

## Joshua L. Payne

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CONTACT INFORMATION	Roche, pRED Data & Analytics Roche Innovation Center Zurich Wagistrasse 10 CH-8952 Schlieren, Switzerland	<i>Phone:</i> 079 501 59 17 <i>E-mail:</i> <a href="mailto:joshua.payne@roche.com">joshua.payne@roche.com</a> <i>Website:</i> <a href="http://joshualevipayne.com">joshualevipayne.com</a>
INTERESTS	Computational biology, evolution, evolutionary computation, gene regulation, genotype-phenotype maps, machine learning, networks, translation	
EDUCATION	Ph.D., Computer Science, The University of Vermont, VT USA (2009) <ul style="list-style-type: none"><li>• Dissertation: Interaction Topologies and Information Flow</li><li>• Advisor: Professor Margaret J. Eppstein</li></ul> M.Eng, Operations Research, Rensselaer Polytechnic Institute, NY USA (2004) B.S., Mathematics and Computer Science, Regis University, CO USA (2003)	
SUMMER PROGRAMS	International Institute for Applied Systems Analysis (IIASA), Austria (2008) Santa Fe Institute, NM USA (2007) New England Complex Systems Institute, MA USA (2005)	
RESEARCH EXPERIENCE	2023 - Present, Principal Scientist, pRED, Roche, Zurich, CH 2018 - 2023, Group Leader, Swiss Institute of Bioinformatics, Lausanne, CH 2017 - 2023, SNSF Assistant Professor of Computational Biology, ETH Zurich, CH 2015 - 2017, Junior Group Leader, University of Zurich, CH 2012 - 2015, Postdoctoral Research Fellow, University of Zurich, CH 2009 - 2011, Postdoctoral Research Fellow, Dartmouth, NH, USA 2009 - 2010, Visiting Scientist, IIASA, Austria 2004 - 2009, Graduate Research Fellow, The University of Vermont, VT, USA	
TEACHING EXPERIENCE	2020 - 2023, Lecturer in Environmental Systems Data Science, ETH 2018 - 2023, Lecturer in the Computational Biology and Bioinformatics Seminar, ETH 2017 - 2023, Guest lecturer in BIO445: Quantitative Life Sciences, University of Zurich 2017 - 2018, Guest lecturer in BIO241: Gene Regulation, University of Zurich 2017, Guest lecturer in Summer School on Polygenic Adaptation, WSL 2015, Lecturer in SystemsX/SIB Joint Autumn School on Systems Modeling 2015, Guest lecturer in BL.0123: Cellular and Genetic Networks, University of Fribourg 2013 - 2015, Guest lecturer in BIO673: Computational Biology, University of Zurich 2012 - 2013, Faculty of the Citizen Science Program, Bard College, NY, USA	
MENTORING	2022 -, Alexander Klug, Postdoc, ETH 2020 -, Hana Rozhoňová, Ph.D. student, ETH 2020 -, Malvika Srivastava, Ph.D. student, ETH 2020 - 2023, Magdalena San Roman, Postdoc, ETH 2017 - 2022, Paco Majic, Ph.D. student, ETH 2017 - 2022, Alejandro Cano, Ph.D. student, ETH 2015 - 2016, Fahad Khalid, Research scientist, University of Zurich 2013 - 2017, José Aguilar-Rodríguez, Ph.D student, University of Zurich 2010 - 2014, Dov Pechenick, Ph.D. student, Dartmouth College	

INVITED TALKS (RECENT) Vienna Graduate School of Population Genetics Seminar Series, Vienna, May 3, 2022  
 Milner Center for Evolution Seminar Series, University of Bath, March 2, 2022  
 Week of Evolution, Boğaziçi University, February 4, 2022  
 Departmental Seminar, University of Bern, Switzerland, March 31, 2021  
 Departmental Seminar, University of Lausanne, Switzerland, January 12, 2020  
 Departmental Seminar, Center for Advanced Study, Oslo, Norway, December 3, 2019  
 Departmental Seminar, Oxford, UK, July 3, 2019

CONFERENCE TALKS (SELECTED) Predicting Evolution, EMBL Workshop, Heidelberg, July 13, 2023  
 LS<sup>2</sup> Life Sciences Switzerland, Zurich, April 21, 2022  
 Predicting Evolution, EMBL Workshop, Heidelberg, June 14, 2021  
 Society for Molecular Biology and Evolution, Manchester, UK, July 22, 2019  
 CECAM Workshop on Genotype-Phenotype Maps, Zaragoza, Spain, March 14, 2019  
 European Society for Evolutionary Biology, Montpellier, France, August 21, 2018  
 European Society for Evolutionary Biology, Groningen, Netherlands, August 23, 2017

