

Russell S Schwartz

List of Publications by Year in descending order

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Version: 2024-02-01

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	Reconstructing tumor clonal lineage trees incorporating single-nucleotide variants, copy number alterations and structural variations. <i>Bioinformatics</i> , 2022, 38, i125-i133.	4.1	2
2	Semi-deconvolution of bulk and single-cell RNA-seq data with application to metastatic progression in breast cancer. <i>Bioinformatics</i> , 2022, 38, i386-i394.	4.1	0
3	3D Collagen Vascular Tumor-on-a-Chip Mimetics for Dynamic Combinatorial Drug Screening. <i>Molecular Cancer Therapeutics</i> , 2021, 20, 1210-1219.	4.1	6
4	Assessing the contribution of tumor mutational phenotypes to cancer progression risk. <i>PLoS Computational Biology</i> , 2021, 17, e1008777.	3.2	2
5	RECOMB 2020 Special Issue. <i>Journal of Computational Biology</i> , 2021, 28, 345-345.	1.6	0
6	RECOMB 2020 Special Issue. <i>Journal of Computational Biology</i> , 2021, 28, 433-434.	1.6	0
7	Tumor heterogeneity assessed by sequencing and fluorescence <i>in situ</i> hybridization (FISH) data. <i>Bioinformatics</i> , 2021, 37, 4704-4711.	4.1	5
8	Joint Clustering of Single-Cell Sequencing and Fluorescence In Situ Hybridization Data for Reconstructing Clonal Heterogeneity in Cancers. <i>Journal of Computational Biology</i> , 2021, 28, 1035-1051.	1.6	2
9	ConTreeDP: A consensus method of tumor trees based on maximum directed partition support problem. , 2021, , .		2
10	Neural Network Deconvolution Method for Resolving Pathway-Level Progression of Tumor Clonal Expression Programs With Application to Breast Cancer Brain Metastases. <i>Frontiers in Physiology</i> , 2020, 11, 1055.	2.8	3
11	Robust and accurate deconvolution of tumor populations uncovers evolutionary mechanisms of breast cancer metastasis. <i>Bioinformatics</i> , 2020, 36, i407-i416.	4.1	7
12	Tumor Copy Number Deconvolution Integrating Bulk and Single-Cell Sequencing Data. <i>Journal of Computational Biology</i> , 2020, 27, 565-598.	1.6	10
13	Tumor Copy Number Deconvolution Integrating Bulk and Single-Cell Sequencing Data. <i>Lecture Notes in Computer Science</i> , 2019, , 174-189.	1.3	3
14	Computational Models for Cancer Phylogenetics. <i>Computational Biology</i> , 2019, , 243-275.	0.2	3
15	Phylogenies Derived from Matched Transcriptome Reveal the Evolution of Cell Populations and Temporal Order of Perturbed Pathways in Breast Cancer Brain Metastases. <i>Lecture Notes in Computer Science</i> , 2019, , 3-28.	1.3	3
16	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
17	Tumor Copy Number Data Deconvolution Integrating Bulk and Single-cell Sequencing Data. , 2018, , .		0
18	Deconvolution and phylogeny inference of structural variations in tumor genomic samples. <i>Bioinformatics</i> , 2018, 34, i357-i365.	4.1	40

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19	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
20	A method for efficient Bayesian optimization of self-assembly systems from scattering data. <i>BMC Systems Biology</i> , 2018, 12, 65.	3.0	5
21	Machine Learning and Radiogenomics: Lessons Learned and Future Directions. <i>Frontiers in Oncology</i> , 2018, 8, 228.	2.8	54
22	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
23	Derivative-Free Optimization of Rate Parameters of Capsid Assembly Models from Bulk in Vitro Data. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 844-855.	3.0	1
24	The evolution of tumour phylogenetics: principles and practice. <i>Nature Reviews Genetics</i> , 2017, 18, 213-229.	16.3	240
25	Quantitative computational models of molecular self-assembly in systems biology. <i>Physical Biology</i> , 2017, 14, 035003.	1.8	13
26	Automated deconvolution of structured mixtures from heterogeneous tumor genomic data. <i>PLoS Computational Biology</i> , 2017, 13, e1005815.	3.2	8
27	Applying, Evaluating and Refining Bioinformatics Core Competencies (An Update from the Curriculum) <i>TJ ETQq1 1 0.784314 10 BT /Ov</i>	3.2	29
28	Modeling Effects of RNA on Capsid Assembly Pathways via Coarse-Grained Stochastic Simulation. <i>PLoS ONE</i> , 2016, 11, e0156547.	2.5	7
29	Medoidshift clustering applied to genomic bulk tumor data. <i>BMC Genomics</i> , 2016, 17, 6.	2.8	4
30	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
31	Classifying the Progression of Ductal Carcinoma from Single-Cell Sampled Data via Integer Linear Programming: A Case Study. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2016, 13, 643-655.	3.0	33
32	FISHtrees 3.0: Tumor Phylogenetics Using a Ploidy Probe. <i>PLoS ONE</i> , 2016, 11, e0158569.	2.5	13
33	Applying Derivative-Free Optimization to Fit Kinetic Parameters of Viral Capsid Self-Assembly Models from Multi-Source Bulk in vitro Data. <i>Biophysical Journal</i> , 2015, 108, 470a-471a.	0.5	1
34	Structurally Governed Cell Mechanotransduction through Multiscale Modeling. <i>Scientific Reports</i> , 2015, 5, 8622.	3.3	10
35	Reference-free inference of tumor phylogenies from single-cell sequencing data. <i>BMC Genomics</i> , 2015, 16, S7.	2.8	10
36	Computationally Projecting the Influence of Nucleic Acid on Pathways of Nucleation-Limited Virus Capsid Assembly. <i>Biophysical Journal</i> , 2015, 108, 319a.	0.5	0

