



# David Koslicki

## Education and Employment

- 2013-Current **Assistant Professor**, *Mathematics*, Oregon State University, Corvallis, OR.
- 2012-2013 **Postdoctoral Researcher**, *Mathematical Biosciences Institute*, Ohio State University, Columbus, OH.
- 2012-2012 **Postdoctoral Researcher**, *Mathematics*, Drexel University, Philadelphia, PA.
- 2007-2012 **Ph.D.**, *Mathematics*, Pennsylvania State University, State College, PA.
- 2004-2006 **B.S.**, *Theoretical Mathematics*, Washington State University, Pullman, WA.

## Research Area

Mathematical and computational approaches to \*-omics problems using techniques such as: probability, Markov chains, compressive sensing, and probabilistic data analysis. Emphasis areas include: metagenomics/microbial community analysis, alignment-free genomic analysis, and entropy techniques.

## Publications

21. The Biomedical Data Translator Consortium. Toward A Universal Biomedical Data Translator. *Clin Transl Sci*, (doi.org/10.1111/cts.12591):1–5, 2018.
20. The Biomedical Data Translator Consortium. The Biomedical Data Translator Program: Conception, Culture, and Community. *Clin Transl Sci*, (doi.org/10.1111/cts.12592):1–4, 2018.
19. N. LaPierre, S. Mangul, M. Alser, I. Mandric, N.C. Wu, **D. Koslicki**, and E. Eskin. MiCoP: Microbial community profiling method for detecting viral and fungal organisms in metagenomic samples. *BMC Bioinformatics*, Accepted, 2018.
18. D. McDonald, Vasquez Baeza Y., **D. Koslicki**, J. McClelland, N. Reeve, Z. Xu, A. Gonzalez, and R. Knight. Striped UniFrac: enabling microbiome analysis at unprecedented scale. *Nature, Methods*, In print, 2018.
17. L. Olde Loohuis, S. Mangul, A.P.S. Ori, G. Jospin, **D. Koslicki**, H.T. Yang, T. Wu, M.P. Boks, C. Lomen-Hoerth, M. Wiedau-Pazos, R.M. Cantor, W.M. de Vos, R.S.

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Kahn, E. Eskin, and R.A. Ophoff. Transcriptome analysis in whole blood reveals increased microbial diversity in schizophrenia. *Nature, Translational Psychiatry*, 8(96), 2018.

16. J. McClelland and **D. Koslicki**. EMDUnifrac: Exact linear time computation of the Unifrac metric and identification of differentially abundant organisms. *Journal of Mathematical Biology*, 77(4):935–949, 2018.
15. M. Ansariola, M. Megraw, and **D. Koslicki**. IndeCut evaluates performance of network motif discovery algorithms. *Bioinformatics*, 34(9):1514–1521, 2017.
14. Sczyrba, A., Hofmann, P., Belmann, P., **D. Koslicki** . . . and McHardy, A. Critical assessment of metagenome interpretation - a benchmark of metagenomics software. *Nature, Methods*, 14(11):1063–1071, 2017.
13. **D. Koslicki** and M. Novak. Exact probabilities for the indeterminacy of complex networks as perceived through press perturbations. *Journal of Mathematical Biology*, Online ahead of print: doi.org/10.1007/s00285-017-1163-0, Jul 2017.
12. S. Mangul and **Koslicki, D.** Reference-free comparison of microbial communities via de bruijn graphs. *ACM-BCB, IEEE/ACM Trans. on Computational Biol. and Bioinf.*, 2016.
11. **D. Koslicki** and D. Falush. Metapalette: A k-mer painting approach for metagenomic taxonomic profiling and quantification of novel strain variation. *mSystems*, 1(3):e00020–16, 2016.
10. **D. Koslicki** and M. Denker. Substitution markov chains and martin boundaries. *Rocky Mountain Journal of Mathematics*, 46(6):1963–1985, 2016.
9. **D. Koslicki**, S. Chatterjee, D. Shahrivar, A. Walker, S. Francis, L. Fraser, M. Vehkaperä, Y. Lan, and J. Corander. Ark: Aggregation of reads by k-means for estimation of bacterial community composition. *PLoS ONE*, 10(10):e0140644, 2015.
8. Holzinger, A., Hörtenhuber, M., Mayer, C., Bachler, M., Wassertheurer, S., Pinho, A.J., and **D. Koslicki**. On entropy-based data mining. In *Interactive Knowledge Discovery and Data Mining in Biomedical Informatics*, pages 209–226. Springer Berlin Heidelberg, 2014.
7. **D. Koslicki**, Foucart, S., and Rosen, G. WGSQuikr: fast whole-genome shotgun metagenomic classification. *PLoS ONE*, 9(3):e91784, 2014.
6. S. Foucart and **D. Koslicki**. Sparse recovery by means of nonnegative least squares. *IEEE Signal Processing Letters*, 21(14):498–502, 2014.
5. Chatterjee, S., **D. Koslicki**, Dong, S., Innocenti, N., Cheng, L., Lan, Y., Vehkaperä, M., Skoglund, M., Rasmussen, L.K., Aurell, E., and Corander, J. SEK: sparsity