GRANTS SNSF Professorship Extension, 2021-2023, CHF 788,205  
 Cogito Foundation Grant 2021, CHF 90,000 (w/J. Winkler, L. Keller, & A. Wagner)  
 EMBO Workshop Grant 2021, EUR 39,000 (w/A. Walczak, P. Wittkopp, & J. Crocker)  
 SNSF Project Grant 2020-2024, CHF 471,928  
 SNSF Professorship, 2017-2021, CHF 1,560,160  
 SystemsX iPhD Project, 2016-2019, CHF 199,463 (w/Y. Schaerli & A. Wagner)  
 SNSF Ambizione Fellowship, 2015-2018, CHF 574,921  
 Forschungskredit, University of Zurich, 2014, CHF 100,000  
 NSF International Research Fellowship, 2012-2014, \$138,734  
 Collaborative Research Travel Grant, Burroughs Wellcome Fund, 2011, \$10,250.  
 Walter Karplus Summer Research Grant, IEEE CIS, 2009, \$2700

AWARDS AND HONORS Fellow of the Center for Advanced Study, Oslo, Norway, 2019-2020  
 Dan David Prize Scholarship in Bioinformatics, 2015 (\$15,000)  
 SIB Young Bioinformatician Award, 2014 (CHF 10,000)  
 Winner of Best Paper Award in the European Conference on Artificial Life, 2011  
 Graduate Award, Department of Computer Science, UVM, 2008, 2009  
 Vermont EPSCoR (NSF) Graduate Research Fellowship, 2008 - 2009  
 Association of Computing Machinery Faculty Award, 2007  
 Winner of Best Student Paper Award in the IEEE Symposium on Artificial Life, 2007  
 Vermont EPSCoR (DOE) Graduate Research Fellowship, 2005 - 2007

SERVICE **Program Committee Member:** IEEE Symposium on Artificial Life 2013-2017; Evo-Complex 2010-2014; European Conference on Artificial Life 2011-2017; Latsis Symposium, “Origin and Prevalence of Life”, ETH, 2022; LS<sup>2</sup> “PI’s of tomorrow” jury member, 2022. **Thesis Tribunal Member:** Luzia Stadler, ETH, 2019; Amel Bekkar, University of Lausanne, 2018; Pablo Catalan Fernandez, Universidad Carlos III de Madrid, 2017; Marcel Weiss, Cambridge, 2020; Christian Feregrino, University of Basel, 2020. **Thesis Committee member:** Cauã Westmann, University of Zurich, 2019-; Stefan Butz, University of Zurich, 2018-2021; Victor Boussange, ETH, 2019-; Michael Schmutzer, UZH, 2020-. **Public Liaison:** UVM’s Computer Science Student Association, 2005 - 2008. **Editorial Work:** Guest editor for *PLoS Computational Biology*, 2019, *eLife*, 2021, and *Philosophical Transactions B*. **Editorial Board:** Review Editor in Bioinformatics and Computational Biology at *Frontiers in Genetics*; Review Editor at *Journal of Evolutionary Biology*. **Conference organization:** Predicting Evolution, EMBO Workshop, June, 2021, 2023; Latsis Symposium on The Origin and Prevalence of Life, 2022.

EXTERNAL PEER  
REVIEWER

**Journals:** Applied Network Science; Artificial Life; BioEssays; Bioinformatics; BMC Bioinformatics; Cell Reports; Developmental Cell; Ecological Modelling; eLife; Evolution; Genetics; Genetic Programming and Evolvable Machines; Genome Biology; IEEE Transactions on Evolutionary Computation; IEEE Transactions on Nanobioscience; Journal of Evolutionary Biology; Journal of Experimental Zoology B; Journal of the Royal Society Interface; Molecular Biology and Evolution; Molecular Systems Biology; Nature; Nature Communications; Nature Ecology & Evolution; Nature Genetics; Nature Reviews Genetics; Philosophical Transactions of the Royal Society B; PLoS Computational Biology; PLoS Genetics; PNAS; Science Advances; Scientific Reports; Soft Computing. **Conferences:** ALIFE 2014, 2016; BMIC 2010; ECAL 2011-2017; Evo\* 2010 - 2013; IEEE SSCI 2013. **Books:** Handbook of Research on Computational and Systems Biology (IGI Global, 2010). **Grants:** Issachar Fund; FWF Project Grants; NWO Innovational Research Incentives Scheme Veni; SNSF Project Grants; DFG Priority Programme “Genomic basis of evolutionary innovations.”

