Layla Oesper

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Department of Computer Science
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Publications: [Google Scholar] [dblp]
Webpage: www.cs.carleton.edu/faculty/loesper/

Education

Ph.D. in Computer Science, Brown University, 2015.
Dissertation Title: *Computational Characterization of Heterogeneity and Rearrangements in Cancer.*
Advisor: Benjamin J. Raphael.

Sc.M. in Computer Science, Brown University, 2012.

Certificate in Computer Science, University of Wisconsin-Madison, 2010.

B.A. in Mathematics, *Magna Cum Laude*, *Phi Beta Kappa*, Pomona College, 2005.

Experience

Associate Professor, Department of Computer Science, Carleton College, 2021 - Present.

Assistant Professor, Department of Computer Science, Carleton College, 2015 - 2021.

Postdoctoral Research Assistant, Department of Computer Science, Brown University, 2015.

Funding & Grants

Alliance to Advance Liberal Arts Colleges (AALAC) Workshop Grant, 2022-2024.
Bioinformatics and Computational Biology in the Liberal Arts.
Role: Workshop Leader, Total Amount: $20,000

Large Faculty Development Endowment (FDE) Grant, Carleton College, 2022-2023.

NSF Division of Information and Intelligent Systems (IIS) #2046011, 6/1/2021 - 5/31/2026.
CAREER: Algorithmic Approaches for Phylogenetic Analysis of Tumor Evolution
Role: PI, Total Amount: $536,321

ACM Faculty Career Enhancement Program (FaCE), 6/1/2019 - 1/31/21.
Exploring Solutions for High-Performance Computing at ACM Institutions.
Role: Project Team, Total Amount: $25,637

NSF Division of Information and Intelligent Systems (IIS) #1657380, 3/1/2017 - 2/28/2022.
CRII: III: RUI: Computational Approaches for Inferring the Evolutionary Histories of Cancer Genomes
Role: PI, Total Amount: $142,783

Elledge, Eugster and Class of '49 Fellowships, Carleton College, 2018-2019.

HHMI/Towsley Fund Award for Faculty-Student Summer Research, Carleton College, 2016.

Google Anita Borg Memorial Scholarship, 2014. Total Amount: $10,000

National Science Foundation Graduate Research Fellowship, 2011-2014.

Honors & Awards

CRA Outstanding Undergraduate Research Mentoring Award, CRA 2025. [website]
SIGBio Best Paper Award, ACM-BCB 2018.
Best Presentation Award, HitSeq 2014.

Teaching Experience

Introduction to Computer Science (CS111): Spring 2016, Fall 2016, Winter 2017, Winter 2018, Winter 2020, Spring 2020, Winter 2021.
Data Structures (CS201): Fall 2017 (2 sections), Winter 2022.
Mathematics of Computer Science (CS202): Fall 2015, Winter 2016, Spring 2016, Spring 2021, Fall 2021, Spring 2022.
Algorithms (CS252): Fall 2016, Winter 2017, Spring 2018, Spring 2020, Fall 2020, Winter 2021, Spring 2021, Winter 2022, Fall 2023, Spring 2024, Fall 2024.
Computability & Complexity (CS254): Spring 2025.
CS Tea Colloquium (CS294): Fall 2023, Winter 2024, Spring 2024.
Data Mining (CS324): Spring 2017.
Computational Biology (CS362): Winter 2016, Winter 2018, Fall 2019, Fall 2021,Winter 2024.
Senior Seminar (CS399): Fall 2019 (3 groups of 6 students each), Fall 2023 (19 students - across 3 groups), Winter 2025 (18 students - across 5 groups).
Integrative Exercise (CS400): Winter 2020 (3 groups of 6 students each), Fall 2023 (19 students - across 3 groups), Winter 2025 (18 students - across 5 groups).
Computational Molecular Biology (CSCI1810): Fall 2013 (at Brown University).
Reading Group on Topics in Computational Biology (CS392): Spring 2020 (3 students), Fall 2020 (5 students), Winter 2022 (9 students).

