

## References

- [1] Eddie Aamari et al. “Estimating the reach of a manifold.” 2017. arXiv: 1705.04565.
- [2] Francesco Abate et al. “Distinct viral and mutational spectrum of endemic Burkitt lymphoma.” *PLoS Pathog.* 11.10 (2015), e1005158.
- [3] Henry Adams and Joshua Mirth. Metric thickenings of euclidean submanifolds. 2017. arXiv: 1709.02492 [math.AT].
- [4] Henry Adams et al. “Persistence images: a stable vector representation of persistent homology.” *J. Mach. Learn. Res.* 18.1 (2017), 218–252.
- [5] Aaron Adcock, Erik Carlsson, and Gunnar Carlsson. “The ring of algebraic functions on persistence bar codes.” *Homology Homotopy Appl.* 18.1 (2016), 381–402.
- [6] Sophie H. Adjalley et al. “Genome-wide transcriptome profiling reveals functional networks involving the *Plasmodium falciparum* drug resistance transporters PfCRT and PfMDR1.” *BMC Genomics* 16.1 (2015), 1090.
- [7] R. J. Adler, O. Bobrowski, and S. Weinberger. “Crackle: the homology of noise.” *Discrete Comput. Geom.* 52.4 (2014), 680–704.
- [8] R. J. Adler and J. E. Taylor. *Random Fields and Geometry*. Springer Monographs in Mathematics. Springer Verlag, 2007.
- [9] R. Adler et al. “Persistent homology for random fields and complexes.” 2010. arXiv: 1003.1001 [math.PR].
- [10] Sebastian E. Ahnert et al. “Unbiased pattern detection in microarray data series.” *Bioinformatics* 22.12 (2006), 1471–1476.
- [11] A. D. Alexandrov. “Über eine Verallgemeinerung der Riemannschen Geometrie.” *Schr. Ortschungsinst. Math. Berlin* 1 (1957), 33–84.
- [12] Ludmil B. Alexandrov et al. “Signatures of mutational processes in human cancer.” *Nature* 500.7463 (2013), 415–421.
- [13] El-ad David Amir et al. “visNE enables visualization of high dimensional single-cell data and reveals phenotypic heterogeneity of leukemia.” *Nature Biotechnol.* 31.6 (2013), 545–552.
- [14] David Anick. “The computation of rational homotopy groups is #P-hard.” *Lecture Notes in Pure and Applied Mathematics*, volume 114, pp. 1–56. Springer, 1989.
- [15] Luis Aparicio et al. “Quasi-universality in single-cell sequencing data.” 2018. biorXiv: [www.biorxiv.org/content/early/2018/10/05/426239](http://www.biorxiv.org/content/early/2018/10/05/426239).
- [16] Peter Armitage and Richard Doll. “The age distribution of cancer and a multi-stage theory of carcinogenesis.” *Br. J. Cancer* 8.1 (1954), 1.
- [17] Luis Arnes et al. “Comprehensive characterisation of compartment-specific long non-coding RNAs associated with pancreatic ductal adenocarcinoma.” *Gut* (2018). doi: 10.1136/gutjnl-2017-314353.

- [18] Norman Arnheim, Peter Calabrese, and Irene Tiemann-Boege. “Mammalian meiotic recombination hot spots.” *Annu. Rev. Genet.* 41 (2007), 369–399.
- [19] Javier Arsuaga et al. “Identification of copy number aberrations in breast cancer subtypes using persistence topology.” *Microarrays* 4.3 (2015), 339–369.
- [20] Javier Arsuaga et al. “Knotting probability of DNA molecules confined in restricted volumes: DNA knotting in phage capsids.” *Proc. Natl. Acad. Sci. USA* 99.8 (2002), 5373–5377.
- [21] Javier Arsuaga et al. “Topological analysis of gene expression arrays identifies high risk molecular subtypes in breast cancer.” *Appl. Alg. Eng. Commun. Comput.* 23.1–2 (2012), pp. 3–15.
- [22] Michael Artin. *Algebra*. Prentice Hall, Englewood Cliffs, NJ, 1991.
- [23] Kevin Atteson. “The performance of neighbor-joining algorithms of phylogeny reconstruction.” *Computing and Combinatorics: Third Annual International Conference, COCOON ’97 Shanghai, China, August 20–22, 1997*, pp. 101–110. Ed. by Tao Jiang and D. T. Lee. Springer, Berlin, 1997.
- [24] Sheldon Jay Axler. *Linear Algebra Done Right*. Third edition. Undergraduate Texts in Mathematics. Springer International Publishing, 2015.
- [25] Ferhat Ay and William S Noble. “Analysis methods for studying the 3D architecture of the genome.” *Genome Biol.* 16.1 (2015), 1306.
- [26] Gayane Badalian-Very et al. “Recurrent BRAF mutations in Langerhans cell histiocytosis.” *Blood* 116.11 (2010), 1919–1923.
- [27] David J. Balding, Richard A. Nichols, and David M. Hunt. “Detecting gene conversion: primate visual pigment genes.” *Proc. R. Soc. London, Ser. B* 249.1326 (1992), 275–280.
- [28] David Baltimore. “Expression of animal virus genomes.” *Bacteriol. Rev.* 35.3 (1971), 235.
- [29] David Baltimore. “RNA-dependent DNA polymerase in virions of RNA tumour viruses.” *A Century of Nature: Twenty-One Discoveries that Changed Science and the World*, p. 173. Ed. by Laura Garwin and Tim Lincoln. University of Chicago Press, Chicago, IL, 2003.
- [30] Hans-Jürgen Bandelt and Andreas W. M. Dress. “Split decomposition: a new and useful approach to phylogenetic analysis of distance data.” *Mol. Phylogen. Evol.* 1.3 (1992), 242–252.
- [31] Hans-Jürgen Bandelt, Peter Forster, and Arne Röhl. “Median-joining networks for inferring intraspecific phylogenies.” *Mol. Biol. Evol.* 16.1 (1999), 37–48.
- [32] Hans-Jürgen Bandelt, Vincent Macaulay, and Martin Richards. “Median networks: speedy construction and greedy reduction, one simulation, and two case studies from human mtDNA.” *Mol. Phylogen. Evol.* 16.1 (2000), 8–28.
- [33] Hans-J. Bandelt et al. “Mitochondrial portraits of human populations using median networks.” *Genetics* 141.2 (1995), 743–753.
- [34] Ziv Bar-Joseph. “Analyzing time series gene expression data.” *Bioinformatics* 20.16 (2004), 2493–2503.
- [35] Ziv Bar-Joseph, Anthony Gitter, and Itamar Simon. “Studying and modelling dynamic biological processes using time-series gene expression data.” *Nature Rev. Genet.* 13.8 (2012), 552–564.
- [36] F. Barre-Sinoussi et al. “Isolation of a T-lymphotropic retrovirus from a patient at risk for acquired immune deficiency syndrome (AIDS).” *Science* 220.45995 (1983), 868–871.
- [37] Frédéric Baudat, Yukiko Imai, and Bernard de Massy. “Meiotic recombination in mammals: localization and regulation.” *Nature Rev. Genet.* 14.11 (2013), 794–806.

- [38] F. Baudat et al. “PRDM9 is a major determinant of meiotic recombination hotspots in humans and mice.” *Science* 327.5967 (2010), 836–840.
- [39] Ulrich Bauer. Ripser. 2016. <https://github.com/Ripser/ripser>.
- [40] Ulrich Bauer, Michael Kerber, and Jan Reininghaus. DIPHA. 2014. <https://github.com/DIPHA/dipha>.
- [41] Ulrich Bauer, Michael Kerber, and Jan Reininghaus. “Distributed computation of persistent homology.” *Proceedings of the Sixteenth Workshop on Algorithm Engineering and Experiments, ALENEX 2014, Portland, OR, USA, January 5, 2014*, pp. 31–38. doi.org/10.1137/1.9781611973198.4.
- [42] Ulrich Bauer and Michael Lesnick. “Induced matchings of barcodes and the algebraic stability of persistence.” *Proceedings of the Thirtieth Annual Symposium on Computational Geometry, SOCG’14, Kyoto, Japan*, pp. 355:355–355:364. ACM, 2014. doi: 10.1145/2582112.2582168.
- [43] Ulrich Bauer et al. PHAT: Persistent homology algorithms toolbox. 2013. <https://bitbucket.org/phat-code/phat>.
- [44] Ulrich Bauer et al. “Phat – Persistent Homology Algorithms Toolbox.” *J. Symbol. Comput.* 78.Supplement C (2017), 76–90.
- [45] Mikhail Belkin and Partha Niyogi. “Laplacian eigenmaps for dimensionality reduction and data representation.” *Neural Comput.* 15.6 (2003), 1373–1396. doi: 10.1162/089976603321780317.
- [46] Mikhail Belkin and Partha Niyogi. “Towards a theoretical foundation for Laplacian-based manifold methods.” *J. Comput. Syst. Sci.* 74.8 (2008), 1289–1308. doi: 10.1016/j.jcss.2007.08.006.
- [47] Sean C. Bendall et al. “Single-cell trajectory detection uncovers progression and regulatory coordination in human B cell development.” *Cell* 157.3 (2014), 714–725.
- [48] Paul Bendich, Bei Wang, and Sayan Mukherjee. “Local homology transfer and stratification learning.” *Proceedings of the Twenty-Third Annual ACM-SIAM Symposium on Discrete Algorithms*, pp. 1355–1370.
- [49] P. Bendich et al. “Topological and statistical behavior classifiers for tracking applications.” *IEEE Trans. Aero. Electron. Syst.* 52.6 (2016), 2644–2661.
- [50] Yoshua Bengio, Aaron Courville, and Pascal Vincent. “Representation learning: a review and new perspectives.” *IEEE Trans. Pattern Anal. Mach. Intell.* 35.8 (2013), 1798–1828. doi: 10.1109/TPAMI.2013.50.
- [51] Mira Bernstein et al. *Graph Approximations to Geodesics on Embedded Manifolds*. Stanford University technical report. 2000.
- [52] Rameen Beroukhim et al. “Assessing the significance of chromosomal aberrations in cancer: methodology and application to glioma.” *Proc. Natl. Acad. Sci. USA* 104.50 (2007), 20007–20012.
- [53] Eva Bianconi et al. “An estimation of the number of cells in the human body.” *Ann. Human Biol.* 40.6 (2013), 463–471.
- [54] Peter J. Bickel and David A. Freedman. “Some asymptotic theory for the bootstrap.” *Ann. Stat.* 9.6 (1981), 1196–1217. doi: 10.1214/aoas/1176345637.
- [55] Louis J. Billera, Susan P. Holmes, and Karen Vogtmann. “Geometry of the space of phylogenetic trees.” *Adv. Appl. Math.* 27.4 (2001), 733–767. doi: 10.1006/aama.2001.0759.
- [56] P. Billingsley. *Convergence of Probability Measures*. Wiley, New York, 1968.
- [57] Patrick Billingsley. *Probability and Measure*. Third edition. John Wiley and Sons, 1995.
- [58] Andrew J. Blumberg and Michael Lesnick. “Universality of the homotopy interleaving distance.” 2017. arXiv: 1705.01690 [math.AT].

