Gregory Ian Lang

Associate Professor & Director of Graduate Studies
Department of Biological Sciences
Lehigh University, Iacocca Hall
111 Research Drive, Bethlehem, PA 18015
610.758.6359

glang@lehigh.edu
www.glanglab.com

Education:

Harvard University, Cambridge, MA (2002 – 2007)
Ph.D. Molecular Biology
Thesis: Mutation rate variation in the yeast *Saccharomyces cerevisiae*
Advisor: Andrew Murray
Thesis Committee: Erin O'Shea (chair), Dan Hartl, Roy Kishony, Matt Michael

Millersville University of Pennsylvania, Millersville, PA (1997 – 2001)
B.S. Molecular Biology
Minors: Physics, Biochemistry

Positions and Appointments:

2021 –	Director of Graduate Studies, Department of Biological Sciences, Lehigh University
2019 –	Associate Professor, Department of Biological Sciences, Lehigh University, Bethlehem, PA
2024 –	Senior Editor, *Journal of Molecular Evolution*
2018 –	Instructor: Cold Spring Harbor Laboratory Yeast Genetics and Genomics Course
2019 – 2021	Co-Director of Graduate Studies, Department of Biological Sciences, Lehigh University
2019 – 2024	Associate Editor, *Journal of Molecular Evolution*
2013 – 2019	Assistant Professor, Department of Biological Sciences, Lehigh University, Bethlehem, PA
2007 – 2013	Postdoctoral Fellow, with David Botstein, Lewis-Sigler Institute of Integrative Genomics and the Department of Molecular Biology, Princeton University, Princeton, NJ

Publications (as an Associate Professor, since 2019):

28. Jhuang HY, Aggeli D, Lang GI. **2025**. Cytoduction preserves genetic diversity following plasmid transfer into pooled yeast libraries. ***Yeast***. 7 April. doi: https://doi.org/10.1002/yea.4001

In this manuscript we develop a method that uses cytoduction (mating without nuclear fusion) to transfer plasmids directionally from a "Donor" to a diverse pool of yeast strains. We demonstrate that this method is efficient such that entire libraries can be genetically modified at one time without losing diversity.

27. Geiler-Samerotte K and Lang GI. **2023**. Best Practices in Microbial Experimental Evolution. ***J Mol Evol***. Jun;91(3):237-240. doi: 10.1007/s00239-023-10119-y.

This is an invited article for a special issue of the Journal of Molecular Evolution *on "Best practices in experimental evolution." I am co-editor of this special issue along with my co-author Kerry Geiler-Samerotte.*

26. Martínez AA and Lang GI. **2023**. Identifying targets of selection in laboratory evolution experiments. ***J Mol Evol***. Feb 21. doi: 10.1007/s00239-023-10096-2.

In this "Best Practices" paper we describe how our laboratory identifies and validates putative beneficial mutations from yeast "Evolve-and-Resequence" experiments. This is an invited article for a special issue of the Journal of Molecular Evolution *on "Best practices in experimental evolution." I am co-editor of this special issue.*

25. Martínez AA, Conboy A, Buskirk SW, Marad DA, Lang GI. **2022**. Long-term adaptation to galactose as a sole carbon source selects for mutations in nutrient signaling pathways. ***J Mol Evol***. Feb;91(1):46-59. doi: 10.1007/s00239-022-10079-9.

In this paper we show that adaptation galactose as a sole carbon source is driven primarily by mutations outside of the canonical galactose pathway. I am the corresponding author.

24. Vignogna RC, Allocca M, Monticelli M, Norris JW, Steet R, Andreotti G, Perlstein EO, Lang GI. **2022**. Evolutionary rescue of phosphomannomutase deficiency in yeast models of human disease. ***Elife***. Oct 10;11:e79346. doi: 10.7554/eLife.79346.

In this paper we use experimental evolution to identify genetic interactions with human disease-associated alleles of PMM2, the most common cause of congenital disorders of glycosylation (CDG). We identify both known and previously unknown genetic interactors with SEC53 (the yeast homolog of PMM2). Interestingly, we observe an enrichment for mutations in other CDG-associated genes. I am the corresponding author.

23. Aggeli D, Marad DA, Liu X, Buskirk SW, Levy SF, Lang GI. **2022**. Overdominant and partially dominant mutations drive short-term adaptation in diploid yeast. ***Genetics***. May 31;221(2):iyac061. doi: 10.1093/genetics/iyac061. PMID: 18202359.

In this paper we use measure the effect of heterozygous mutations in laboratory-evolved diploid yeast. We find that diploid populations contain fewer beneficial mutations relative to haploid populations. Consistent with theory, beneficial mutations in diploids are at least partially dominant, and half are overdominant. I am the corresponding author.

22. Fisher KJ, Vignogna RC, Lang GI. **2021**. Overdominant mutations restrict adaptive loss of heterozygosity at linked loci. ***Genome Biol Evol***. Aug 3;13(8):evab181. doi: 10.1093/gbe/evab181. PMID: 34363476.

In this paper we show that overdominant and partially dominant heterozygous beneficial mutations may interfere with one another if they arise on the same chromosome arm. This is because loss-of-heterozygosity will convert both mutations to the homozygous state, increasing fitness for one and reducing fitness for the other. I am the corresponding author.

21. Vignogna RC, Buskirk SW, Lang GI. **2021**. Exploring a local genetic interaction network using evolutionary replay experiments. ***Mol Biol Evol***. Mar 22:msab087. doi: 10.1093/molbev/msab087. PMID: 33749796.