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exploiting  $k$ -mer based estimation of bacterial community composition. *Bioinformatics*, 30(17):2423–2431, 2014.

4. **D. Koslicki** and Thompson, D.J. Coding sequence density estimation via topological pressure. *Journal of Mathematical Biology*, pages 1–25, 2014.
3. **D. Koslicki**, Foucart, S., and Rosen, G. Quikr: a Method for Rapid Reconstruction of Bacterial Communities via Compressive Sensing. *Bioinformatics*, 29(17):2096–2102, 2013.
2. **D. Koslicki**. *Substitution Markov chains with applications to molecular evolution*. PhD thesis, Pennsylvania State University, State College, PA, USA, 2012.
1. **D. Koslicki**. Topological entropy of DNA sequences. *Bioinformatics*, 27(8):1061–1067, 2011.

## Preprints and Submitted Manuscripts

- Meyer, F., Bremges, A., Belmann, P., Janssen, S., McHardy, A.C., and **Koslicki, D.** Assessing metagenomic taxonomic profiling with OPAL. Under review at *PLoS Computational Biology*. 2018
- **Koslicki, D.** and Zabeti, H. Improving Min Hash via the Containment Index with applications to Metagenomic Analysis. Under revision at *Applied Mathematics and Computation*. 2017
- **Koslicki, D.** An alignment-free indel model of molecular evolution. arXiv, <http://arxiv.org/abs/1102.1897>. 2011.

## Other Published Material

- Wrote and self-published a 207 page, partially interactive book for MTH 321 covering MATLAB, Mathematica, and  $\LaTeX$ .
- Published over 30 research software repositories on GitHub, with over 48K unique lines of Python, Julia, C++, C, Mathematica, MATLAB, and bash code (excluding comments, manuals, licenses etc.)

## Funding

- NIH NCATS Biomedical Data Translator: *RTX: a Markov chain-based reasoning tool integrated with NCATS Blackboard and the Translator system*. Co-PI along with Stephen Ramsey (Oregon State), Eric Deutsch (Institute for Systems Biology), and Arnab Nandi (Ohio State). December 29, 2017-unspecified. Award number: 1OT2TR002520-01. Total award amount to date (1/16/2019): \$788,863.
- NSF DMS QuBBB, *Fast, efficient mathematical approach to the analysis of the human microbiome through biodiversity optimization*, PI with subawards to Simon Foucart (Texas A&M) and Ivan Ivanov (Texas A&M). June 6, 2018 - May 31, 2021. Award number 1664803. Award amount: \$292,041.