- [59] Andrew J. Blumberg and Michael A. Mandell. “Quantitative homotopy theory in topological data analysis.” *Found. Comput. Math.* 13.6 (2013), 885–911.
- [60] Andrew J. Blumberg et al. “Robust statistics, hypothesis testing, and confidence intervals for persistent homology on metric measure spaces.” *Found. Comput. Math.* 14.4 (2014), 745–789.
- [61] O. Bobrowski and M. Kahle. “Topology of random geometric complexes: a survey.” *Topology in Statistical Inference*. Proceedings of Symposia in Applied Mathematics. 2014.
- [62] Omer Bobrowski and Sayan Mukherjee. “The topology of probability distributions on manifolds.” *Prob. Theor. Relat. Fields* 161.3 (2015), 651–686.
- [63] O. Bobrowski, M. Kahle, and P. Skraba. “Maximally persistent cycles in random geometric complexes.” *Ann. Appl. Prob.* (2017). arXiv: 1509.04347 [math.PR].
- [64] B. Bollobas. *Modern Graph Theory*. Graduate Texts in Mathematics, volume 184. Springer Verlag, 1998.
- [65] Magnus Bordewich and Charles Semple. “Computing the minimum number of hybridization events for a consistent evolutionary history.” *Discrete Appl. Math.* 155.8 (2007), 914–928.
- [66] Magnus Bordewich and Charles Semple. “On the computational complexity of the rooted subtree prune and regraft distance.” *Ann. Combinatorics* 8.4 (2005), 409–423.
- [67] Magnus Bakke Botnan and Michael Lesnick. “Algebraic stability of zigzag persistence modules.” 2016. arxiv.org/abs/1604.00655.
- [68] Theodor (Biologe) Boveri and Henry Harris. *Concerning the Origin of Malignant Tumours*. Cold Spring Harbor Laboratory Press, 2008.
- [69] Matthew Brand. “Charting a manifold.” *Adv. Neur. Inf. Process. Syst.* 15 (2002), 961–968.
- [70] J. R. Bray and J. T. Curtis. “An ordination of the upland forest communities of Southern Wisconsin.” *Ecol. Monogr.* 27 (1957), 325–349.
- [71] Cameron W. Brennan et al. “The somatic genomic landscape of glioblastoma.” *Cell* 155.2 (2013), 462–477.
- [72] Bryn A. Bridges. “Microbial genetics: hypermutation under stress.” *Nature* 387.6633 (1997), 557–558.
- [73] M. R. Bridson and A. Häfliger. *Metric Spaces of Non-Positive Curvature*. Grundlehren der Mathematischen Wissenschaften. Springer, Berlin, 2011.
- [74] Peter J. Brockwell and Richard A. Davis. *Time Series: Theory and Methods*. Springer Science & Business Media, 2013.
- [75] David Bryant and Vincent Moulton. “Neighbor-net: an agglomerative method for the construction of phylogenetic networks.” *Mol. Biol. Evol.* 21.2 (2004), 255–265.
- [76] Peter Bubenik. “Statistical topological data analysis using persistence landscapes.” *J. Mach. Learn. Res.* 16.1 (2015), 77–102.
- [77] Peter Bubenik and Paweł Dłotko. A persistence landscapes toolbox for topological statistics. 2015. [www.math.upenn.edu/~dlotko/persistenceLandscape.html](http://www.math.upenn.edu/~dlotko/persistenceLandscape.html).
- [78] Peter Bubenik and Paweł Dłotko. “A persistence landscapes toolbox for topological statistics.” *J. Symb. Comput.* 78 (2017), 91–114. doi: 10.1016/j.jsc.2016.03.009.
- [79] Mickaël Buchet et al. “Efficient and robust persistent homology for measures.” *Comput. Geom.* 58 (2016), 70–96.
- [80] Dorothy Buck. “DNA topology.” Applications of Knot Theory. *Proc. Symp. Appl. Math.*, 66 (2009), 47–79.

- [81] O. Peter Buneman. “The recovery of trees from measures of dissimilarity.” *Math. Archaeol. Hist. Sci.* (1971), 387–395.
- [82] Peter Buneman. “A note on the metric properties of trees.” *J. Combinatorics Theor. Ser. B* 17.1 (1974), 48–50.
- [83] Dmitri Burago, Yuri Burago, and Sergei Ivanov. *A Course in Metric Geometry*. Graduate Studies in Mathematics, volume 33. American Mathematical Society, Providence, RI, 2001.
- [84] Denis Burkitt. “A sarcoma involving the jaws in African children.” *Hematology: Landmark Papers of the Twentieth Century* 1.8 (2000), 353.
- [85] Martin Cadek et al. “Polynomial-time computation of homotopy groups and Postnikov systems in fixed dimension.” *SIAM J. Comput.* 43.5 (2014), 1728–1780. doi: 10.1137/120899029.
- [86] John Cairns, Julie Overbaugh, and Stephan Miller. “The origin of mutants.” *Nature* 335.6186 (1988), 142–145.
- [87] Pablo G. Cámarra. “Topological methods for genomics: present and future directions.” *Curr. Opin. Syst. Biol.* 1 (2017), 95–101.
- [88] Pablo G. Cámarra, Arnold J. Levine, and Raúl Rabadán. “Inference of ancestral recombination graphs through topological data analysis.” *PLoS Comput. Biol.* 12.8 (2016), e1005071.
- [89] Emmanuel J. Candès et al. “Robust principal component analysis?” *J. ACM* 58.3 (2011), 11:1–11:37. doi: 10.1145/1970392.1970395.
- [90] Gunnar Carlsson. “Topological pattern recognition for point cloud data.” *Acta Num.* 23 (2014), 289–368.
- [91] Gunnar E. Carlsson, Vin de Silva, and Dmitriy Morozov. “Zigzag persistent homology and realvalued functions.” *Proceedings of the 25th ACM Symposium on Computational Geometry, Aarhus, Denmark, June 8–10, 2009*, pp. 247–256.
- [92] Gunnar E. Carlsson and Afra Zomorodian. “The theory of multidimensional persistence.” *Discrete Comput. Geom.* 42.1 (2009), pp. 71–93. doi: 10.1007/s00454-009-9176-0.
- [93] Gunnar Carlsson and Vin De Silva. “Zigzag persistence.” *Found. Comput. Math.* 10.4 (2010), 367–405.
- [94] Gunnar Carlsson and Sara Kališnik Verovšek. “Symmetric and r-symmetric tropical polynomials and rational functions.” *J. Pure Appl. Algebra* 220.11 (2016), 3610–3627. doi: 10.1016/j.jpaa.2016.05.002.
- [95] Gunnar Carlsson et al. “On the local behavior of spaces of natural images.” *Int. J. Comput. Vision* 76.1 (2008), 1–12.
- [96] Manfredo Perdigão do Carmo. *Riemannian Geometry. Mathematics: Theory & Applications*. Translated from the second Portuguese edition by Francis Flaherty. Birkhauser Boston, MA, 1992. doi: 10.1007/978-1-4757-2201-7.
- [97] Mathieu Carrière, Steve Y. Oudot, and Maks Ovsjanikov. “Stable topological signatures for points on 3D shapes.” *Proceedings of the Eurographics Symposium on Geometry Processing. SGP ’15. Graz, Austria*, pp. 1–12. Eurographics Association, 2015. doi: 10.1111/cgf.12692.
- [98] Ben Cassidy, Caroline Rae, and Victor Solo. “Brain activity: conditional dissimilarity and persistent homology.” *Biomedical Imaging (ISBI), Proceedings of the IEEE 12th International Symposium on Biomedical Imaging*, pp. 1356–1359. IEEE, 2015
- [99] Andrea Cerri et al. “Betti numbers in multidimensional persistent homology are stable functions.” *Math. Methods Appl. Sci.* 36.12 (2013), 1543–1557.

- [100] Joseph Minhow Chan, Gunnar Carlsson, and Raúl Rabadán. “Topology of viral evolution.” *Proc. Natl. Acad. Sci. USA* 110.46 (2013), 18566–18571.
- [101] Yuan Chang et al. “Identification of herpesvirus-like DNA sequences in AIDS-associated Kaposi’s sarcoma.” *Science* 266.5192 (1994), 1865.
- [102] Chris Chatfield. *The Analysis of Time Series: An Introduction*. CRC Press, 2013.
- [103] Frédéric Chazal. “Higher-dimensional topological data analysis.” To appear in *Handbook of Discrete and Computational Geometry*. 2017.
- [104] Frédéric Chazal, David Cohen-Steiner, and Quentin Mérigot. “Geometric inference for probability measures.” *Found. Comput. Math.* 11.6 (2011), 733–751. doi: 10.1007/s10208-011-9098-0.
- [105] Frédéric Chazal, Vin de Silva, and Steve Oudot. “Persistence stability for geometric complexes.” *Geometriae Dedicata* 173.1 (2014), 193–214.
- [106] Frédéric Chazal and Jian Sun. “Gromov-Hausdorff approximation of filament structure using Reeb-type graph.” *Proceedings of the Thirtieth Annual Symposium on Computational Geometry, SOCG’14, Kyoto, Japan, June 08–11, 2014*, p. 491. ACM, 2014. doi: 10.1145/2582112.2582129.
- [107] Frédéric Chazal et al. “Proximity of persistence modules and their diagrams.” *Proceedings of the Twenty-fifth Annual Symposium on Computational Geometry, SOCG ’09, Aarhus, Denmark*, pp. 237–246. ACM, 2009. doi: 10.1145/1542362.1542407.
- [108] Frédéric Chazal et al. “Robust topological inference: distance to a measure and kernel distance.” *J. Mach. Learn. Res.* 18.159 (2018), 1–40. arXiv: 1412.7197 [math.ST].
- [109] Frédéric Chazal et al. “Stochastic convergence of persistence landscapes and silhouettes.” *Proceedings of the Thirtieth Annual Symposium on Computational Geometry, SOCG’14, Kyoto, Japan*, pp. 474:474–474:483. ACM, 2014. doi: 10.1145/2582112.2582128.
- [110] Frédéric Chazal et al. “Subsampling methods for persistent homology.” 2014. arXiv: 1406.1901 [math.AT].
- [111] Frédéric Chazal et al. *The Structure and Stability of Persistence Modules*. Springer Briefs in Mathematics. Springer, 2016. doi: 10.1007/978-3-319-42545-0.
- [112] Andrew X. Chen and Raúl Rabadán. “A fast semi-automatic segmentation tool for processing brain tumor images.” *Towards Integrative Machine Learning and Knowledge Extraction*, pp. 170–181. Lecture Notes in Computer Science, volume 10344. Springer, 2017.
- [113] Chao Chen and Daniel Freedman. “Hardness results for homology localization.” *Discrete Comput. Geom.* 45.3 (2011), 425–448.
- [114] Gary K. Chen, Paul Marjoram, and Jeffrey D. Wall. “Fast and flexible simulation of DNA sequence data.” *Genome Res.* 19.1 (2009), 136–142.
- [115] Benny Chor and Tamir Tuller. “Maximum likelihood of evolutionary trees: hardness and approximation.” *Bioinformatics* 21.suppl 1 (2005), i97–i106.
- [116] Fan R. K. Chung. *Spectral Graph Theory*. American Mathematical Society, 1997.
- [117] David Cohen-Steiner, Herbert Edelsbrunner, and John Harer. “Stability of persistence diagrams.” *Discrete Comput. Geom.* 37.1 (2007), 103–120.
- [118] David Cohen-Steiner et al. “Lipschitz functions have L p-stable persistence.” *Found. Comput. Math.* 10.2 (2010), 127–139.
- [119] Ronald R. Coifman and Mauro Maggioni. “Diffusion wavelets.” *Appl. Comput. Harmonic Anal.* 21.1 (2006), 53–94. doi: 10.1016/j.acha.2005.09.006.
- [120] Rodney Colina et al. “Evidence of intratypic recombination in natural populations of hepatitis C virus.” *J. Gen. Virol.* 85.1 (2004), 31–37.

- [121] Michael Collins and Nigel Du\_y. "Convolution kernels for natural language." *Proceedings of the 14th International Conference on Neural Information Processing Systems: Natural and Synthetic. NIPS'01. Vancouver, British Columbia, Canada*, pp. 625–632. MIT Press, 2001.
- [122] 1000 Genomes Project Consortium et al. "An integrated map of genetic variation from 1,092 human genomes." *Nature* 491.7422 (2012), 56–65.
- [123] ENCODE Project Consortium et al. "An integrated encyclopedia of DNA elements in the human genome." *Nature* 489.7414 (2012), 57–74.
- [124] J. E. Cooper and Edward J. Feil. "The phylogeny of *Staphylococcus aureus* – which genes make the best intra-species markers?" *Microbiology* 152.5 (2006), 1297–1305.
- [125] Thomas H. Cormen et al. *Introduction to Algorithms*. Third edition. MIT Press, 2009.
- [126] Nicholas R. Cozzarelli and James C. Wang. *DNA Topology and its Biological Effects*. Cold Spring Harbor Laboratory Press, 1990.
- [127] Lorin Crawford et al. "Functional data analysis using a topological summary statistic: the smooth Euler characteristic transform." 2016. arXiv: 1611.06818.
- [128] Lorin Crawford et al. "Topological summaries of tumor images improve prediction of disease free survival in glioblastoma multiforme." 2016. arXiv: 1611.06818.
- [129] José M. Cuevas et al. "Extremely high mutation rate of HIV-1 in vivo." *PLoS Biol.* 13.9 (2015), e1002251.
- [130] Carina Curto. "What can topology tell us about the neural code?" *Bull. Am. Math. Soc.* 54.1 (2017), 63–78.
- [131] Riccardo Dalla-Favera et al. "Human c-myc oncogene is located on the region of chromosome 8 that is translocated in Burkitt lymphoma cells." *Proc. Natl. Acad. Sci. USA* 79.24 (1982), 7824–7827.
- [132] Robert Dallmann et al. "The human circadian metabolome." *Proc. Natl. Acad. Sci. USA* 109.7 (2012), 2625–2629.
- [133] Charles Darwin. *On the Origin of Species*. Murray, London, 1859.
- [134] Julian Davies and Dorothy Davies. "Origins and evolution of antibiotic resistance." *Microbiol. Mol. Biol. Rev.* 74.3 (2010), 417–433.
- [135] William H. E. Day. "Computational complexity of inferring phylogenies from dissimilarity matrices." *Bull. Math. Biol.* 49.4 (1987), 461–467.
- [136] Ulrik De Lichtenberg et al. "Comparison of computational methods for the identification of cell cycle-regulated genes." *Bioinformatics* 21.7 (2005), 1164–1171.
- [137] Anastasia Deckard et al. "Design and analysis of large-scale biological rhythm studies: a comparison of algorithms for detecting periodic signals in biological data." *Bioinformatics* 29.24 (2013), 3174–3180.
- [138] Job Dekker, Marc A. Marti-Renom, and Leonid A. Mirny. "Exploring the three-dimensional organization of genomes: interpreting chromatin interaction data." *Nature Rev. Genet.* 14 (2013), 390–403.
- [139] Albert B. DeLeo et al. "Detection of a transformation-related antigen in chemically induced sarcomas and other transformed cells of the mouse." *Proc. Natl. Acad. Sci. USA* 76.5 (1979), 2420–2424.
- [140] Mary-Lee Dequeant et al. "Comparison of pattern detection methods in microarray time series of the segmentation clock." *PLoS One* 3.8 (2008), e2856.
- [141] Satyan L. Devadoss, Daoji Huang, and Dominic Spadacene. "Polyhedral covers of tree space." *SIAM J. Discrete Math.* 28.3 (2014), 1508–1514. doi: 10.1137/130947532.