Guest Lectures

Ph.D. School on Evolution in Pangenomics, Lake Como School of Advanced Studies, Italy: Fall 2024 (4 lectures) [Website].
Computational Biology (CS320/BIOL320), Macalester College: Fall 2022 (1 lecture).
The Genetics and Cell Biology of Cancer (BIO431), Reed College: Spring 2020 (Cancelled due to COVID-19).
Tutorial in Systems Pharmacology (MPET 6813), Mayo Clinic: Fall 2017 (1 lecture).
Bioinformatics and Genomics Workshop, Reed College: October 2015 (module leader).
Seminar in Computer Science (CSOC 450), Amherst College: Fall 2014 (1 lecture).
Topics in Computational Biology (CSCI2950-C), Brown University: Spring 2013 (1 lecture).
Computational Molecular Biology (CSCI1810), Brown University: Fall 2012, Fall 2014 (6 lectures).
CS: An Integrated Introduction (CSCI0180), Brown University: Spring 2012 (2 lectures).

Publications

*undergraduate author. †joint first authorship. ‡alphabetical author list.

Peer-Reviewed Conference and Journal Publications

*Quoc Nguyen and **Layla Oesper**. Generalized Matching Distance: Tumor Phylogeny Comparison Beyond the Infinite Sites Assumption. *Proceedings of the 14th ACM International Conference on Bioin-*

formatics, Computational Biology, and Health Informatics (ACM-BCB), Article No.: 10, pp 1-9, 2023. (Regular papers: 10% acceptance rate.) [publisher link]

*Ziyun (Cathy) Guang, *Matthew Smith-Erb and **Layla Oesper**. A Weighted Distance-based Approach for Deriving Consensus Tumor Evolutionary Trees. *Bioinformatics,* 39 (Supplement_1), i204-i212, 2023. [Proceedings of ISMB/ECCB 2023 (17% acceptance rate).] [publisher link]

‡Mohammed El-Kebir, Quaid Morris, **Layla Oesper** and S Cenk Sahinalp. Emerging Topics in Cancer Evolution. *Pacific Symposium on Biocomputing*, 397-401, 2022. [publisher link]

*Kiya Govek, *Camden Sikes, *Yangqiaoyu Zhou and **Layla Oesper**. GraPhyC: A Consensus Approach to Infer Tumor Evolutionary Histories. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2020. [publisher link]

†*Zach DiNardo, †*Kiran Tomlinson, Anna Ritz and **Layla Oesper**. Distance Measures for Tumor Evolutionary Trees. *Bioinformatics*, 36(7):2090-2097, 2020. [publisher link]

Layla Oesper and Anya Vostinar. Expanding Undergraduate Exposure to Computer Science Subfields: Resources and Lessons from a Hands-on Computational Biology Workshop. *Proceedings of the 51st ACM Technical Symposium on Computer Science Education (SIGCSE)*, 1214-1219, 2020. [publisher link]

The ICGC/TCGA Pan-Cancer Analysis of Whole Genomes Consortium (includes **Layla Oesper**). Pancancer analysis of whole genomes. *Nature*, 578, 82-93, 2020. [publisher link]

Gerstung, Mortiz, PCAWG Evolution & Heterogeneity Working Group, *et al.* (**Layla Oesper** is listed as a member of the working group). The evolutionary history of 2,658 cancers. *Nature*, 578 (7793), 122-128 2020. [publisher link]

*Kiran Tomlinson and **Layla Oesper**. Parameter, Noise, and Tree Topology Effects in Tumor Phylogeny Inference. *BMC Medical Genomics*, 12 (10):1-14, 2019. [Extended Version of 2018 IEEE BIBM paper.] [publisher link] [data]

*Kiran Tomlinson and **Layla Oesper**. Examining Tumor Phylogeny Inference in Noisy Sequencing Data. *Proceedings of the IEEE International Conference on Bioinformatics and Biomedicine* (BIBM), 36-43, 2018. [PDF]

*Kiya Govek, *Camden Sikes, and **Layla Oesper**. A Consensus Approach to Infer Tumor Evolutionary Histories. *Proceedings of the 9th ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics* (ACM-BCB), 63-72, 2018. **Best Paper Award**. [publisher link]

