JONATHAN ARNOLD

Professor: Erdos Number: 2

Curriculum VIta

CONTENTS

FIELD OF ENDEAVOR

Systems Biology

VIDEO OF RESEACH

http://www.youtube.com/watch?v=A18OnmSsCAA

INTERNATIONAL LEADERSHIP

Fungal Genome Initiative Steering Committee
Neurospora Genomics Working Group
Pneumocystis Genome Project Steering Committee
Aspergillus fumigatus Genomics Steering Committee
Advisor to Burroughs-Wellcome Fund on Fungal Genomics
NIH Genome Study Section (ad hoc)
NIH Genetics Study Section (ad hoc)
NIH GCAT Study Section (ad hoc)
Charter Member of NIH Genetic Variation and Evolution (GVE) study section, 2005-2008

ACADEMIC DEGREES

PhD	1982	Statistics	Yale University
MPhil	1978	Statistics	Yale University
BS	1975	Mathematics	Yale University

TITLE OF DOCTORAL DISSERTATION

Statistics of Natural Populations: Seasonal Variation in Inversion Frequencies of Mexican *Drosophila pseudoobscura*.
Thesis Advisor: I. R. Savage, deceased

FACULTY POSITIONS

2002 – Dept of Genetics, Statistics, and Physics/Astronomy, UGA
1997 – Dept of Genetics and Statistics, UGA
1981 – Department of Statistics, Rutgers University

AREAS OF RESEARCH

Systems Biology
Fungal Genomics
Computational Genomics
Molecular Evolutionary Genetics
Theoretical Population Genetics
Chromosomal Evolution

GRANTS RECEIVED

Collective behavior of cellular oscillators, NSF, 3/01/2021, 807,190 (PI: Jonathan Arnold, Co-PIs: H.-B. Schuttler, Leidong Mao, & Art Edison, Award NSF MCB-2041546

Systems analysis of the beneficial associations of sorghum and arbuscular mycorrhizal fungi studied with genetics, genomics, imaging, and microbiomics, DOE, 9/15/2020, 11,711,865 (PI: Jeff Bennetzen, Co-PIs: Jonathan Arnold, Annie Chung, Katrien Devos, and Nancy Johnson). Award DE-SC0021386. Project FP000201496

RAPID: finding virulence genes as therapeutic targets in Covid-19. DBI-2029595, 4/19/2020-4/18/2021, $200,000 (PI: Jonathan Arnold, Co-PIs: Liang Liu and Justin Bahl)

"REU site, Genomics and Computational biology". DBI-1946937,03/30/2020-03/30/2023, $364,707 (PI: Jonathan Arnold, Co-PI David Logan, Clark Atlanta University).

"REU site, interdisciplinary experiences in nanotechnology and Biomedicine. EEC-1950581, 04/01/2020-4/01/2023, $404,071 (PI: Leidong Ma, Co-PI, Jonathan Arnold)

"Measuring and Modeling how Clocks in Single Cells Communicate: an interdisciplinary approach". MCB-SSB/PHY-POLS-1713746, 08/01/2017-07/31/2020, $838,000 (PI: Jonathan Arnold, Co-PI, H. Bernd Schuttler, Leidong Mao, and Art Edison). This is two separate awards combined administratively into one NSF award.

"EAGER: ALICE, MCB-1645325, "Adaptive Learning for Interdisciplinary Collaborative Environments", 7/10/2016-7/09/2018, $299,899 (PI: Juan Gutierrez, Co-PI: Jonathan Arnold, Pedro Portes

"REU site: Interdisciplinary research experiences in Nanotechnology and Biomedicine", NSF EEC-1659525, 2017-2020, $411,338 (PI: Leidong Mao, Co-PI: Jonathan Arnold)

"REU site: collaborative research: genomics and computational biology", NSF DBI-1426834, 3/18/2014-3/17/2019, $538,095 (PI: Jonathan Arnold, Co-PI: Richard B. Meagher, PI: David A. Logan)

"REU site: Interdisciplinary research experiences in Nanotechnology and Biomedicine", NSF EEC-1359095, 2014-2017, $359,998 (PI: Leidong Mao, Co-PI: Jonathan Arnold)

"REU site: genomics and computational biology", NSF DBI-1062213, 2011-2014, $379,000
(PI: Jonathan Arnold, Co-PI: Richard B. Meagher)

"Creativity Extension Award to DBI-0646315", NSF DBI-01041715, 2010-2011, $91,350 (PI:
Jonathan Arnold, Co-PI: D.A. Logan).

"Workshop on Mathematical Biology and Numerical Analysis", NSF DMS-0906557, 2009-2010, $30,000 (PI: T. Taha, Co-PIs: J. Arnold, J. Prestegard, & A Summers).

“Genomics and Computational Biology, an REU site”, NSF DBI-0646315, 2007-2011, \$318,012+\$91,350 (PI: J. Arnold, Co-PIs: D.A. Logan, C. Teare Ketter).

“CAA: Identification of genetic networks in *Neurospora crassa*: a systems biology approach”, NSF MCB-0542915, Mar 1, 2006- Feb 29, 2008, \$157,115, (PI: D. A. Logan and Co-PI: J. Arnold)

“Computing Life and the Kinetics of the Cell”, NSF QSB-0425762, 2004-2008, \$499,994, (PI: J. Arnold and Co-PI: H.-B. Schuttler)

“A population based, multi-disciplinary study of Centenarians”, NIH 5P01 AG017553-03, 2003-2009, \$159,720 (PI: L. Poon and Co-PIs: J. Arnold, R. Green, M. Jazwinski, M.A. Johnson, W. Markesbery, and W. Rogers)

“Genomics and Computational Biology, an REU site”, NSF DBI-0243754, 2003-2007, \$337,000 (PI: J. Arnold, Co-PIs: D.A. Logan, C. Teare Ketter, & S. Datta).

"Novel statistical methods for generation of integrated genomics maps", USDA-2002-35300-12475, 2002-2007, \$280,000 (Co-PIs: S. Bhandarkar and J. Arnold)

“3rd International Symposium on Fungal Genomics and Computational Biology”, Burroughs-Wellcome Fund 1001657, 2000-2001, \$5,000 (PI: J. Arnold)

“3rd International Symposium on Fungal Genomics and Computational Biology”, DOE- 021463, 2000-2001, \$10,000 (PI: J. Arnold)

"*Pneumocystis* Genome Project”, NIH 018275-01, 1999-2004, \$206,440, (subcontract from Dr. M. T. Cushion, University of Cincinnati).

"Parallel computing of physical maps for fungal genomes,” USDA-9710389, 1997-2000, \$200,000 (Co-PIs, S. Bhandarkar and J. Arnold).

" *In vitro* reconstruction of fungal chromosomes", NSF, 1996-2000, \$467,917, 11/01/96-10/31/00, Microbial Genetics, MCB-9630910 (PI: J. Arnold)

" Robotics system for physical mapping fungal genomes", NSF, 1996-1998, \$107,150, 3/15/96-3/15/98, BIR-9512887 (PI: J. Arnold)

" Development of fungal-resistant peanut varieties", Georgia Research Alliance, 1996-1997, \$350,000, 7/01/96-6/30/97 (Co-PIs: L. Ljungdahl, J. Arnold, and P. Ozias-Akins).

" Parallel computing of physical maps", NSF, 1994-1995, \$50,000, 11/15/94 - 11/15/95, BIR-9422896.

" Novel data parallel algorithms and neural networks for computer vision, image processing, and genetics on the MasPar MP-2, MASPAR Corp., 1993-1994, \$420,656.

" *In vitro* reconstruction of fungal chromosomes", NIH grant, W. E. Timberlake and J. Arnold, 8/1/89-7/31/94, \$837,037.

" Instrumentation for a biological sequence/structure computational facility (BS/SCF), NSF grant, J. Arnold, 1989-1990, 2 years, \$188,090.

" Mitochondrial-nuclear interactions in hybrid zones", NSF grant, J. Arnold, 1988-1991, 3 years, \$130,000.

" Statistical problems in population genetics", NSF grant, J. Arnold, 1983-1987, 3 years, $125,000.

" Statistical computing and genetic engineering", Army Research Office (ARO) training grant, J. Arnold and R. Bradley, 1983-1986, 3 years, $60,000.