SUBMITTED

Rozhoňová, H., Martí-Gómez, C., McCandlish, D.M., **Payne**<sup>®</sup>, **J.L.** “Protein evolvability under rewired genetic codes.”

Cano, A., Couce, A., Masel, J., **Payne, J.L.**, Stoltzfus, A., & Storz, J. F. “Misrepresenting biases in arrival.”

REFEREED  
JOURNAL  
PUBLICATIONS

Srivastava<sup>®</sup>, M., Rozhoňová, H., & **Payne, J.L.** “Alphabet cardinality and adaptive evolution.” (2023) *Journal of Physics A*, to appear.

Majic<sup>®</sup>, P. & **Payne, J.L.** “Developmental selection and the perception of mutation bias.” (2023) *Molecular Biology & Evolution*, 40, masad179.

Baier, F., Gauye, F., Perez-Carrasco, R., **Payne**<sup>®</sup>, **J.L.**, Schaerli<sup>®</sup>, Y. (2023) “Environment-dependent epistasis increases phenotypic diversity in gene regulatory networks.” *Science Advances*, 9, eadf1773.

Gitschlag<sup>=</sup>, B., Cano<sup>=</sup>, A., **Payne, J.L.**, McCandlish<sup>®</sup>, D.M., & Stoltzfus<sup>®</sup>, A. (2023) “Mutation and selection induce correlations between selection coefficients and mutation rates.” *The American Naturalist*, to appear.

Crocker<sup>®</sup>, J., & **Payne, J.L.**, Walczak, A. M., & Wittkopp, P. J. (2023) “Interdisciplinary approaches to predicting evolutionary biology.” *Philosophical Transactions B*, 378, 20220042.

Cano<sup>=</sup>, A., Gitschlag<sup>=</sup>, B., Rozhonova, H., Stoltzfus<sup>®</sup>, A., McCandlish<sup>®</sup>, D.M., & **Payne**<sup>®</sup>, **J.L.** (2023) “Mutation bias and the predictability of evolution.” *Philosophical Transactions B*, 378, 20220055.

Srivastava, M. & **Payne**<sup>®</sup>, **J.L.** (2022) “On the incongruence of genotype-phenotype and fitness landscapes.” *PLoS Computational Biology*, 18, e1010524.

Majic P., Erten, Y., & **Payne**<sup>®</sup>, **J.L.** (2022) “The adaptive potential of non-heritable somatic mutations.” *The American Naturalist*, 200, 755-772.

Cano, A., Rozhoňová, H., Stoltzfus, A., McCandlish<sup>=,®</sup>, D. & **Payne**<sup>=,®</sup>, **J.L.** (2022) “Mutation bias shapes the spectrum of adaptive substitutions.” *Proceedings of the National Academy of the Sciences*, 119, e2119720119.

Rozhoňová, H. & **Payne**<sup>®</sup>, **J.L.** (2021) “Little evidence the standard genetic code is optimized for resource conservation.” *Molecular Biology & Evolution*, 38, 5127-5133.

Manrubia, S. et al. (including **Payne**, **J.L.**) (2021) “From genotypes to organisms: State-of-the-art and perspectives of a cornerstone in evolutionary dynamics.” *Physics of Life Reviews*, 38, 55-106.

Cano, A. & **Payne**<sup>®</sup>, **J.L.** (2020) “Mutation bias interacts with composition bias to influence adaptive evolution.” *PLoS Computational Biology*, 16, e1008296.

Majic, P. & **Payne**<sup>®</sup>, **J.L.** (2020) “Enhancers facilitate the birth of *de novo* genes and gene integration into regulatory networks.” *Molecular Biology & Evolution*, 37, 1165-1178.

**Payne**<sup>™</sup>, **J.L.**, Menardo<sup>™</sup>, F., Trauner, A., Borrell, S., Gygli, S.M., Loiseau, C., Gagneux<sup>™,®</sup>, S., & Hall<sup>™,®</sup>, A.R. (2019) “Transition bias influences the evolution of antibiotic resistance in *Mycobacterium tuberculosis*.” *PLoS Biology*, 17(5), e3000265.