In this paper we use "evolutionary replay" experiments to identify mutations that have a positive genetic interaction with an allele of interest. We identify both known and unknown genetic interactors and show that many could not have been detected using traditional methods. I am the corresponding author.

20. Buskirk SW, Rokes AB, Lang GI. **2020**. Adaptive evolution of nontransitive fitness in yeast. ***Elife***. Dec 29;9:e62238. doi: 10.7554/eLife.62238. Online ahead of print. PMID: 33372653.

In this paper we identify a nontransitive sequence along a direct line of evolutionary descent where a 1,000-generation evolved clone outcompetes its immediate predecessor, but loses in competition against it's distance ancestor. Therefore, evolution is nontransitive: a series of selective events, each improving fitness relative to the immediate predecessor, may not translate into a cumulative increase in fitness relative. This provides empirical evidence against the common misconception that evolution is a linear "march of progress," where each organism along a line of descent is more fit than all those that came before it. I am the corresponding author.

19. McCandlish DM, Lang GI. **2020**. Evolution of Epistasis: Small Populations Go Their Separate Ways. ***J Mol Evol.*** May 20;. doi: 10.1007/s00239-020-09950-4. [Epub ahead of print] PubMed PMID: 32435963.

In this perspective piece, we describe findings from Sydykova et al. (Journal of Molecular Evolution, 2020). We explain that if the epistasis, as a parameter, could evolve, it would do so in two alternative ways: towards either Drift Robustness or towards Mutational Robustness, depending on the amount of epistasis present in the starting population.

18. Song G, Lee J, Kim J, Kang S, Lee H, Kwon D, Lee D, Lang GI, Cherry JM, Kim J. **2019**. Integrative Meta-Assembly Pipeline (IMAP): Chromosome-level genome assembler combining multiple de novo assemblies. ***PLoS One***. Aug 27;14(8):e0221858. PMID: 31454399.

In this paper we present a new pipeline for building chromosomal-level sequence assemblies of simple eukaryotic genomes using short read sequencing data. I became involved in this project because our lab wanted to generate a better reference genome for our evolution experiments. My role as middle author was to provide short read sequence data and to edit the manuscript.

17. Fisher KJ, Kryazhimskiy S, Lang GI. **2019**. Detecting genetic interactions using parallel evolution in experimental populations. ***Philos Trans R Soc Lond B Biol Sci***. Jul 22;374(1777):20180237. doi: 10.1098/rstb.2018.0237. PMID: 31154981.

In this paper we report produce a new computational method for identifying genetic interactions in laboratory evolved populations. Briefly, we use mutual information to identify variants that co-occur more often than expected by chance. Take home is that there are lots of weak interactions and a handful of strong pairwise interactions. We validate one of them: TRK1 & PHO84. This work was a collaboration with Sergey Kryazhimskiy at UCSD. I am a corresponding author.

Book Reviews (as an Assistant Professor, 2013 – 2018):

16 Lang GI, and Rice AM. **2019**. Evolution unscathed: Darwin Devolves argues on weak reasoning that unguided evolution is a destructive force, incapable of innovation. ***Evolution***. 13 March 2019. https://doi.org/10.1111/evo.13710. *Review of Behe, Michael J. "Darwin Devolves: The New Science About DNA that Challenges Evolution." (2019; HarperOne; New York, NY).*

In this book review, Amber Rice and I assert that Michael Behe misrepresents the scientific literature and commits several critical errors in logic, thus undermining his central premise that degradative mutations cripple evolution.

Publications (as an Assistant Professor, 2013 – 2018):

15. Fisher KJ, Buskirk SW, Vignogna RC, Marad DA, and Lang GI. **2018**. Adaptive genome duplication affects patterns of molecular evolution in *Saccharomyces cerevisiae*. ***PLoS Genetics.*** May 25;14(5):e1007396. doi: 10.1371/journal.pgen.1007396. PMID: 29799840

In this paper we report recurrent genome duplication in 46 haploid yeast populations evolved for 4,000 generations. We find that genome duplication confers a fitness advantage, and that this immediate fitness gain is accompanied by a shift in *genomic and phenotypic evolution. My role as senior author was to design and direct the project, to supervise the students performing the experiments, and to edit the manuscript. All authors are Lang Lab members. I am the corresponding author.*

14. Marad DM, Buskirk SW, and Lang GI. **2018**. Altered access to beneficial mutations slows adaptation and biases fixed mutations in diploids. ***Nature Ecology & Evolution***. May;2(5):882-889. doi: 10.1038/s41559-018-0503-9. PMID: 29581586

    In this paper we perform a 4,000-generation evolution experiment using diploid strains of the yeast Saccharomyces cerevisiae. We show that the rate of adaptation and spectrum of beneficial mutations are influenced by ploidy. My role as senior author was to design and direct the project, to supervise the students performing the experiments, and to write the manuscript. All authors are Lang Lab members. I am the corresponding author.

13. Lang GI. **2018**. Measuring mutation rates using the Luria-Delbrück fluctuation assay**.** ***Methods Mol Biol***. 1672:21-31. doi: 10.1007/978-1-4939-7306-4_3. PMID: 29043614

    In this methods paper I outline the essential features of performing Luria-Delbrück fluctuation assays—one of the most commonly used methods for measuring the mutation rate in microorganisms. I describe common missteps and tips for improving the accuracy of mutation rate estimates. In addition, I provide tools for analyzing data from fluctuation assays.