Layla Oesper, Simone Dantas and Benjamin J. Raphael. Identifying Simultaneous Rearrangements in Cancer Genomes. *Bioinformatics*, 34(2):346-352, 2017. [Full paper at RECOMB Satellite Workshop on Computational Cancer Biology (RECOMB-ccb).] [publisher link]

†Mohammed El-Kebir, †Gryte Satas, **Layla Oesper** and Benjamin J. Raphael. Inferring the Mutational History of a Tumor Using Multi-state Perfect Phylogeny Mixtures. *Cell Systems*, 3(1): 43-53, 2016. [publisher link]

†Mohammed El-Kebir, †Gryte Satas, **Layla Oesper** and Benjamin J. Raphael. Multi-State Perfect Phylogeny Mixture Deconvolution and Applications to Cancer Sequencing. *20th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*. LNBI 9649, 251, 2016. [published abstract] [full paper]

†Mohammed El-Kebir, †**Layla Oesper**, *Hannah Acheson-Field and Benjamin J. Raphael. Reconstruction of clonal trees and tumor composition from multi-sample sequencing data. *Bioinformatics*, 31(12):i62-i70, 2015. [Proceedings of ISMB/ECCB.] [publisher link]

[†]**Layla Oesper**, [†]Gryte Satas and Benjamin J. Raphael. Quantifying Tumor Heterogeneity in Whole-Genome and Whole-Exome Sequencing Data. *Bioinformatics*, 30(24): 3532-40, 2014. [publisher link]

[†*]Caleb Weinreb, [†]**Layla Oesper** and Benjamin J. Raphael. Open adjacencies and k-breaks: detecting simultaneous rearrangements in cancer genomes. *BMC Genomics*, 15(Suppl 6):S4, 2014. [Proceedings for the 12th Annual Research in Computational Molecular Biology Satellite Workshop on Comparative Genomes (RECOMB-CG).] [publisher link]

Benjamin J. Raphael, Jason R. Dobson, **Layla Oesper** and Fabio Vandin. Identifying Driver Mutations in Sequenced Cancer Genomes: Computational Approaches to Enable Precision Medicine. *Genome Medicine*, 6:5, 2014. [pdf]

Layla Oesper, Ahmad Mahmoody and Benjamin J. Raphael. THetA: Inferring intra-tumor heterogeneity from high-throughput DNA sequencing data. *Genome Biology*, 14:R80, 2013. [publisher link]

Layla Oesper, Ahmad Mahmoody and Benjamin J. Raphael. Inferring Intra-tumor Heterogeneity from High-Throughput DNA Sequencing Data. *17th Annual International Conference on Research in Computational Molecular Biology (RECOMB).* LNCS 7821, 171-172, 2013. [publisher link]

Layla Oesper, Anna Ritz, Sarah J. Aerni, [*]Ryan Drebin and Benjamin J. Raphael. Reconstructing Cancer Genomes from Paired-end Sequencing Data. *BMC Bioinformatics*, 13(Suppl 6):S10, 2012. [Proceedings of 2nd Annual RECOMB Satellite Workshop on Massively Parallel Sequencing (RECOMB-seq).] [publisher link]

Layla Oesper, Daniele Merico, Ruth Isserlin and Gary D. Bader. WordCloud: a Cytoscape plugin to create a visual semantic summary of networks. *Source Code for Biology and Medicine*, 6(1) 7, 2011. [pdf]

[‡]Anna-Lisa Breiland, **Layla Oesper** and Laura Taalman. p-Coloring Classes of Torus Knots. *Missouri Journal of Mathematical Sciences*, 21(2), 120-125, 2009. [publisher link]

Invited Journal Publications

Layla Oesper. What is the Role for Algorithmics and Computational Biology in Responding to the COVID-19 Pandemic? Interdisciplinary Science. *Cell Systems*, 10(5): 379-380, 2020. [publisher link]

Presentations

[*]undergraduate author. <u>Presenter.</u>

Conference Talks

[*]<u>Thea Traw</u>, Quoc Nguyen, **Layla Oesper** and Eric Alexander. VECTr: Facilitating Visual Comparison of Clonal Trees. *Great Lakes Bioinformatics Conference*, May 2025.