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## Students

### Graduate

- Benjamin Sebastian, 2018, Masters, math
- Zihao (Kevin) Zhang, 2018-present, Masters, math
- Andrew Jensen, 2017-2018, Masters, math
- Hooman Zabeti, 2015-2017, Masters, math
- Ryan Melson, 2015-2017, Masters, math
- Jason McClelland, 2014-2018, PhD, math
- Abby Pecoske, 2014-2015, Masters, math
- Ian McKay, 2014-2015, Masters, math

### Undergraduate

- Michael Kupperman, 2016-present, undergraduate research
- Makenzie Brian, 2015, undergraduate research
- Morgan Shirley, 2014, undergraduate research

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## Department and University Service

- OSU Microbiome Initiative Workshop Committee Member 2016-present
- Graduate committee 2017-present
- Alumni Newsletter committee 2016-present
- Assisted in the creation of a new course series on mathematical biology: MTH 427/527 MTH 428/528 2015-present
- Undergraduate advising committee 2015-2017
- Mathematics department computer committee 2013-present (chair 2016-present)
- Mathematical biology seminar organizer 2014-present
- Created and continue to teach MTH 321, *Introductory applications of Mathematical Software* 2014-present
- CGRB Spring Conference: *Dealing with the Data Deluge*. Served on organizing committee April 7, 2014
- Undergraduate curriculum committee 2013-2015

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## Synergistic Activities

- UCLA Computational Genomics Summer Institute (CGSI) organizer. 2018
- UCLA Computational Genomics Summer Institute (CGSI) organizer. 2017
- Critical Assessment of Metagenomic Interpretation (CAMI) advisory board member. 2015-present
- Member of the messaging and funding committees for the OSU crowd-funded effort to sequence the beaver genome. This project successfully raised \$30,000 to sequence the beaver genome. Fall, 2015

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- Member of Math Alliance, a community dedicated to serving underrepresented groups of students in the mathematical sciences. 2015-present

## Consulting Experience

- Omnigen Research <http://www.omnigenresearch.com/>
- Maurentia Analytics <http://www.maurentia.com/>

## Refereeing Experience

- Nature, Scientific Reports
- Oxford Journal of Bioinformatics
- Advances in Mathematics
- MDPI Entropy
- Evolutionary Bioinformatics
- Genome Biology
- PeerJ
- MDPI Journal of Molecular Sciences
- RECOMB
- Journal of Theoretical Biology
- BMC Bioinformatics
- PLoS ONE
- MDPI Biology
- Molecular Ecology
- mSystems
- Molecular BioSystems
- PLoS Computational Biology
- Israeli Science Foundation

## Awards

- Awardee, College of Science Impact Award, SciRIS level 1, *Oregon State University* Fall 2018
- Nominated for the Carter Award for Outstanding and Inspirational Teaching in Science at the undergraduate level, *Oregon State University* Winter 2016
- Residence Life "First Year Experience" recognition recipient, *Penn State* 2011
- Graduate assistant teaching award, *Penn State* 2009

## Courses Taught

- MTH 321: Introductory applications of mathematical software OSU, Fall, 2018
- MTH 311: Advanced Calculus OSU, Winter, 2018
- MTH 361: Introduction to Probability OSU, Fall, 2017
- MTH 321: Introductory Applications of Mathematical Software OSU, Fall, 2017
- MTH 665: Probability Theory II OSU, Spring, 2017
- MTH 664: Probability Theory OSU, Winter, 2017
- MTH 311: Advanced Calculus OSU, Winter, 2017
- MTH 427/527: Introduction to Mathematical Biology OSU, Fall, 2016
- MTH 321: Introductory Applications of Mathematical Software OSU, Fall, 2016
- MTH 465/565: Probability III OSU, Spring, 2016
- MTH 464/564: Probability II OSU, Winter, 2016