12. Buskirk SW, Peace RE, and Lang GI. **2017**. Hitchhiking and epistasis give rise to cohort dynamics in adapting populations. ***Proc Natl Acad Sci U S A***. 2017 Jul 18. pii: 201702314. doi: 10.1073/pnas.1702314114. PMID: 28720700

    In this paper we utilize a bulk-segregant approach to identify beneficial mutations across 11 lineages of experimentally-evolved yeast populations. In total, we determine the fitness effects for 116 mutations. We identify a striking example of synergistic epistasis in one of the populations. I am the corresponding author.

11. Fisher KJ, and Lang GI. **2016**. *Invited Review Article:* Experimental evolution in fungi: An untapped resource. ***Fungal Genetics and Biology***. Sep;94:88-94. doi: 10.1016/j.fgb.2016.06.007. Epub 2016 Jun 30. PMID: 27375178

    In this invited review article we describe the current state of fungal experimental evolution and why fungi are uniquely positioned to answer many of the outstanding questions in our field. We also review which fungal species are most well suited for experimental evolution. Both authors are Lang Lab members. I am the corresponding author.

10. Frenkel EM, McDonald MJ, Van Dyken JD, Kosheleva K, Lang GI, and Desai MM. **2015**. Crowded growth leads to the spontaneous evolution of semistable coexistence in laboratory yeast populations. ***Proc Natl Acad Sci U S A*** Aug 3. pii: 201506184. PMID: 26240355

    In this paper we report spontaneous diversification during experimental evolution in the yeast Saccharomyces cerevisiae. We demonstrate that stable sub-populations are maintained by negative frequency-dependent selection, in which dispersal reduces interference competition for nutrients among kin. My role as middle author was to consult on the design and implementation of the experiments and to edit the manuscript.

9. Lang GI, and Desai MM. **2014**. *Invited Review Article:* The spectrum of adaptive mutations in experimental evolution. ***Genomics***. Dec;104(6 Pt A):412-6. doi: 10.1016/j.ygeno.2014.09.011. Epub 2014 Sep 28. PMID: 25269377

    In this invited review article we describe our current understanding of the spectrum of mutations observed across systems used in the field of experimental evolution, with a focus on epistatic interactions between beneficial mutations and constraints on evolutionary outcomes. I am a corresponding author.

8. Lang GI, Parsons L, and Gammie A. **2013**. Mutation rates, spectra, and genome-wide distribution of spontaneous mutations in mismatch repair deficient yeast. ***G3***, Sep 4;3(9):1453-65. PMID: 23821616

    In this paper we performed mutation accumulation assays to generate a genome-wide view of the rates, spectra, and distribution of mutation in the yeast Saccharomyces cerevisiae in the absence of mismatch repair. My role as first author was to design and perform the experiments and to edit the manuscript, which was written primarily by the senior author.

7. Lang GI, Rice DP, Hickman MJ, Sodergren E, Weinstock GM, Botstein D, and Desai MM. **2013**. Pervasive genetic hitchhiking and clonal interference in forty evolving yeast populations. ***Nature***, Aug 29;500(7464):571-4. PMID: 23873039

    In this paper we use whole-genome whole-population timecourse sequencing to examine the dynamics of genome sequence evolution at high temporal resolution in 40 replicate Saccharomyces cerevisiae populations. This was the first demonstration that many mutations arise and move synchronously through populations as mutational "cohorts." As co-first author I was involved in all aspects of performing the experiments, data analysis, and writing the manuscript. I am a corresponding author. This work is featured in the second edition of Bergstrom and Dugatkin's "Evolution" textbook (pages 335-337), for which I provided a figure (Figure 9.26) and accompanying text.

Publications Prior to My Lehigh Appointment:

6. Lang GI, Botstein D, and Desai MM. **2011**. Genetic variation and the fate of beneficial mutations in asexual populations. ***Genetics***. Jul;188(3):647-61. PMID: 21546542
5. Lang GI, Murray AW. **2011**. Mutation rates across budding yeast Chromosome VI are correlated with replication timing. ***Genome Biol Evol***. 3:799-811. PMID: 21666225
4. Lang GI, and Botstein D. **2011**. A test of the coordinated expression hypothesis for the origin and maintenance of the *GAL* cluster in yeast. ***PLoS ONE***. Sep 22; 10.1371/journal.pone.0025290. PMID: 21966486
3. Lang GI, Murray AW, and Botstein D. **2009**. The cost of gene expression underlies a fitness trade-off in yeast. ***Proc Natl Acad Sci U S A***. Apr 7;106(14):5755-60. PMID: 19299502
2. Lang GI, Murray AW. **2008**. Estimating the per-base-pair mutation rate in the yeast *Saccharomyces cerevisiae*. ***Genetics***. Jan;178(1):67-82. PMID: 18202359
1. Hepfer CE, Arnold-Croop S, Fogell H, Steudel KG, Moon M, Roff A, Zaikoski S, Rickman A, Komsisky K,Harbaugh DL, Lang GI, Keil RL. **2005**. *DEG1*, encoding the tRNA:pseudouridine synthase Pus3p, impacts *HOT1*-stimulated recombination in *Saccharomyces cerevisiae*. ***Mol Genet Genomics***. Dec;274(5):528-38. PMID: 16231152

Competitively Awarded Research Support

Active

Source:	**National Institutes of Health R35GM149540**
Total Costs:	$2,087,228 ($265,000 Direct Costs per year for five years)
Name:	Genetic interactions and the evolution of complex traits in yeast (**05/01/23 – 04/31/28**)
Description:	We will perform evolution experiments following a series of genetic and environmental perturbations to determine how genetic changes give rise to complex phenotypes. In addition, we will develop a fast and reliable method for performing multiple rounds of pooled gene editing in yeast. Our work will connect genotype to phenotype in an evolutionary context, provide a mechanistic understanding of complex trait evolution.