AWARDS AND HONORS

The UGA Excellence in undergraduate research mentoring award, 2002
National Science Foundation Creativity Extension Award for work on the biological clock, 2010.
AAAS Fellow, 2011
Franklin Diversity Leadership Development Award, 2013

INSTRUCTION

Undergraduate

“Genomics and Society” 12-credit core cluster course for freshmen with new Genomics laboratory for undergraduates in partnership with Drs. Celeste Condit, William Barstow, Scott Kleiner, and Nelson Hilton in the Departments of Speech Communication, Botany, Philosophy, and English, respectively, 2001-2005

10-week NSF-funded summer institute for undergraduates from underrepresented groups in fungal genomics and computational biology in partnership with Clark Atlanta University, Fort Valley State University. and Georgia State University in partnership with Drs. David Logan, Richard B. Meagher, William Seffens, Susmita Datta and Catherine Teare-Ketter. 2000-2009

Introductory Genetics (60→350+ students each fall) for last 23 years. 1985-2008

Annual Academic Affairs Faculty Symposium, “Why do I need to learn this: Science and Math for the Non-Science Majors”

Graduate

Genomics
Genomic Analysis
Nucleic Acids
Bioinformatics
Advanced Molecular Genetics
Genetic Data Analysis
Statistical Genetics
Advanced Population Genetics
Bioethics
C++

Past Courses Taught

Molecular Evolution
Theoretical Population Genetics
Nucleic Acids
Advanced Molecular Genetics
Advanced Population Genetics
Advanced Ecological Genetics
Statistical Methods
Statistical Theory
Regression Methods
Data Analysis
Experimental Design
Statistical Computing with APL
Bioinformatics
Genetics
Systems biology
Mathematical Biology
Introduction to Bioinformatics

OTHER SERVICES

Departmental Committees

Head Search, Statistics, 2001 – 2003
Bioinformatics faculty search, Statistics, 2000-2002
Graduate Affairs Committee, 2000 – 2003
IOB Graduate Affairs Committee – 2012-2019
Undergraduate Affairs Committee, 1997 – 2018
Complex Traits Search, 2006

Systems Biology Search, 2006
Computational Biology Search, 2008
Genetics Department Executive Committee, 2009-2012
Web page committee, 2010-present
Awards Committee – 2011-present

University Committees

Executive Committee of Institute of Bioinformatics
Institute of Bioinformatics Advisory Board
University Wide Genome Committee,
University Computing Advisory Committee
University Computational Science Program Advisory Committee
Carmon Fellowship Selection Committee
3 recruiting committees in computational biology
Georgia Advanced Computing Resource Center Advisory Committee 2011-2014
College Promotion and Tenure – 2013-2014

Other University Services

Graduate Coordinator, Institute of Bioinformatics, University of Georgia, 2013-2019
Director, NSF REU site in Fungal Genomics & Computational Biology, 2000-2019
Director, Fungal Genome Resource, UGA, 1995-present.
Founding Director, Biological Sequence/Structure Computational Facility (BS/SCF), UGA, 1988-1992.

Federal Services

NSF Computational Biology Panel, 1997-1999
DOE Genome Panel, 1993-1994
NIH Genomics Study Section (ad hoc), 2003
NIH Genetics Study Section (ad hoc), 2004-2005
NIH Genetic Variation and Evolution Study Section, charter member, 2005-2008
NIH GCAT Study Section (ad hoc), 2010
NSF Systems and Synthetic Biology Panel, 2018-2019

Editorships

Associate editor, *Frontiers in Genetics of Aging*, 2011-
Editor, Special issue of *Genetics* 157 devoted to Fungal Genomics and Computational Biology, March, 2001
Genome Editor, *Fungal Genetics & Biology*, 1997
Associate Editor, *Evolution*, 1988-1991

Journal volumes edited

Fungal Genetics and Biology, vol. 21 (Genome Issue), 1997
Genetics, vol. 157, March, 2001
Xiong, M, Z Zhao, J Arnold, and F Yu (2010). Next-generation sequencing. *Journal of Biomedicine and Biotechnology*, Hindawi Publishing Corporation.

REFEREED JOURNAL ARTICLES

JR Powell, WJ Tabachnick, and J Arnold (1980). Genetics and the origin of a vector population: *Aedes aegypti*, a case study. *Science* 201: 1385-1387.
J Arnold, (1981). Statistics of natural populations, I: estimating an allele probability in cryptic fathers with a fixed number of offspring. *Biometrics* 37: 495-504.
J Arnold, and DR Kankel (1981). Fate mapping multi-focus phenotypes. *Genetics* 99: 211-229.
RG Harrison, and J Arnold (1982). A narrow hybrid zone between closely related cricket species. *Evolution* 36: 535-552.

WW Anderson, and J Arnold (1983). Genotypic interactions in a model of density- regulated selection. *American Naturalist* 121: 649-655.

J Arnold, and WW Anderson (1983). Density-regulated selection in a heterogeneous environment. *American Naturalist* 121: 656-668.

JC Avise, JE Neigel, and J Arnold (1984). The demographics of mitochondrial lineage survivorship. *Journal of Molecular Evolution* 20: 99-105.

J Arnold, and ML Morrison (1985). Statistics of natural populations. II. Estimating an allele probability in cryptic mothers with a fixed number of offspring. *Genetics* 109: 785-798.

VK Eckenrode, J Arnold, and RB Meagher (1985). Comparison of the 18s rRNA with the sequence of other ribosomal small subunit rRNAs. *Journal of Molecular Evolution* 21:259-269.

WW Anderson, J Arnold, SA Sammons, and DG Yardley (1986). Frequency-dependent viabilities of *Drosophila pseudoobscura* karyotypes, *Heredity* 56: 7-17.

IF Goldman, J Arnold, and BC Carlton (1986). Selection for resistance to *Bacillus thuringiensis* subspecies *israelensis* in field and laboratory populations of the mosquito *Aedes aegypti*, *Journal of Invertebrate Pathology* 47: 317-324.

J Arnold, VK Eckenrode, K Lemke, GJ Phillips, and SW Schaeffer. (1986). A comprehensive package for DNA sequence analysis in Fortran-IV for the PDP-11. *Nucleic Acids Research* 14: 239-254.

MJ Sobel, J Arnold, and M Sobel (1986). Statistics of natural populations. III. Sequential sampling plans for the estimation of gene frequencies. *Biometrics* 42: 45-65.

MA Asmussen, J Arnold, and JC Avise (1987). Statistics of natural populations. IV. Definition and properties of disequilibrium statistics for associations between nuclear and cytoplasmic genotypes. *Genetics*115: 755-768.

GJ Phillips, J Arnold, and R Ivarie (1987). Mono- through hexanucleotide composition of the *Escherichia coli* genome: a Markov chain analysis. *Nucleic Acids Research* 15: 2611-2626.

GJ Phillips, J Arnold, and R Ivarie (1987). The effect of codon usage on the oligonucleotide composition of the *E. coli* genome and identification of over- and underrepresented sequences by Markov chain analysis. *Nucleic Acids Research* 15: 2627-2638.

JC Avise, J Arnold, RM Ball, E Bermingham, T Lamb, JE Neigel, CA Reeb, and N. C. Saunders (1987). Intraspecific phylogeography: the mitochondrial DNA bridge between population genetics and systematics. *Annual Review of Ecology and Systematics* 18: 489-522.

SG Wellso, DJ Howard, JL Adams, and J Arnold (1988). Electrophoretic monomorphism in six biotypes and two populations of the Hessian fly (*Diptera*: *cedidouryiidae*). *Annals of Entomological Society of America* 80 (1): 50-53.

J Arnold, MA Asmussen, and JC Avise (1988). An epistatic mating system model can produce permanent cytonuclear disequilibria in a hybrid zone. *Proceedings of the National Academy of Sciences USA* 85: 1893-1896.

JC Avise, RM Ball, and J Arnold (1988). 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. *Molecular Biology and Evolution* 5: 331-344.

J Arnold, AJ Cuticchia, DA Newsome, WW Jennings III, and R Ivarie (1988). Mono- through hexanucleotide composition of the sense strand of yeast DNA: a Markov chain analysis. *Nucleic Acids Research* 16: 7145-7157.

PA Adams, A Falek, and J Arnold (1988). Huntington's Disease in Georgia: Age at onset. *American Journal of Human Genetics* 43: 695-704.

RB Meagher, MD McLean, and J Arnold (1988). Recombination within a subclass of restriction fragment polymorphisms may help link classical and molecular genetics. *Genetics* 120: 809-818.

MA Asmussen, J Arnold, and JC Avise (1989). The effects of assortative mating and migration on cytonuclear associations in hybrid zones", *Genetics* 122, 923-934.

CJ Williams, WW Anderson, CJ Brown, and J Arnold (1989). An analysis of density-dependent viability selection, *Journal of the American Statistical Association* 84, September, 84, 662-668.

CJ Williams, WW Anderson, and J Arnold (1990). Generalized linear modeling methods for selection component experiments. *Theoretical Population Biology* 35 (2): 389-423.

JC Avise, WS Nelson, J Arnold, RK Koehn, GC Williams, and V Thorsteinsson (1990). The evolutionary genetic status of Icelandic eels. *Evolution* 44: 1254-1262.

SE Surles, J Arnold, A Schnabel, JC Hamrick, and BC Bongarten (1990). Genetic relatedness in open-pollinated families of two leguminous tree species, *Robinia pseudoacacia L*. and *Gleditsia tricanthos L*., *Theoretical and Applied Genetics* 80: 49-56.

MA Asmussen, and J Arnold (1991). The effects of admixture and population subdivision on cytonuclear disequilibria, *Theoretical Population Biology* 39: 273-300.

Y-X Fu, and J Arnold (1991). On the association of RFLP's across species boundaries. *Proceedings of the National Academy of Sciences USA* 88: 3967-3971.

H Brody, J Griffith, AJ Cuticchia, J Arnold, and WE Timberlake (1991).Chromosome-specific recombinant DNA libraries from the fungus *Aspergillus nidulans*. *Nucleic Acids Research* 19: 3105-3109.

