

# Jonathan Arnold

## List of Publications by Year in descending order

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134  
papers

8,231  
citations

81743

39  
h-index

48187

88  
g-index

136  
all docs

136  
docs citations

136  
times ranked

7395  
citing authors

#	ARTICLE	IF	CITATIONS
1	“How Do We Do This at a Distance?” A Descriptive Study of Remote Undergraduate Research Programs during COVID-19. <i>CBE Life Sciences Education</i> , 2022, 21, ar1.	1.1	17
2	Ensemble Methods for Identifying RNA Operons and Regulons in the Clock Network of <i>Neurospora crassa</i> . <i>IEEE Access</i> , 2022, 10, 32510-32524.	2.6	3
3	Characterizing the gene-environment interaction underlying natural morphological variation in <i>Neurospora crassa</i> conidiophores using high-throughput phenomics and transcriptomics. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	2
4	The macroscopic limit to synchronization of cellular clocks in single cells of <i>Neurospora crassa</i> . <i>Scientific Reports</i> , 2022, 12, 6750.	1.6	1
5	Uncovering in vivo biochemical patterns from time-series metabolic dynamics. <i>PLoS ONE</i> , 2022, 17, e0268394.	1.1	3
6	Are we there yet? A machine learning architecture to predict organotropic metastases. <i>BMC Medical Genomics</i> , 2021, 14, 281.	0.7	0
7	RTExtract: time-series NMR spectra quantification based on 3D surface ridge tracking. <i>Bioinformatics</i> , 2020, 36, 5068-5075.	1.8	7
8	Wild Isolates of <i>Neurospora crassa</i> Reveal Three Conidiophore Architectural Phenotypes. <i>Microorganisms</i> , 2020, 8, 1760.	1.6	2
9	Identifying a stochastic clock network with light entrainment for single cells of <i>Neurospora crassa</i> . <i>Scientific Reports</i> , 2020, 10, 15168.	1.6	3
10	Single Cells of <i>Neurospora Crassa</i> Show Circadian Oscillations, Light Entrainment, Temperature Compensation, and Phase Synchronization. <i>IEEE Access</i> , 2019, 7, 49403-49417.	2.6	6
11	Continuous in vivo Metabolism by NMR. <i>Frontiers in Molecular Biosciences</i> , 2019, 6, 26.	1.6	41
12	What is Phase in Cellular Clocks?. <i>Yale Journal of Biology and Medicine</i> , 2019, 92, 169-178.	0.2	3
13	Discovering Regulators in Post-Transcriptional Control of the Biological Clock of <i>Neurospora crassa</i> Using Variable Topology Ensemble Methods on GPUs. <i>IEEE Access</i> , 2018, 6, 54582-54594.	2.6	6
14	Ensemble methods for stochastic networks with special reference to the biological clock of <i>Neurospora crassa</i> . <i>PLoS ONE</i> , 2018, 13, e0196435.	1.1	9
15	Aging and the Biological Clock. <i>Healthy Ageing and Longevity</i> , 2017, , 211-234.	0.2	5
16	Measuring synchronization of stochastic oscillators in biology. <i>Journal of Physics: Conference Series</i> , 2016, 750, 012001.	0.3	5
17	<i>lac1</i> and <i>lag1</i> with <i>ras1</i> affect aging and the biological clock in <i>Neurospora crassa</i> . <i>Ecology and Evolution</i> , 2016, 6, 8341-8351.	0.8	6
18	Synchronizing stochastic circadian oscillators in single cells of <i>Neurospora crassa</i> . <i>Scientific Reports</i> , 2016, 6, 35828.	1.6	17