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37	A simplicial complex-based approach to unmixing tumor progression data. BMC Bioinformatics, 2015, 16, 254.	2.6	11
38	Inferring models of multiscale copy number evolution for single-tumor phylogenetics. Bioinformatics, 2015, 31, i258-i267.	4.1	28
39	Machine Learning Approaches for Predicting Radiation Therapy Outcomes: A Clinician's Perspective. International Journal of Radiation Oncology Biology Physics, 2015, 93, 1127-1135.	0.8	153
40	Identification of novel mutations by exome sequencing in African American colorectal cancer patients. Cancer, 2015, 121, 34-42.	4.1	36
41	Abstract 2182: Reconstructing evolutionary models of tumor progression from single-cell heterogeneity data. , 2015, , .		0
42	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
43	Abstract 1934: Improved deconvolution of heterogeneous tumor data to reconstruct clonal evolution from bulk genomic samples. , 2015, , .		0
44	Bioinformatics Curriculum Guidelines: Toward a Definition of Core Competencies. PLoS Computational Biology, 2014, 10, e1003496.	3.2	102
45	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
46	Phenotypic Signatures Arising from Unbalanced Bacterial Growth. PLoS Computational Biology, 2014, 10, e1003751.	3.2	10
47	Editorial. Bioinformatics, 2014, 30, i1-i2.	4.1	6
48	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
49	A Novel Subset of Human tumors that Simultaneously Overexpress Multiple E2F-responsive Genes Found in Breast, Ovarian, and Prostate Cancers. Cancer Informatics, 2014, 13s5, CIN.S14062.	1.9	17
50	Applying Molecular Crowding Models to Simulations of Virus Capsid Assembly In Vitro. Biophysical Journal, 2014, 106, 310-320.	0.5	31
51	Reply to 'Complexity of molecular crowding in cell-free enzymatic reaction networks'. Nature Nanotechnology, 2014, 9, 407-408.	31.5	0
52	Network and Pathway Analysis of Cancer Susceptibility (A). Cancer Informatics, 2014, 13s5, CIN.S24095.	1.9	9
53	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
54	Molecular crowding shapes gene expression in synthetic cellular nanosystems. Nature Nanotechnology, 2013, 8, 602-608.	31.5	215

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55	Tumor Phylogenetics in the NGS Era: Strategies, Challenges, and Future Prospects. , 2013, , 335-357.		0
56	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
57	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
58	Phylogenetic analysis of multiprobe fluorescence in situ hybridization data from tumor cell populations. Bioinformatics, 2013, 29, i189-i198.	4.1	40
59	A Report of the Curriculum Task Force of the ISCB Education Committee. PLoS Computational Biology, 2012, 8, e1002570.	3.2	10
60	Inference of Tumor Phylogenies from Genomic Assays on Heterogeneous Samples. Journal of Biomedicine and Biotechnology, 2012, 2012, 1-16.	3.0	12
61	Stochastic steady state gain in a gene expression process with mRNA degradation control. Journal of the Royal Society Interface, 2012, 9, 1589-1598.	3.4	16
62	Novel Multi-sample Scheme for Inferring Phylogenetic Markers from Whole Genome Tumor Profiles. Lecture Notes in Computer Science, 2012, , 250-262.	1.3	1
63	Coalescent-based method for learning parameters of admixture events from large-scale genetic variation data. , 2012, , .		0
64	Biological colloid engineering: Self-assembly of dipolar ferromagnetic chains in a functionalized biogenic ferrofluid. Applied Physics Letters, 2012, 101, 063701.	3.3	12
65	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. American Journal of Pathology, 2012, 181, 1807-1822.	3.8	104
66	Surveying Capsid Assembly Pathways through Simulation-Based Data Fitting. Biophysical Journal, 2012, 103, 1545-1554.	0.5	31
67	Modeling Nuclear Blebs in a Nucleoskeleton of Independent Filament Networks. Cellular and Molecular Bioengineering, 2012, 5, 73-81.	2.1	20
68	Three-Dimensional Stochastic Off-Lattice Model of Binding Chemistry in Crowded Environments. PLoS ONE, 2012, 7, e30131.	2.5	3
69	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
70	Unified regression model of binding equilibria in crowded environments. Scientific Reports, 2011, 1, 97.	3.3	7
71	An Optimization-Based Sampling Scheme for Phylogenetic Trees. Journal of Computational Biology, 2011, 18, 1599-1609.	1.6	0
72	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