- [142] D. DeWoskin et al. “Applications of computational homology to the analysis of treatment response in breast cancer patients.” *Topol. Appl.* 157.1 (2010), 157–164.
- [143] Tamal K. Dey, Facundo Mémoli, and Yusu Wang. “Topological analysis of nerves, Reeb spaces, mappers, and multiscale mappers.” *Proceedings of the 33rd International Symposium on Computational Geometry, SoCG 2017. July 4–7, 2017, Brisbane, Australia*, pp. 36:1–36:16. 2017.
- [144] Persi Diaconis, Susan Holmes, and Mehrdad Shahshahani. “Sampling from a manifold.” *Advances in Modern Statistical Theory and Applications: A Festschrift in honor of Morris L. Eaton*. Contemporary Mathematics, volume 453, pp. 102–125. Institute of Mathematical Statistics, 2013.
- [145] Persi Diaconis and Bernd Sturmfels. “Algebraic algorithms for sampling from conditional distributions.” *Ann. Stat.* 26.1 (1998), 363–397. doi: 10.1214/aos/1030563990.
- [146] David L. Donoho and Carrie Grimes. “Hessian eigenmaps: locally linear embedding techniques for high-dimensional data.” *Proc. Natl. Acad. Sci. USA* 100.10 (2003), 5591–5596.
- [147] W. Ford Doolittle. “Phylogenetic classification and the universal tree.” *Science* 284.5423 (1999), 2124–2128. doi: 10.1126/science.284.5423.2124.
- [148] Boryana Doyle et al. “Chromatin loops as allosteric modulators of enhancer-promoter interactions.” *PLoS Comput. Biol.* 10.10 (2014), e1003867.
- [149] John W. Drake. “A constant rate of spontaneous mutation in DNA-based microbes.” *Proc. Natl. Acad. Sci. USA* 88.16 (1991), 7160–7164.
- [150] John W. Drake et al. “Rates of spontaneous mutation.” *Genetics* 148.4 (1998), 1667–1686.
- [151] Andreas Dress, Katharina T. Huber, and Jacobus Koolen. *Basic Phylogenetic Combinatorics*. Cambridge University Press, 2012.
- [152] Brian J. Druker. “Perspectives on the development of imatinib and the future of cancer research.” *Nature Med.* 15.10 (2009), 1149–1152.
- [153] Alexei J. Drummond and Andrew Rambaut. “BEAST: Bayesian evolutionary analysis by sampling trees.” *BMC Evol. Biol.* 7.1 (2007), 1.
- [154] H. Edelsbrunner, D. Letscher, and A. Zomorodian. “Topological persistence and simplification.” *Proceedings of the 41st Annual Symposium on Foundations of Computer Science, FOCS ’00*, pp. 454–463. IEEE Computer Society, Washington, DC, 2000.
- [155] Herbert Edelsbrunner and John Harer. *Computational Topology – an Introduction*. American Mathematical Society, 2010.
- [156] Herbert Edelsbrunner and John Harer. “Persistent homology – a survey.” *Survey on Discrete and Computational Geometry. Twenty Years Later*. Contemporary Mathematics, volume 453. Ed. by J. E. Goodman, J. Pach, and R. Pollack. American Mathematical Society, 2008.
- [157] Herbert Edelsbrunner and Dmitriy Morozov. “Persistent homology.” To appear in *Handbook of Discrete and Computational Geometry*. 2017.
- [158] Editorial. “Microbiology by numbers.” *Nature Rev. Microbiol.* 9.9 (2011), 628.
- [159] Peter Eirew et al. “Dynamics of genomic clones in breast cancer patient xenografts at single-cell resolution.” *Nature* 518.7539 (2014), 422–426.
- [160] Gábor Elek. “Betti numbers are testable.” *Fete of Combinatorics and Computer Science*, pp. 139–149. Ed. by Gyula O. H. Katona et al. Springer, Berlin, 2010.,
- [161] Kevin J. Emmett and Raúl Rabadán. “Characterizing scales of genetic recombination and antibiotic resistance in pathogenic bacteria using topological data analysis.” *Brain Informatics and Health*, pp. 540–551. Springer, 2014.

- [162] Kevin Emmett and Raúl Rabadán. “Quantifying reticulation in phylogenetic complexes using homology.” *Proceedings of the 9th EAI International Conference on Bio-inspired Information and Communications Technologies (formerly BIONETICS)*, pp. 193–196. ICST (Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering), 2016.
- [163] Kevin Emmett, Benjamin Schweinhart, and Raúl Rabadán. “Multiscale topology of chromatin folding.” *Proceedings of the 9th EAI International Conference on Bio-inspired Information and Communications Technologies (formerly BIONETICS)*, pp. 177–180. ICST (Institute for Computer Sciences, Social-Informatics and Telecommunications Engineering), 2016.
- [164] Kevin Emmett et al. “Parametric inference using persistence diagrams: a case study in population genetics.” *ICML Workshop on Topological Methods in Machine Learning*. 2014. arXiv: 1406.4582.
- [165] Michael Anthony Epstein, Bert G. Achong, and Yvonne M. Barr. “Virus particles in cultured lymphoblasts from Burkitt’s lymphoma.” *The Lancet* 283.7335 (1964), 702–703.
- [166] Warren J. Ewens. *Mathematical Population Genetics 1: Theoretical Introduction*. Springer Science & Business Media, 2012.
- [167] Gregory Ewing and Joachim Hermisson. “MSMS: a coalescent simulation program including recombination, demographic structure and selection at a single locus.” *Bioinformatics* 26.16 (2010), 2064–2065.
- [168] Jittat Fakcharoenphol, Satish Rao, and Kunal Talwar. “A tight bound on approximating arbitrary metrics by tree metrics.” *Proceedings of the Thirty-Fifth Annual ACM Symposium on Theory of Computing. STOC ’03. San Diego, CA, USA*, pp. 448–455. ACM, 2003. doi: 10.1145/780542.780608.
- [169] Nuno R. Faria et al. “The early spread and epidemic ignition of HIV-1 in human populations.” *Science* 346.6205 (2014), 56–61.
- [170] Brittany T. Fasy et al. “Confidence sets for persistence diagrams.” *Ann. Stat.* 42.6 (2014), 2301–2339. doi: 10.1214/14-AOS1252.
- [171] Brittany T. Fasy et al. TDA: Statistical tools for topological data analysis. 2017. <https://cran.r-project.org/web/packages/TDA/index.html>.
- [172] J. Felsenstein. *Inferring Phylogenies*. Sinauer Associates, Sunderland, MA, 2003.
- [173] Joseph Felsenstein. “Evolutionary trees from DNA sequences: a maximum likelihood approach.” *J. Mol. Evol.* 17.6 (1981), 368–376.
- [174] Joseph Felsenstein. *Inferring Phylogenies*, volume 2. Sinauer Associates Sunderland, MA, 2004.
- [175] Huichen Feng et al. “Clonal integration of a polyomavirus in human Merkel cell carcinoma.” *Science* 319.5866 (2008), 1096–1100.
- [176] Walter M. Fitch. “Toward defining the course of evolution: minimum change for a specific tree topology.” *Systematic Biol.* 20.4 (1971), 406–416.
- [177] Walter M. Fitch, Emanuel Margoliash et al. “Construction of phylogenetic trees.” *Science* 155.3760 (1967), 279–284.
- [178] Erica Flapan. *When Topology meets Chemistry: A Topological Look at Molecular Chirality*. Cambridge University Press, 2000.
- [179] S. Jane Flint et al. *Principles of Virology*. Third edition. ASM Press, 2009.
- [180] Leslie R. Foulds and Ronald L. Graham. “The Steiner problem in phylogeny is NP-complete.” *Adv. Appl. Math.* 3.1 (1982), 43–49.
- [181] Kyle R. Fowler et al. “Evolutionarily diverse determinants of meiotic DNA break and recombination landscapes across the genome.” *Genome Res.* 24.10 (2014), 1650–1664.

- [182] Christophe Fraser, William P. Hanage, and Brian G. Spratt. “Recombination and the nature of bacterial speciation.” *Science* 315.5811 (2007), 476–480.
- [183] Veronique Frattini et al. “The integrated landscape of driver genomic alterations in glioblastoma.” *Nature Genet.* 45.10 (2013), 1141–1149.
- [184] David A. Freedman. *Statistical Models: Theory and Practice*. Second edition. Cambridge University Press, 2009.
- [185] A. E. Friedman-Kien et al. “Kaposi’s sarcoma and *Pneumocystis pneumonia* among homosexual men – New York City and California.” *MMWR. Morbidity and Mortality Weekly Report* 30.25 (1981), 305–308.
- [186] S. S. Froland et al. “HIV-1 infection in a Norwegian family before 1970.” *The Lancet* 331.8598 (1988), 1344–1345.
- [187] P. Frosini. “Discrete computation of size functions.” *J. Combinatorics Inf. Syst. Sci.* 17.3–4 (1992), 232–250.
- [188] André Fujita et al. “Modeling gene expression regulatory networks with the sparse vector autoregressive model.” *BMC Syst. Biol.* 1.1 (2007), 39.
- [189] André Fujita et al. “Time-varying modeling of gene expression regulatory networks using the wavelet dynamic vector autoregressive method.” *Bioinformatics* 23.13 (2007), 1623–1630.
- [190] Robert C. Gallo et al. “Frequent detection and isolation of cytopathic retroviruses (HTLV-III) from patients with AIDS and at risk for AIDS.” *Science* 224.4648 (1984), 500–503.
- [191] Rongbao Gao et al. “Human infection with a novel avian-origin influenza A (H7N9) virus.” *N. Engl. J. Med.* 368.20 (2013), 1888–1897. doi: 10.1056/NEJMoa1304459.
- [192] Charles Gawad, Winston Koh, and Stephen R. Quake. “Single-cell genome sequencing: current state of the science.” *Nature Rev. Genet.* 17.3 (2016), 175–188.
- [193] Robert Ghrist. “Barcodes: the persistent topology of data.” *Bull. Am. Math. Soc.* 45 (2008), 61–75.
- [194] Robert Ghrist. *Elementary Applied Topology*. Createspace, 2014.
- [195] Alison L. Gibbs and Francis Edward Su. “On choosing and bounding probability metrics.” *Int. Stat. Rev.* 70.3 (2002), 419–435. doi: 10.1111/j.1751-5823.2002.tb00178.x.
- [196] Anna C. Gilbert and Lalit Jain. “If it ain’t broke, don’t fix it: sparse metric repair.” *Allerton Conf. on Communication, Control, and Computing*. 2017.
- [197] Brian J. Gill et al. “MRI-localized biopsies reveal subtype-specific differences in molecular and cellular composition at the margins of glioblastoma.” *Proc. Natl. Acad. Sci. USA* 111.34 (2014), 12550–12555.
- [198] John H. Gillespie. *Population Genetics: A Concise Guide*. JHU Press, 2010.
- [199] Janet R. Gilsdorf, Carl F. Marrs, and Betsy Foxman. “Haemophilus influenzae: genetic variability and natural selection to identify virulence factors.” *Infect. Immun.* 72.5 (2004), 2457–2461.
- [200] M. Ginsberg et al. “Swine influenza A (H1N1) infection in two children – Southern California, March–April 2009.” *MMWR. Morbidity and Mortality Weekly Report* 58.15 (2009), 400–402.
- [201] Chad Giusti et al. “Clique topology reveals intrinsic geometric structure in neural correlations.” *Proc. Natl. Acad. Sci. USA* 112.44 (2015), 13455–13460.
- [202] Earl F. Glynn, Jie Chen, and Arcady R. Mushegian. “Detecting periodic patterns in unevenly spaced gene expression time series using Lomb–Scargle periodograms.” *Bioinformatics* 22.3 (2005), 310–316.