[*]<u>Bryce Bernstein</u>, [*]<u>Kendra Winhall</u> and **Layla Oesper**. Enumerating and Exploring the Space of Clonal Trees. *Great Lakes Bioinformatics Conference*, May 2025. **Awarded Best Talk**

[*]<u>Quoc Nguyen</u> and **Layla Oesper**. Generalized Matching Distance: Tumor Phylogeny Comparison Beyond the Infinite Sites Assumption. *14th ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB)*, September 2023.

[*]<u>Ziyun (Cathy) Guang</u>, [*]Matthew Smith-Erb and **Layla Oesper**. A Weighted Distance-based Approach for Deriving Consensus Tumor Evolutionary Trees. *Intelligent Systems in Molecular Biology (ISMB/ECCB)*, July 2023.

*Ziyun (Cathy) Guang, *Matthew Smith-Erb and **Layla Oesper**. A Weighted Distance-based Approach for Deriving Consensus Tumor Evolutionary Trees. *RECOMB Satellite Workshop on Computational Cancer Biology (RECOMB-ccb)*, April 2023.

*Zach DiNardo, *Kiran Tomlinson, Anna Ritz and **Layla Oesper**. Distance Measures for Tumor Evolutionary Trees. *24th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, June 2020. (Highlights Talk - presented virtually.)

Layla Oesper and Anya Vostinar. Expanding Undergraduate Exposure to Computer Science Subfields: Resources and Lessons from a Hands-on Computational Biology Workshop, *ACM Technical Symposium on Computer Science Education (SIGCSE)*, March 2020. (In-person conference cancelled due to COVID-19, [talk video].)

*Kiya Govek, *Camden Sikes, and **Layla Oesper**. GraPhyC: Using Consensus to Infer Tumor Evolutionary Histories, *Great Lakes Bioinformatics Conference*, May 2019.

*Zach DiNardo, *Kiran Tomlinson, Anna Ritz and **Layla Oesper**. Distance Measures for Tumor Evolutionary Trees. *RECOMB Satellite Workshop on Computational Cancer Biology (RECOMB-ccb)*, May 2019.

*Kiran Tomlinson and **Layla Oesper**. Examining Tumor Phylogeny Inference in Noisy Sequencing Data. *IEEE International Conference on Bioinformatics and Biomedicine* (BIBM), Accepted as a Long paper, December 2018.

*Kiya Govek, *Camden Sikes, and **Layla Oesper**. A Consensus Approach to Infer Tumor Evolutionary Histories. *The 9th ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics* (ACM-BCB), August 2018.

Layla Oesper, Simone Dantas and Benjamin J. Raphael. Identifying Simultaneous Rearrangements in Cancer Genomes. *RECOMB Satellite Workshop on Computational Cancer Biology (RECOMB-ccb)*, Accepted as a Full Talk, July 2017.

Layla Oesper. Racial/Ethnic Disparities in DNA Sequencing Data and the Potential Impact on Computational Cancer Research. *AALAC Workshop on Data Ethics*, Pomona College, February 2017.

†Mohammed El-Kebir, †Gryte Satas, **Layla Oesper** and Benjamin J. Raphael. Multi-State Perfect Phylogeny Mixture Deconvolution and Applications to Cancer Sequencing. *20th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, April 2016.

Mohammed El-Kebir, **Layla Oesper**, *Hannah Acheson-Field and Benjamin J. Raphael. Reconstruction of clonal trees and tumor composition from multi-sample cancer sequencing data. *Intelligent Systems in Molecular Biology (ISMB)*, July 2016.

Mohammed El-Kebir, **Layla Oesper**, *Hannah Acheson-Field and Benjamin J. Raphael. Reconstruction of clonal trees and tumor composition from multi-sample cancer sequencing data. *RECOMB Satellite Workshop on Computational Cancer Biology (RECOMB-ccb)*, April 2015.