Zheng, J., **Payne**, **J.L.**, & Wagner<sup>®</sup>, A. (2019) “Cryptic genetic variation accelerates evolution by opening access to diverse adaptive peaks.” *Science*, 365, 347-353.

**Payne**, **J.L.** & Wagner<sup>®</sup>, A. (2019) “The causes of evolvability and their evolution.” *Nature Reviews Genetics*, 20, 24-38.

Aguilar-Rodríguez, J., Peel, L., Stella, M., Wagner<sup>®</sup>, A., & **Payne**<sup>®</sup>, **J.L.** (2018) “The architecture of an empirical genotype-phenotype map.” *Evolution*, 72, 1242-1260.

**Payne**<sup>®</sup>, **J.L.**, Khalid, F., & Wagner, A. (2018) “RNA-mediated gene regulation is less evolvable than transcriptional regulation.” *Proceedings of the National Academy of the Sciences*, 115, E3481-E3490. (**recommended by the Faculty of 1000.**)

Aguilar-Rodríguez<sup>™</sup>, J., **Payne**<sup>™</sup>, **J.L.**, & Wagner<sup>®</sup>, A. (2017) “A thousand empirical adaptive landscapes and their navigability.” *Nature Ecology & Evolution*, 1, 0045.

Khalid, F., Aguilar-Rodríguez, J., Wagner<sup>®</sup>, A., & **Payne**<sup>®</sup>, **J.L.** (2016) “Genonets server — a web server for the construction, analysis, and visualization of genotype networks.” *Nucleic Acids Research*, 44, W70-W76.

**Payne**<sup>®</sup>, **J.L.** (2016) “No tradeoff between versatility and robustness in gene circuit motifs.” *Physica A*, 449, 192-199.

SIB Swiss Institute of Bioinformatics Members (including **Payne**, **J.L.**) (2016) “The SIB Swiss Institute of Bioinformatics’ resources: focus on curated databases.” *Nucleic Acids Research*, 44, D27-D37.

**Payne**<sup>®</sup>, **J.L.** & Wagner, A. (2015) “Mechanisms of mutational robustness in transcriptional regulation.” *Frontiers in Genetics*, 6, 332.

**Payne**, **J.L.** & Wagner<sup>®</sup>, A. (2015) “Function does not follow form in gene regulatory circuits” *Scientific Reports*, 5, 13015.

Pechenick, D.A., **Payne**, **J.L.** & Moore<sup>®</sup>, J.H. (2014) “Phenotypic robustness and the assortativity signature of human transcription factor networks.” *PLoS Computational Biology*, 10, e1003780.

**Payne, J.L.** & Wagner<sup>®</sup>, A. (2014) “Latent phenotypes pervade gene regulatory circuits.” *BMC Systems Biology*, 8, p. 64.

**Payne, J.L.**, & Wagner<sup>®</sup>, A. (2014) “The robustness and evolvability of transcription factor binding sites.” *Science*, 343, pp. 875-877. (**recommended by the Faculty of 1000.**)

**Payne<sup>®</sup>, J.L.**, Moore, J.H., & Wagner, A. (2014) “Robustness, evolvability, and the logic of genetic regulation.” *Artificial Life*, 20, pp. 111-126.

**Payne, J.L.**, & Wagner<sup>®</sup>, A. (2013) “Constraint and contingency in multifunctional gene regulatory circuits.” *PLoS Computational Biology*, 9, p. e1003071.

Pechenick, D.A., Moore<sup>®</sup>, J.H., & **Payne, J.L.** (2013) “The influence of assortativity on the robustness and evolvability of gene regulatory networks upon gene birth.” *Journal of Theoretical Biology*, 330, pp. 26-36.

**Payne<sup>®</sup>, J.L.**, Giacobini<sup>®</sup>, M., & Moore<sup>®</sup>, J.H. (2013) “Complex and dynamic population structures: synthesis, open questions, and future directions.” *Soft Computing*, 17, pp. 1109-1120.

Hu<sup>=</sup>, T., **Payne<sup>=,®</sup>, J.L.**, Banzhaf, W., & Moore, J.H. (2012) “Evolutionary dynamics on multiple scales: a quantitative analysis of the interplay between genotype, phenotype, and fitness in linear genetic programming.” *Genetic Programming and Evolvable Machines*, 13, pp. 305-337.

Pechenick<sup>=,®</sup>, D.A., **Payne<sup>=</sup>, J.L.**, Moore, J.H. (2012) “The influence of assortativity on the robustness of signal-integration logic in gene regulatory networks.” *Journal of Theoretical Biology*, 296, pp. 21-32.