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19	Discovering Regulatory Network Topologies Using Ensemble Methods on GPGPUs With Special Reference to the Biological Clock of <i>Neurospora crassa</i> . IEEE Access, 2015, 3, 27-42.	2.6	16
20	Secondary structural entropy in RNA switch (Riboswitch) identification. BMC Bioinformatics, 2015, 16, 133.	1.2	15
21	The aging biological clock in <i>Neurospora crassa</i> . Ecology and Evolution, 2014, 4, 3494-3507.	0.8	16
22	APOE $\epsilon$ 4, rated life experiences, and affect among centenarians. Aging and Mental Health, 2014, 18, 240-247.	1.5	9
23	A MINE Alternative to D-Optimal Designs for the Linear Model. PLoS ONE, 2014, 9, e110234.	1.1	5
24	Solving Nonlinear Systems of First Order Ordinary Differential Equations Using a Galerkin Finite Element Method. IEEE Access, 2013, 1, 408-417.	2.6	10
25	Solving Large Nonlinear Systems of First-Order Ordinary Differential Equations With Hierarchical Structure Using Multi-GPGPUs and an Adaptive Runge Kutta ODE Solver. IEEE Access, 2013, 1, 770-777.	2.6	20
26	Understanding Dementia Prevalence Among Centenarians. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2012, 67A, 358-365.	1.7	52
27	Telomere maintenance genes SIRT1 and XRCC6 impact age-related decline in telomere length but only SIRT1 is associated with human longevity. Biogerontology, 2012, 13, 119-131.	2.0	85
28	Systems Biology of the qa Gene Cluster in <i>Neurospora crassa</i> . PLoS ONE, 2011, 6, e20671.	1.1	24
29	<i>HRAS1</i> and <i>LASS1</i> with <i>APOE</i> are associated with human longevity and healthy aging. Aging Cell, 2010, 9, 698-708.	3.0	75
30	Predicting Successful Aging in a Population-Based Sample of Georgia Centenarians. Current Gerontology and Geriatrics Research, 2010, 2010, 1-9.	1.6	45
31	Cognitive Performance in Centenarians and the Oldest Old: Norms from the Georgia Centenarian Study. Aging, Neuropsychology, and Cognition, 2010, 17, 575-590.	0.7	47
32	Next-Generation Sequencing. Journal of Biomedicine and Biotechnology, 2010, 2010, 1-2.	3.0	437
33	KINSOLVER: A simulator for computing large ensembles of biochemical and gene regulatory networks. Computers and Mathematics With Applications, 2009, 57, 420-435.	1.4	38
34	LIKELIHOOD OF A PARTICULAR ORDER OF GENETIC MARKERS AND THE CONSTRUCTION OF GENETIC MAPS. Journal of Bioinformatics and Computational Biology, 2008, 06, 125-162.	0.3	1
35	Systems Biology of the Clock in <i>Neurospora crassa</i> . PLoS ONE, 2008, 3, e3105.	1.1	86
36	DESIGN AND ANALYSIS OF AN EFFICIENT RECURSIVE LINKING ALGORITHM FOR CONSTRUCTING LIKELIHOOD BASED GENETIC MAPS FOR A LARGE NUMBER OF MARKERS. Journal of Bioinformatics and Computational Biology, 2007, 05, 201-250.	0.3	1

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37	A genetic network for the clock of <i>Neurospora crassa</i> . Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 2809-2814.	3.3	93
38	Systems biology of the <i>Neurospora</i> biological clock. IET Systems Biology, 2007, 1, 257-265.	0.8	6
39	Exact Sample Size Needed to Detect Dependence in $2 \times 2$ Tables. Biometrics, 2007, 63, 1245-1252.	0.8	10
40	Transcriptome of <i>Pneumocystis carinii</i> during Fulminate Infection: Carbohydrate Metabolism and the Concept of a Compatible Parasite. PLoS ONE, 2007, 2, e423.	1.1	58
41	Genome-wide expression analysis of genetic networks in <i>Neurospora crassa</i> . Bioinformatics, 2007, 1, 390-395.	0.2	4
42	Methodological Considerations in Studying Centenarians: Lessons Learned From the Georgia Centenarian Studies. Annual Review of Gerontology and Geriatrics, 2007, 27, 231-264.	0.5	73
43	Exact sample sizes needed to detect dependence in $2 \times 3$ tables. Theoretical Population Biology, 2006, 69, 111-120.	0.5	4
44	Competitive coexistence of two <i>Pneumocystis</i> species. Infection, Genetics and Evolution, 2006, 6, 177-186.	1.0	16
45	EFFICIENT RECURSIVE LINKING ALGORITHM FOR COMPUTING THE LIKELIHOOD OF AN ORDER OF A LARGE NUMBER OF GENETIC MARKERS. , 2006, , .		0
46	GCSDB: an integrated database system for the Georgia Centenarian Study. Bioinformatics, 2006, 1, 214-9.	0.2	3
47	The human commensal yeast, <i>Candida albicans</i> , has an ancient origin. Fungal Genetics and Biology, 2005, 42, 444-451.	0.9	47
48	ESSENTIAL EUKARYOTIC CORE. Evolution; International Journal of Organic Evolution, 2004, 58, 441.	1.1	0
49	ESSENTIAL EUKARYOTIC CORE. Evolution; International Journal of Organic Evolution, 2004, 58, 441-446.	1.1	8
50	Quality of service for workflows and web service processes. Web Semantics, 2004, 1, 281-308.	2.2	723
51	Metabolomics. Mycology, 2004, , 597-633.	0.5	1
52	IntelliGEN: A Distributed Workflow System for Discovering Protein-Protein Interactions. Distributed and Parallel Databases, 2003, 13, 43-72.	1.0	67
53	Revelations from a bread mould. Nature, 2003, 422, 821-822.	13.7	13
54	Mapping by Sequencing the <i>Pneumocystis</i> Genome Using the Ordering DNA Sequences V3 Tool. Genetics, 2003, 163, 1299-1313.	1.2	10