- [203] Mitchell Goldfarb et al. “Isolation and preliminary characterization of a human transforming gene from T 24 bladder carcinoma cells.” *Nature* 296.5856 (1982), 404–409.
- [204] Oded Goldreich and Dana Ron. “Property testing in bounded degree graphs.” *Proceedings of the Twenty-ninth Annual ACM Symposium on Theory of Computing. STOC ’97. El Paso, Texas, USA*, pp. 406–415. ACM, 1997.
- [205] P. Grassberger and I. Procaccia. “Measuring the strangeness of strange attractors.” *Physica D* 9 (1983), 170–189.
- [206] Benjamin D. Greenbaum et al. “Viral reassortment as an information exchange between viral segments.” *Proc. Natl. Acad. Sci. USA* 109.9 (2012), 3341–3346.
- [207] Andreas Greven, Peter Pfaffelhuber, and Anita Winter. “Convergence in distribution of random metric measure spaces ( $\Lambda$ -coalescent measure trees).” *Prob. Theor. Relat. Fields* 145.1 (2009), 285–322.
- [208] Robert C. Griffiths and Paul Marjoram. “An ancestral recombination graph.” *Inst. Math. Appl.* 87 (1997), 257.
- [209] Robert C. Griffiths and Paul Marjoram. “Ancestral inference from samples of DNA sequences with recombination.” *J. Comput. Biol.* 3.4 (1996), 479–502.
- [210] N. R. Grist. “Pandemic influenza 1918.” *Br. Med. J.* 2.6205 (1979), 1632–1633.
- [211] Ann Griswold. “Genome packaging in prokaryotes: the circular chromosome of *E. coli*.” *Nature Educ.* 1.1 (2008), 57.
- [212] Mikhail Gromov. *Metric Structures for Riemannian and Non-Riemannian Spaces*. Ed. by J. LaFontaine and P. Pansu. Modern Birkhauser Classics. Birkhauser, Boston, MA, 2007.
- [213] Mikhail Gromov. “Hyperbolic groups.” *Essays in Group Theory*, pp. 75–263. Ed. by S. M. Gersten. Mathematical Sciences Research Institute Publications, volume 8. Springer, New York, 1987. doi: 10.1007/978-1-4613-9586-7\_3.
- [214] Dominic Grün et al. “Single-cell messenger RNA sequencing reveals rare intestinal cell types.” *Nature* 525.7568 (2015), 251–255.
- [215] Leonidas J. Guibas and Steve Oudot. “Reconstruction using witness complexes.” *Discrete Comput. Geom.* 40.3 (2008), 325–356. doi: 10.1007/s00454-008-9094-6.
- [216] Stéphane Guindon and Olivier Gascuel. “A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood.” *Systematic Biol.* 52.5 (2003), 696–704.
- [217] Stephane Guindon et al. “PHYML Online – a web server for fast maximum likelihood-based phylogenetic inference.” *Nucleic Acids Res.* 33.suppl 2 (2005), W557–W559.
- [218] Vishal Gupta, David J. Earl, and Michael W. Deem. “Quantifying influenza vaccine efficacy and antigenic distance.” *Vaccine* 24.18 (2006), 3881–3888.
- [219] Dan Gusfield. “Optimal, efficient reconstruction of root-unknown phylogenetic networks with constrained and structured recombination.” *J. Comput. Syst. Sci.* 70.3 (2005), 381–398.
- [220] Dan Gusfield. *ReCombinatorics: The Algorithmics of Ancestral Recombination Graphs and Explicit Phylogenetic Networks*. MIT Press, 2014.
- [221] Dan Gusfield, Satish Eddhu, and Charles Langley. “Optimal, efficient reconstruction of phylogenetic networks with constrained recombination.” *J. Bioinformatics Comput. Biol.* 2.01 (2004), 173–213.
- [222] Daniel A. Haber and Jeff Settleman. “Cancer: drivers and passengers.” *Nature* 446.7132 (2007), 145–146.

- [223] Laleh Haghverdi, Florian Buettner, and Fabian J. Theis. “Diffusion maps for high-dimensional single-cell analysis of differentiation data.” *Bioinformatics* 31.18 (2015), 2989–2998.
- [224] Paul R. Halmos. *Naive Set Theory*. Reprint of the 1960 edition. Undergraduate Texts in Mathematics. Springer-Verlag, New York, 1974.
- [225] Jihun Ham et al. “A kernel view of the dimensionality reduction of manifolds.” *Proceedings of the Twenty-First International Conference on Machine Learning, ICML '04, Banff, Alberta, Canada*, p. 47. ACM, 2004. doi: 10.1145/1015330.1015417.
- [226] James Douglas Hamilton. *Time Series Analysis*, volume 2. Princeton University Press, Princeton, NJ, 1994.
- [227] Douglas Hanahan and Robert A. Weinberg. “The hallmarks of cancer.” *Cell* 100.1 (2000), 57–70.
- [228] Shaun Harker et al. “Discrete Morse theoretic algorithms for computing homology of complexes and maps.” *Found. Comput. Math.* 14.1 (2014), 151–184.
- [229] John A. Hartigan. *Clustering Algorithms*. John Wiley & Sons, New York, 1975.
- [230] Daniel L. Hartl and Andrew G Clark. *Principles of Population Genetics*. Sinauer Associates, Sunderland, MA, 1997.
- [231] Masami Hasegawa, Hirohisa Kishino, and Taka-aki Yano. “Dating of the human-ape splitting by a molecular clock of mitochondrial DNA.” *J. Mol. Evol.* 22.2 (1985), 160–174.
- [232] Tamar Hashimshony et al. “CEL-Seq: single-cell RNA-Seq by multiplexed linear amplification.” *Cell Rep.* 2.3 (2012), 666–673.
- [233] Trevor Hastie, Robert Tibshirani, and Jerome Friedman. *The Elements of Statistical Learning: Data Mining, Inference and Prediction*. Second edition. Springer, 2009.
- [234] W. Keith Hastings. “Monte Carlo sampling methods using Markov chains and their applications.” *Biometrika* 57.1 (1970), 97–109.
- [235] Allen Hatcher. *Algebraic Topology*. Cambridge University Press, Cambridge, 2002.
- [236] Ingrid Hedenfalk et al. “Gene-expression profiles in hereditary breast cancer.” *N Engl. J. Med.* 344.8 (2001), 539–548.
- [237] Jotun Hein, Mikkel Schierup, and Carsten Wiuf. *Gene Genealogies, Variation and Evolution: A Primer in Coalescent Theory*. Oxford University Press, 2004.
- [238] Gregory Henselman. Eirene. <http://gregoryhenselman.org/eirene/>. 2016.
- [239] Gregory Henselman and Robert Ghrist. “Matroid filtrations and computational persistent homology.” 2016. arXiv: 1606.00199.
- [240] Sander Herfst et al. “Airborne transmission of influenza A/H5N1 virus between ferrets.” *Science* 336.6088 (2012), 1534–1541. doi: 10.1126/science.1213362.
- [241] Carlos Xavier Hernández et al. “Understanding the origins of a pandemic virus.” 2011. arXiv: 1104.4568.
- [242] Geoffrey Hinton and Sam Roweis. “Stochastic neighbor embedding.” *Proceedings of the 15th International Conference on Neural Information Processing Systems, NIPS'02, Cambridge, MA, USA*, pp. 857–864. MIT Press, 2002.
- [243] Yorio Hinuma et al. “Adult T-cell leukemia: antigen in an ATL cell line and detection of antibodies to the antigen in human sera.” *Proc. Natl. Acad. Sci. USA* 78.10 (1981), 6476–6480.
- [244] The Joint United Nations Programme on HIV/AIDS (UNAIDS). *Global AIDS Update 2016*. World Health Organization, 2016.
- [245] E. Hodis et al. “A landscape of driver mutations in melanoma.” *Cell* 150.2 (2012), 251–63. doi: 10.1016/j.cell.2012.06.024.
- [246] Edward C. Holmes. *The Evolution and Emergence of RNA Viruses*. Oxford University Press, 2009.

- [247] Susan Holmes. “Bootstrapping phylogenetic trees: theory and methods.” *Stat. Sci.* 2003), 241–255.
- [248] Susan Holmes. “Statistical approach to tests involving phylogenies.” *Mathematics of Evolution and Phylogeny*, pp. 91–120. Ed. by Olivier Gascuel. Oxford University Press, Oxford, 2005.
- [249] Hugo M. Horlings et al. “Integration of DNA copy number alterations and prognostic gene expression signatures in breast cancer patients.” *Clin. Cancer Res.* 16.2 (2010), 651–663.
- [250] Katharina T. Huber et al. “Pruned median networks: a technique for reducing the complexity of median networks.” *Mol. Phylogenet. Evol.* 19.2 (2001), 302–310.
- [251] Peter J. Huber and Elvezio M. Ronchetti. *Robust Statistics*. Second edition. Wiley Series in Probability and Statistics. Wiley, Hoboken, NJ, 2009.
- [252] Richard R. Hudson. “Generating samples under a Wright–Fisher neutral model of genetic variation.” *Bioinformatics* 18.2 (2002), 337–338.
- [253] Richard R. Hudson. “Properties of a neutral allele model with intragenic recombination.” *Theor. Population Biol.* 23.2 (1983), 183–201.
- [254] Richard R. Hudson and Norman L. Kaplan. “Statistical properties of the number of recombination events in the history of a sample of DNA sequences.” *Genetics* 111.1 (1985), 147–164.
- [255] R. R. Hudson, D. Dr Boos, and N. L. Kaplan. “A statistical test for detecting geographic subdivision.” *Mol. Biol. Evol.* 9.1 (1992), 138–151.
- [256] John P. Huelsenbeck and David M. Hillis. “Success of phylogenetic methods in the four-taxon case.” *Systematic Biol.* 42.3 (1993), 247–264.
- [257] John P. Huelsenbeck, Fredrik Ronquist et al. “MRBAYES: Bayesian inference of phylogenetic trees.” *Bioinformatics* 17.8 (2001), 754–755.
- [258] Michael E. Hughes, John B. Hogenesch, and Karl Kornacker. “JTK CYCLE: an efficient nonparametric algorithm for detecting rhythmic components in genome-scale data sets.” *J. Biol. Rhythms* 25.5 (2010), 372–380.
- [259] Devon P. Humphreys et al. “Fast estimation of recombination rates using topological data analysis.” *Genetics* 211.4 (2019), 1191–1204.
- [260] Daniel H. Huson. “SplitsTree: analyzing and visualizing evolutionary data.” *Bioinformatics* 14.1 (1998), 68–73.
- [261] Daniel H. Huson and David Bryant. “Application of phylogenetic networks in evolutionary studies.” *Mol. Biol. Evol.* 23.2 (2006), 254–267.
- [262] Daniel H. Huson, Regula Rupp, and Celine Scornavacca. *Phylogenetic Networks: Concepts, Algorithms and Applications*. Cambridge University Press, 2010.
- [263] Daniel H. Huson and Celine Scornavacca. “A survey of combinatorial methods for phylogenetic networks.” *Genome Biol. Evol.* 3 (2011), 23–35.
- [264] Daniel H. Huson and Celine Scornavacca. “Dendroscope 3: an interactive tool for rooted phylogenetic trees and networks.” *Systematic Biol.* 61.6 (2012), 1061–1067.
- [265] Francisco J. Iborra et al. “Active RNA polymerases are localized within discrete transcription ‘factories’ in human nuclei.” *J. Cell Sci.* 109.6 (1996), 1427–1436.
- [266] Masaki Imai et al. “Experimental adaptation of an influenza H5 HA confers respiratory droplet transmission to a reassortant H5 HA/H1N1 virus in ferrets.” *Nature* 486.7403 (2012), 420–428.
- [267] Ayasdi Inc. Ayasdi Iris. [www.ayasdi.com](http://www.ayasdi.com).
- [268] Ayasdi Inc. Iris. 2015. [www.ayasdi.com](http://www.ayasdi.com).