WW Anderson, J Arnold, DG Baldwin, AT Beckenbach, CJ Brown, SH Bryant, JA Coyne, LG Harshman, WB Heed, DE Jeffrey, LB Klaczko, BC Moore, JM Porter, JR Powell, T Prout, SW Schaeffer, JC Stephens, CE Taylor, ME Turner, GO Williams, JA Moore (1991). Four decades of inversion polymorphism in *Drosophila pseudoobscura*. *Proceedings of the National Academy of Sciences USA* 88: 10367-10371.

JM Brewer, J Arnold, GG Beach, WL Ragland, and JK Wunderlich. (1991). Comparison of the amino acid sequences of tissue-specific parvalbumins from chicken muscle and thymus and possible evolutionary significance. *Biochemical and Biophysical Research Communications* 181: 226-231.

Y-X Fu, and J Arnold (1992). Dynamics of cytonuclear disequilibria in finite populations and a comparison with a two-locus nuclear system. *Theoretical Population Biology* 41, No. 1, 1-25.

Y-X Fu, and J Arnold (1992). A table of exact sample sizes for use with Fisher's exact test for 2 x 2 tables. *Biometrics* 48 (December) 48: 1103-1112.

AJ Cuticchia, J Arnold, and WE Timberlake (1992). The use of simulated annealing in chromosome reconstruction experiments based on binary scoring of clones. *Genetics* 132: 591-601.

AJ Cuticchia, J Arnold, H Brody, and WE Timberlake (1992) CMAP: Contig mapping and analysis package: a relational database for chromosome reconstruction, *CABIOS* 8: 467-474.

Y-X Fu, WE Timberlake, and J Arnold (1992). On the design of genome mapping experiments using short synthetic oligonucleotides. *Biometrics* 48: 337-359.

AJ Cuticchia, R Ivarie, and J Arnold (1992). The application of Markov chain analysis to oligonucleotide frequency prediction and physical mapping of *Drosophila melanogaster*. *Nucleic Acids Research* 20: 3651-3657.

AJ Cuticchia, J Arnold, and WE Timberlake (1993). ODS: Ordering DNA sequences, a physical mapping algorithm based on simulated annealing. *CABIOS* 9, 2, 215-219.

AJ Cuticchia, J Arnold, and WE Timberlake (1993). PCAP: Probe choice and analysis package: a set of programs to aid in choosing synthetic oligomers for contig mapping, *CABIOS* 9, 2, 201-203.

ML Cellino, and J Arnold (1993). The effects of male sterility on cytonuclear disequilibria in hybrid zones. *Genetica* 88: 37-50.

J Arnold. (1993). Cytonuclear disequilibria in hybrid zones. *Annual Review of Ecology and Systematics* 24: 521-554.

SK Hollingshead, J Arnold, T Readdy, and DE Bessen (1994). Molecular evolution of a multi-gene family in group A *streptococci*, *Molecular Biology and Evolution* 11: 208-219.

Y Wang, RA Prade, J Griffith, WE Timberlake, and J Arnold (1994). A fast random cost algorithm for physical mapping. *Proc. Natl. Acad. Sci. USA* 91: 11094-11098.

Y Wang, RA Prade, J Griffith, WE Timberlake, and J. Arnold (1994). ODS_BOOTSTRAP: Assessing the statistical reliability of physical maps by resampling. *CABIOS* 10: 625-634.

M Xiong, HJ Chen, RA Prade, Y Wang, J Griffith, WE Timberlake, and J. Arnold (1996). On the consistency of a physical mapping algorithm to reconstruct a chromosome. *Genetics* 142: 267-284.

R Dean and J Arnold (1996). Cytonuclear disequilibria in hybrid zones using RAPD markers. *Evolution* 50(4): 1702-1705.

S Datta, Y-X Fu, and J Arnold (1996). Dynamics and equilibrium behavior of cytonuclear disequilibria under genetic drift, mutation, and migration. *Theoretical Population Biology* 50: 298-324.

R Dean and J. Arnold (1996). Small sample properties for estimators of cytonuclear disequilibria. *Heredity* 77: 396-399.

M Bhandarkar, S Chirravuri, and J Arnold (1996). Parallel computing of physical maps--a comparative study in SIMD and MIMD parallelism. *J. Computational Biology* 3: 503-528.

S Datta and J Arnold (1996). Diagnostics and a statistical test of neutrality hypotheses using the dynamics of cytonuclear disequilibria, *Biometrics* 52: 1042-1054.

SM Bhandarkar, S Chirravuri, and J Arnold (1996). PARODS - A study of parallel algorithms for ordering DNA sequences. *CABIOS* 12, No. 4, 269-280.

Wollenberg, J Arnold, and JC Avise (1996). Recognizing the forest for the trees: testing temporal patterns of cladogenesis using a null model of stochastic diversification. *Molecular Biology and Evolution* 13: 833-849.

S Datta, M Kiparsky, DM Rand, and J Arnold (1996). A statistical test of a neutral model using the dynamics of cytonuclear disequilibria. *Genetics* 144: 1985-1992.

RA Prade, J Griffith, K Kochut, J Arnold, and WE Timberlake (1997). *In vitro* reconstruction of the *Aspergillus (=Emericella) nidulans* genome. *Proc. Natl. Acad. Sci. USA* 94: 14564-14569

R Dean and J Arnold (1997). The effects of unidirectional incompatibility on cytonuclear disequilibria in a hybrid zone. *Genetica* 101: 215-223

M Sanchez, J Arnold, and MA Asmussen (1997). Effects of vertical transmission rates on the survival, maintenance of genetic variability and association of viral parasite and host genotypes. *Gibier Faune Sauvage* 14: 477-492

J Arnold and MT Cushion (1997). Constructing a physical map of the *Pneumocystis* genome, *J. Euk. Microbiol.*_44:8s

MT Cushion, and J Arnold (1997). Proposal for a *Pneumocystis* Genome Project, *J. Euk. Microbiol* 44: 7s

SM Bhandarkar, S Machaka, S Chirravuri, and J Arnold (1998). Parallel computing for chromosome reconstruction via ordering of DNA sequences. *Parallel Computing* 24: 1177-1204.

S Datta and J Arnold (1998). Dynamics of cytonuclear disequilibria in subdivided populations. *J. Theor. Biol.*, 192: 99-111

KT Scribner, S Datta, J Arnold and JC Avise (1999). Empirical evaluation of cytonuclear models incorporating genetic drift and tests for neutrality of mtDNA variants: data from experimental *Gambusia* hybrid zones, *Genetica* 105: 101-108

TJ Lott, BP Holloway, DA Logan, R Fundyga, and J Arnold (1999). Towards understanding the evolution of the human commensal yeast, *Candida albicans*. *Microbiology* 145: 1137-1143

MS Sanchez, J Arnold, and MA Asmussen (2000). Symbiont survival and host-symbiont disequilibria under differential vertical transmission. *Genetics* 154: 1347-1365

Kelkar, HS, J Griffith, ME Case, S Covert, R D Hall, C Keith, JS Oliver, MJ Orbach, MS Sachs, J Wagner, MJ Weise, J Wunderlich, and J Arnold. (2001). The *Neurospora crassa* genome: cosmid libraries sorted by chromosome. *Genetics* 157 (March issue), 979-990

Hoyer, LL, R Fundyga, JE Hecht, JC Kapetyn, FM Klis, and J Arnold. (2001). Characterization of ALS genes from non-albicans *Candida* and phylogenetic analysis of the ALS family, *Genetics* 157 (April issue), 1555-1567

RD Hall,, SM Bhandarkar, J. Arnold, and T. Jiang (2001). Physical mapping with automatic capture of hybridization data. *Bioinformatics* 17 (3): 205-213

Zhang, Y, H Tian, E Kraemer, and J Arnold (2002). Visualization of protein interaction mapping using Java 3D. *Bioinformatics*, submitted

Kraemer, E, J Wang, J Guo, S Hopkins, and J Arnold (2001). An analysis of gene-finding approaches for *Neurospora crassa*. *Bioinformatics* 17: 901-912

Fang, X, JA Miller, and J Arnold (2002). J3DV: a Java-based 3D database visualization tool. Software – *Practice and Experience* 32: 443-463

Battogtokh, D, DK Asch, ME Case, J Arnold, & H-B Schuttler (2002). An ensemble method for identifying regulatory circuits with special reference to the *qa* gene cluster of *Neurospora crassa*. *PNAS USA* 99: 16904-16909

Fundyga, R, TJ Lott, and J Arnold (2002). Population structure of *Candida albicans*, a member of the human flora, as determined by microsatellite loci, *Infection, Genetics, and Evolution* 2: 57-68.