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73	Generalized Buneman Pruning for Inferring the Most Parsimonious Multi-State Phylogeny. <i>Journal of Computational Biology</i> , 2011, 18, 445-457.	1.6	7
74	Inference of tumor phylogenies from genomic assays on heterogeneous samples. , 2011, , .		2
75	Approximate Dynamic Programming using Halfspace Queries and Multiscale Monge Decomposition. , 2011, , .		1
76	An Optimization-Based Sampling Scheme for Phylogenetic Trees. <i>Lecture Notes in Computer Science</i> , 2011, , 252-266.	1.3	1
77	Phylogenetics of Heterogeneous Samples. <i>Lecture Notes in Computer Science</i> , 2011, , 1-1.	1.3	0
78	Applying unmixing to gene expression data for tumor phylogeny inference. <i>BMC Bioinformatics</i> , 2010, 11, 42.	2.6	54
79	Response of an Actin Filament Network Model Under Cyclic Stretching Through a Coarse Grained Monte Carlo Approach. , 2010, , .		0
80	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
81	Discrete, continuous, and stochastic models of protein sorting in the Golgi apparatus. <i>Physical Review E</i> , 2010, 81, 011914.	2.1	18
82	Robust unmixing of tumor states in array comparative genomic hybridization data. <i>Bioinformatics</i> , 2010, 26, i106-i114.	4.1	28
83	A Consensus Tree Approach for Reconstructing Human Evolutionary History and Detecting Population Substructure. <i>Lecture Notes in Computer Science</i> , 2010, , 167-178.	1.3	1
84	Generalized Buneman Pruning for Inferring the Most Parsimonious Multi-state Phylogeny. <i>Lecture Notes in Computer Science</i> , 2010, , 369-383.	1.3	1
85	Parameter effects on binding chemistry in crowded media using a two-dimensional stochastic off-lattice model. <i>Physical Review E</i> , 2009, 80, 041918.	2.1	4
86	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
87	A human genome-wide library of local phylogeny predictions for whole-genome inference problems. <i>BMC Genomics</i> , 2008, 9, 389.	2.8	0
88	Exploring the Parameter Space of Complex Self-Assembly through Virus Capsid Models. <i>Biophysical Journal</i> , 2008, 94, 772-783.	0.5	59
89	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
90	Mixed Integer Linear Programming for Maximum-Parsimony Phylogeny Inference. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2008, 5, 323-331.	3.0	50