Source:	**National Institutes of Health R35GM149540-02S1 (*2024 Administrative Supplement*)**
Total Costs:	$249,188
Name:	Equipment Supplement to Genetic interactions and the evolution of complex traits in yeast
Description:	Funds are being used to upgrade my lab's liquid handling capabilities. Specifically, we are purchasing from Beckman Coulter a new Biomek i7 liquid handler with a 96-well head and a Span-8. The instrument is expected to arrive late fall 2024.

Source:	**National Science Foundation 2233124 (PI: Meyer)**
Total Costs:	$478,374
Name:	BRC-BIO: Exploring the genetic basis of adaptation through convergent dietary specialization in mammals (**01/01/23 – 12/31/25**)
Description:	The overall objectives are to define quantitative phenotypes representing dietary variation across mammals, to identify genes underlying selection on dietary phenotypes across mammals, and to demonstrate the cellular mechanisms underlying dietary adaptation. My role is to provide laboratory space, reagents, and guidance on the yeast reconstruction experiments.

Completed

Source:	**National Institutes of Health R01GM127420**
Total Costs:	$1,654,069 ($210,000 Direct Costs per year for five years).
Name:	Mapping genetic interactions between growth-promoting mutations in yeast (**05/01/18 – 04/31/23**)
Major Goals:	The major goals of this proposal are to (1) leverage the power of evolutionary "replay" experiments to identify a local network of genetic interactions, (2) to extend this analysis genome-wide, and (3) to determine the extent to which genetic interactions persist across environments.
Description:	Annual salary support for PI, two post-doctoral fellows, and graduate students. Research support for consumables, equipment usage fees, travel expenses, and support for publication costs.

Source:	**National Institutes of Health R01GM127420-04S1 (*2022 Administrative Supplement*)**
Total Costs:	$10,368
Name:	Equipment Supplement to Mapping genetic interactions between growth-promoting mutations in yeast
Description:	Administrative Supplements to Support Undergraduate Summer Research. Funds were used to support one undergraduate student (Grace Allen) in the Summer of 2022.

Source:	**Faculty Innovation Grant, Lehigh University 459785**
Total Costs:	$30,000
Name:	A fast and reliable method for multiple rounds of pooled gene editing in yeast (**06/01/21 – 05/31/22**)

Major Goals: We are developing a new method for CRISPR/Cas9 genome editing in yeast using cytoduction (mating without nuclear fusion) to introduce gRNA plasmids directionally from a “Donor” cell to a “Recipient” cell. The goals of this project are to expand the set of selectable markers on our gRNA plasmid, benchmark our system, and perform a proof-of-concept experiment.
Description: Research support and 25% salary support for my post-doctoral fellow Han-Ying Jhuang to perform pilot experiments and generate preliminary data for a future grant submission to the NIH.

Source: **National Institutes of Health R01GM127420-04S1 (*2021 Administrative Supplement*)**
Total Costs: $49,980
Name: Equipment Supplement to Mapping genetic interactions between growth-promoting mutations in yeast
Description: Funds were used for the purchase of a Sony SH800 FACS Cell Sorter, which was installed in the Fall of 2021. This is the first cell sorter in the department. This piece of equipment is crucial to my future research vision, and it greatly expands the capabilities in the Department of Biological Sciences.

Source: **Faculty Innovation Grant, Lehigh University 459664**
Total Costs: $30,000
Name: Host-virus coevolution and the resolution of intragenomic conflict (**09/01/17 – 08/31/18**)
Major Goals: The goals of this proposal are to (1) isolate and sequence the yeast Killer virus and (2) determine the mechanism of Killer loss in yeast experimental evolution.
Description: Research support and 50% salary support for my post-doctoral fellow Sean Buskirk in order to perform pilot experiments and generate preliminary data for a future grant submission to either the NIH or NSF.

Source: **The Charles E. Kaufman Foundation of The Pittsburgh Foundation KA2014-73925**
Total Costs: $150,000
Name: Epistatic interactions and constraints on evolutionary outcomes in yeast experimental evolution (**09/01/14 – 12/31/16**)
Major Goals: The goals of this proposal are to (1) determine how fitness effects and epistatic interactions contribute to the fitness gains during experimental evolution and (2) determine how epistasis constrains evolutionary paths.
Description: Research support for consumables and equipment usage fees. This grant also provided graduate student summer support, travel expenses, and support for publication costs.

In-Kind Current

Source: **Cold Spring Harbor Laboratories**
Total Costs: $3,000 per year
Summary: Instructor Honorarium
Description: I am an instructor for the Cold Spring Harbor Laboratory Yeast Genetics & Genomics Course.
Commitment: **0.05** person months per year

Professional Societies, Honors, and Awards:

- Nominated for the CAS Diane Hyland Award for Service, 2024
- Lehigh CAS Career Research Enhancement Award, 2022
- Lehigh Graduate Student Senate Champion Award, 2021
- Member of the Society for the Study of Evolution, 2019 – present
- Nominated for the CAS Dean's Award for Teaching, 2018
- Nominated for Lehigh University Graduate Mentorship Award, 2017
- Class of ’68 Junior Faculty Fund Award, 2017
- Eugene Mercy, Jr. President and Provost's Fund for Faculty Development Travel Grant, 2016
- EMBO CPP Travel Fellowship, 2016
- Member of the American Society of Microbiology, 2015 – present
- GSA Chair’s Choice Plenary Talk at the Fungal Genetics Meeting, 2015
- Charles E. Kaufman New Investigator, 2014
- Member of the Society for Molecular Biology and Evolution, 2014 – present
- Eugene Mercy, Jr. President and Provost's Fund for Faculty Development Travel Grant, 2014
- EMBO CPP Travel Fellowship, 2014
- Member of the Genetics Society of America, 2010 – present

Scholarly Presentations at National and International Scientific Conferences (Since 2013):

15. Journal of Molecular Evolution, Evolution Advances Meeting. (17 – 19 March, 2023)
Washington, DC.
Talk: Rock, Paper, Scissors: Nontransitivity in experimental evolution.