Kochut, KJ, J Arnold, A Sheth, J Miller, E Kraemer, B Arpinar, and J Cardoso. (2003). INTELLIGEN: a distributed workflow system for discovering protein-protein interactions. *Parallel and Distributed Databases* 13, 43-72

Xu, Z, B Lance, C Vargas, B Arpinar, S Bhandarkar, E Kraemer, KJ Kochut, JA Miller, JR Wagner, MJ Weise, JK Wunderlich, J Stringer, G Smulian, MT Cushion, & J Arnold (2003). Mapping by sequencing the Pneumocystis genome using the ODS3 tool. *Genetics* 163: 1299-1313

Cardoso, J, A Sheth, JA Miller, J Arnold, and KJ Kochut (2004). Quality of service for workflows and web service processes. *J. Web Semantics: Science, Services, and Agents on the World Wide Web* 1: 281-308

Strobel, G. and J. Arnold (2004). Essential eukaryotic core. *Evolution* 58, No. 2, 441-446

Lott, TJ, RE Fundyga, RJ Kuykendall, and J Arnold (2005). The human commensal yeast, *Candida albicans*, has an ancient origin. *Fungal Genetics and Biology* 42: 444-451

Sanchez, MS., CJ Basten, AM Ferrenberg, MA Asmussen, and J Arnold (2006). Exact sample sizes needed to detect dependence in 2 x 3 tables. *Theoretical Population Biology* 69: 111-120

Icenhour, CR, J Arnold, M Medvedovic, and MT Cushion (2006). Competitive coexistence of two *Pneumocystis* species, *Infection, Genetics, and Evolution* 6: 177-186

Dai, J, A Davey, IC Siegler, J Arnold, and LW Poon (2006). GCSDB: an integrated database system for the Georgia Centenarian Study. *Bioinformation* 1: 214-219

Dai, J, L. Li, S. Kim, B. Kimball, M. Jazwinski, and J Arnold for the Georgia Centenarian Study (2007). Exact sample size needed to detect dependence in 2 x 2 x 2 tables. *Biometrics* 63: 1245-1253

Tewari, S, SM Bhandarkar, and J Arnold (2007). 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* 5 (No 2), 201-250

Yu, Y, W Dong, C Altimus, X Tang, J Griffith, M Morello, L Dudek, J Arnold, and H-B Schuttler (2007). A genetic network for the clock of *Neurospora crassa*. *PNAS USA* 104: 2809-2814

Logan, DA, AL Koch, W Dong, J Griffith, R Nilsen, ME Case, H-B Schuttler and J Arnold (2007). Genome-wide expression analysis of genetic networks in *Neurospora crassa*. *Bioinformation* 1 (10), 390-395

Cushion, MT, AG Smulian, BE Slaven, T Sesterhenn, J Arnold, C Staben, A Porollo, R Adamczyk, and J Meller. (2007). Transcriptome of *Pneumocystis carinii* during fulminate infection: carbohydrate metabolism and the concept of a compatible parasite, *PloS one 2(5):* e423. doi:10.1371/journal.pone.0000423

Dong, W, X Tang, Y Yu, J Griffith, R Nilsen, D Choi, J Baldwin, L Hilton, K Kelps, J McGuire, R Morgan, M Smith, M Case, J Arnold, H-B Schuttler, Q Wang, J Liu, J Reeves, and D Logan (2007). Systems biology of the Neurospora biological clock, *IET Systems Biology* 1 (No 5): 257-265

Dong, W, X Tang, Y Yu, R. Nilsen, J Griffith, R Kim, J Arnold, and H.-B. Schuttler (2008). Systems biology of the clock in *Neurospora crassa*, *PLoS ONE* 3: e3105, http://dx.plos.org/10.1371/journal.pone.0003105

Tewari, S, J Arnold, and SM Bhandarkar (2008). Likelihood of a particular order of genetic markers and the construction of genetic maps. *Journal of Bioinformatics and Computational Biology* 6, 125-162

Aleman-Meza, B, Y Yu, H-B Schuttler, J Arnold, and TR Taha (2009) KINSOLVER: a simulator for computing large ensembles of biochemical and gene regulatory networks. *Computers and Mathematics with Applications* 57: 430-435, doi:10.1016/j.camwa.2008.10.086

Randall GK, Martin P, McDonald M, Poon LW; Georgia Centenarian Study, Jazwinski SM, Green RC, Gearing M, Markesbery WR, Woodard JL, Johnson MA, Tenover JS, Siegler IC, Rodgers WL, Hausman DB, Rott C, Davey A, Arnold J. (2010). Social resources and longevity: findings from the Georgia centenarian study. *Gerontology* 56(1): 106-111

Jazwinski, SM, S Kim, J. Dai, L Li, X Bi, JC Jiang, J Arnold, MA Batzer, JA Walker, DA Welsh, CM Lefante, J Volaufova, L Myers, LJ Su, DB Hausman, MV Miceli, E Ravussin, LW Poon, KE Cherry & MA Welsch for the Georgia Centenarian Study and the Louisiana Healthy Aging Study (2010). HRAS1 and LASS1 with APOE are associated with human longevity and healthy aging, *Aging Cell* 9: 698-708, doi:10.1111/j.1474-9726.2010.00600.x

Arnold, J, J Dai, L Nahapetyan, A Arte, MA Johnson, D Hausman, WL Rodgers, R Hensley, PM MacDonald, SM Jazwinski & LW Poon for the Georgia Centenarians Study. (2010) Predicting successful aging in a population-based sample of Georgia centenarians. *Current Gerontology and Geriatrics Research*, Volume 2010, doi:10.1155/2010/989315

Tang, X, W Dong, J Griffith, R Nilsen, A Matthes, KB Cheng, J Reeves, H-B Schuttler, ME Case, J Arnold, & DA Logan (2011). Systems biology of the *qa* gene cluster of *Neurospora crassa*. *PLoS ONE* 6(6): e20671 http://dx.plos.org/10.1371/journal.pone.0020671

Kim, S, X Bi, M Czarny-Ratajczak, J Dai, DA Welsh, L Myers, MA Welsch, KE Cherry, J Arnold, LW Poon, SM Jazwinski for the Louisiana Healthy Aging Study and The Georgia Centenarian Study 2012. Telomere maintenance genes SIRT1 and XRCC6 impact age-related decline in telomere length but only SIRT1 is associated with human longevity. *Biogerontology* 13, 119-131, DOI 10.1007/s10522-011-9360-5

Arnold, J, T R Taha, & L Deligiannidis 2012. GKIN: a tool for drawing genetic networks, *Network Biology* 2(1): 26-37

Poon, L. W., J. L Woodard, L. S. Miller, R. Green, M. Gearing, A. Davey, J. Arnold, P. Martin, I. Siegler, L. Nehapetyan, Y S. Kim, & W. Markesbery for the Georgian Centenarian Study. (2012) Understanding dementia prevalence among Centenarians. *J. Gerontology A: Biological Sciences Medical Sciences* 67A, 358-365, *doi: 10.1093/gerona/glr250*.

Al-Omari, A, H-B Schuttler, J Arnold, & T Taha 2013. Solving nonlinear systems of first order differential equations using a Galerkin finite element method. *IEEE Access* 1(1), 408-417, DOI 10.1109/ACCESS.2013.2269192

Al-Omari, A, J Arnold, T Taha, & H-B Schuttler 2013. 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* 1(1), 770-777 DOI 10.1109/ACCESS.2013.2290623

Martin, P, SM Jazwinski, A Davey, R Green, M MacDonald, JA Margrett, IC Siegler, J. Arnold, J Woodard, MA Johnson, S Kim, J Dai, L Li, MA Batzer, LW Poon 2014. APOE ε4, rated life experiences, and affect among centenarians. *Aging and Mental Health* 18, 240-247, DOI: 10.1080/13607863.2013.827624

Case, ME, J Griffith, W Dong, IL Tigner, K Gaines, JC Jiang, SM Jazwinski, & J Arnold for the Georgia Centenarian Study 2014. The aging biological clock in *Neurospora crassa*, *Ecology & Evolution* 4, 3494-3507, http://onlinelibrary.wiley.com/doi/10.1002/ece3.1202/full

Bouffier, A. M., J. Arnold, & H-Bernd Schuttler 2014. A MINE alternative to D-optimal designs for the linear model. 2014. *PLoS ONE* 9(10): e110234, http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0110234

Manzourolajdad, A. & J Arnold 2015. Secondary structural entropy RNA switch (riboswitch) identification. *BMC Bioinformatics* 16:133, DOI: 10.1186/s12859-015-0523-2 http://www.biomedcentral.com/1471-2105/16/133

Al-Omari, A, J Griffith, M Judge, T Taha, J Arnold, & H-B Schuttler 2015. Discovering regulatory network topologies using ensemble methods on GPGPUs with special reference to the biological clock of *Neurospora crassa*, *IEEE Access* 3, 27-42, DOI 10.1109/ACCESS.2015.2399854, http://ieeexplore.ieee.org/xpl/articleDetails.jsp?tp=&arnumber=7029612&queryText%3Ddiscovering+regulatory+network+topologies+with+ensemble+methods

Brunson, JK, J Griffith, D. Bowles, ME Case, & J Arnold 2016. *lac-1* and *lag-1* with *ras-1* affect aging and the biological clock in *Neurospora crassa*. *Ecology and Evolution* 6: 8341-8351, DOI: 10.1002/ece3.2554

Deng, Z., S Arsenault, C Caranica, J Griffith, T Zhu, A Al-Omari, H-B Schuttler, J Arnold, & L Mao 2016. Synchronizing stochastic circadian oscillators in single cells of *Neurospora crassa*, *Scientific Reports 6*, 35828, DOI: 10.1038/srep35828, www.nature.com/articles/srep35828

Al-Omari, A. D., J. Griffith, C. Caranica, T. Taha, H.-B. Schuttler & J. Arnold 2018. Discovering regulators in post transcriptional control of the biological clock of *Neurospora crassa* using Variable Topology Ensemble Methods on GPUs. *IEEE Access* 6, doi:10.1109/ACCESS.2018.2871876 6: 54582-54594