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91	Pathway Complexity of Model Virus Capsid Assembly Systems. Computational and Mathematical Methods in Medicine, 2008, 9, 277-293.	1.3	18
92	Efficient stochastic sampling of first-passage times with applications to self-assembly simulations. Journal of Chemical Physics, 2008, 129, 204109.	3.0	7
93	Stochastic off-lattice modeling of molecular self-assembly in crowded environments by Green's function reaction dynamics. Physical Review E, 2008, 78, 031911.	2.1	17
94	Network-Based Inference of Cancer Progression from Microarray Data. , 2008, , 268-279.		1
95	RECONSTRUCTING TUMOR PHYLOGENIES FROM HETEROGENEOUS SINGLE-CELL DATA. Journal of Bioinformatics and Computational Biology, 2007, 05, 407-427.	0.8	35
96	Modeling molecular interactions to understand spatial crowding effects on heterodimer formations. Physical Review E, 2007, 76, 041904.	2.1	6
97	Algorithms for Efficient Near-Perfect Phylogenetic Tree Reconstruction in Theory and Practice. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2007, 4, 561-571.	3.0	20
98	Investigating Scaling Effects on Virus Capsid-Like Self-Assembly Using Discrete Event Simulations. IEEE Transactions on Nanobioscience, 2007, 6, 235-241.	3.3	6
99	Evolution of genes and genomes on the Drosophila phylogeny. Nature, 2007, 450, 203-218.	27.8	1,886
100	Direct maximum parsimony phylogeny reconstruction from genotype data. BMC Bioinformatics, 2007, 8, 472.	2.6	13
101	A comparative genomics approach to identifying the plasticity transcriptome. BMC Neuroscience, 2007, 8, 20.	1.9	24
102	Computational models of molecular self-organization in cellular environments. Cell Biochemistry and Biophysics, 2007, 48, 16-31.	1.8	12
103	Efficiently Finding the Most Parsimonious Phylogenetic Tree Via Linear Programming. , 2007, , 37-48.		15
104	Simulation Study of the Contribution of Oligomer/Oligomer Binding to Capsid Assembly Kinetics. Biophysical Journal, 2006, 90, 57-64.	0.5	67
105	Frequencies of hydrophobic and hydrophilic runs and alternations in proteins of known structure. Protein Science, 2006, 15, 102-112.	7.6	42
106	Evaluating Spatial Constraints in Cellular Assembly Processes Using a Monte Carlo Approach. Cell Biochemistry and Biophysics, 2006, 45, 195-202.	1.8	8
107	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
108	Simple Reconstruction of Binary Near-Perfect Phylogenetic Trees. Lecture Notes in Computer Science, 2006, , 799-806.	1.3	9

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109	Fixed Parameter Tractability of Binary Near-Perfect Phylogenetic Tree Reconstruction. Lecture Notes in Computer Science, 2006, , 667-678.	1.3	14
110	OPTIMAL IMPERFECT PHYLOGENY RECONSTRUCTION AND HAPLOTYPING (IPPH). , 2006, , .		9
111	Optimal imperfect phylogeny reconstruction and haplotyping (IPPH). Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference, 2006, , 199-210.	0.4	3
112	RELAXING HAPLOTYPE BLOCK MODELS FOR ASSOCIATION TESTING. , 2005, , .		0
113	Queue-based method for efficient simulation of biological self-assembly systems. Journal of Computational Physics, 2005, 204, 100-120.	3.8	28
114	Optimal Haplotype Block-Free Selection of Tagging SNPs for Genome-Wide Association Studies. Genome Research, 2004, 14, 1633-1640.	5.5	113
115	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
116	Haplotype Parsing. Applied Bioinformatics, 2004, 3, 181-191.	1.6	1
117	Inferring Piecewise Ancestral History from Haploid Sequences. Lecture Notes in Computer Science, 2004, , 62-73.	1.3	3
118	Bridging Mechanical Stimulation of Cellular and Molecular Structure Through Lattice Based Computational Simulations. , 2004, , .		0
119	Algorithms for association study design using a generalized model of haplotype conservation. Proceedings, 2004, , 90-7.	0.0	1
120	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
121	Robustness of Inference of Haplotype Block Structure. Journal of Computational Biology, 2003, 10, 13-19.	1.6	54
122	Haplotypes and informative SNP selection algorithms. , 2003, , .		52
123	Haplotype motifs: an algorithmic approach to locating evolutionarily conserved patterns in haploid sequences. Proceedings, 2003, 2, 306-14.	0.1	0
124	Epitope prediction algorithms for peptide-based vaccine design. Proceedings, 2003, 2, 17-26.	0.1	16
125	The Sequence of the Human Genome. Science, 2001, 291, 1304-1351.	12.6	12,623
126	Frequencies of amino acid strings in globular protein sequences indicate suppression of blocks of consecutive hydrophobic residues. Protein Science, 2001, 10, 1023-1031.	7.6	83

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127	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
128	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
129	Local rule mechanism for selecting icosahedral shell geometry. <i>Discrete Applied Mathematics</i> , 2000, 104, 97-111.	0.9	14
130	“Local Rules” Theory Applied to Polyomavirus Polymorphic Capsid Assemblies. <i>Virology</i> , 2000, 268, 461-470.	2.4	44
131	Lattice Simulations of Aggregation Funnels for Protein Folding. <i>Journal of Computational Biology</i> , 1999, 6, 143-162.	1.6	48
132	Local Rules Simulation of the Kinetics of Virus Capsid Self-Assembly. <i>Biophysical Journal</i> , 1998, 75, 2626-2636.	0.5	148
133	Implementation of a Discrete Event Simulator For Biological Self-Assembly Systems. , 0, , .		4