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55	Using Workflow to Build an Information Management System for a Geographically Distributed Genome Sequencing Initiative. , 2003, , .		9
56	An ensemble method for identifying regulatory circuits with special reference to the qa gene cluster of <i>Neurospora crassa</i> . Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 16904-16909.	3.3	110
57	Population structure of <i>Candida albicans</i> , a member of the human flora, as determined by microsatellite loci. Infection, Genetics and Evolution, 2002, 2, 57-68.	1.0	32
58	J3DV: A Java-based 3D database visualization tool. Software - Practice and Experience, 2002, 32, 443-463.	2.5	3
59	SOME COMPARISONS OF CLUSTERING AND CLASSIFICATION TECHNIQUES APPLIED TO TRANSCRIPTIONAL PROFILING DATA. , 2002, , .		5
60	An analysis of gene-finding programs for <i>Neurospora crassa</i> . Bioinformatics, 2001, 17, 901-912.	1.8	14
61	Physical mapping with automatic capture of hybridization data. Bioinformatics, 2001, 17, 205-213.	1.8	6
62	Genomics for Fungi. , 2001, , 267-297.		15
63	Foreword to the Special Section on Fungal Genomics. Genetics, 2001, 157, 933-933.	1.2	2
64	The <i>Neurospora crassa</i> Genome: Cosmid Libraries Sorted by Chromosome. Genetics, 2001, 157, 979-990.	1.2	51
65	Characterization of Agglutinin-like Sequence Genes From Non- <i>albicans</i> <i>Candida</i> and Phylogenetic Analysis of the ALS Family. Genetics, 2001, 157, 1555-1567.	1.2	75
66	Symbiont Survival and Host-Symbiont Disequilibria Under Differential Vertical Transmission. Genetics, 2000, 154, 1347-1365.	1.2	10
67	Towards understanding the evolution of the human commensal yeast <i>Candida albicans</i> . Microbiology (United Kingdom), 1999, 145, 1137-1143.	0.7	71
68	Title is missing!. Genetica, 1999, 105, 101-108.	0.5	6
69	Dynamics of Cytonuclear Disequilibria in Subdivided Populations. Journal of Theoretical Biology, 1998, 192, 99-111.	0.8	4
70	Parallel computing for chromosome reconstruction via ordering of DNA sequences. Parallel Computing, 1998, 24, 1177-1204.	1.3	6
71	In vitro reconstruction of the <i>Aspergillus</i> (= <i>Emericella</i> ) <i>nidulans</i> genome. Proceedings of the National Academy of Sciences of the United States of America, 1997, 94, 14564-14569.	3.3	62
72	Editorial. Fungal Genetics and Biology, 1997, 21, 254-257.	0.9	10