14. Genetics Society of America, Yeast Genetics Meeting. (17 – 21 August, 2022)
Los Angeles, CA.
Talk: Vignogna RC, Allocca M, Monticelli M, Norris JW, Steet R, Andreotti G, Perlstein EO, Lang GI, Evolutionary rescue of phosphomannomutase deficiency in yeast models of human disease.

13. Society for the Study of Evolution, Evolution Meeting. (21 – 25 June, 2019)
Providence, RI.
Poster: Buskirk SW, Rokes A, Lang GI, Host-virus genome coevolution in laboratory populations of yeast.

12. Genetics Society of America, Yeast Genetics Meeting. (22 – 26 August, 2018)
Palo Alto, CA.
Talk: Buskirk SW, Lang GI, Host-virus genome coevolution in laboratory populations of yeast.

11. Genetics Society of America, Population Evolution and Quantitative Genetics Conference. (13 – 16 May, 2018)
Madison, WI
Poster: Buskirk SW, Lang GI, Host-virus genome coevolution in laboratory populations of yeast.

10. Genetics Society of America, Fungal Genetics Meeting. (14 – 19 March, 2017)
Pacific Grove, CA
Invited Speaker: Lang GI, Fitness and epistasis in yeast experimental evolution.

9. Experimental Approaches to Evolution and Ecology using Yeast and other Model Systems. (19 – 23 October, 2016)
Heidelberg, Germany
Talk: Lang GI, Linking the emergence of epistatic interactions to the dynamics of adaptation.

8. American Society for Microbiology: 2nd Conference on Experimental Microbial Evolution. (4 – 7 August, 2016)
Washington, DC
Talk (*presented by Sean Buskirk*): Buskirk SW, Peace RE, Lang GI, Characterizing patterns of epistasis in experimentally-evolved yeast.
Poster (*presented by Daniel Marad*): Marad DA, Lang GI, Rate of adaptation and spectrum of beneficial mutations in haploids and diploids.
Poster (*presented by Chris Graves from Brown University*): Graves CJ, Bauer C, Siegal ML, Lang GI, Weinreich DM, Yeast populations adapted to periodic stress trade fast growth for stress resistance.

7. Genetics Society of America, The Allied Genetics Conference. (13 – 27 July, 2016)
Orlando, FL
Talk: Lang GI, Buskirk SW, Peace RE, Characterizing patterns of epistasis in yeast experimental evolution.
Poster (*presented by Katie Fisher*): Fisher K, Lang GI, Quantifying host genome response to gene drive.

6. Genetics Society of America, Fungal Genetics Meeting. (17 – 22 March, 2015)
Pacific Grove, CA
Chair's Choice Plenary Talk: Lang GI, Genome sequence evolution in experimental populations of *S. cerevisiae.*

5. Experimental Approaches to Evolution and Ecology using Yeast and other Model Systems. (12 – 16 October, 2014)
Heidelberg, Germany
Talk: Lang GI, Genome sequence evolution in experimental populations of *S. cerevisiae*

4. American Society for Microbiology: 1st Conference on Experimental Microbial Evolution. (19 – 22 June, 2014)
Washington, DC
Invited Speaker: Lang GI, The dynamics of genomic sequence evolution in experimental populations of *S. cerevisiae.*

3. Annual Meeting for the Society of Molecular Biology and Evolution. (8 – 12 June, 2014)
San Juan, Puerto Rico
Symposium Organizer: *Genome Scale Approaches to Experimental Evolution*.
Poster: Lang GI, The dynamics of genomic sequence evolution in experimental populations of *S. cerevisiae.*

2. Comparative Genomics of Eukaryotic Microorganisms: Patterns of Complexity in Eukaryotic Genomes. (19 – 24 Oct, 2013)
San Feliu de Guixols, Spain
Invited Speaker: Lang GI, Hickman M, Parsons L, Desai MM, Weinstock GM, Botstein D. The dynamics of genomic sequence evolution in experimental populations of *S. cerevisiae.*

1. Gordon Research Conference on Microbial Population Biology. (21 – 26 July, 2013)
Proctor Academy, Andover, NH
Poster: Lang GI, Rice DP, Hickman MJ, Sodergren E, Weinstock GM, Botstein D, and Desai MM. The dynamics of genomic sequence evolution in experimental populations of *Saccharomyces cerevisiae*.