Layla Oesper and Rajmonda Caceres. Using Consensus to Inform Stochastic Graph Aggregation. *Part of the Minisymposium "Analysis of Noisy Networks in Theory and Practice" at the 2015 SIAM Conference on Computational Science and Engineering*, March 2015.

Layla Oesper, Gryte Satas and Benjamin J. Raphael. Quantifying Tumor Heterogeneity in Whole-Genome and Whole-Exome Sequencing Data. *HitSeq 2014: High-throughput Sequencing Algorithms*, July 2014. **Best Presentation Award.**

Layla Oesper, Gryte Satas and Benjamin J. Raphael. Inferring Intra-Tumor Heterogeneity from Whole-Genome/Exome Sequencing Data. *The Cancer Genome Atlas (TCGA) Third Annual Scientific Symposium*, May 2014.

*Caleb Weinreb, **Layla Oesper** and Benjamin J. Raphael. Open adjacencies and k-breaks: detecting simultaneous rearrangements in cancer genomes. *Research in Computational Molecular Biology Satellite Workshop on Comparative Genomes* (RECOMB-CG), October 2014.

Layla Oesper, Gryte Satas, *Max Song, Simone Dantas and Benjamin J. Raphael. Analysis of Complex Genomic Rearrangements using High-Throughput DNA Sequencing Data. *Wellcome Trust Scientific Conferences/Cold Spring Harbor Laboratory conference on Genome Informatics*, November 2013.

Layla Oesper, Ahmad Mahmoody and Benjamin J. Raphael. Inferring Intra-tumor Heterogeneity from High-Throughput DNA Sequencing Data. 17th *International Conference on Research in Molecular Biology (RECOMB)*, April 2013.

Layla Oesper, Ahmad Mahmoody and Benjamin J. Raphael. Estimating Tumor Clonal Populations from Copy Number Data. *Pacific Symposium on Biocomputing (PSB)*, January 2013.

Layla Oesper, Ahmad Mahmoody and Benjamin J. Raphael. Estimating Tumor Purity and Cancer Subpopulations from High-Throughput DNA Sequencing Data. *Women in Machine Learning Workshop (WiML)*, December 2012.

Layla Oesper, Anna Ritz, Sarah J. Aerni, *Ryan Drebin and Benjamin J. Raphael. Reconstructing Cancer Genomes from Paired-end Sequencing Data. *RECOMB Satellite Workshop on Massively Parallel Sequencing (RECOMB-seq)*, April 2012.

Layla Oesper, Sarah Aerni, *Ryan Drebin and Benjamin J. Raphael. Reconstructing Cancer Genome Organization from Paired End Sequencing. *RECOMB Satellite Workshop on Computational Cancer Biology (RECOMB-ccb)*, March 2011.

Layla Oesper, Anna-Lisa Breiland and Laura Taalman. p-Coloring Classes of Torus Knots. *Joint Mathematics Meetings Session on research by undergraduates*, January 2005.

Layla Oesper, Anna-Lisa Breiland and Laura Taalman. p-Coloring Classes of Torus Knots. *Big Sky Conference on Discrete Mathematics*, September 2004.

Invited Talks

Computational Genomics Summer Institute (CGSI), July 2025.
Great Lakes Bioinformatics Conference, Keynote Lecture, May 2025. [website]
Carleton College Biology Seminar, January 2025.
NCI Spring School on Algorithmic Cancer Biology, April 2024.
Carleton Connects Webinar, January 2024.
Computational Genomics Summer Institute (CGSI), July 2023. [Video]
St. Olaf College, Department of Mathematics, Statistics and Computer Science Colloquium, March 2023.
Heywood Society Lecture, Carleton College, 2022. [Video]
Computational Genomics Summer Institute (CGSI), July 2022.
Bioinformatics: From Algorithms to Applications (BiATA), July 2021. [website]
Computational Genomics Summer Institute (CGSI), July 2020. (Cancelled due to COVID-19)
Computational Genomics Summer Institute (CGSI), July 2019. [Video]
Great Lakes Bioinformatics Conference, Special Session on Education, May 2019. [Slides]
Rhodes College, Department of Computer Science Seminar, April 2019.
Reed College, Department of Biology Seminar, November 2018.

