



# David Koslicki

## Education/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 Probability, Markov chains, Martin boundaries, symbolic dynamics, applications of compressive sensing, thermodynamic formalism, mathematical approaches to Big Data problems
- Biological High throughput sequencing technology, metagenomics/microbial community analysis, entropy techniques, alignment-free genomic analysis

## Publications

- J. McClelland and **Koslicki, D.** Emdunifrac: Exact linear time computation of the unifrac metric and identification of differentially abundant organisms. *Journal of Mathematical Biology*, (Accepted), 2017.
- M. Ansariola, M. Megraw, and **Koslicki, D.** Indecut evaluates performance of network motif discovery algorithms. *Bioinformatics*, (Accepted), 2017.
- A. Sczyrba, P. Hofmann, P. Belmann, **Koslicki, D.**, et al. Critical assessment of metagenome interpretation - a benchmark of metagenomics software. *Nature methods*, 14(11):1063–1071, 2017.
- Koslicki, D.** and M. Novak. Exact probabilities for the indeterminacy of complex networks as perceived through press perturbations. *Journal of Mathematical Biology*, Online ahead of print, Jul 2017.

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.

**Koslicki, D.** 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.

**Koslicki, D.** and M. Denker. Substitution markov chains and martin boundaries. *Rocky Mountain Journal of Mathematics*, 46(6):1963–1985, 2016.

**Koslicki, D.**, 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.

Holzinger, A., Hörtenhuber, M., Mayer, C., Bachler, M., Wassertheurer, S., Pinho, A.J., and **Koslicki, D.** On entropy-based data mining. In *Interactive Knowledge Discovery and Data Mining in Biomedical Informatics*, pages 209–226. Springer Berlin Heidelberg, 2014.

**Koslicki, D.**, Foucart, S., and Rosen, G. WGSQuikr: fast whole-genome shotgun metagenomic classification. *PLoS ONE*, 9(3):e91784, 2014.

S. Foucart and **Koslicki, D.** Sparse recovery by means of nonnegative least squares. *IEEE Signal Processing Letters*, 21(14):498–502, 2014.

Chatterjee, S., **Koslicki, D.**, Dong, S., Innocenti, N., Cheng, L., Lan, Y., Vehkaperä, M., Skoglund, M., Rasmussen, L.K., Aurell, E., and Corander, J. SEK: sparsity exploiting  $k$ -mer based estimation of bacterial community composition. *Bioinformatics*, 30(17):2423–2431, 2014.

**Koslicki, D.** and Thompson, D.J. Coding sequence density estimation via topological pressure. *Journal of Mathematical Biology*, pages 1–25, 2014.

**Koslicki, D.**, Foucart, S., and Rosen, G. Quikr: a Method for Rapid Reconstruction of Bacterial Communities via Compressive Sensing. *Bioinformatics*, 29(17):2096–2102, 2013.

**Koslicki, D.** *Substitution Markov chains with applications to molecular evolution*. PhD thesis, Pennsylvania State University, State College, PA, USA, 2012.

**Koslicki, D.** Topological entropy of DNA sequences. *Bioinformatics*, 27(8):1061–1067, 2011.

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## Preprints and Submitted Manuscripts

- **Koslicki, D.** and Zabeti, H. Improving Min Hash via the Containment Index with applications to Metagenomic Analysis. Under review. 2017

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☎ (541) 737 5172 • ✉ david.koslicki@math.oregonstate.edu

🌐 koslicki.math.oregonstate.edu • 🌐 dkoslicki

- Mangul, S., Loohuis, L., Ori, A. Jospin, G., **Koslicki, D.** et. al. Total RNA Sequencing reveals microbial communities in human blood and disease specific effects. Under revision., 2016
- **Koslicki, D.** An alignment-free indel model of molecular evolution. arXiv, <http://arxiv.org/abs/1102.1897>. 2011.

## Students

### Graduate

- Hooman Zabeti, 2015-2017, Masters, math
- Ryan Melson, 2015-2017, Masters
- Jason McClelland, 2014-present, PhD, math
- Abby Pecoske, graduated August, 2015 with Masters in math. Pursuing PhD at University of Pittsburgh.
- Ian McKay, graduated May, 2015 with Masters in math. Currently employed by Salesforce.

### Undergraduate

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

## Consulting Experience

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

## Presentations/Seminars/Workshops

- 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
- 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

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- 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
- 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

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- *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
- 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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## Refereeing Experience

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

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## Professional Memberships

- American Mathematical Society (AMS)
- Mathematical Association of America (MAA)
- International Society for Computational Biology (ISCB)
- Society for Industrial and Applied Mathematics (SIAM)

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## Awards

- 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
- Commencement highlight student, *Washington State* 2006
- Vantsdal memorial math scholarship, *Washington State* 2006
- Excellent performance fellowship, *Penn State MASS program* 2005
- Graber endowment math scholarship, *Washington State* 2005

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## University Service

- OSU Microbiome Initiative Workshop Committee Member 2016-present
- Graduate committee 2017-present
- Alumni Newsletter committee 2016-present
- Undergraduate advising committee 2015-2017
- Mathematics department computer committee 2013-present (chair 2016-present)
- Mathematical biology seminar organizer 2014-present
- CGRB Spring Conference: *Dealing with the Data Deluge*. Served on organizing committee April 7, 2014
- Mathematics department undergraduate committee 2013-2015
- Mathematics department graduate teaching association committee 2009-2010

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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. <https://create.osufoundation.org/project/619> Fall, 2015
- Member of Math Alliance, a community dedicated to serving underrepresented groups of students in the mathematical sciences. 2015-present

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## Courses Taught

- 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
- 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

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- 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

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