Scholarly Presentations at Regional Meetings (number of presentations from our lab):

Evolution in Philadelphia Conference, Temple University, 14 September 2019 (2 talks, 2 posters)
Lehigh Valley Ecology and Evolution Symposium, Lafayette College, 13 April 2019 (4 talks)
Evolution in Philadelphia Conference, University of Pennsylvania, 8 September 2019 (3 talks)

Lehigh Valley Ecology and Evolution Symposium, Cedar Crest College, 7 April 2018 (3 talks)
Three Rivers Evolution Event, University of Pittsburgh, 9 September 2017 (1 talk)
Evolution in Philadelphia Conference, University of Pennsylvania, University of Pennsylvania, 15 April 2017 (4 talks)
Lehigh Valley Ecology and Evolution Symposium, DeSales University, 8 April 2017 (4 talks)
Lehigh Valley Ecology and Evolution Symposium, Muhlenberg College, 18 April 2015 (2 posters)

Invited Seminars with Lehigh Affiliation:

33. *Upcoming:* Johns Hopkins University. *Departmental Seminar*. 13 March 2025.
32. Université Laval. Quebec City, Canada. *Departmental Seminar*. 16 May 2024.
31. NIH/NIGMS. *Yeast Scientific Interest Group Meeting*. 10 April 2024.
30. University of Pittsburgh. *Departmental Seminar*. 11 October 2023.
29. Stockton University. *Departmental Seminar*. 22 September 2023.
28. Pennsylvania State University. *Departmental Seminar*. 22 February 2021 (*virtual*).
27. Gettysburg College. *Departmental Seminar*. 3 March 2020.
26. Institute of Molecular Biology, Academia Sinica. Taipei, Taiwan. *Departmental Seminar*. 16 April 2019.
25. *Invited Keynote Address.* Temple University, Department of Biology. *Annual Retreat*. 20 October 2018.
24. International Laboratory for Human Genome Research, Queretaro, Mexico. 24 September 2018.
24. Siena College, Albany, NY. 5 October 2018.
23. Carnegie Mellon University, Pittsburgh, PA. *Departmental Seminar*. 11 April 2018.
22. Millersville University of Pennsylvania. *Departmental Seminar*. 28 March 2018.
21. University of Michigan, Ann Arbor. *Departmental Seminar*. 18 January 2018.
20. University of California, San Diego. *Departmental Seminar*. 3 November 2017.
19. Georgetown University. *Departmental Seminar*. 12 October 2017.
18. DuPont. Wilmington DE. *Seminar*. 29 September 2017.
17. Kavli Institute of Theoretical Physics, University of California, Santa Barbara. *Seminar*. 3 August 2017.
16. Cold Spring Harbor, Yeast Genetics Course. *Seminar*. 28 July 2017.
15. Stony Brook University. *Departmental Seminar*. 12 May 2017.
14. Villanova University. *Departmental Seminar*. 2 February 2017.
13. Dartmouth College. *Graduate-student Invited Departmental Seminar*. 19 December 2016.
12. Penn State, Hershey Medical Center. *Departmental Seminar*. 5 December 2016.
11. Brown University. *Departmental Seminar*. 15 November 2016.
10. Cornell University. *Departmental Seminar*. 15 April 2016.
9. Rowan University. *Departmental Seminar*. 11 November 2015.
8. Princeton University. *Princeton Area Yeast Meeting*. 4 April 2015.
7. University of Alabama, Birmingham. *Departmental Seminar*. 1 April 2015.
6. Calico (California Life Company). South San Francisco. *Seminar*. 5 March 2015.
5. University of Nebraska, Lincoln. *Departmental Seminar*. 5 March 2015.
4. Bryn Mawr College. *Departmental*. 29 October 2014.
3. University of New Hampshire. *Departmental Seminar*. 6 March 2014.
2. Princeton Plasma Physics Laboratory. *Seminar*. 26 February 2014.
1. Cedar Crest College. *Departmental Seminar*. 20 February 2014.

Courses Taught:

Molecular Genetics Lab/SEA-GENES Lab. BIOS297/346. (Spring 2024).
Methods & Logic. BIOS495. (Fall 2023, Instructor of Record only—this course is taught collectively).
Microbiology. BIOS324. (Fall 2014, Fall 2015, Fall 2016, Fall 2017, Fall 2018, Fall 2019, Fall 2020, Spring 2022, Fall 2023).
Molecular Evolution. BIOS330/428 (formerly BIOS396/496). (Spring 2014, Spring 2015, Spring 2016, Fall 2019, Spring 2021, Spring 2023).
Molecular Cell Biology II. BIOS422 (Fall 2022)
Microbiology Lab. BIOS325 (formerly BIOS398). (Spring 2017, Spring 2018, Spring 2019).
Understanding the Human Genome. BIOS090. (Fall 2013).

Summary of Course Evaluations:

Term	Course	Enrollment	Instructor presented content in an organized manner.	The instructor's teaching methods contributed to my understanding of the course material.	The instructor was responsive when I had difficulties or questions.	The instructor gave me constructive feedback.	The instructor's assignments provided opportunities for participative learning within the course.	The course increased my knowledge of the subject matter.
SP 2024	BIOS 297/346: Mol Gen Lab/SEA-GENES Lab	13	5.00	5.00	5.00	5.00	5.00	5.00
FA 2023	BIOS 324: Microbiology	24	4.88	5.00	4.75	5.00	4.88	5.00
SP 2023	BIOS 330/428: Molecular Evolution	13	5.00	4.83	4.83	4.67	4.83	5.00
FA 2022	BIOS 422: Molecular Cell Biology II	18	5.00	4.50	4.67	4.00	4.50	4.50
SP 2022	BIOS 324: Microbiology	77	4.88	4.79	4.61	4.25	4.75	4.81
SP 2021	BIOS 330/428: Molecular Evolution	5	5.00	5.00	4.20	4.20	4.20	4.80
FA 2020	BIOS 324: Microbiology	48	4.94	4.75	4.50	4.44	4.63	4.81
FA 2019	BIOS 330/428: Molecular Evolution	7	4.33	4.67	5.00	4.33	4.67	5.00
FA 2019	BIOS 324: Microbiology	50	4.89	4.83	4.76	4.39	4.89	4.89
SP 2019	BIOS 325: Microbiology Laboratory	24	5.00	5.00	5.00	5.00	5.00	5.00
FA 2018	BIOS 324: Microbiology	57	4.97	4.97	4.88	4.72	4.94	4.88