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- MTH 463/563: Probability I OSU, Fall, 2015
- MTH 321: Introductory Applications of Mathematical Software OSU, Fall, 2015
- MTH 255: Vector Calculus II OSU, Summer, 2015
- MTH 361: Introduction to Probability OSU, Summer, 2015
- MTH 361: Introduction to Probability OSU, Spring, 2015
- MTH 321: Introduction to Mathematical Software OSU, Spring, 2015
- MTH 306H: Honors Matrix and Power Series Methods OSU, Winter, 2015
- MTH 252: Integral Calculus OSU, Summer, 2014
- MTH 252H: Honors Integral Calculus OSU, Winter, 2014
- MTH 252H: Honors Integral Calculus OSU, Fall, 2014
- MTH 399: Introduction to Mathematical Software OSU, Fall, 2014
- MTH 268: Mathematical Ideas in Biology OSU, Fall, 2013
- Techniques in Bioinformatics Working Seminar, Drexel, Winter 2013
- Molecular Evolution Working Seminar Penn State, Spring, 2011
- Math 140: Calculus with Analytic Geometry Penn State, Fall, 2010
- Math 35: General View of Mathematics Penn State, Summer, 2010
- Math 140: Calculus with Analytic Geometry Penn State, Spring, 2010
- Math 41: Trigonometry and Analytic Geometry Penn State, Fall, 2009
- Math 35: General View of Mathematics Penn State, Summer, 2009
- Math 41: Trigonometry and Analytic Geometry Penn State, Spring, 2008
- Math 18: Elementary Linear Algebra Penn State, Fall, 2008
- Math 35: General View of Mathematics Penn State, Summer, 2008
- Math 17: Finite Mathematics Penn State, Spring, 2008
- Math 171: Calculus I (Recitation) Washington State, Fall, 2006

## Presentations, Seminars, and Workshops

- Compressive sensing and metagenomics *Mathematics department colloquium, Oregon State University, Corvallis, OR* October 15, 2018
- IndeCut: Evaluating performance of motif discovery algorithms, *Mathematical biology seminar, Oregon State University, Corvallis, OR* October 3, 2018
- IndeCut: Evaluating performance of motif discovery algorithms, *UCLA CGSI, Los Angeles, CA* July 16, 2018
- Multi-resolution k-mer classification of metagenomic samples, *UCLA CGSI, Los Angeles, CA* July 12, 2018
- Probabilistic Analysis of Metagenomic Data, *Statistics seminar, Oregon State University, Corvallis, OR* October 16, 2017
- Using the earth-mover's distance to compare microbial communities, *UCLA CGSI, Los Angeles, CA* July 20, 2017

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- The CAMI Project: Assessment of computational techniques in metagenomics, *UCLA CGSI, Los Angeles, CA* July 12, 2017
- Improving Min Hash for Metagenomic Classification, *UCLA CGSI, Los Angeles, CA* July 7, 2017
- The CAMI Project: Assessment of computational techniques in metagenomics, *Microbiome Initiative Conference, Oregon State University, Corvallis, OR* May 12, 2017
- Optimizing biodiversity in metagenomics via compressive sensing, *Joint Mathematics Meeting, Seattle, WA* January 1, 2017
- Topological pressure with applications to genomics, *Mathematics department seminar, Brigham Young University, Provo, UT* November 10, 2016
- Reference-free and reference-based metrics for metagenomics community comparison, *Genomics In Action Seminar, University of Oregon, Eugene, OR* November 4, 2016
- Probabilities for the indeterminacy of ecological interactions as perceived through perturbation experiments, *Mathematical biology seminar, Oregon State University, Corvallis, OR* October 12, 2016
- Reference-free comparison of microbial Communities via de Bruijn graphs, *ACM-BCB Conference, Seattle, WA* October 3, 2016
- Quantifying strain-level variation in metagenomic profiling with MetaPalette, *Applied Math Seminar, Texas A&M University, College Station, TX* September 12, 2016
- Bacterial community reconstruction via compressed sensing, *Computational Genomics Summer Institute (CGSI), UCLA, Los Angeles, CA* August 11, 2016
- Mathematical Methods in (Meta)Genomics, *Computational Genomics Summer Institute (CGSI), UCLA, Los Angeles, CA* July 28, 2016
- Participant, speaker, journal club leader, *Computational Genomics Summer Institute (CGSI), UCLA, Los Angeles, CA* July 18-August 12, 2016
- CAMI profiling results, *CAMI evaluation workshop, Isaac Newton Institute, Cambridge University, Cambridge, UK* May 11, 2016
- Quantifying strain level variation in metagenomic profiling with MetaPalette, *CGRB Spring Conference, Oregon State University, Corvallis, OR* April 11, 2016
- Testing independence in motif finding algorithms, *Mathematical biology seminar, Oregon State University, Corvallis, OR* March 30, 2016
- Topological pressure with applications to genomics, *US Naval Academy Applied Math Seminar, Annapolis, MD* January 14, 2016
- Symbolic dynamical (and other) approaches to the analysis of biological data, *US Naval Academy Math Department Colloquium, Annapolis, MD* January 13, 2016
- Optimizing biodiversity in metagenomics via compressed sensing, *Joint Mathematics Meeting, Seattle, WA* January 9, 2016
- Mathematical Methods in Metagenomics, *Science Seminar Series, WSU Vancouver, WA* September 21, 2015
- Assessment Metrics for Metagenomic profiling, *CAMI Evaluation Meeting, Berlin, Germany* May 28, 2015