Caranica, C., A. D. Al-Omari, Z. Deng, J. Griffith, R. Nilsen, L. Mao, J. Arnold, and H.-B. Schuttler 2018. Ensemble methods for stochastic networks with special reference to the biological clock of *Neurospora crassa*, *PLoS ONE* 13(5):e0196435

Deng, Z., J. H. Cheong, C. Caranica, L. Wu, X. Qiu, M. Judge, B. Hull, C. Rodriguez, J. Griffith, A. Al-Omari, S. Arsenault, H.-B. Schuttler, L. Mao, & J. Arnold 2019. Single cells of *Neurospora crassa* show circadian oscillations, light entrainment, temperature compensation, and phase synchronization. *IEEE Access* 7, 49403-49417, DOI (identifier) 10.1109/ACCESS.2019.2910731

Judge, M. T., Y. Wu, F. Tayyari, J. Glushka, T. Ito, J. Arnold, & A. Edison 2019. Continuous *in vivo* metabolism by NMR. *Frontiers Molecular Biosciences | Metabolomics* 6, doi: 10.3389/fmolb.2019.00026

Caranica, C., J. Hwei-Cheong, X. Qiu, E. Krach, Z. Deng, L. Mao, H.-B. Schuttler[6], J. Arnold 2019. What is phase in cellular clocks? *Yale Journal of Biology and Medicine* 92, 169-178.

Aguar, K., C C Sanchez, D. Boada Beltran, S Safaei, M Asefi, J Arnold, P Portes, H R Arabnia, J Gutierrez 2019. Considerations on Interdisciplinary Instruction and Design influenced by Adaptive Learning. SAIL-SB: A case study involving Biology, Computer Science, Mathematics, and Statistics. *Computers and Education*, submitted, https://arxiv.org/submit/1831769

Caranica, C., A. Al-Omari, H.-B. Schuttler, & J. Arnold 2020. Identifying a clock stochastic network with light entrainment for single cells of *Neurospora crassa* by ensemble methods. *Nature Scientific Reports* 10, 15168, https://doi.org/10.1038/s41598-020-72213-1

Wu, Y., M. T. Judge, J. Arnold, S. M. Bhandarkar, & A. S. Edison (2020) RTextract: Time-series NMR spectra quantification based on 3D surface ridge tracking, *Bioinformatics* 36, 5068-5075 https://doi.org/10.1093/bioinformatics/btaa631

Montenegro, T. D. P., S. Kleindienst, A. E. Allen, A. M. Eren, J. McCrow, J. D. S. Calderon, J. Arnold, & S. B. Joye 2020. Colwellia and Marinobacter metapangenomes reveal species-specific responses to oil and dispersant exposure in deep sea microbial communities. *bioRχiv*, doi: 10.1101/2020.09.28.317438

Krach, E. K., Y. Wu, M. Skaro, L. Mao, & J. Arnold (2020). Wild isolates of *Neurospora crassa* reveal three conidiophore architectural phenotypes. *Microorganisms* 8(11), 1760, https://doi.org/10.3390/microorganisms8111760 (registering DOI)

Arnold, J, J Griffith, & ME Case 2021. Microevolution of the clock genetic network in *Neurospora crassa*, submitted.

Huang, Y, J. Arnold, & H-B Schuttler 2022. Modeling of biological and chemical reaction networks: the super-ensemble approach, submitted

Tewari, S, J Griffith, SM Bhandarkar, & J Arnold 2021. Likelihood-based integrated genetic and physical map of *Neurospora crassa*, submitted

Wu, Lingyun, J. Arnold, & H.-B. Schuttler (2022). Collective synchronization of stochastic biological clocks, *Physical Review Letters*, submitted

Skaro, M.S., M. Hill, Y. Zhou, S. Quinn, M. Davis, L. Cai, A. Sboner, M. Murph, and J. Arnold (2021). Are we there yet? A machine learning architecture to predict organotropic metastases. *BMC Medical Genomics 14*, 281, https://doi.org/10.1186/s12920-021-01122-7

Montenegro, T. D. P., S. Kleindienst, A. E. Allen, A. M. Eren, J. McCrow, J. D. S. Calderon, J. Arnold, & S. B. Joye 2022. Species-specific responses of *Colwellia* and *Marinobacter* to differential organic carbon exposure in deep sea microbial communities. *PNAS USA*, submitted doi: 10.1101/2020.09.28.317438

Cheong, J. W., X. Qiu, Y. Liu, A. Al-Omari, J. Griffith, H.-B. Schuttler, L. Mao, & J. Arnold (2022). The macroscopic limit to synchronization of cellular clocks in single cells of *Neurospora crassa*. *Nature Scientific Reports* **12**: 6750 , https://rdcu.be/cL5cL

Erickson, O. A, R. B. Cole, J. M. Isaacs, S. Alvarez-Clare, J. Arnold, A. Augustus-Wallace, J. Ayoob, A. Berkowitz, J. Branchaw, K. Burgio, C. Cannon, S. Cohen, H. Coller, J. Disney, Van Doze, M. Eggers, S. Farina, E. Ferguson, J. Gray, J. Greenberg, A. Hoffman, D. Jensen-Ryan, R. Kao, A. Keene, D. Levesque, J. Kowalko, S. A. Lopez, C. Mathis, M. Minkara, C. Murren, M. J. Ondrechen, P.Ordoñez, A. Osano, E. Padilla-Crispo, S.

Palchoudhury, H. Qin, J. Ramírez-Lugo, J. Reithel, C. Shaw, A. Smith, R. Smith, A. Summers, F. Tsien, A. Turkewitz, R. M. Ceballos, Erin L. Dolan (2022). "How do we do this at a distance?!" A descriptive study of remote Research Experiences for Undergraduates sites during COVID19. CBE-*Life Sciences Education*, https://doi.org/10.1187/cbe.21-05-0125

Torres, I., S. Zhang, M. Skaro, Z. Wang, Yue Wu, L. Stupp, T. Pendergast, N. Johnson, J. Arnold, A. Chung, K. Devos, J. Bennetzen, J. Townsend, & H.-B. Schuttler (2022). MINE: a new way to design genetics experiments for discovery. In preparation.

Wu, Y., M. T. Judge, A. S. Edison, & J. Arnold (2022). Uncovering *in vivo* biochemical patterns from time-series metabolic dynamics. *PLoS ONE* 17(5): e0268394. https://doi.org/10.1371/journal.pone.0268394

Krach, E., M. Skaro, Y. Wu, & J. Arnold (2022). Characterizing the gene-environment interaction underlying natural morphological variation in *Neurospora crassa* conidiophores using high-throughput phenomics and transcriptomics. *G3*, 10.1093/g3journal/jkac050

Al-Omari, A. M., J. Griffith, A. Scruse, R. W. Robinson, H.-B. Schuttler, & J Arnold (2022). Ensemble methods for identifying RNA operons and Regulons in the Clock Network of *Neurospora crassa*. *IEEE Access 10:32510-32524* , doi:10.1109/ACCESS.2022.3160481.

Hess, R. A., O. A. Erickson, R. B. Cole, J. M. Isaacs, S. Alvarez-Clare, J. Arnold, Al. Augustus-Wallace, J. C. Ayoob, A. Berkowitz, J. Branchaw, K. R. Burgio, C. H. Cannon, R. M. Ceballos, C. S. Cohen, H. Coller, J. Disney, Van A. Doze, M. J. Eggers, E. L. Ferguson, J. J. Gray, J. T. Greenberg, A. Hoffmann, D. Jensen-Ryan, R. M. Kao, A. C. Keene, J.E. Kowalko, S. A. Lopez, C. Mathis, M. Minkara, C. J. Murren, M. J. Ondrechen, P. Ordo.ez, A. Osano, El. Padilla-Crespo, S. Palchoudhury, H. Qin, J. Ramirez-Lugo, J. Reithel, C. A. Shaw, A. Smith, R. Smith, F. Tsien, E. L. Dolan (2022). Virtually the same? Evaluating the effectiveness of remote undergraduate research, Life Sciences Education, submitted

Skaro, M., A. Sboner, & J. Arnold (2022). SPARCE: Statistical preprocessing of attributes via recursive cross elimination. *IEEE Transactions on Journal Computational Biology and Bioinformatics*, submitted

INVITED JOURNAL ARTICLES / CHAPTERS

Arnold, J (1997). Editorial. *Fungal Genetics and Biology*, 21: 254-57.

Arnold, J (2001). Genetic Drift. *Encyclopedia of Genetics*, pp. 831-834, Academic Press, NY, NY

Bennett, J and J Arnold (2001). Genomics of Fungi. *The Mycota VIII. Biology of the Fungal Cell.* Howard and Gow (eds). pp. 267-297 Springer-Verlag, NY, NY

Arnold, J and N Hilton (2003). Revelations from a bread mould. *Nature* 422: 821-822

Poon, LW, M Jazwinski, RC Green, JL Woodard, P Martin, WL Rodgers, MA Johnson, D Hausman, J Arnold, J, A Davey, MA Batzer, WR Markesbery, M Gearing, IC Siegler, S Reynolds, and J Dai. (2007). Methodological considerations in studying Centenarians: lessons learned from the Georgia Centenarian Studies. In *Annual Reviews of Gerontology and Geriatrics: Biopsychosocial Approaches to Longevity, Vol. 27*. LW Poon and TT Perls (ed.s), Springer-Verlag, NY, NY. pp. 231-264

CONVENTION PAPERS / BOOK CHAPTERS REFEREED AND PUBLISHED

Arnold, J and DR Kankel (1982). Mapping contingency tables. In Computer Science and Statistics: *Proceedings of the 14th Symposium on the Interface*. Springer-Verlag, New York, pp. 140-149.