Carleton College Summer Computer Science Institute (SCSI), July 2018.
University of Minnesota, Computer Science and Engineering Colloquia, October 2017.
Macalester College MSCS Seminar, October 2016.
Carleton College Summer Computer Science Institute (SCSI), July 2016.
Carleton College Biology Seminar, January 2016.
St. Olaf College MSCS Research Seminar, November 2015.
SciLifeLab, Stockholm, Sweden, June 2015.
Carleton College, Department of Computer Science, February 2015.
Amherst College, Department of Computer Science, January 2015.
Williams College, Department of Computer Science, January 2015.
Western Washington University, Department of Computer Science, January 2015.
University of Richmond, Department of Computer Science, December 2014.
The College of New Jersey, Department of Computer Science, December 2014.
James Madison University Mathematics REU Program, June 2013.
IEEE Conference on Computational Advances in Bio and Medical Sciences (ICCABS), June 2013.

Other Talks

Carleton College Faculty Retreat, September 2017 and September 2023.
Carleton College, Computer Science Tea Talk, November 2016.

Posters

*undergraduate author. Presenter.

*Quoc Nguyen, *Thea Traw, **Layla Oesper**, and Eric Alexander. Facilitating Visual Comparison of Clonal Trees. *14th ACM International Conference on Bioinforamtics, Computational Biology, and Health Informatics (ACM-BCB), September 2023.*

*Matthew Smith-Erb, *Cathy Guang and **Layla Oesper**. Deriving Consensus Tumor Trees Using Integer Linear Programming. *IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, December 2022. [Abstract Link].

*Quoc Nguyen and **Layla Oesper**. An Approach to Relax the Infinite Sites Assumption in Tumor Phylogeny Distance Measures. *IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, December 2022. [Abstract Link].

*Cecilia Ehrlichman and **Layla Oesper**. Combining Distance Measures on Tumor Evolutionary Trees. *IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, December 2022. [Abstract Link].

*Qianzi Li and **Layla Oesper**. A Matching Based Approach to Relax the Infinite Sites Assumption in Tumor Phylogeny Distance Measures. *Great Lakes Bioinformatics Conference (GLBIO)*, May 2021.

*Zach DiNardo, *Kiran Tomlinson, Anna Ritz and **Layla Oesper**. Distance Measures for Tumor Evolutionary Trees. *26th International Conference on Intelligent Systems for Molecular Biology (ISMB)*, July 2019.

*Zach DiNardo, *Kiran Tomlinson, Anna Ritz and **Layla Oesper**. Distance Measures for Tumor Evolutionary Trees. *23rd International Conference on Research in Computational Molecular Biology (RE-COMB)*, May 2019.

*Yangqiaoyu Zhou and **Layla Oesper**. A Topology-Aware Edit Distance Measure For Cancer Evolutionary Trees. *RECOMB Satellite Workshop on Computational Cancer Biology (RECOMB-ccb)*, May 2019.

*Kiya Govek, *Camden Sikes and **Layla Oesper**. Finding Consensus Phylogenetic Trees for Tumor Evolution. *26th International Conference on Intelligent Systems for Molecular Biology (ISMB)*, July 2018.

*Kiya Govek, *Camden Sikes and **Layla Oesper**. Finding Consensus Phylogenetic Trees for Tumor Evolution. *22nd Annual International Conference on Research in Computational Molecular Biology (RE-COMB)*, April 2018.

*Kiya Govek, *Camden Sikes and **Layla Oesper**. Finding Consensus Phylogenetic Trees for Tumor Evolution. *RECOMB Satellite Workshop on Computational Cancer Biology (RECOMB-ccb)*, July 2017.

*Allie Warren and **Layla Oesper**. Methods for Inferring Consensus Across Tumor Phylogenetic Histories. *14th Annual Rocky Bioinformatics Conference*, December 2016.

Layla Oesper, Mohammed El-Kebir, *Hannah Acheson-Field and Benjamin J. Raphael. Reconstruction of clonal trees and tumor composition from multi-sample cancer sequencing data. *19th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, April 2015.