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- Advances in Metagenomic Analysis, *Penn State University, State College, PA*  
January 12, 2015
- Metagenomics: State of the Art, *Omnigen Research scientific workshop, Corvallis, OR*  
September 3, 2014
- Advances in Metagenomic Analysis, *Bioinformatics Users Group, Oregon State University, Corvallis, OR*  
July 2, 2014
- Reference-free comparison of metagenomic samples via de Bruijn graph metrics, *High throughput genomics reunion conference, UCLA*  
June 12, 2014
- *Workshop: Mathematical, statistical and computational aspects of the new science of metagenomics, Isaac Newton Institute of Mathematical Sciences, Cambridge University, Cambridge, UK, Visiting Fellow*  
March 24–April 17, 2014
- Reference-free methods in metagenomics analysis, *Mathematical Methods in Metagenomics, Cambridge University, Cambridge, UK*  
April 2, 2014
- Quikr: Rapid bacterial community reconstruction via compressive sensing, *Mathematical Methods in Metagenomics, Cambridge University, Cambridge, UK*  
March 27, 2014
- Random substitutions, Martin boundaries, and molecular evolution, *Probability seminar, University of Oregon, Eugene, OR*  
November 12, 2013
- Substitution Markov chains with applications to molecular evolution, *Pacific Northwest Probability Seminar, Seattle, WA*  
October 19, 2013
- Quikr: a method for rapid reconstruction of bacterial communities via compressive sensing, *Applied math seminar, Oregon State University*  
October 4, 2013
- Quikr: a method for rapid reconstruction of bacterial communities via compressive sensing, *Math, Bio, and physiology seminar, Penn State University, State College, PA*  
April 16, 2013
- Quikr: a method for rapid reconstruction of bacterial communities via compressive sensing, *Mathematical life sciences seminar, Case Western Reserve University, Cleveland, OH*  
March 4, 2013
- Bacterial community reconstruction via compressive sensing, *DTRA/NSF/NGA Algorithms conference, San Diego, CA*  
November 27, 2012
- Topological pressure, *Ergodic theory seminar, The Ohio State University, Columbus, OH*  
October 24, 2012
- Topological pressure, *Mathematical Biosciences Institute postdoc seminar, Ohio State University, Columbus, OH*  
September 27, 2012
- Symbolic dynamics and DNA, *Drexel University, Philadelphia*  
April 5, 2012
- Symbolic dynamics and DNA, *Oregon State University*  
February 21, 2012
- *UCLA IPAM Mathematical approaches to High-throughput genomics core participant.*  
September–December, 2011
- Topological entropy, *UCLA, Los Angeles, CA*  
March 7, 2011
- Topological entropy of finite sequences, *Pennsylvania State University, State College, PA*  
January 22, 2011

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- Random substitutions: applications to molecular evolution, *Penn State University, State College, PA* March 26, 2010
- Random substitutions and Martin boundaries, *Penn State University, State College, PA* April 2, 2010
- Problem session, *Georg-August-Universität, Göttingen, Germany* July 12-26, 2009
- Topological pressure, *Georg-August-Universität, Göttingen, Germany* July 24, 2009
- Random Substitutions: poster presentation, *Chern Institute, Nankai Univ., Tianjin, China* June 8-9, 2009

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