Miller, JA, J Arnold, KJ Kochut, AJ Cuticchia, and WD Potter (1991). Query driven simulation as a tool for genetic engineers. *Proceedings of the International Conference on Simulation in Engineering Education*. Newport Beach, California. pp. 67-72.

Xiong, M, P Wang, J Arnold, and HJ Chen. (1992). Hybrid Kohonen self-organizing neural network and multilayer feed-forward network for nonlinear regression and pattern recognition. *Proceedings of Artificial Neural Networks in Engineering* (ANNIE'92). St. Louis, Missouri. pp. 439-444.

Xiong, M, J Arnold, and HJ Chen (1993). A neural network model based on differential-algebraic equations for nonlinear programming. *IEEE International Conference on Neural Networks.* San Francisco. March 28-April 13. pp. 923-928.

Xiong, M, J Arnold, and HJ Chen (1993). O(n^3L) neural network model for linear programming. *Proceedings World Congress on Neural Networks*. Portland, OR. July 11-15. Volume 1, pp. 654-657.

Kochut, KJ, J Arnold, JA Miller, and WD Potter (1993). Design of an object-oriented database for reverse genetics. *Proceedings First International Conference on Intelligient Systems for Molecular Biology*. AAAI Press. Menlo Park, CA. pp. 234-242.

Bhandarkar, SM and J Arnold (1994). Parallel simulated annealing on the hypercube for chromosome reconstruction. *Proc. 14th IMACS World Congress at Georgia Tech on Computational and Applied Mathematics*. Volume 3, pp. 1109-1112.

Bhandarkar, SM, S Chirravuri, J Arnold, and D Whitmire (1996). Massively parallel algorithms for chromosome reconstruction. *Proc. Pacific Symp. on Biocomputing*, Jan. 3-6, Hawaii, USA, pp. 85-92.

Kececioglu, J, S Shete, and J Arnold (2000). Reconstructing order and distance in physical maps using non-overlapping probes. RECOMB 2000, 183-192z

Hall, RD, SM Bhandarkar, and J Arnold (2000). Creating physical maps with automatic capture of hybridization data, *ACM Conf. Computational Molecular Biology* (RECOMB), Tokyo, Japan, April 8-11, 2000, published in *Currents in Computational Molecular Biology*, S. Miyano, R. Shamir and T. Takagi (eds.) Universal Academy Press, Tokyo, Japan, pp. 163- 164

Hall, RD, SM Bhandarkar, SA Machaka, SS Shete, and J Arnold (2000). Parallel computation for chromosome reconstruction on a cluster of workstations. *Proc. Intl. Parallel and Distributed Processing Symposium (IPDS)*, Cancun, Mexico, May 2000, p. 63-70

Bhandarkar, SM, SA Machaka, SS Shete, and J Arnold (2000). Parallel computation for chromosome reconstruction on a cluster of workstations. *Proc. Intl Parallel and Distributed Processing Symposium (IPDS)*, Cancun, Mexico, May 1-5, 2000. pp. 63-70

Bhandarkar, SM, J Huang, and J Arnold (2002). Parallel Monte Carlo methods for physical mapping of chromosomes. *Proc. IEEE Computer Society Bioinformatics Conference*, Stanford University, Palo Alto, CA Aug 14-16, pp. 64-75.

Datta, S and J Arnold (2002). Some comparisons of clustering and classification techniques applied to transcriptional profiling data. *In Advances in Statistics, Combinatorics, and Related Areas*. C. Gulati, Y.-X. Lin, S. Mishra, and J. Rayner. World Scientific, Singapore, pp. 63-74

Hall, RD, JA Miller, J Arnold, KJ Kochut, A Sheth, and MJ Weise (2003). Using workflow to build an information management system for a geographically distributed genome sequencing initiative. In *Genomics of Plants and Fungi*. RA Prade and HJ Bohnert (eds). Marcel Dekker, Inc, NY, NY. Chapter 12, 359-371

Bhandarkar, SM, J Huang, and J Arnold (2003). A parallel genetic algorithm for physical mapping of chromosomes. *Bioinformatics Conference 2003. CSB 2003. Proc. 2003 IEEE*. pp. 567-572

Arnold, J, H-B Schuttler, D A Logan, D Battogtokh, J Griffith, B Arpinar, S Bhandarkar, S Datta, K,J Kochut, E. Kraemer, J A Miller, A Sheth, G Strobel, T Taha, B Aleman-Meza, J Doss, L Harris, and A Nyong (2004). Chapter 22 in Metabolomics. In *Handbook of Industrial Mycology*. 597-634 Marcel-Dekker, NY, NY

Deligiannidis, L, TR Taha, B Aleman-Meza, Y Yu, H-B Schuttler, and J Arnold (2005). GKIN: a graphical user interface for KINSOLVER. *Proc. 2005 International Arabic Conference on Information Technology(ACIT'2005)*, Dec. 6-8, 2005, Amman, Jordan. Pp. 245-251

Bhandarkar, SM, J Huang, and J Arnold (2006). An Information theoretic approach to genome reconstruction. Chapter 11 in *Handbook of Computational Molecular Biology*. 11-1-11-26 CRC Press, Boca Raton, FL

Tewari, S, J Arnold and SM Bhandarkar (2006) "Efficient Recursive Linking Algorithm for Computing the Likelihood of an Order of a Large Number of Genetic Markers" *Proc. of the IEEE LSS Computational Systems Bioinformatics Conference* (CSB 2006), Aug. 14-18, 2006, Stanford University, Palo Alto, CA., P Markstein and Y. Xu (ed.s), Imperial College Press, London. Pp. 191-198

Arnold, J, W Dong, J Griffith, D Choi, J Baldwin, L Hilton, K Kelps, J McGuire, R Morgan, M Smith, Q Wang, J Liu, J Reeves, DA Logan, ME Case, and H-B Schuttler. (2006).

Systems Biology of the Biological Clock. *IEEE Proceedings of the First International Conference on Computational Systems Biology (ICCSB-2006)*, pp. 119-125.

Xiong, M and J Arnold (2006). Do genetic networks obey Kirchhoff's and Ohm's Laws? *Proc. IASTED International Conf. on Comp. & Systems Biology*, Dallas, TX, November 13-14, 2006, pp. 13-19.

Deng, Z, S Arsenault, T Zhu, R Cheng, J Griffith, J Arnold, & L Mao (2014). Single cell measurements on the biological clock by microfluidics. *Proc. of the 18nth International Conference on Miniaturized Systems for Chemistry and Life Sciences (MicroTAS)*. San Antonio, TX 881-883.

Deng, Z, S Arsenault, L Mao, & J Arnold 2016. Measuring synchronization of stochastic oscillators in Biology. *J. Physics Conference Series* 750: 012001, doi:10.1088/1742-6596/750/1/012001

Judge, M, J Griffith, & J Arnold. 2017. Aging and the Biological Clock. In "*Circadian Rhythms and Their Impact on Aging*". Jazwinski, S M, Belancio, V P, & Hill, S M (ed.s). In "*Healthy Aging and Longevity*". Rattan, S. (ed.). Springer Science + Business Media B.V., Dordrecht, Netherlands. 978-3-319-64542-1. Ch. 10. Pp. 211-234

Deng, Z, J. Arnold, & L Mao (2017). Light entrainment of single cell circadian oscillator measured by a high-throughput microfluidic droplet platform. *Proc. of the 21st International Conference on Miniaturized Systems for Chemistry and Life Sciences (MicroTAS)*. Savannah, GA October 22-26, 2017.

Judge, M., S. Zhang, Y. Wue, J. Glushka, J. Arnold, & A. Edison (2018). Developments in the detection of oscillating metabolites in *Neurospora crassa*. *59nth Experimental Nuclear Magnetic Resonance Conference (ENC)*, Apr 29 – May 4, 2018. Orlando, FL.

Cheong, J. H, X. Qiu, Y. Liu, J. Griffith, H-B Schuttler, J. Arnold, & L. Mao (2020). Microfluidic Chamber Device to Test Quorum Sensing Theory. MicroTAS2020. Oct 4-9, 2020, online.

Cheong, J. H, X. Qiu, Y. Liu, J. Griffith, H-B Schuttler, J. Arnold, & L. Mao (2021). Measuring how clocks in single cells of *Neurospora crassa* communicate in microfluidic devices. MicroTAS2021. Oct 10-14, 2021, Palm Springs, CA 1/5/22, 12:18 PM RPPR - Preview Report https://reporting.research.gov/rppr-web/rppr?execution=e1s20 13/28

Qiu X, Cheong J, Liu Y, Schuttler H-B, Mao L, Arnold J. (2021) Quorum sensing in single cells of *Neurospora crassa*. 25th International Conference on Miniaturized Systems for Chemistry and Life Sciences (MicroTAS2021), Palm Springs, CA, USA, 10 Oct 2021 - 14 Oct 2021. 04 Oct 2021 (Proceedings of conference (published))

INVITED SEMINARS AND SYMPOSIUMS (1993-PRESENT)

Colloquium talk on "Towards a map of the human genome," Dept. of Statistics, UC Santa Barbara, April 8, 1993

"*In vitro* reconstruction of *A. nidulans* chromosome IV," June 8-11, 1994, NIH Mycology Workshop, Flagstaff, AZ. Symposium.