Term	Course	Enrollment	Overall, the instructor's teaching was effective	Overall the quality of the course was good.	I learned a great deal in this course
SP 2018	BIOS 325: Microbiology Laboratory	23	5.00	5.00	4.87
FA 2017	BIOS 324: Microbiology	52	4.86	4.90	4.83
SP 2017	BIOS 398: Microbiology Laboratory	21	5.00	5.00	4.81
FA 2016	BIOS 324: Microbiology	57	4.68	4.71	4.61
SP 2016	BIOS 396/496: Molecular Evolution	12	5.00	5.00	4.89
FA 2015	BIOS 324: Microbiology	49	4.93	4.93	4.89
SP 2015	BIOS 396/496: Molecular Evolution	12	4.89	5.00	4.89
FA 2014	BIOS 324: Microbiology	31	4.96	4.96	5.00
SP 2014	BIOS 396/496: Molecular Evolution	15	4.93	5.00	4.79
FA 2013	BIOS 090: Understanding the Human Genome	18	4.94	4.88	4.76

Undergraduate Research Advising:

Completed: William Yaeger. Spring 2022 (1 credit of BIOS391), Fall 2022 (2 credits of BIOS391), Spring 2023 (2 credits of BIOS391), Fall 2023 (2 credits of BIOS391), Spring 2024 (2 credits of BIOS391).

Completed: Cal Shutack. Fall 2023 (2 credits of BIOS391), Spring 2024 (2 credits of BIOS391).

Completed: Mary Grace Allen. Fall 2020 (1 credit of BIOS391), Spring 2021 (2 credits of BIOS391), Fall 2021 (2 credits of BIOS391), Spring 2022 (1 credit of BIOS391), Fall 2022 (2 credits of BIOS391).

Completed: Kaya Harper. Spring 2020 (1 credit of BIOS391), Fall 2020 (1 credit of BIOS391), Spring 2021 (2 credits of BIOS391), Fall 2021 (2 credits of BIOS391), Spring 2022 (2 credits of BIOS391).

Completed: Alexis Hampton. Spring 2021 (1 credit of BIOS391), Fall 2021 (1 credit of BIOS391).

Completed: Ginger Gerhold. Fall 2019 (1 credit BIOS391), Spring 2020 (2 credits of BIOS391).

Completed: Bryan Novak. Fall 2019 (2 credits BIOS391).

Completed: Jasper Jeffrey. Fall 2017 (3 credits BIOS391), Spring 2018 (2 credits of BIOS391), Fall 2018 (3 credits of BIOS391), Spring 2019 (3 credits of BIOS391).

Completed: Alecia Rokes. Spring 2018 (2 credits of BIOS391), Fall 2018 (3 credits of BIOS391), Spring 2019 (3 credits of BIOS391).

Completed: Kenneth Brill. Fall 2014 (1 credit BIOS 161), Spring 2015 (2 credits BIOS 161), Fall 2015 (2 credits BIOS 161), Spring 2016 (2 credits BIOS391), Fall 2016 (3 credits BIOS391 as a writing intensive course), Spring of 2017 (3 credit Thesis).

Completed: Rebecca Unterborn. Fall 2016 (2 credits BIOS391), Spring 2017 (2 credits of BIOS391).

Completed: Ali O'Donnell. Spring 2015 (1 credit BIOS 161), Fall 2015 (2 credits BIOS 161).

Completed: Ryan Emily Peace. Spring 2014 (2 credits, BIOE142), Fall 2014 (2 credits, BIOE132), Spring 2015 (4 credits, BIOE242).

Completed: Jessica Moore. Summer of 2014. Jessica was supported by a Grants for Experiential Learning in Health (GELH) Grant from Lehigh University.

Graduate Research Advising:

Completed: Ryan Vignogna, Graduate Student (Biochemistry), 2016 – 2022.

Completed: Thesis committee member for Caitlin Zuilkoski (Molecular Biology, Skibbens Lab). 2018 – 2021.

Completed: Andrew Conboy, Graduate Student (Terminal Masters), 2019 – 2020.

Completed: Thesis committee member for Alex Huynh (Integrative Biology, Rice Lab). 2017 – 2020.

Completed: Daniel Marad, Graduate Student (Molecular Biology), 2014 – 2019.

Completed: Kaitlin Fisher, Graduate Student (Biology, Lang Lab), 2014 – 2019.

Completed: External thesis committee member for Stephanie Lauer in The Center for Genomics and Systems Biology, New York University. Stephanie was advised by David Gresham, 2015 – 2018.

Completed: Thesis committee member for Donglai Shen (Molecular Biology, Skibbens Lab). 2016 – 2018.

Completed: Thesis committee member for Michael McQuillan (Integrative Biology, Rice Lab). 2016 – 2018.

Completed: Thesis committee member for Katie Mageeney (Molecular Biology, Ware Lab). 2015 – 2018.

Completed: Thesis committee member for Bita Khalili (Physics, Vavylonis Lab). 2015 – 2017.

Completed: External thesis committee member for Christopher Graves in the Department of Ecology and Evolutionary Biology, Brown University. Chris was advised by Daniel Weinreich, 2016 – 2017.