- [269] Toshihiro Ito et al. “Molecular basis for the generation in pigs of influenza A viruses with pandemic potential.” *J. Virol.* 72.9 (1998), 7367–7373.
- [270] Aniek Janssen et al. “Chromosome segregation errors as a cause of DNA damage and structural chromosome aberrations.” *Science* 333.6051 (2011), 1895–1898.
- [271] Jose A. Jarillo et al. “An *Arabidopsis* circadian clock component interacts with both CRY1 and phyB.” *Nature* 410.6827 (2001), 487–490.
- [272] Lars Juhl Jensen et al. “Co-evolution of transcriptional and post-translational cell-cycle regulation.” *Nature* 443.7111 (2006), 594–597.
- [273] Slade O. Jensen and Bruce R. Lyon. “Genetics of antimicrobial resistance in *Staphylococcus aureus*.” *Future Microbiol.* 4.5 (2009), 565–582.
- [274] Fulai Jin et al. “A high-resolution map of the three-dimensional chromatin interactome in human cells.” *Nature* 503 (2013), 290–294.
- [275] Daniel Johansson, Petter Lindgren, and Anders Berglund. “A multivariate approach applied to microarray data for identification of genes with cell cycle-coupled transcription.” *Bioinformatics* 19.4 (2003), 467–473.
- [276] Niall P. A. S. Johnson and Juergen Mueller. “Updating the accounts: global mortality of the 1918–1920 ‘Spanish’ influenza pandemic.” *Bull. Hist. Med.* 76.1 (2002), 105–115.
- [277] Keith A. Jolley and Martin C. J. Maiden. “BIGSdb: Scalable analysis of bacterial genome variation at the population level.” *BMC Bioinformatics* 11.1 (2010), 595.
- [278] Aimable R. Jonckheere. “A distribution-free k-sample test against ordered alternatives.” *Biometrika* 41.1/2 (1954), 133–145.
- [279] Thomas H. Jukes, Charles R. Cantor et al. “Evolution of protein molecules.” *Mammal. Protein Metabol.* 3.21 (1969), 132.
- [280] Tomasz Kaczynski, Konstantin Mischaikow, and Marian Mrozek. *Computational Homology*. Applied Mathematical Sciences, volume 157. Springer, 2004.
- [281] Matt Kahle. “Random simplicial complexes.” To appear in *Handbook of Discrete and Computational Geometry*. 2017.
- [282] Matthew Kahle and Elizabeth Meckes. “Limit theorems for Betti numbers of random simplicial complexes.” *Homology Homotopy Appl.* 15.1 (2013), 343–374.
- [283] Sara Kališnik Verovšek. “Tropical coordinates on the space of persistence barcodes.” *Found. Comput. Math.* (2018), 1–29.
- [284] Irving Kaplansky. *Set Theory and Metric Spaces*. Second edition. Chelsea Publishing Co., New York, 1977.
- [285] H. Karcher. “Riemannian center of mass and mollifier smoothing.” *Commun. Pure Appl. Math.* 30.5 (1977), 509–541. doi: 10.1002/cpa.3160300502.
- [286] T. Kasahara et al. “Mice with neuron-specific accumulation of mitochondrial DNA mutations show mood disorder-like phenotypes.” *Mol. Psychiatry* 11.6 (2006), 577–593.
- [287] Marcus Kaul. “HIV-1 associated dementia: update on pathological mechanisms and therapeutic approaches.” *Curr. Opin. Neurol.* 22.3 (2009), 315.
- [288] Liisa Kauppi, Alec J. Jeffreys, and Scott Keeney. “Where the crossovers are: recombination distributions in mammals.” *Nature Rev. Genet.* 5.6 (2004), 413–424.
- [289] Michael Kerber, Dmitriy Morozov, and Arnur Nigmetov. “Geometry helps to compare persistence diagrams.” *Proceedings of the Eighteenth Workshop on Algorithm Engineering and Experiments (ALENEX)*, pp. 103–112. 2016.
- [290] Michael Kerber, Dmitriy Morozov, and Arnur Nigmetov. Hera. [https://bitbucket.org/grey\\_narn/hera](https://bitbucket.org/grey_narn/hera). 2015.

- [291] Firas A. Khasawneh and Elizabeth Munch. "Utilizing topological data analysis for studying signals of time-delay systems." *Time Delay Systems: Theory, Numerics, Applications, and Experiments*, pp. 93–106. Ed. by Tamás Insperger, Tulga Ersal, and Gábor Orosz. Springer International Publishing, 2017.
- [292] Hossein Khiabanian, Vladimir Trifonov, and Raúl Rabadán. "Reassortment patterns in swine influenza viruses." *PloS One* 4.10 (2009), e7366.
- [293] Hossein Khiabanian et al. "Viral diversity and clonal evolution from unphased genomic data." *BMC Genomics* 15.Suppl 6 (2014), S17.
- [294] Pavel P. Khil et al. "Sensitive mapping of recombination hotspots using sequencing-based detection of ssDNA." *Genome Res.* 22.5 (2012), 957–965.
- [295] Bong-Rae Kim et al. "Wavelet-based functional clustering for patterns of high-dimensional dynamic gene expression." *J. Comput. Biol.* 17.8 (2010), 1067–1080.
- [296] Sunyong Kim, Seiya Imoto, and Satoru Miyano. "Dynamic Bayesian network and nonparametric regression for nonlinear modeling of gene networks from time series gene expression data." *Biosystems* 75.1 (2004), 57–65.
- [297] Edna T. Kimura et al. "High prevalence of BRAF mutations in thyroid cancer genetic evidence for constitutive activation of the RET/PTC-RAS-BRAF signaling pathway in papillary thyroid carcinoma." *Cancer Res.* 63.7 (2003), 1454–1457.
- [298] Motoo Kimura. "A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences." *J. Mol. Evol.* 16.2 (1980), 111–120.
- [299] Motoo Kimura. "Diffusion models in population genetics." *J. Appl. Probab.* 1.2 (1964), 177–232.
- [300] Motoo Kimura. *The Neutral Theory of Molecular Evolution*. Cambridge University Press, 1984.
- [301] John Frank Charles Kingman. "The coalescent." *Stochastic Process. Appl.* 13.3 (1982), 235–248.
- [302] Allon M. Klein et al. "Droplet barcoding for single-cell transcriptomics applied to embryonic stem cells." *Cell* 161.5 (2015), 1187–1201.
- [303] Nobuya Koike et al. "Transcriptional architecture and chromatin landscape of the core circadian clock in mammals." *Science* 338.6105 (2012), 349–354.
- [304] Andrei Nikolaevich Kolmogorov. "Three approaches to the definition of the concept 'quantity of information'." *Probl. Peredachi Inf.* 1.1 (1965), 3–11.
- [305] Eugene V. Koonin, Kira S. Makarova, and L. Aravind. "Horizontal gene transfer in prokaryotes: quantification and classification." *Annu. Rev. Microbiol.* 55 (2001), 709–742.
- [306] Arthur Kornberg, Tania A. Baker et al. *DNA Replication*. W. Freeman, San Francisco, CA, 1980.
- [307] Dmitry N. Kozlov. *Combinatorial Algebraic Topology*. Algorithms and Computation in Mathematics, volume 21. Springer, 2008. doi: 10.1007/978-3-540-71962-5.
- [308] Mark A. Krasnow et al. "Determination of the absolute handedness of knots and catenanes of DNA." *Nature* 304.5926 (1983), 559–560.
- [309] Martin Kreitman. "Nucleotide polymorphism at the alcohol dehydrogenase locus of *Drosophila melanogaster*." *Nature* 304, (1983), 412–417.
- [310] Susanna L. Lamers et al. "Extensive HIV-1 intra-host recombination is common in tissues with abnormal histopathology." *PLoS One* 4.3 (2009), e5065.
- [311] Susanna L. Lamers et al. "Human immunodeficiency virus-1 evolutionary patterns associated with pathogenic processes in the brain." *J. Neurovirol.* 16.3 (2010), 230–241.

- [312] Sangeet Lamichhaney et al. “Evolution of Darwin’s finches and their beaks revealed by genome sequencing.” *Nature* 518.7539 (2015), 371–375.
- [313] D. P. Lane and L. V. Crawford. “T antigen is bound to a host protein in SY40-transformed cells.” *Nature* 278 (1979), 261–263.
- [314] Serge Lang. *Undergraduate Algebra*. Undergraduate Texts in Mathematics. Springer, 2005.
- [315] J. Latschev. “Vietoris-Rips complexes of metric spaces near a closed Riemannian manifold.” *Arch. Math.* 77.6 (2001), 522–528.
- [316] Michael S. Lawrence et al. “Mutational heterogeneity in cancer and the search for new cancer associated genes.” *Nature* 499.7457 (2013), 214–218.
- [317] Tung B. K. Le et al. “High-resolution mapping of the spatial organization of a bacterial chromosome.” *Science* 342.6159 (2013), 731–734.
- [318] Joshua Lederberg and Edward L. Tatum. “Gene recombination in *Escherichia coli*.” *Nature* 158 (1946), 558.
- [319] Daniel D. Lee and H. Sebastian Seung. “Algorithms for non-negative matrix factorization.” *Advances in Neural Information Processing Systems*, volume 13, pp. 556–562. Ed. by T. K. Leen, T. G. Dietterich, and V. Tresp. MIT Press, 2001.
- [320] Jin-Ku Lee et al. “Spatiotemporal genomic architecture informs precision oncology in glioblastoma.” *Nature Genet.* 49.4 (2017), 594–599.
- [321] Jin-Ku Lee et al. “Pharmacogenomic landscape of patient-derived tumor cells informs precision oncology therapy.” *Nature Genet.* 50.10 (2018), 1399–1411.
- [322] Christina Leslie et al. “Mismatch string kernels for SVM protein classification.” *Proceedings of the 15th International Conference on Neural Information Processing Systems. NIPS’02. Cambridge, MA, USA*, pp. 1441–1448. MIT Press, 2002.
- [323] Michael Lesnick, Raúl Rabadán, and Daniel Rosenbloom. “Quantifying genetic innovation: mathematical foundations for the topological study of reticulate evolution.” 2018. arXiv: 1804.01398 [math.AT].
- [324] Michael Lesnick and Mathew Wright. Rivet. <http://rivet.online/>. 2015.
- [325] Michael Lesnick and Matthew Wright. “Interactive visualization of 2-D persistence modules.” 2015. arXiv: 1512.00180.
- [326] Mike Lesnick. *Studying the Shape of Data Using Topology*. IAS Letter, 2013.
- [327] Elizaveta Levina and Peter J. Bickel. “Maximum likelihood estimation of intrinsic dimension.” *Advances in Neural Information Processing Systems*, volume 17, pp. 777–784. Ed. by L. K. Saul, Y. Weiss, and L. Bottou. MIT Press, 2005.
- [328] Arnold J. Levine. *Viruses*. Scientific American Library, New York, 1992.
- [329] Dan Levy and Lior Pachter. “The neighbor-net algorithm.” *Adv. Appl. Math.* 47.2 (2011), 240–258.
- [330] E. Lieberman-Aiden et al. “Comprehensive mapping of long-range interactions reveals folding principles of the human genome.” *Science* 326.5950 (2009), 289–293.
- [331] Daniel I. H. Linzer and Arnold J. Levine. “Characterization of a 54K dalton cellular SV40 tumor antigen present in SV40-transformed cells and uninfected embryonal carcinoma cells.” *Cell* 17.1 (1979), 43–52.
- [332] A. V. Little, M. Maggioni, and L. Rosasco. Multiscale geometric methods for data sets I: multiscale SVD, noise, and curvature. MIT-CSAIL-TR-2012-029. 2012.
- [333] Nicholas R. Lomb. “Least-squares frequency analysis of unequally spaced data.” *Astrophys. Space Sci.* 39.2 (1976), 447–462.
- [334] P. Y. Lum et al. “Extracting insights from the shape of complex data using topology.” *Sci. Rep.* 3 (2013). doi: 10.1038/srep01236.