Layla Oesper, Gryte Satas and Benjamin J. Raphael. Inferring Intra-Tumor Heterogeneity from Whole-Genome/Exome Sequencing Data. *International Conference on Intelligent Systems for Molecular Biology (ISMB)*, 2014.

Layla Oesper, Gryte Satas and Benjamin J. Raphael. Inferring Intra-Tumor Heterogeneity from Whole-Genome/Exome Sequencing Data. *The Cancer Genome Atlas (TCGA) Third Annual Scientific Symposium*, 2014.

Layla Oesper, Gryte Satas, *Max Song, Simone Dantas and Benjamin J. Raphael. Analysis of Complex Rearrangements in Cancer. *Microsoft Research - Computational Aspects of Biological Information*, 2013.

Layla Oesper, Ahmad Mahmoody and Benjamin J. Raphael. Inferring Intra-tumor Heterogeneity from High-Throughput DNA Sequencing Data. *Rhode Island Healthcare Symposium*, 2013.

Layla Oesper, Ahmad Mahmoody and Benjamin J. Raphael. Inferring Intra-tumor Heterogeneity from High-Throughput DNA Sequencing Data. *CSHL Meeting on the Biology of Genomes*, 2013.

Layla Oesper, Ahmad Mahmoody and Benjamin J. Raphael. Inferring Intra-tumor Heterogeneity from High-Throughput DNA Sequencing Data. *RECOMB Satellite Workshop on Massively Parallel Sequencing (RECOMB-Seq)*, 2013.

Layla Oesper, Ahmad Mahmoody and Benjamin J. Raphael. Estimating Tumor Clonal Populations from Copy Number Data. *Pacific Symposium on Biocomputing (PSB)* 2013.

Layla Oesper, Anna Ritz, Sarah Aerni, *Ryan Drebin and Benjamin J. Raphael. Reconstructing Cancer Genomes from Paired-end Sequencing Data. *16th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, 2012.

Layla Oesper, Sarah Aerni, *Ryan Drebin and Benjamin J. Raphael. Reconstructing Cancer Genome Organization from Paired-end Sequencing. *15th Annual International Conference on Research in Computational Molecular Biology (RECOMB)*, 2011.

Layla Oesper, Anna-Lisa Breiland and Laura Taalman. p-Coloring Classes of Torus Knots. *Joint Mathematics Meetings Undergraduate Research Poster Session*, 2005. **Outstanding undergraduate poster award.**

Software

Software Released at Carleton College

Generalized Matching Distance (GMD) - a generalizable approach that allows ISA dependent distance measures to be applied to non-ISA trees. [Download Link]

TuELiP - a consensus approach to inferring tumor evolutionary histories that allows for input histories to be weighted. [Download Link]

CASet and DISC Distances - distance measures on tumor evolutionary histories. [Download Link]

GraPhyC - a consensus approach to inferring tumor evolutionary histories. [Download Link]

H/T Alternating Fraction - a measurement of one potential signature of chromothripsis that can be computed using DNA sequencing data. [Download Link]

Software Released Elsewhere

AncesTree - an algorithm that infers the clonal evolution and tumor composition, including mixing fractions, of a tumor from multi-sample DNA sequence data.
[Download Link] [Software page] [Google Group]

THetA/THetA2 - an algorithm that estimates the tumor purity and clonal/sublconal copy number aberrations directly from high-throughput DNA sequencing data.
[Download Link] [Software page] [Google Group]

PREGO - an algorithm that reconstructs a cancer genome as a rearrangement of segments, or intervals, from the reference genome using paired-end sequencing data. [Software page]

WordCloud - a Cytoscape plugin that generates a word tag cloud from a user-defined node selection, summarizing an attribute of choice. [Software page]