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73	Proposal for a Pneumocystis Genome Project. <i>Journal of Eukaryotic Microbiology</i> , 1997, 44, 7s-7s.	0.8	23
74	Constructing a Physical Map of the Pneumocystis Genome. <i>Journal of Eukaryotic Microbiology</i> , 1997, 44, 8s-8s.	0.8	15
75	The effects of unidirectional incompatibility on cytonuclear disequilibria in a hybrid zone. <i>Genetica</i> , 1997, 101, 215-224.	0.5	6
76	Dynamics and Equilibrium Behavior of Cytonuclear Disequilibria under Genetic Drift, Mutation, and Migration. <i>Theoretical Population Biology</i> , 1996, 50, 298-324.	0.5	17
77	Diagnostics and a Statistical Test of Neutrality Hypotheses Using the Dynamics of Cytonuclear Disequilibria. <i>Biometrics</i> , 1996, 52, 1042.	0.8	10
78	CYTONUCLEAR DISEQUILIBRIA IN HYBRID ZONES USING RAPD MARKERS. <i>Evolution; International Journal of Organic Evolution</i> , 1996, 50, 1702-1705.	1.1	1
79	Small sample properties for estimators of cytonuclear disequilibria. <i>Heredity</i> , 1996, 77, 396-399.	1.2	6
80	Parallel Computing of Physical Maps—A Comparative Study in SIMD and MIMD Parallelism. <i>Journal of Computational Biology</i> , 1996, 3, 503-528.	0.8	6
81	PARODS—a study of parallel algorithms for ordering DNA sequences. <i>Bioinformatics</i> , 1996, 12, 269-280.	1.8	2
82	Recognizing the forest for the trees: testing temporal patterns of cladogenesis using a null model of stochastic diversification. <i>Molecular Biology and Evolution</i> , 1996, 13, 833-849.	3.5	44
83	Cytonuclear Disequilibria in Hybrid Zones Using RAPD Markers. <i>Evolution; International Journal of Organic Evolution</i> , 1996, 50, 1702.	1.1	3
84	On the Consistency of a Physical Mapping Method to Reconstruct a Chromosome <i>in Vitro</i> . <i>Genetics</i> , 1996, 142, 267-284.	1.2	30
85	A Statistical Test of a Neutral Model Using the Dynamics of Cytonuclear Disequilibria. <i>Genetics</i> , 1996, 144, 1985-1992.	1.2	15
86	ODS_BOOTSTRAP: assessing the statistical reliability of physical maps by bootstrap resampling. <i>Bioinformatics</i> , 1994, 10, 625-634.	1.8	12
87	A fast random cost algorithm for physical mapping. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994, 91, 11094-11098.	3.3	43
88	The effects of cytoplasmic male sterility on cytonuclear disequilibria in hybrid zones. <i>Genetica</i> , 1993, 88, 37-50.	0.5	10
89	PCAP: probe choice and analysis package—a set of programs to aid in choosing synthetic oligomers for contig mapping. <i>Bioinformatics</i> , 1993, 9, 201-203.	1.8	8
90	ODS: ordering DNA sequences—a physical mapping algorithm based on simulated annealing. <i>Bioinformatics</i> , 1993, 9, 215-219.	1.8	20

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91	Cytonuclear Disequilibria in Hybrid Zones. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 1993, 24, 521-553.	6.7	128
92	The application of markov chain analysis to oligonucleotide frequency prediction and physical mapping of <i>Drosophila melanogaster</i> . <i>Nucleic Acids Research</i> , 1992, 20, 3651-3657.	6.5	15
93	CMAP: contig mapping and analysis package, a relational database for chromosome reconstruction. <i>Bioinformatics</i> , 1992, 8, 467-474.	1.8	2
94	A Table of Exact Sample Sizes for Use with Fisher's Exact Test for 2 x 2 Tables. <i>Biometrics</i> , 1992, 48, 1103.	0.8	24
95	On the Design of Genome Mapping Experiments Using Short Synthetic Oligonucleotides. <i>Biometrics</i> , 1992, 48, 337.	0.8	16
96	Dynamics of cytonuclear disequilibria in finite populations and comparison with a two-locus nuclear system. <i>Theoretical Population Biology</i> , 1992, 41, 1-25.	0.5	28
97	The use of simulated annealing in chromosome reconstruction experiments based on binary scoring. <i>Genetics</i> , 1992, 132, 591-601.	1.2	46
98	The effects of admixture and population subdivision on cytonuclear disequilibria. <i>Theoretical Population Biology</i> , 1991, 39, 273-300.	0.5	61
99	Chromosome-specific recombinant DNA libraries from the fungus <i>Aspergillus nidulans</i> . <i>Nucleic Acids Research</i> , 1991, 19, 3105-3109.	6.5	231
100	On the association of restriction fragment length polymorphisms across species boundaries. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1991, 88, 3967-3971.	3.3	12
101	THE EVOLUTIONARY GENETIC STATUS OF ICELANDIC EELS. <i>Evolution; International Journal of Organic Evolution</i> , 1990, 44, 1254-1262.	1.1	118
102	Genetic relatedness in open-pollinated families of two leguminous tree species, <i>Robinia pseudoacacia</i> L. and <i>Gleditsia triacanthos</i> L.. <i>Theoretical and Applied Genetics</i> , 1990, 80, 49-56.	1.8	43
103	The Evolutionary Genetic Status of Icelandic Eels. <i>Evolution; International Journal of Organic Evolution</i> , 1990, 44, 1254.	1.1	48
104	Generalized linear modeling methods for selection component experiments. <i>Theoretical Population Biology</i> , 1990, 37, 389-423.	0.5	20
105	An Analysis of Density-Dependent Viability Selection. <i>Journal of the American Statistical Association</i> , 1989, 84, 662-668.	1.8	2
106	The effects of assortative mating and migration on cytonuclear associations in hybrid zones. <i>Genetics</i> , 1989, 122, 923-934.	1.2	105
107	Mono- through hexanucleotide composition of the sense strand of yeast DNA: a Markov chain analysis. <i>Nucleic Acids Research</i> , 1988, 16, 7145-7158.	6.5	51
108	An epistatic mating system model can produce permanent cytonuclear disequilibria in a hybrid zone. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1988, 85, 1893-1896.	3.3	73