Completed: External thesis committee member for Marcus Dillon in the Department of Molecular, Cellular, and Biomedical Sciences at the University of New Hampshire. Marcus was co-advised by Vaughn Cooper (UNH) and Michael Lynch (Indiana University), 2013 – 2016.

Artemiza Martinez. Graduate Student (Biology, Molecular & Cell), Fall 2019 – present.

Brooke Dubyna. Graduate Student (Biology, Molecular & Cell), Spring 2023 – present.

Dominick Costanzo. Graduate Student (Biology, Molecular & Cell), Spring 2023 – present.

Brooke Coonrod. Graduate Student (Biology, Molecular & Cell), Spring 2024 – present.

Thesis committee member for Kayli Silimperi (Biology, Molecular & Cell, Zappulla Lab). 2022 – present.

Thesis committee member for Austin Russell (Biology, Evolution, Rice Lab). 2023 – present.

Thesis committee member for Sara Aden (Biology, Molecular & Cell, Ware Lab). 2024 – present.

Thesis committee member for Stephen Mensah (Biology, Molecular & Cell, Ware Lab). 2024 – present.

Thesis committee member for Michael Tene (Biology, Molecular & Cell, Meyer Lab). 2024 – present.

Thesis committee member for Arpana Upadhyay (Biology, Molecular & Cell, Zappulla Lab). 2024 – present.

Thesis committee member for Gurvir Singh (Biology, Molecular & Cell, Skibbens Lab). 2024 – present.

Postdoctoral Student Mentoring:

Completed: Dimitra Aggeli (Ph.D. Biochemistry and Molecular Biology, SUNY Upstate), June 2018 – August 2023.

Completed: Sean W. Buskirk (Ph.D. Infectious Diseases, University of Georgia), September 2015 – 2019.
Dr. Buskirk is now an Assistant Professor of Biology at West Chester University.

Han-Ying Jhuang (Ph.D. Life Sciences, Institute of Molecular Biology, Academia Sinica, Taiwan), January 2021 – present.
Dr. Jhuang will be an Assistant Professor at Taipei Medical University starting in September 2024.

Faculty Advising:

Mentor to Dylan Shropshire, Biological Sciences. 2024 – present.
Mentor to Albert Liu, College of Health (at the request of Dean Beth Dolan). 2022 – present.

Departmental Service:

Director of Graduate Studies, 2021 – present.
Acting Director of Graduate Studies, 2020.
Co-Director of Graduate Studies, 2019 – 2021.
Chair of Faculty Search Committee, Biostatistics, Assistant Professor, 2018.
Faculty Search Committee, Infectious Disease, Assistant Professor, 2016.
Graduate Committee, 2015 – present.
Coordinator for the Cell & Molecular graduate student qualifying exam, 2015 – 2018.
Infrastructure Committee, 2014 – present.
Co-organizer of the Graduate Research Seminar Series, Fall 2013 – Spring 2016.

College & University Service:

CAS Tenure Committee. 2024 – present.
Internal Review Committee, Lehigh Office of Research. 2022 – present.
Alternate Lehigh Faculty Representative to the Federal Demonstration Partnership. 2020 – present.
Ad hoc Reviewer, Lehigh CORE Grants, 2020.
Data X Innovation Grant Committee, 2015.
Faculty Search Committee, DataX/Connected Health, Assistant Professor, 2015.

Professional Service:

External Program Reviewer, NHGRI Genomics and Data Science Research Quadrennial Review, 2024

External Program Reviewer, Millersville University Biology Department 5-year Program Review, 2023

Senior Editor, *Journal of Molecular Evolution*, 2024 – present.

Associate Editor, *Journal of Molecular Evolution*, 2019 – 2024.

Instructor for the Cold Spring Harbor Laboratory Yeast Genetics and Genomics Course, 2018 – present.

Instructor for the European Molecular Biological Organization (EMBO) Practical Course: Measuring intra-species diversity using high-throughput sequencing, Oeiras, Portugal, July 2015.

Symposium Organizer for *Genome Scale Approaches to Experimental Evolution* at the Annual Meeting for the Society of Molecular Biology and Evolution in San Juan, Puerto Rico. June 2014.

Reviewer for *BioEssays*, *Bioinformatics*, *BMC Genomics*, *BMC Systems Biology*, *Cell Genomics*, *Current Biology*, *eLife*, *Evolution*, *G3*, *Genetics*, *Genome Biology and Evolution, Journal of Molecular Evolution*, *Molecular Biology and Evolution*, *Nature Communications*, *Nature Ecology and Evolution*, *Nucleic Acids Research*, *Philosophical Transactions of the Royal Society B*, *PLoS Biology*, *PLoS Genetics*, *PLoS ONE*, *Proceedings of the National Academy of Sciences*, *Proceedings of the Royal Society B*, *Science, Trends in Cell Biology*, and *Yeast*.

Grant Reviewer on the NIH GVE Study Section (February 2018 & June 2020), the NIH GCAT Study Section (January 2021 & June 2022), NIH F08 Fellowship Study Section (February 2022, October 2022, & April 2023), NIH R15 Study Section (March 2024), NIH MRAF Study Section (June 2024 & February 2025), the NSF DEB DDIG Review Panel (January 2015) and the NASA Filamentous Fungi and Yeast Panel (June 2020). In addition, I have served as an *ad hoc* grant reviewer for MRC, DOD, NSF DEB, NSF MCB, NSF CAREER, NSF LTREB, and NASA Exobiology.

Professional Development related to Teaching:

2nd Avida-ED Active LENS Workshop. 9 – 11 June 2016. NSF BEACON Center for the Study of Evolution in Action, Michigan State University, East Lansing, MI