- [335] Laurens J. P. van der Maaten, Eric O. Postma, and H. Jaap van den Herik. “Dimensionality reduction: a comparative review.” *J. Mach. Learn. Res.* 10.1-41 (2009), 66–71.
- [336] L. J. P. van der Maaten and G. E. Hinton. “Visualizing high-dimensional data using t-SNE.” *J. Mach. Learn. Res.* 9 (2008), 2579–2605.
- [337] Saunders MacLane. *Categories for the Working Mathematician*. Graduate Texts in Mathematics, volume 5. Springer-Verlag, New York, 1971.
- [338] Evan Z. Macosko et al. “Highly parallel genome-wide expression profiling of individual cells using nanoliter droplets.” *Cell* 161.5 (2015), 1202–1214.
- [339] Robert MacPherson and Benjamin Schweinhart. “Measuring shape with topology.” *J. Math. Phys.* 53.7 (2012), 073516.
- [340] Eugenio Marco et al. “Bifurcation analysis of single-cell gene expression data reveals epigenetic landscape.” *Proc. Natl. Acad. Sci. USA* 111.52 (2014), E5643–E5650.
- [341] Clément Maria et al. “The Gudhi Library: simplicial complexes and persistent homology.” *Mathematical Software – ICMS 2014: Proceedings of the Fourth International Congress, Seoul, South Korea, August 5–9, 2014*, pp. 167–174. Ed. by Hoon Hong and Chee Yap. Springer, Berlin, 2014.
- [342] J. P. May. *A Concise Course in Algebraic Topology*. Chicago Lectures in Mathematics. University of Chicago Press, Chicago, IL, 1999.
- [343] Roger McLendon et al. “Comprehensive genomic characterization defines human glioblastoma genes and core pathways.” *Nature* 455.7216 (2008), 1061–1068.
- [344] Gilean A. T. McVean et al. “The fine-scale structure of recombination rate variation in the human genome.” *Science* 304.5670 (2004), 581–584.
- [345] Emma Meats et al. “Characterization of encapsulated and nonencapsulated *Haemophilus influenzae* and determination of phylogenetic relationships by multilocus sequence typing.” *J. Clin. Microbiol.* 41.4 (2003), 1623–1636.
- [346] Facundo Mémoli. “A spectral notion of Gromov-Wasserstein distances and related methods.” *Appl. Comput. Math.* 30 (2011), 363–401. doi: 10.1016/j.apm.2011.07.001.
- [347] Facundo Mémoli. “Gromov-Wasserstein distances and the metric approach to object matching.” *Found. Comput. Math.* (2011), 1–71. doi: 10.1007/s10208-011-9093-5.
- [348] Ignacio Mena et al. “Origins of the 2009 H1N1 influenza pandemic in swine in Mexico.” *eLife* (2016), e16777.
- [349] Carl D. Meyer (editor). *Matrix Analysis and Applied Linear Algebra*. Society for Industrial and Applied Mathematics, Philadelphia, PA, 2000.
- [350] Folker Meyer, Ross Overbeek, and Alex Rodriguez. “FIGfams: yet another set of protein families.” *Nucleic Acids Res.* 37.20 (2009), 6643–6654.
- [351] Radu Mihaescu, Dan Levy, and Lior Pachter. “Why neighbor-joining works.” *Algorithmica* 54.1 (2009), 1–24.
- [352] Yuriy Mileyko, Sayan Mukherjee, and John Harer. “Probability measures on the space of persistence diagrams.” *Inverse Probl.* 27.12 (2011), 124007.
- [353] Lance D. Miller et al. “An expression signature for p53 status in human breast cancer predicts mutation status, transcriptional effects, and patient survival.” *Proc. Natl. Acad. Sci. USA* 102.38 (2005), 13550–13555.
- [354] J. Milnor. *Morse Theory. Based on lecture notes by M. Spivak and R. Wells*. Annals of Mathematics Studies, No. 51. Princeton University Press, Princeton, NJ, 1963.
- [355] John W. Milnor. *Topology from the Differentiable Viewpoint. Based on notes by David W. Weaver*. Princeton Landmarks in Mathematics. Revised reprint of the 1965 original. Princeton University Press, Princeton, NJ, 1997.

- [356] Mark J. Minichiello and Richard Durbin. “Mapping trait loci by use of inferred ancestral recombination graphs.” *Am. J. Human Genet.* 79.5 (2006), 910–922.
- [357] Anthea Monod et al. “Tropical sufficient statistics for persistent homology.” 2017. arXiv: 1709.02647.
- [358] Patrick Alfred Pierce Moran. “A general theory of the distribution of gene frequencies. I. Overlapping generations.” *Proc. R. Soc. London, Ser. B* 149.934 (1958), 102–112.
- [359] Thomas Hunt Morgan. *A Critique of the Theory of Evolution*. Princeton University Press, 1916.
- [360] Dmitriy Morozov. Dionysus. 2017. [www.mrzv.org/software/dionysus2/](http://www.mrzv.org/software/dionysus2/).
- [361] Dmitriy Morozov. *Persistence algorithm takes cubic time in the worst case*. 2005.
- [362] David A. Morrison. *Introduction to Phylogenetic Networks*. RJR Productions, 2011.
- [363] Siddhartha Mukherjee. *The Emperor of all Maladies: A Biography of Cancer*. Simon and Schuster, 2011.
- [364] Hermann J. Muller. “The production of mutations by X-rays.” *Proc. Natl. Acad. Sci. USA* 14.9 (1928), 714.
- [365] Daniel Müllner and Aravindakshan Babu. Python mapper. 2016. <http://danifold.net/mapper/>.
- [366] Bei Munch and Elizabeth Wang. “Convergence between categorical representations of Reeb space and Mapper.” *32nd International Symposium on Computational Geometry, SoCG 2016*, pp. 53:1–53:16. Ed. by Sándor Fekete and Anna Lubiw. Leibniz International Proceedings in Informatics (LIPIcs), volume 51. Leibniz-Zentrum fuer Informatik, Dagstuhl, 2016. doi: 10.4230/LIPIcs.SoCG.2016.53.
- [367] Elizabeth Munch et al. “Probabilistic Fréchet means and statistics on vineyards.” 2013. arXiv: 1307.6530.
- [368] James R. Munkres. *Elements of Algebraic Topology*. Addison-Wesley, Menlo Park, CA, 1984.
- [369] James R. Munkres. *Topology: A First Course*. Prentice-Hall, Englewood Cliffs, NJ, 1975.
- [370] Simon R. Myers and Robert C. Griffiths. “Bounds on the minimum number of recombination events in a sample history.” *Genetics* 163.1 (2003), 375–394.
- [371] Simon Myers et al. “A fine-scale map of recombination rates and hotspots across the human genome.” *Science* 310.5746 (2005), 321–324.
- [372] Simon Myers et al. “Drive against hotspot motifs in primates implicates the PRDM9 gene in meiotic recombination.” *Science* 327.5967 (2010), 876–879.
- [373] Peter Mysling, Soren Hauberg, and Kim S. Pedersen. “An empirical study on the performance of spectral manifold learning techniques.” *Artificial Neural Networks and Machine Learning – ICANN 2011*, pp. 347–354. Lecture Notes in Computer Science, volume 6791. Springer, Berlin, 2011.
- [374] Takashi Nagano et al. “Single-cell Hi-C for genome-wide detection of chromatin interactions that occur simultaneously in a single cell.” *Nature Protocols* 10.12 (2015), 1986–2003.
- [375] Takashi Nagano et al. “Single-cell Hi-C reveals cell-to-cell variability in chromosome structure.” *Nature* 502.7469 (2013), 59–64.
- [376] Vudit Nanda. Perseus. 2017. <http://people.maths.ox.ac.uk/nanda/perseus/index.html>.
- [377] Nicholas E. Navin. “The first five years of single-cell cancer genomics and beyond.” *Genome Res.* 25.10 (2015), 1499–1507.
- [378] Nicholas Navin et al. “Tumour evolution inferred by single-cell sequencing.” *Nature* 472.7341 (2011), 90–94.

- [379] Saul B. Needleman and Christian D. Wunsch. “A general method applicable to the search for similarities in the amino acid sequence of two proteins.” *J. Mol. Biol.* 48.3 (1970), 443–453.
- [380] Masatoshi Nei and Sudhir Kumar. *Molecular Evolution and Phylogenetics*. Oxford University Press, 2000.
- [381] Cancer Genome Atlas Research Network et al. “Comprehensive, integrative genomic analysis of diffuse lower-grade gliomas.” *N. Engl. J. Med.* 372 (2015), 2481–2498.
- [382] Harold C. Neu. “The crisis in antibiotic resistance.” *Science* 257.5073 (1992), 1064–1073.
- [383] Monica Nicolau, Arnold J. Levine, and Gunnar Carlsson. “Topology based data analysis identifies a subgroup of breast cancers with a unique mutational profile and excellent survival.” *Proc. Natl. Acad. Sci. USA* 108.17 (2011), 7265–7270.
- [384] Partha Niyogi, Stephen Smale, and Shmuel Weinberger. “Finding the homology of submanifolds with high confidence from random samples.” *Discrete Comput. Geom.* 39.1–3 (2008), 419–441.
- [385] Takeshi Noda et al. “Architecture of ribonucleoprotein complexes in influenza A virus particles.” *Nature* 439.7075 (2006), 490–492.
- [386] C. O. Nordling. “A new theory on the cancer-inducing mechanism.” *Br. J. Cancer* 7.1 (1953), 68.
- [387] Peter C. Nowell. “A minute chromosome in human granulocytic leukemia.” *Science* 132 (1960), 1497–1501.
- [388] Peter C. Nowell. “The clonal evolution of tumor cell populations.” *Science* 194.4260 (1976), 23–28.
- [389] Howard Ochman, Jeffrey G. Lawrence, and Eduardo A. Groisman. “Lateral gene transfer and the nature of bacterial innovation.” *Nature* 405.6784 (2000), 299–304.
- [390] John O’Keefe and Jonathan Dostrovsky. “The hippocampus as a spatial map. Preliminary evidence from unit activity in the freely-moving rat.” *Brain Res.* 34.1 (1971), 171–175.
- [391] World Health Organization. *Antimicrobial Resistance: global report on surveillance 2014*. Technical Report. World Health Organization, 2014.
- [392] Steve Y. Oudot. *Persistence Theory – From Quiver Representations to Data Analysis*. Mathematical Surveys and Monographs, volume 209. American Mathematical Society, 2015.
- [393] Steve Y. Oudot and Donald R. Sheehy. “Zigzag zoology: rips zigzags for homology inference.” *Proceedings of the 29th Annual Symposium on Computational Geometry*, pp. 387–396. 2013.
- [394] Megan Owen and J. Scott Provan. “A fast algorithm for computing geodesic distances in tree space.” *IEEE/ACM Trans. Comput. Biol. Bioinformatics* 8.1 (2011), 2–13.
- [395] L. Pachter and B. Sturmfels. *Algebraic Statistics for Computational Biology*. Cambridge University Press, New York, 2005.
- [396] Kenneth Paigen and Petko Petkov. “Mammalian recombination hot spots: properties, control and evolution.” *Nature Rev. Genet.* 11.3 (2010), 221–233.
- [397] Jing Pan et al. “A hierarchical combination of factors shapes the genome-wide topography of yeast meiotic recombination initiation.” *Cell* 144.5 (2011), 719–731.
- [398] Luis F. Parada et al. “Human EJ bladder carcinoma oncogene is homologue of Harvey sarcoma virus ras gene.” *Nature* 297.5866 (1982), 474–478.

- [399] Donald Maxwell Parkin. “The global health burden of infection-associated cancers in the year 2002.” *Int. J. Cancer* 118.12 (2006), 3030–3044.
- [400] Emil D. Parvanov, Petko M. Petkov, and Kenneth Paigen. “Prdm9 controls activation of mammalian recombination hotspots.” *Science* 327.5967 (2010), 835–835.
- [401] Anoop P. Patel et al. “Single-cell RNA-seq highlights intratumoral heterogeneity in primary glioblastoma.” *Science* 344.6190 (2014), 1396–1401.
- [402] Paul Pearson. TDAmapper. 2017. <https://cran.r-project.org/web/packages/TDAmapper/README.html>.
- [403] M. Penrose. *Random Geometric Graphs*. Oxford Studies in Probability. Oxford University Press, 2003.
- [404] Jose A. Perea and John Harer. “Sliding windows and persistence: an application of topological methods to signal analysis.” *Found. Comput. Math.* 15.3 (2015), 799–838.
- [405] Jose A. Perea et al. “SW1PerS: sliding windows and 1-persistence scoring; discovering periodicity in gene expression time series data.” *BMC Bioinformatics* 16.1 (2015), 257.
- [406] K. Petren et al. “Comparative landscape genetics and the adaptive radiation of Darwin’s finches: the role of peripheral isolation.” *Mol. Ecol.* 14.10 (2005), 2943–2957.
- [407] Giovanni Petri et al. “Homological scaffolds of brain functional networks.” *J. R. Soc. Interface* 11.101 (2014), 20140873.
- [408] Sophie Petropoulos et al. “Single-Cell RNA-Seq reveals lineage and X chromosome dynamics in human preimplantation embryos.” *Cell* 165.4 (2016), 1012–1026.
- [409] Brett E. Pickett and Elliot J. Lefkowitz. “Recombination in West Nile Virus: minimal contribution to genomic diversity.” *Virol. J.* 6.1 (2009), 1.
- [410] Peter Piot et al. “Acquired immunodeficiency syndrome in a heterosexual population in Zaire.” *The Lancet* 324.8394 (1984), 65–69.
- [411] Joshua B. Plotkin and Hunter B. Fraser. “Assessing the determinants of evolutionary rates in the presence of noise.” *Mol. Biol. Evol.* 24.5 (2007), 1113–1121.
- [412] Dimitris N. Politis and Joseph P. Romano. “Large sample confidence regions based on subsamples under minimal assumptions.” *Ann. Stat.* 22.4 (1994), 2031–2050. doi: 10.1214/aos/1176325770.
- [413] M. Porter et al. “A roadmap for the computation of persistent homology.” *EPJ Data Sci.* 6.17 (2017).
- [414] David Posada. “Evaluation of methods for detecting recombination from DNA sequences: empirical data.” *Mol. Biol. Evol.* 19.5 (2002), 708–717.
- [415] Lisa Postow et al. “Topological domain structure of the *Escherichia coli* chromosome.” *Genes Dev.* 18.14 (2004), 1766–1779.
- [416] Raúl Rabadán, Arnold J. Levine, and Michael Krasnitz. “Non-random reassortment in human influenza A viruses.” *Influenza Other Respir. Viruses* 2.1 (2008), 9–22.
- [417] Raúl Rabadán and Harlan Robins. “Evolution of the influenza A virus: some new advances.” *Evol. Bioinformatics Online* 3 (2007), 299.
- [418] Marco F. Ramoni, Paola Sebastiani, and Isaac S. Kohane. “Cluster analysis of gene expression dynamics.” *Proc. Natl. Acad. Sci. USA* 99.14 (2002), 9121–9126.
- [419] Daniel Ransköld et al. “Full-length mRNA-Seq from single-cell levels of RNA and individual circulating tumor cells.” *Nature Biotechnol.* 30.8 (2012), 777–782.
- [420] Suhas S. P. Rao et al. “A 3D map of the human genome at kilobase resolution reveals principles of chromatin looping.” *Cell* 159.7 (2014), 1665–1680.
- [421] Matthew D. Rasmussen et al. “Genome-wide inference of ancestral recombination graphs.” *PLoS Genet.* 10.5 (2014), e1004342.