**Payne<sup>®</sup>, J.L.**, Decker-Harris<sup>®</sup>, K., & Dodds<sup>®</sup>, P.S. (2011) “Exact solutions for social and biological contagion models on mixed directed and undirected, degree-correlated random networks.” *Physical Review E*, 84, p.016110.

Dodds<sup>®</sup>, P.S., Decker-Harris<sup>®</sup>, K., & **Payne<sup>®</sup>, J.L.** (2011) “Direct, physically motivated derivation of the contagion condition for spreading processes on generalized random networks.” *Physical Review E*, 83, p.056122.

**Payne<sup>®</sup>, J.L.**, Mazzucco, R., & Dieckmann, U. (2011) “The evolution of conditional dispersal and reproductive isolation along environmental gradients.” *Journal of Theoretical Biology*, 273, pp. 147-155.

**Payne<sup>=,®</sup>, J.L.**, Sinnott-Armstrong<sup>=‡</sup>, N., & Moore, J.H. (2010) “Exploiting graphics processing units for computational biology and bioinformatics.” *Interdisciplinary Sciences: Computational Life Sciences*, Springer-Verlag, 2(3), pp. 213-220.

**Payne<sup>®</sup>, J.L.**, Dodds, P.S., & Eppstein, M.J. (2009) “Information cascades on degree-correlated random networks.” *Physical Review E*, 80, p. 026125.

**Payne<sup>®</sup>, J.L.**, & Eppstein<sup>®</sup>, M.J. (2009) “Evolutionary dynamics on scale-free interaction networks.” *IEEE Transactions on Evolutionary Computation*, 13(4), pp. 895-912.

**Payne<sup>®</sup>, J.L.**, & Eppstein<sup>®</sup>, M.J. (2009) “Pair approximations of takeover dynamics in regular population structures.” *Evolutionary Computation*, 17(2), pp. 203-229.

Eppstein<sup>®</sup>, M.J., **Payne, J.L.**, & Goodnight, C.J. (2009) “Underdominance, multi-scale interactions, and self-organizing barriers to gene flow.” *Artificial Evolution and Applications*, p. 725049.

Dodds<sup>®</sup>, P.S., & **Payne<sup>®</sup>, J.L.** (2009) “Analysis of a threshold model of social contagion on degree-correlated networks.” *Physical Review E*, 79, p. 066115.

Eppstein<sup>®</sup>, M.J., **Payne, J.L.**, White, Bill C., & Moore J.H. (2007) “Genomic mining for complex disease traits with ‘random chemistry.’” *Genetic Programming and Evolvable Machines*, Special Issue on Medical Applications, 8(4), pp. 395 - 411.

REFEREED  
CONFERENCE  
PUBLICATIONS

Peckenick<sup>®</sup>, D.A., **Payne, J.L.**, & Moore, J.H. (2013) “An alternative route to robustness: the relationship between assortativity, in-components, and characteristic path length in gene regulatory networks.” *Proceedings of the European Conference on Artificial Life*, ECAL-2013, pp. 364-371.

**Payne<sup>®</sup>, J.L.** & Moore, J.H. (2011) “Robustness, evolvability, and accessibility in the signal-integration space of gene regulatory circuits.” *Proceedings of the European Conference on Artificial Life*, ECAL-2011, pp. 638-645. **(best paper award.)**

Pan, Q., Darabos, C., Tyler, A., Moore<sup>®</sup>, J.H., & **Payne, J.L.** (2011) “The influence of whole genome duplication and subsequent diversification on environmental robustness and evolutionary innovation in gene regulatory networks.” *Proceedings of the European Conference on Artificial Life*, ECAL-2011, pp. 614-621.

Hu<sup>®</sup>, T., **Payne<sup>®</sup>, J.L.**, Banzhaf, W., & Moore<sup>®</sup>, J.H. (2011) “Robustness, evolvability, and accessibility in linear genetic programming.” *Proceedings of the 14th European Conference on Genetic Programming*, EuroGP, Evo\*2011, Lecture Notes in Computer Science vol. 6621, Springer-Verlag, pp. 13-24. **(nominated for a best paper award.)**

**Payne<sup>®</sup>, J.L.** & Moore, J.H. (2010) “Sexual recombination in self-organizing interaction networks.” *Proceedings of the EvoComplex Conference*, Evo\*2010, Lecture Notes in Computer Science vol. 6024, Springer-Verlag, pp. 41-50.