"*In vitro* reconstruction of fungal chromosomes," seminar speaker, Bristol-Meyer, Princeton, NJ, June 25, 1994.

"*In vitro* reconstruction of fungal chromosomes," seminar speaker, National Science Foundation, Arlington, VA, Sept. 8, 1994.

"*In vitro* reconstruction of fungal chromosomes,", seminar speaker, Department of Energy, Germantown, MD, October 19, 1994.

"*In vitro* reconstruction of fungal chromosomes and genomes," Fungal Genetics meeting, Asilomar, CA, March 21-26, 1995.

"*In vitro* reconstruction of fungal genomes," Georgia Institute of Technology, May 23,1995.

"*In vitro* reconstruction of fungal chromosomes," seminar speaker, School of Biological Sciences, Georgia Tech., Spring, 1995.

"*In vitro* reconstruction of fungal chromosomes," seminar speaker, Dept. of Biological Sciences, Clark Atlanta University, November, 1995.

"*In vitro* reconstruction of fungal chromosomes," symposium speaker, First Fungal Genome Workshop, Stillwater, OK, August 19, 1996.

"Fungal Genomics," symposium speaker, Plant Molecular Biology Retreat, December, 1996.

" Fungal Genomics", seminar, University of Cincinnati Medical Center, August, 1997.

" Fungal Genomics", Second International Symposium on Fungal Genomics, Athens, GA, March 26-27, 1998.

"Statistical Genomics", Sixth International Symposium/Statistics, Purdue, Lafayette, IN, June 21-23, 1998.

"*Neurospora crassa* physical mapping project", Gordon Conference on Cellular and Molecular Mycology, Holderness School, Plymouth, NH, July 19 – 24, 1998.

"Statistical Genomics", Part II, Fall Colloquia, Purdue, Lafayette, IN, Oct. 21-23, 1998.

"Genomics", Human Genetics Center, University of Texas at Houston, March 16- 18, 1999.

"Fungal Genomics", 20th Fungal Genetics Conference, Asilomar Conference, Pacific Grove, CA, March 23 – 25, 1999.
"Physical mapping of *Pneumocystis carinii*", Society of Protozoologists, Raleigh, NC May 26-29, 1999.
"Physical Mapping", Burroughs Wellcome Meeting following the American Society of Microbiology, Chicago, IL June 3 – 4, 1999.
" Fungal Genomics", International Botanical Congress, St. Louis, MI, August 1-7, 1999
" Microsatellite variation in *Candida albicans*", invited talk, General Society of Microbiology, University of Warwick, Warwick, England, April 13, 2000.
"*In vitro* reconstruction of fungal chromosomes", Clark Atlanta University, Spring 2000.
"Computing Life", Joint Statistical Meetings (JSM) 2001, Atlanta, GA, August 9, 2001
"Metabolomics", North Carolina State University, Raleigh, NC, Feb 19, 2002
"Fungal Genomics", Centers for Disease Control, Atlanta, GA, May 15, 2002
"Computing Life", Purdue University, April, 2003
"Computing Life", National Science Foundation Workshop on
"Computational Resources for Microbial Systems, Arlington, VA, October 27-29, 2003
"Computing Life", University of Minnesota, Bioinformatics: Building Bridges, April 16, 2004
"Genetic Networks", Dept. Biochemistry & Molecular Biology, Louisiana Health Science Center, January 13, 2006, rescheduled, New Orleans.
"Systems Biology of the Biological Clock", keynote address, First International Conference on Computational Systems Biology, July 20-23, 2006, Shanghai, China.
"Design of Case-Control studies of Centenarians", invited talk, International Conference on Centenarians, October 18, 2006, Sunchang, KoreaZ
Systems Biology of the Biological Clock", Yale Department of Ecology and Evolutionary Biology, November 14, 2007, New Haven, CT
"Biological clock and aging", 20th Anniversary Celebration of the Georgia Centenarian Study, August 12, 2008, Atlanta, GA
"Biological Clock and Aging, IAGG Meeting, July 8, 2009, Paris, France
"Systems Biology of the Clock", Yale Systems Biology Symposium, October 15, 2010, New Haven, CT
"Systems Biology of the Clock", seminar, Department of Organismal and Evolutionary Biology, Harvard University, March 21, 2012, Cambridge, MA
"Systems Biology of the Clock", seminar, Department of Bioinformatics and Biostatistics, University of Louisville, March 27, 2015, Louisville, KY
"Measuring synchronization of stochastic oscillators in biology", in *Recent Developments in Computer Simulation Studies in Condensed Matter Physics*. UGA. February 22-26, 2016, Center for Simulational Physics.
"ALICE: New approaches to undergraduate and graduate education in systems biology, March 12, 2016, Spelman College, NSF Quantitative Biology Workshop
"Are there clocks in single cells that synchronize?", Laboratory of Genetics, University of Wisconsin – Madison, January 25, 2017
"Are there clocks in single cells that synchronize?", Georgia Scientific Computing Symposium, University of Georgia, February 25, 2017

RECOGNITION AND OUTSTANDING ACHIEVEMENTS

Member of Sigma Xi
Yale University Graduate Fellowship
Yale Stanley Prize in Mathematics (undergraduate)

PRE AND POSTDOCTORAL FELLOWS

Current graduate students

Zhang, S., (co-advised with Leidong Mao) "Clock Filaments and their Synchronization in *Neurospora crassa*"

Hossain, Z. (co-advised with Art Edison). "Quorum sensing in the clock in *Neurospora crassa*".
Asher, Olivia (co-advised with Jeff Bennetzen), "Competition between arbuscular mycorrhizal fungi"
Bouffier-Landrum, Amanda, "MINE for Mapping Populations of Sorghum"
Zhang, Shufan, "Mapping Arbuscular Mycorrhizal Fungi traits to the Sorghum genome"
Torres, Isaac, "MINE for structural equation models"
Skaro, Michael, PhD candidate, IOB, "Applications of machine learning in omics and computer vision"
Scruse, Ashley, PhD candidate, IOB, "Network Motifs"
Qiu, Xiao, PhD candidate, Institute of Bioinformatics,"contact networks for cellular clock synchronization"
Wu, Yue, PhD candidate, Institute of Bioinformatics, "metabolomics network models in Neurospora crassa using CIVM-NMR"
Hwei-Cheong, Jia, PhD candidate, Chemistry Department, "quorum sensing to synchronize cellular clocks".

Current undergraduates

Lincoln, Brooke, (2021-). "Living Mulch"

Felt, Camryn (2021-). "N and P ratios and AMF colonization of sorghum roots".

Gay, Skylar (2021-). "Coalescent Theory and the 2020 Pandemic"

Prestel, Anna (2022-). "High throughput phenotyping of AMF in sorghum roots and their GWAS"

Lantz, William (2022-). "High throughput phenotyping of AMF in sorghum and their GWAS"

Meinster, Andrew (2022-). "High throughput phenotyping of AMF in sorghum"

Prestel, Anna (2022-). "High throughput imaging of AMF in sorghum"

Lantz, William (2022-). "High throughput imaging of AMF in sorghum"

Current postdoctoral fellows

Past postdoctoral fellows

Weaver, Geoffrey, (2020-2021) "High-throughput imaging of arbuscular mycorrhizal fungi in sorghum"
Dong, Wubei (2007), Genetics, UGA, "Systems biology of Neurospora" –Professor, Huazhong Agricultural University, Wuhan, China
Dai, Jianliang (2007). "Sample size problem for 2 x 2 x 2 table" – now Biostastician/Bioinformatician, Department of Medicine, Tulane Center of Aging, Tulane University, New Orleans, LA
Arpinar, B (2001). "Adaptive workflows for protein-protein interaction mapping" – UGA, now associate professor, Computer Science Department, University of Georgia
Hall, D. (2000), "Fungal Genome Database", Assistant Computational Biologist – UGA, now
Head of Computational Biology at Rho, Inc., Chapel Hill, NC
Kelkar, H. (1999), "*In vitro* reconstruction of the *Neurospora crassa* and *Aspergillus flavus* genomes.", now Director of Scientific Computing, Bioinformatics Center, University of North Carolina – Chapel Hill
Prade, R., (1995). "Physical mapping of *Aspergillus nidulans*". Associate Professor, Dept. Microbiology and Molecular Genetics, Oklahoma State University, Stillwater, OK.
Wang, Y., (1994). "Neural Networks for physical mapping". Bioinformatics Department, Merck , Inc.
Fu, Y.-X. (1990). "Cytonuclear disequilibria in finite populations". Professor, University of Texas at Houston Human Genetics Center, University of Texas at Houston, Houston, TX.