- [422] Roberto Refinetti, Germaine Cornélissen, and Franz Halberg. “Procedures for numerical analysis of circadian rhythms.” *Biol. Rhythm Res.* 38.4 (2007), 275–325.
- [423] Ann H. Reid et al. “Origin and evolution of the 1918 ‘Spanish’ influenza virus hemagglutinin gene.” *Proc. Natl. Acad. Sci. USA* 96.4 (1999), 1651–1656.
- [424] Michael W. Reimann et al. “Cliques of neurons bound into cavities provide a missing link between structure and function.” *Front. Comput. Neurosci.* 11 (2017), 48.
- [425] J. Reininghaus et al. “A stable multi-scale kernel for topological machine learning.” *Proceedings of the 2015 IEEE Conference on Computer Vision and Pattern Recognition (CVPR)*, pp. 4741–4748. IEEE, 2015.
- [426] Rebeca Rico-Hesse. “Microevolution and virulence of dengue viruses.” *Adv. Virus Res.* 59 (2003), 315–341.
- [427] Emily Riehl. Categorical Homotopy Theory. New Mathematical Monographs, volume 24. Cambridge University Press, Cambridge, 2014.
- [428] Emily Riehl. *Category Theory in Context*. Aurora: Modern Math Originals. Dover Publications, 2016.
- [429] Philippe Rigollet and Régis Vert. “Optimal rates for plug-in estimators of density level sets.” *Bernoulli* 15.4 (2009), 1154–1178. doi: 10.3150/09-BEJ184.
- [430] Christian Rinke et al. “Insights into the phylogeny and coding potential of microbial dark matter.” *Nature* 499.7459 (2013), 431–437.
- [431] Abbas H. Rizvi et al. “Single-cell topological RNA-seq analysis reveals insights into cellular differentiation and development.” *Nature Biotechnol.* 35.6 (2017), 551–560.
- [432] David L. Robertson, Beatrice H. Hahn, and Paul M. Sharp. “Recombination in AIDS viruses.” *J. Mol. Evol.* 40.3 (1995), 249–259.
- [433] Vanessa Robins. “Toward computing homology from finite approximations.” *Topology Proc.* 24 (1999), 503–532.
- [434] Mark D. Robinson and Alicia Oshlack. “A scaling normalization method for differential expression analysis of RNA-seq data.” *Genome Biol.* 11.3 (2010), R25.
- [435] Holger Rohde et al. “Open-source genomic analysis of shiga-toxin-producing *E. coli* O104:H4.” *N. Engl. J. Med.* 365.8 (2011), 718–724.
- [436] Fredrik Ronquist and John P. Huelsenbeck. “MrBayes 3: Bayesian phylogenetic inference under mixed models.” *Bioinformatics* 19.12 (2003), 1572–1574.
- [437] Peyton Rous. “A sarcoma of the fowl transmissible by an agent separable from the tumor cells.” *J. Exp. Med.* 13.4 (1911), 397–411.
- [438] Peyton Rous. “A transmissible avian neoplasm (sarcoma of the common fowl)” *J. Exp. Med.* 12.5 (1910), 696–705.
- [439] S. Roweis and L. Saul. “Nonlinear dimensionality reduction by locally linear embedding.” *Science* 290.5500 (2000), 2323–2326.
- [440] Walter Rudin. *Principles of Mathematical Analysis*. Third edition. International Series in Pure and Applied Mathematics. McGraw-Hill, New York, 1976.
- [441] T. Ruf. “The Lomb-Scargle periodogram in biological rhythm research: analysis of incomplete and unequally spaced time-series.” *Biol. Rhythm Res.* 30.2 (1999), 178–201.
- [442] Naruya Saitou and Masatoshi Nei. “The neighbor-joining method: a new method for reconstructing phylogenetic trees.” *Mol. Biol. Evol.* 4.4 (1987), 406–425.
- [443] Marco Salemi, Philippe Lemey, and Anne-Mieke Vandamme. *The Phylogenetic Handbook: A Practical Approach to Phylogenetic Analysis and Hypothesis Testing*. Cambridge University Press, 2009.

- [444] Eugenio Santos et al. “T24 human bladder carcinoma oncogene is an activated form of the normal human homologue of BALB-and Harvey-MSV transforming genes.” *Nature* 298 (1982), 343–347.
- [445] Rahul Satija et al. “Spatial reconstruction of single-cell gene expression data.” *Nature Biotechnol.* 33.5 (2015), 495–502.
- [446] Joao Ricardo Sato et al. “A method to produce evolving functional connectivity maps during the course of an fMRI experiment using wavelet-based time-varying Granger causality.” *Neuroimage* 31.1 (2006), 187–196.
- [447] Nathaniel Saul and Hendrik Jacob van Veen. “MLWave/kepler-mapper: 186f.” 2017. doi: 10.5281/zenodo.1054444.
- [448] Jeffrey D Scargle. “Studies in astronomical time series analysis. II – Statistical aspects of spectral analysis of unevenly spaced data.” *Astrophys. J.* 263 (1982), 835–853.
- [449] Benjamin Schweinhart. *Statistical Topology of Embedded Graphs*. PhD thesis. Princeton University Press, 2015.
- [450] Lars Seemann, Jason Shulman, and Gemunu H. Gunaratne. “A robust topology-based algorithm for gene expression profiling.” *ISRN Bioinformatics* 2012 (2012), 381023.
- [451] Stefan Semrau and Alexander van Oudenaarden. “Studying lineage decision-making in vitro: emerging concepts and novel tools.” *Annu. Rev. Cell Dev. Biol.* 31 (2015), 317–345.
- [452] Manu Setty et al. “Wishbone identifies bifurcating developmental trajectories from single-cell data.” *Nature Biotechnol.* 34.6 (2016), 637–645.
- [453] Paul M. Sharp and Beatrice H. Hahn. “Origins of HIV and the AIDS pandemic.” *Cold Spring Harbor Persp. Med.* 1.1 (2011), a006841.
- [454] Ann M. Sheehy, Nathan C. Gaddis, and Michael H. Malim. “The antiretroviral enzyme APOBEC3G is degraded by the proteasome in response to HIV-1 Vif.” *Nature Med.* 9.11 (2003), 1404–1407.
- [455] Donald R. Sheehy. “Linear-size approximations to the Vietoris-Rips filtration.” *Discrete Comput. Geom.* 49.4 (2013), 778–796.
- [456] Chiaho Shih and Robert A. Weinberg. “Isolation of a transforming sequence from a human bladder carcinoma cell line.” *Cell* 29.1 (1982), 161–169.
- [457] Rebecca Siegel et al. “Cancer statistics, 2014.” *CA Cancer J. Clin.* 64.1 (2014), 9–29. doi: 10.3322/caac.21208.
- [458] Vin de Silva and Gunnar Carlsson. “Topological estimation using witness complexes.” *Proceedings of the First Eurographics Conference on Point-Based Graphics* , pp. 157–166. Ed. by Marc Alex et al. Eurographics Association, Zurich, 2004.
- [459] Vin de Silva, Elizabeth Munch, and Amit Patel. “Categorified Reeb graphs.” *Discrete Comput. Geom.* 55.4 (2016), 854–906. doi: 10.1007/s00454-016-9763-9.
- [460] Vin de Silva and Joshua B. Tenenbaum. “Global versus local methods in nonlinear dimensionality reduction.” *Advances in Neural Information Processing Systems*, volume 15, pp. 705–712. MIT Press, 2002.
- [461] Devendra Singh et al. “Transforming fusions of FGFR and TACC genes in human glioblastoma.” *Science* 337.6099 (2012), 1231–1235. doi: 10.1126/science.1220834.
- [462] Gurjeet Singh, Facundo Mémoli, and Gunnar Carlsson. “Topological methods for the analysis of high dimensional data sets and 3d object recognition.” *Eurographics Symposium on Point-Based Graphics*, pp. 91–100. The Eurographics Association, 2007.

- [463] Gurjeet Singh et al. “Topological analysis of population activity in visual cortex.” *J. Vision* 8.8 (2008), 11–11.
- [464] Ann Sizemore et al. “Closures and cavities in the human connectome.” 2016. arXiv: 1608.03520 (2016).
- [465] J. Skryzalin and G. Carlsson. “Numeric invariants from multidimensional persistence.” *J. Appl. Comput. Topology* 1.1 (2017), 89–119.
- [466] Fatima Smagulova et al. “Genome-wide analysis reveals novel molecular features of mouse recombination hotspots.” *Nature* 472.7343 (2011), 375–378.
- [467] Derek J. Smith et al. “Mapping the antigenic and genetic evolution of influenza virus.” *Science* 305.5682 (2004), 371–376.
- [468] Temple F. Smith and Michael S. Waterman. “Identification of common molecular subsequences.” *J. Mol. Biol.* 147.1 (1981), 195–197.
- [469] Gordon K. Smyth. “Limma: linear models for microarray data.” *Bioinformatics and Computational Biology Solutions using R and Bioconductor*, pp. 397–420. Springer, 2005.
- [470] Peter H. A. Sneath, Michael J. Sackin, and Richard P. Ambler. “Detecting evolutionary incompatibilities from protein sequences.” *Systematic Biol.* 24.3 (1975), 311–332.
- [471] Alexandra Snyder et al. “Genetic basis for clinical response to CTLA-4 blockade in melanoma.” *N. Engl. J. Med.* 371.23 (2014), 2189–2199.
- [472] American Cancer Society. *Cancer Facts and Figures 2015*. American Cancer Society, Atlanta, GA, 2015.
- [473] Ray J. Solomonoff. “A formal theory of inductive inference. Part II.” *Inf. Control* 7.2 (1964), 224–254.
- [474] A. Solovyov et al. “Cluster analysis of the origins of the new influenza A (H1N1) virus.” *Euro Surveill.* 14.21 (2009), 19224.
- [475] Jiuzhou Z Song et al. “The wavelet-based cluster analysis for temporal gene expression data.” *EURASIP J. Bioinformatics Syst. Biol.* 2007 (2007), 2–2.
- [476] Yun S. Song and Jotun Hein. “Constructing minimal ancestral recombination graphs.” *J. Comput. Biol.* 12.2 (2005), 147–169. doi: 10.1089/cmb.2005.12.147.
- [477] Yun S. Song, Yufeng Wu, and Dan Gusfield. “Efficient computation of close lower and upper bounds on the minimum number of recombinations in biological sequence evolution.” *Bioinformatics* 21.suppl 1 (2005), i413–i422.
- [478] Andrea Sottoriva et al. “Intratumor heterogeneity in human glioblastoma reflects cancer evolutionary dynamics.” *Proc. Natl. Acad. Sci. USA* 110.10 (2013), 4009–4014.
- [479] David Speyer and Bernd Sturmfels. “The tropical grassmannian.” *Adv. Geom.* 4.3 (2004), 389–411.
- [480] David I. Spivak. *Category Theory for the Sciences*. MIT Press, 2014.
- [481] B. St. Thomas et al. “Learning subspaces of different dimensions.” 2014. arXiv: 1404.6841.
- [482] Alexandros Stamatakis. “RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models.” *Bioinformatics* 22.21 (2006), 2688–2690.
- [483] Oliver Stegle, Sarah A. Teichmann, and John C. Marioni. “Computational and analytical challenges in single-cell transcriptomics.” *Nature Rev. Genet.* 16.3 (2015), 133–145.
- [484] Dominique Stehelin et al. “DNA related to the transforming gene(s) of avian sarcoma viruses is present in normal avian DNA.” *Nature* 260 (1976), 170–173.