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109	Current versus historical population sizes in vertebrate species with high gene flow: a comparison based on mitochondrial DNA lineages and inbreeding theory for neutral mutations.. <i>Molecular Biology and Evolution</i> , 1988, 5, 331-44.	3.5	230
110	Recombination within a subclass of restriction fragment length polymorphisms may help link classical and molecular genetics.. <i>Genetics</i> , 1988, 120, 809-818.	1.2	26
111	Mono-through hexanucleotide composition of the <i>Escherichia coli</i> genome: a Markov chain analysis. <i>Nucleic Acids Research</i> , 1987, 15, 2611-2626.	6.5	102
112	The effect of codon usage on the oligonucleotide composition of the <i>E.coli</i> genome and identification of over-and underepresented sequences by Markov chain analysis. <i>Nucleic Acids Research</i> , 1987, 15, 2627-2638.	6.5	65
113	Intraspecific Phylogeography: The Mitochondrial DNA Bridge Between Population Genetics and Systematics. <i>Annual Review of Ecology, Evolution, and Systematics</i> , 1987, 18, 489-522.	6.7	2,444
114	Definition and Properties of Disequilibrium Statistics for Associations Between Nuclear and Cytoplasmic Genotypes. <i>Genetics</i> , 1987, 115, 755-768.	1.2	190
115	Selection for resistance to <i>Bacillus thuringiensis</i> subspecies <i>israelensis</i> in field and laboratory populations of the mosquito <i>Aedes aegypti</i> . <i>Journal of Invertebrate Pathology</i> , 1986, 47, 317-324.	1.5	83
116	Statistics of Natural Populations. III. Sequential Sampling Plans for the Estimation of Gene Frequencies. <i>Biometrics</i> , 1986, 42, 45.	0.8	3
117	Frequency-dependent viabilities of <i>Drosophila pseudoobscura</i> karyotypes. <i>Heredity</i> , 1986, 56, 7-17.	1.2	32
118	A comprehensive package for DNA sequence analysis in FORTRAN IV for the PDP-11. <i>Nucleic Acids Research</i> , 1986, 14, 239-254.	6.5	15
119	Comparison of the nucleotide sequence of soybean 18S rRNA with the sequences of other small-subunit rRNAs. <i>Journal of Molecular Evolution</i> , 1985, 21, 259-269.	0.8	168
120	STATISTICS OF NATURAL POPULATIONS. II. ESTIMATING AN ALLELE PROBABILITY IN FAMILIES DESCENDED FROM CRYPTIC MOTHERS. <i>Genetics</i> , 1985, 109, 785-798.	1.2	11
121	Demographic influences on mitochondrial DNA lineage survivorship in animal populations. <i>Journal of Molecular Evolution</i> , 1984, 20, 99-105.	0.8	576
122	Density-Regulated Selection with Genotypic Interactions. <i>American Naturalist</i> , 1983, 121, 649-655.	1.0	28
123	Density-Regulated Selection in a Heterogeneous Environment. <i>American Naturalist</i> , 1983, 121, 656-668.	1.0	16
124	Mapping Contingency Tables. , 1983, , 140-149.		0
125	A Narrow Hybrid Zone Between Closely Related Cricket Species. <i>Evolution; International Journal of Organic Evolution</i> , 1982, 36, 535.	1.1	28
126	A NARROW HYBRID ZONE BETWEEN CLOSELY RELATED CRICKET SPECIES. <i>Evolution; International Journal of Organic Evolution</i> , 1982, 36, 535-552.	1.1	68



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127	Statistics of Natural Populations. I: Estimating an Allele Probability in Cryptic Fathers with a Fixed Number of Offspring. <i>Biometrics</i> , 1981, 37, 495.	0.8	16
128	FATE MAPPING MULTI-FOCUS PHENOTYPES. <i>Genetics</i> , 1981, 99, 211-229.	1.2	7
129	Genetics and the origin of a vector population: <i>Aedes aegypti</i> , a case study. <i>Science</i> , 1980, 208, 1385-1387.	6.0	71
130	A neural network model based on differential-algebraic equations for nonlinear programming. , 0, , .		1
131	Parallel computation for chromosome reconstruction on a cluster of workstations. , 0, , .		1
132	Parallel Monte Carlo methods for physical mapping of chromosomes. , 0, , .		3
133	A parallel genetic algorithm for physical mapping of chromosomes. , 0, , .		0
134	An Analysis of Density-Dependent Viability Selection. , 0, .		2