Past students

Skaro, Michael, PhD (2022),, Institute of Bioinformatics, "Applications of machine learning in omics and computer vision", computational biologist, Glaxo-Smith-Kline

Stupp, Lauren (2021-2022). "Imaging of arbuscular mycorrhizal fungi in sorghum roots".

Krach, Emily, PhD (2021), Genetics Department, "Conidio-forms: Identifying and characterizing natural morphological variation in *Neurospora crassa* conidiophores", postdoctoral fellow, NIH

Judge, Michael, PhD (joint with Art Edison) (2021), Genetics Department, "Dynamics of Metabolism in *Neurospora crassa*", Postdoctoral Fellow, Imperial College

Montenegro, Tito Pena, PhD (joint with Mandy Joye) (2021), Institute of Bioinformatics, "Tracking the response of hydrocarbon-degrading microorganisms to environmental forcings"

Lim-Tom, Tatiana BS (2017-2020). "conidiophore development in *Neurospora crassa*.

Wu, Lingyun, PhD (2020), Physics and Astronomy, "Collective Behavior of Stochastic Biological Clocks". Research scientist, Google, San Diego.

Caranica, Cristian PhD (2020) Stochastic Models for Genetic Networks, Department of Statistics, postdoctoral fellow, Jackson Laboratories, Bar Harbour, ME

Hull, Brooke, BS (2018). Genomic editing of *Neurospora crassa* as a tool for studying circadian oscillator synchronization – Now, graduate student at Princeton University

Deng, Zhaojie, PhD (2017), College of Engineering, "Single-cell analysis on the biological clock using microfluidic droplets", College of Engineering. Research Scientist, Department of Genomic Sciences. University of Washington, Seattle, WA

Robinson, Sarah BS (2017). Propagation of errors in single cell oscillatory time series to the periodogram. – Now, graduate student at Rice University

Al-Omari, Ahmad, Ph.D (2015), Institute of Bioinformatics, "Discovering a regulatory network topology by Markov Chain Monte-Carlo on GPGPUs with special reference to the biological clock of *Neurospora crassa*", associate professor, Yarmouk University, Jordan

Cunningham, Sarah, BS (2016). The genetic network of circadian rhythms in *Neurospora crassa*. – Now, graduate student at Duke University

Manzourolajdad, Amirhossein, Ph.D. (2014), Institute of Bioinformatics, UGA: *Ab initio* Identification of regulatory RNAs using information-theoretic uncertainty. Research fellow, NLM, temporary assistant professor, Indiana University - Indianapolis

Brunson, Patrick (2014). Sphingolipid synthesis and the aging biological clock in *Neurospora crassa*. Now graduate student at UC-San Diego.

Bouffier, Amanda M., M.S. (2013), Institute of Bioinformatics, UGA: A MINE alternative to D-optimal designs for the linear model. unknown

Arte, Ankit, M.S (2011), Computer Science, UGA: HiDEW: High-Speed Determination of epigenetic code rendered through a Web Application. Web developer, University of Georgia

Tang, Xiaojia, Ph.D. (2009), Physics and Astronomy, UGA: The Computational Systems Biology for the Biological Clock of *Neurospora crassa*. Postdoctoral fellow, Mayo Clinic with Dr. Krishna Kalari

Tewari, Susanta, Ph.D. (2008), Statistics, UGA: Construction of high-resolution likelihood-based integrated genetic and physical map of *Neurospora crassa*. Assistant Professor, Ahmedabad University, Calcultta, India.

Koch, Allison, B.S. (2007), Genetics, UGA: Systems Biology of the *qa* gene cluster in *Neurospora crassa*, - Now, Regulatory Affairs manager at Astra/Zeneca

Morello, M., B.S. (2005), Genetics, UGA: Half-life of the *wc-1* mRNA in *Neurospora crassa*". Medical College of Georgia physician training program.

Altimus, Cara, B.S. (2003), Honors, Genetics, UGA "What makes a Biological clock in tick?" Honors Thesis. Johns Hopkins University postdoctoral fellow

Whitworth, C., B.S. (2003). Honors, Genetics, UGA, "Integrated genomic and proteomic analysis of the *qa* gene cluster of *Neurospora crassa*". Associate Director, Bloomington Drosophila Stock Center, Bloomington, Indiana.

Xu, Zheng, M.S. (2001), Computer Science, UGA, "Mapping by Sequencing using ODS". University of Chicago Business School

Fundyga, R., Ph.D. (2001), Genetics, UGA, "The population genetics of pathogenic fungi: empirical and theoretical studies. ASM postdoctoral fellow", CDC, now veterinarian, Plymouth, MASS

Hall, D., Ph.D. (1999), Genetics, UGA, "New computational tools for genome mapping". Rho, principal investigator.

Sanchez, M., Ph.D. (1999), Genetics, UGA, "Coevolutionary models of host/pathogen systems." Postdoctoral fellow, Dr. Alan Hastings, University of California - Davis

Shete, S., Ph.D. (1998), Statistics, UGA, "Methods for physical mapping." Professor. University of Texas M.D. Anderson Cancer Center, Houston, Texas.

Wollenberg, K., Ph.D. (1997), Genetics, UGA, "Testing for nonrandomness in phylogenetic trees."Assistant Professor, Tufts University, now NIH

Dean, R., Ph.D. (1996), Genetics, UGA, "Three models for cytonuclear disequilibria". Statistical Geneticist. National Plant Germplasm System, Griffin, GA.

Datta, S., Ph.D. (1995), Statistics, UGA, "Dynamics of cytonuclear disequilibria and related statistical tests for the neutrality of mitochondrial DNA markers for hybrid zone data". Professor, Department of Biostatistics, University of Florida, Gainesville, FL.

Xiong. M., Ph.D. (1993), Statistics, UGA, co-sponsored with H.J. Chen, "Mathematical theory of neural learning and its applications to statistics and molecular biology". Professor, University of Texas at Houston Human Genetics Center, University of Texas at Houston, Houston, TX.

Cellino, M. J., M. S. (1992), Genetics, UGA, "The effects of cytoplasmic male sterility on Cytonuclear Disequilibria in hybrid zones". Networking Professional, NetCom, Inc, Washington, D.C.

Cuticchia, A. J., Ph.D. (1992). Genetics, UGA. "Computational advances in the physical mapping of small eukaryotic genomes". instructor, North Carolina Central University and AJC Legal Services.

Williams, C. J., Ph.D. (1988). Statistics, UGA. "Statistical problems in selection component analysis". full professor, Department of Mathematics & Statistics, University of Idaho.

Phillips, G. J., Ph.D. (1987). Genetics, UGA, Co-sponsored with S. R. Kushner. "Structural and functional characterization of the Exonuclease I (*sbcB)* gene and gene product from *Escherichia coli* and a Markov chain analysis of DNA sequences". Professor, Department of Microbiology, Iowa State University, Ames, Iowa.

Adams, P. B., Ph.D. (1986). Behavior Genetics, Georgia State University, Co-sponsored with A. Falek. "Statistical analysis of age at onset in Huntington's disease". Assistant professor, Department of Genetic Epidemiology, Columbia University Psychiatry and New York Psychiatric Institute.

Sammons, S. A., M.S.T. (1987). Genetics, UGA, "Molecular evolution of homeo boxes". Research Scientist, Bioinformatics, CDC, Atlanta, GA

Lemke, K. M.S. (1985). Statistics, UGA, "Dispersal models for *Drosophila*". Biostatistician, Johns Hopkins University Bloomberg School of Public Health, Center for Heath Services and Outcomes Research.

Porter, J., M.A.M.S. (1985). Computer Science, UGA, "Inversion frequency mapping in *Drosophila pseudoobscura*". Ph.D. candidate, Botany Department, Duke University.

Goldman, I. F., M.S. (1985). Entomology, UGA, "Selection for resistance to *Bacillus thuringiensis* variety *israelensis* in field and laboratory populations of the mosquito *Aedes aegypti*". Molecular Entomologist, Center for Disease Control (CDC, Atlanta).

REVIEWER

ad hoc reviewer, NIA grant in longevity
ad hoc reviewer, NIAID grants in fungal genomics
ad hoc reviewer, NIH Nonmammalian models of Biomedical Research
ad hoc reviewer, NIH GCAT study section
USDA grant proposals
NSF grant proposals
United Kingdom grant proposals
ACS Synthetic Biology
American Journal of Human Genetics
American Naturalist
Applied Mathematics and Computation
Bioinformatics
Bioinformation
Biometrics
Biophysical Journal
BMC Bioinformatics
BMC Genomics
Bulletin of Mathematical Biology
CABIOS
Current Gerontology and Geriatrics Research
Database
Evolution
Evolutionary Theory

FEBS Letters
Frontiers Cell and Developmental Biology
Frontiers in Genetics
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Fungal Biology Reviews
Fungal Genetics & Biology
Genetica
Genetics
Genetics Research
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Journal of Royal Society Series B
Journal of Theoretical Biology
Mathematical Biosciences
Molecular Biology & Evolution
Nature
Nature Communications
Nature Metabolism
Nature Scientific Reports
Nucleic Acids Research
PLoS Computational Biology
PLoS ONE
Proceedings of the National Academy of Sciences USA
Science
SIAM Journal of Applied Mathematics
Statistical Methods in Medical Research
Statistics and Probability Letters
Swiss National Science Foundation
Theoretical Population Biology

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