- [485] J. Claiborne Stephens. “Statistical methods of DNA sequence analysis: detection of intragenic recombination or gene conversion.” *Mol. Biol. Evol.* 2.6 (1985), 539–556.
- [486] Tim J. Stevens et al. “3D structures of individual mammalian genomes studied by single-cell Hi-C.” *Nature* 544.7648 (2017), 59–64.
- [487] Karl-Theodor Sturm. “Probability measures on metric spaces of nonpositive curvature.” *Heat Kernels and Analysis on Manifolds, Graphs, and Metric Spaces*. Contemporary Mathematics, volume 338. American Mathematical Society, 2003.
- [488] Curtis A. Suttle. “Marine viruses major players in the global ecosystem.” *Nature Rev. Microbiol.* 5.10 (2007), 801–812.
- [489] Andrzej Szymczak et al. “Coronary vessel trees from 3D imagery: a topological approach.” *Med. Image Anal.* 10.4 (2006), 548–559.
- [490] Andrew Tausz, Mikael Vejdemo-Johansson, and Henry Adams. “JavaPlex: a research software package for persistent (co)homology.” *Proceedings of ICMS 2014*, pp. 129–136. Ed. by Han Hong and Chee Yap. Lecture Notes in Computer Science, volume 8592. Springer, 2014.
- [491] Dane Taylor et al. “Topological data analysis of contagion maps for examining spreading processes on networks.” *Nature Commun.* 6 (2015), 7723.
- [492] H. M. Temin and S. Mizutani. “RNA-dependent DNA polymerase in virions of Rous sarcoma virus.” *Nature* 226 (1970), 1211–1213.
- [493] Howard M. Temin. “The effects of actinomycin D on growth of Rous sarcoma virus in vitro.” *Virology* 20.4 (1963), 577–582.
- [494] Alan Templeton. “Out of Africa again and again.” *Nature* 416.6876 (2002), 45–51.
- [495] J. B. Tenenbaum, V. de Silva, and J. C. Langford. “A global geometric framework for nonlinear dimensionality reduction.” *Science* 290.5500 (2000), 2319–2323.
- [496] Christoph A. Thaiss et al. “Transkingdom control of microbiota diurnal oscillations promotes metabolic homeostasis.” *Cell* 159.3 (2014), 514–529.
- [497] Christopher M. Thomas and Kaare M Nielsen. “Mechanisms of, and barriers to, horizontal gene transfer between bacteria.” *Nature Rev. Microbiol.* 3.9 (2005), 711–721.
- [498] Enrico Tiacci et al. “BRAF mutations in hairy-cell leukemia.” *N. Engl. J. Med.* 364.24 (2011), 2305–2315.
- [499] Itay Tirosh et al. “Dissecting the multicellular ecosystem of metastatic melanoma by single-cell RNA-seq.” *Science* 352.6282 (2016), 189–196.
- [500] Suxiang Tong et al. “A distinct lineage of influenza A virus from bats.” *Proc. Natl. Acad. Sci. USA* 109.11 (2012), 4269–4274.
- [501] Brenda Y. Torres et al. “Tracking resilience to infections by mapping disease space.” *PLoS Biol.* 14.4 (2016), e1002436.
- [502] Csaba D. Toth, Joseph O’Rourke, and Jacob E. Goodman. *Handbook of Discrete and Computational Geometry*. Third edition. CRC Press, 2017.
- [503] Valerio Tozzi et al. “Persistence of neuropsychologic deficits despite long-term highly active antiretroviral therapy in patients with HIV-related neurocognitive impairment: prevalence and risk factors.” *JAIDS J. Acquir. Immune Defic. Syndr.* 45.2 (2007), 174–182.
- [504] Cole Trapnell et al. “The dynamics and regulators of cell fate decisions are revealed by pseudotemporal ordering of single cells.” *Nature Biotechnol.* 32.4 (2014), 381–386.
- [505] Barbara Treutlein et al. “Reconstructing lineage hierarchies of the distal lung epithelium using single-cell RNA-seq.” *Nature* 509.7500 (2014), 371–375.

- [506] Vladimir Trifonov, Hossein Khiabanian, and Raúl Rabadán. “Geographic dependence, surveillance, and origins of the 2009 influenza A (H1N1) virus.” *N. Engl. J. Med.* 361.2 (2009), 115–119.
- [507] Vladimir Trifonov, Vincent Racaniello, and Raúl Rabadán. “The contribution of the PB1-F2 protein to the fitness of influenza A viruses and its recent evolution in the 2009 influenza A (H1N1) pandemic virus.” *PLOS Curr.* (2009), RRN1006.
- [508] Vladimir Trifonov et al. “MutComFocal: an integrative approach to identifying recurrent and focal genomic alterations in tumor samples.” *BMC Syst. Biol.* 7.1 (2013), 25.
- [509] Federico E. Turkheimer et al. “Chromosomal patterns of gene expression from microarray data: methodology, validation and clinical relevance in gliomas.” *BMC Bioinformatics* 7.1 (2006), 1.
- [510] Katharine Turner, Sayan Mukherjee, and Douglas Boyer. “Persistent homology transform for modeling shapes and surfaces.” *Inform. Inference* 3.4 (2014), 310–344.
- [511] Katharine Turner et al. “Fréchet means for distributions of persistence diagrams.” *Discrete Comput. Geom.* 52.1 (2014), 44–70.
- [512] Marc J. Van De Vijver et al. “A gene-expression signature as a predictor of survival in breast cancer.” *N. Engl. J. Med.* 347.25 (2002), 1999–2009.
- [513] J. Craig Venter et al. “The sequence of the human genome.” *Science* 291.5507 (2001), 1304–1351.
- [514] Annelien Verfaillie et al. “Decoding the regulatory landscape of melanoma reveals TEADS as regulators of the invasive cell state.” *Nature Commun.* 6 (2015), 6683. doi: 10.1038/ncomms7683.
- [515] Roel G. W. Verhaak et al. “Integrated genomic analysis identifies clinically relevant subtypes of glioblastoma characterized by abnormalities in PDGFRA, IDH1, EGFR, and NF1.” *Cancer Cell* 17.1 (2010), 98–110.
- [516] Nicole Vidal et al. “Unprecedented degree of human immunodeficiency virus type 1 (HIV-1) group M genetic diversity in the Democratic Republic of Congo suggests that the HIV-1 pandemic originated in Central Africa.” *J. Virol.* 74.22 (2000), 10498–10507.
- [517] C. Villani. *Optimal Transport – Old and New*. Grundlehren der Mathematischen Wissenschaften, volume 338. Springer, Berlin, 2009.
- [518] John Wakeley. *Coalescent Theory: An Introduction*. Roberts and Company, 2008.
- [519] Jianzhong Wang. “Local tangent space alignment.” *Geometric Structure of High-Dimensional Data and Dimensionality Reduction*, pp. 221–234. Springer, Berlin, 2011.
- [520] Jiguang Wang et al. “Clonal evolution of glioblastoma under therapy.” *Nature Genet.* 48 (2016), 768–776. doi:10.1038/ng.3590.
- [521] Lusheng Wang and Tao Jiang. “On the complexity of multiple sequence alignment.” *J. Comput. Biol.* 1.4 (1994), 337–348.
- [522] Lusheng Wang, Kaizhong Zhang, and Louxin Zhang. “Perfect phylogenetic networks with recombination.” *J. Comput. Biol.* 8.1 (2001), 69–78.
- [523] Xindan Wang, Paula Montero Llopis, and David Z Rudner. “Organization and segregation of bacterial chromosomes.” *Nature Rev. Genet.* 14.3 (2013), 191–203.
- [524] Yong Wang and Nicholas E. Navin. “Advances and applications of single-cell sequencing technologies.” *Mol. Cell* 58.4 (2015), 598–609.
- [525] Zidong Wang et al. “Stochastic dynamic modeling of short gene expression time-series data.” *IEEE Trans. NanoBiosci.* 7.1 (2008), 44–55.

- [526] Larry Wasserman. *All of Statistics: A Concise Course in Statistical Inference*. Springer, 2010.
- [527] A. R. Wattam et al. “PATRIC, the bacterial bioinformatics database and analysis resource.” *Nucleic Acids Res.* 42.D1 (2013), D581–D591.
- [528] G. A. Watterson. “On the number of segregating sites in genetical models without recombination.” *Theor. Population Biol.* 7.2 (1975), 256–276.
- [529] R. G. Webster et al. “Evolution and ecology of influenza A viruses.” *Microbiol. Rev.* 56.1 (1992), 152–179.
- [530] Georg F. Weiller. “Phylogenetic profiles: a graphical method for detecting genetic recombinations in homologous sequences.” *Mol. Biol. Evol.* 15.3 (1998), 326–335.
- [531] Robert Weinberg. *The Biology of Cancer*. Garland Science, 2013.
- [532] Killan Q. Weinberger and Lawrence K. Saul. “An introduction to nonlinear dimensionality reduction by maximum variance unfolding.” *Proceedings of the 21st National Conference on Artificial Intelligence, AAAI'06, Boston, MA*, volume 2, p. 1683. AAAI Press, 2006.
- [533] Shmuel Weinberger. “The complexity of some topological inference problems.” *Found. Comput. Math.* 14.6 (2014), 1277–1285. doi: 10.1007/s10208-013-9152-1.
- [534] Shmuel Weinberger. *The Topological Classification of Stratified Spaces*. Chicago Lectures in Mathematics. University of Chicago Press, Chicago, IL, 1994.
- [535] Shmuel Weinberger. “What is . . . persistent homology?” *Notices AMS* 58.1 (2011), 36–39.
- [536] I. Bernard Weinstein and Andrew Joe. “Oncogene addiction.” *Cancer Res.* 68.9 (2008), 3077–3080. doi: 10.1158/0008-5472.can-07-3293.
- [537] Michael L. Whitfield et al. “Identification of genes periodically expressed in the human cell cycle and their expression in tumors.” *Mol. Biol. Cell* 13.6 (2002), 1977–2000.
- [538] Carl R. Woese, Otto Kandler, and Mark L. Wheelis. “Towards a natural system of organisms: proposal for the domains Archaea, Bacteria, and Eucarya.” *Proc. Natl. Acad. Sci. USA* 87.12 (1990), 4576–4579.
- [539] Michael Worobey, Andrew Rambaut, and Edward C. Holmes. “Widespread intra-serotype recombination in natural populations of dengue virus.” *Proc. Natl. Acad. Sci. USA* 96.13 (1999), 7352–7357.
- [540] Michael Worobey et al. “Direct evidence of extensive diversity of HIV-1 in Kinshasa by 1960.” *Nature* 455.7213 (2008), 661–664.
- [541] Sewall Wright. “Evolution in Mendelian populations.” *Genetics* 16.2 (1931), 97–159.
- [542] Katsusaburo Yamagiwa and Koichi Ichikawa. “Experimental study of the pathogenesis of carcinoma.” *J. Cancer Res.* 3.1 (1918), 1–29.
- [543] D. Yogeshwaran, Eliran Subag, and Robert J. Adler. “Random geometric complexes in the thermodynamic regime.” *Prob. Theor. Relat. Fields* 167.1 (2017), 107–142.
- [544] Xianghui Yu et al. “Induction of APOBEC3G ubiquitination and degradation by an HIV-1 Vif-Cul5-SCF complex.” *Science* 302.5647 (2003), 1056–1060.
- [545] Sakellarios Zairis et al. “Genomic data analysis in tree spaces.” 2016. arXiv: 1607.07503 [q-bio.GN].
- [546] Sakellarios Zairis et al. “Moduli spaces of phylogenetic trees describing tumor evolutionary patterns.” 2014. arXiv: 1410.0980 [q-bio.GN].
- [547] Dmitriy Zamarin, Mila B. Ortigoza, and Peter Palese. “Influenza A virus PB1-F2 protein contributes to viral pathogenesis in mice.” *J. Virol.* 80.16 (2006), 7976–7983.

- [548] H. Zhu et al. “Infectivity, transmission, and pathology of human H7N9 influenza in ferrets and pigs.” *Science* 341.6142 (2013), 183–186. doi: 10.1126/science.1239844.
- [549] Afra Zomorodian. “The tidy set: a minimal simplicial set for computing homology of clique complexes.” *Proceedings of the Twenty-sixth Annual Symposium on Computational Geometry, SoCG ’10, Snowbird, UT, USA*, pp. 257–266. ACM, 2010. doi: 10.1145/1810959.1811004
- [550] Afra J. Zomorodian. *Topology for Computing*. Cambridge University Press, New York, 2009.
- [551] Afra Zomorodian and Gunnar Carlsson. “Computing persistent homology.” *Discrete Comput. Geom.* 33.2 (2005), 249–274.
- [552] Hui Zou, Trevor Hastie, and Robert Tibshirani. “Sparse principal component analysis.” *J. Comput. Graph. Stat.* 15 (2004), 2006.