**Payne, J.L.** & Eppstein<sup>®</sup>, M.J. (2008) “The influence of scaling and assortativity on takeover times in scale-free topologies.” *Proceedings of the Genetic and Evolutionary Computation Conference*, GECCO-2008, Eds. Keijzer et al., pp. 241-248. **(nominated for a best paper award.)**

**Payne, J.L.** & Eppstein<sup>®</sup>, M.J. (2008) “Parameterizing pair approximations for takeover dynamics.” *Proceedings of the Genetic and Evolutionary Computation Conference*, GECCO-2008, late-breaking papers, Eds. Keijzer et al., pp. 2199-2204.

**Payne, J.L.** & Eppstein<sup>®</sup>, M.J. (2007) “Takeover times on scale-free topologies.” *Proceedings of the Genetic and Evolutionary Computation Conference*, GECCO-2007, Eds. Thierens, D. et al., pp. 308 - 315.

**Payne, J.L.**, Eppstein, M.J., & Goodnight<sup>®</sup>, C.J. (2007) “Sensitivity of self-organized speciation to long-distance dispersal.” *Proceedings of the IEEE Symposium on Artificial Life*, 2007, pp. 1 - 7. **(best student paper award.)**

**Payne, J.L.** & Eppstein<sup>®</sup>, M.J. (2007) “Using pair approximations to predict takeover dynamics in spatially structured populations.” *Proceedings of the Genetic and Evolutionary Computation Conference*, GECCO-2007, late-breaking papers, Eds. Thierens, D. et al., pp. 2557 - 2563.

**Payne, J.L.** & Eppstein<sup>®</sup>, M.J. (2006) “Emergent mating topologies in spatially structured genetic algorithms.” *Proceedings of the Genetic and Evolutionary Computation Conference*, GECCO-2006, Eds. Keijzer, M. et al., pp. 207 - 214.

Eppstein, M.J., **Payne, J.L.**, White, B.C., & Moore<sup>®</sup>, J.H. (2006) “Hill climbing through ‘random chemistry’ for detecting epistasis.” *Proceedings of the Genetic and Evolutionary Computation Conference*, GECCO-2006, late-breaking papers, Ed. Grah, J.

Eppstein, M.J., **Payne, J.L.**, & Goodnight<sup>®</sup>, C.J. (2006) “Speciation by self-organizing barriers to gene flow in simulated populations with localized mating.” *Proceedings of the Genetic and Evolutionary Computation Conference*, GECCO-2006.

**Payne J.L.** & Eppstein<sup>®</sup>, M.J. (2005) “A hybrid genetic algorithm with pattern search for finding heavy atoms in protein crystals.” *Proceedings of the Genetic and Evolutionary Computation Conference*, GECCO-2005, Eds. Beyer, H.G. et al., pp. 377 - 384. **(nominated for a best paper award.)**

REFEREED BOOK  
CHAPTERS

Aguilar-Rodríguez, J. & **Payne, J.L.** (2021) “Robustness and evolvability of transcriptional regulation.” *Evolutionary Systems Biology*, Eds. A Crombach & J. Jaeger, Springer-Verlag, pp. 197-219.

Wagner, A., & **Payne, J.L.** (2016) “Robustness and evolvability in molecular evolution.” *Encyclopedia of Evolutionary Biology*, Elsevier, pp. 484 - 488.

**Payne, J.L.** “Pair approximations.” (2012) In *Encyclopedia of Theoretical Ecology*, Eds. A. Hastings & L. Gross, University of California Press, pp. 531-534.

Pattin, K.A.<sup>=</sup>, **Payne, J.L.**<sup>=</sup>, Hill, D.P., Caldwell, T., Fisher, J.M., & Moore, J.H. (2011) “Exploiting expert knowledge of protein-protein interactions in a computational evolution system for detecting epistasis.” In *Genetic Programming Theory and Practice*, Eds. R. Riolo et al., Springer-Verlag, pp. 195-210.

**Payne, J.L.**, Greene, C.S., Hill, D.P., & Moore, J.H. (2010) “Sensible initialization of a computational evolution system using expert knowledge for epistasis analysis in human genetics.” In *Exploiting Linkage Learning in Evolutionary Algorithms*, Ed. Y.P. Chen, Springer-Verlag, pp. 215-226.

<sup>=</sup> denotes equal contribution, <sup>®</sup> denotes corresponding author, <sup>‡</sup> denotes undergraduate student.