2
105	Haplotype Parsing. Applied Bioinformatics, 2004, 3, 181-191.	1.6	1
106	Approximate Dynamic Programming using Halfspace Queries and Multiscale Monge Decomposition. , 2011, , .		1
107	Novel Multi-sample Scheme for Inferring Phylogenetic Markers from Whole Genome Tumor Profiles. Lecture Notes in Computer Science, 2012, , 250-262.	1.3	1
108	Applying Derivative-Free Optimization to Fit Kinetic Parameters of Viral Capsid Self-Assembly Models from Multi-Source Bulk in vitro Data. Biophysical Journal, 2015, 108, 470a-471a.	0.5	1

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109	Derivative-Free Optimization of Rate Parameters of Capsid Assembly Models from Bulk in Vitro Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 844-855.	3.0	1
110	A Consensus Tree Approach for Reconstructing Human Evolutionary History and Detecting Population Substructure. Lecture Notes in Computer Science, 2010, , 167-178.	1.3	1
111	Generalized Buneman Pruning for Inferring the Most Parsimonious Multi-state Phylogeny. Lecture Notes in Computer Science, 2010, , 369-383.	1.3	1
112	An Optimization-Based Sampling Scheme for Phylogenetic Trees. Lecture Notes in Computer Science, 2011, , 252-266.	1.3	1
113	Network-Based Inference of Cancer Progression from Microarray Data. , 2008, , 268-279.		1
114	Algorithms for association study design using a generalized model of haplotype conservation. Proceedings, 2004, , 90-7.	0.0	1
115	RELAXING HAPLOTYPE BLOCK MODELS FOR ASSOCIATION TESTING. , 2005, , .		0
116	A human genome-wide library of local phylogeny predictions for whole-genome inference problems. BMC Genomics, 2008, 9, 389.	2.8	0
117	Response of an Actin Filament Network Model Under Cyclic Stretching Through a Coarse Grained Monte Carlo Approach. , 2010, , .		0
118	An Optimization-Based Sampling Scheme for Phylogenetic Trees. Journal of Computational Biology, 2011, 18, 1599-1609.	1.6	0
119	Coalescent-based method for learning parameters of admixture events from large-scale genetic variation data. , 2012, , .		0
120	Tumor Phylogenetics in the NGS Era: Strategies, Challenges, and Future Prospects. , 2013, , 335-357.		0
121	Coalescent-Based Method for Learning Parameters of Admixture Events from Large-Scale Genetic Variation Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1137-1149.	3.0	0
122	Reply to 'Complexity of molecular crowding in cell-free enzymatic reaction networks'. Nature Nanotechnology, 2014, 9, 407-408.	31.5	0
123	Computationally Projecting the Influence of Nucleic Acid on Pathways of Nucleation-Limited Virus Capsid Assembly. Biophysical Journal, 2015, 108, 319a.	0.5	0
124	Tumor Copy Number Data Deconvolution Integrating Bulk and Single-cell Sequencing Data. , 2018, , .		0
125	RECOMB 2020 Special Issue. Journal of Computational Biology, 2021, 28, 345-345.	1.6	0
126	RECOMB 2020 Special Issue. Journal of Computational Biology, 2021, 28, 433-434.	1.6	0



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127	Bridging Mechanical Stimulation of Cellular and Molecular Structure Through Lattice Based Computational Simulations. , 2004, , .		0
128	Phylogenetics of Heterogeneous Samples. Lecture Notes in Computer Science, 2011, , 1-1.	1.3	0
129	Abstract 2182: Reconstructing evolutionary models of tumor progression from single-cell heterogeneity data. , 2015, , .		0
130	Abstract 4833: Single-cell genetic analysis reveals insights into clonal development of cervical cancer and confirms TERC as an early and dominant aberration. , 2015, , .		0
131	Abstract 1934: Improved deconvolution of heterogeneous tumor data to reconstruct clonal evolution from bulk genomic samples. , 2015, , .		0
132	Haplotype motifs: an algorithmic approach to locating evolutionarily conserved patterns in haploid sequences. Proceedings, 2003, 2, 306-14.	0.1	0
133	Semi-deconvolution of bulk and single-cell RNA-seq data with application to metastatic progression in breast cancer. Bioinformatics, 2022, 38, i386-i394.	4.1	0