Professional Service

Organizer

Lead Organizer - Bioinformatics and Computational Biology in the Liberal Arts Workshop, Carleton College College - Summer 2025.
Organizing Committee - Bioinformatics and Computational Biology in the Liberal Arts Workshop, Reed College - 2023. [website]
Student Travel Chair - Great Lakes Bioinformatics Conferences (GLBio) - 2021, 2023.
Organizer - Emerging Topics in Cancer Evolution - Pacific Symposium on Biocomputing (PSB) - 2022.
Program Chair - RECOMB Workshop on Massively Parallel Sequencing (RECOMB-Seq) - 2021. [website]
Workshop Organizer - High Performance Computing at ACM colleges - 2021.
Workshop Organizer - First Time Conference Attendance Workshop - Great Lakes Bioinformatics Conference (GLBio) - 2021. [website]
Student Fellowship Chair - Great Lakes Bioinformatics Conference (GLBio) - 2021.
Organizer - High Throughput Sequencing Algorithms and Applications (HiTSeq): 2019, 2020.
Sole-Organizer - Undergraduate Computational Biology Workshop: 2018. [website].
Poster Chair - Great Lakes Bioinformatics Conference (GLBio) - 2019.
Discussion Leader - CoBE: Computational Biology Education BoF, ISMB, 2017,
Poster Committee - Grace Hopper Celebration of Women in Computing - 2016.
Poster Committee Research in Computational Molecular Biology (RECOMB) - 2015.

Program Committee

Great Lakes Bioinformatics Conferences (GLBio) - 2023 - 2025.
Research in Computational Molecular Biology (RECOMB): 2018,2020-2023,2025.
RECOMB Workshop on Computational Cancer Biology (RECOMB-CCB): 2016-2020,2023-2025.
Intelligent Systems for Molecular Biology (ISMB): 2017-2021,2023.
RECOMB Satellite Workshops on Massively Parallel Sequencing (RECOMB-seq): 2016, 2019.
International Symposium on Mathematical and Computational Oncology: 2019.
ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB): 2017.

Steering Committee

Great Lakes Bioinformatics Conferences (GLBio) - 2024-Present.

Journal Reviewer

Algorithms for Molecular Biology
Bioinformatics
BMC Bioinformatics
BMC Medical Genomics
IEEE Transactions on Computational Biology and Bioinformatics
Journal of Bioinformatics and Computational Biology
Journal of Graph Algorithms and Applications
Nature Communications
Nucleic Acids Research
PLOS Computational Biology
Scientific Reports

Additional Conference Reviewing

ACM-SIAM Symposium on Discrete Algorithms (SODA)
Genome Informatics Workshop (GIW)
Pacific Symposium on Biocomputing (PSB)
Research in Computational Molecular Biology (RECOMB)
Workshop on Algorithms in Bioinformatics (WABI)

Grant Reviewing

NSF, Division of Information and Intelligent Systems (IIS): 2018,2021,2022.

Other Reviewing

PhD Thesis Committee - Yuanyuan Qi, University of Illinois Urbana-Champaign: 2023-2024.
Harris Fellowship - Grinnell College, 2022.
PhD Thesis Reviewer - Simone Ciccolella, Università di Milano - Bicocca: 2021

Service within Carleton College

College-wide Service

Faculty Personnel Committee: 2024-Present
Interdisciplinary Task Force member: 2024-2025
Computational Resources User Group (CRUG): 2019-Present.
Recreation Center Advisory Committee: 2023-2024
Faculty Judiciary Committee (elected member): 2017 - 2018, 2023-2024
Budget Committee and Liaison to Faculty Compensation Committee (elected position): 2020 - 2022.
Classrooms Committee: 2019 - 2020.
Institutional Review Board (IRB) Committee: 2016 - 2018.

Departmental Service

Broadening Participation/IDE Coordinator: 2025 - Present.
Computer Science Tea Talk Coordinator: 2016 - 2018, 2023-2025.
Official Mentor for Tenure Track Colleague: 2021 - 2022, 2023-Present.
NCWIT Learning Circle Member: 2023-2024.
Associate Chair of Computer Science: 2021 - 2022, 2023-2024.
Department Educational Associate Advisor: 2023-2024.
Visiting Hiring Committee (CS): 2016, 2018, 2019, 2020, 2022.
Richard Tapia Conference Coordinator: 2021.
Grace Hopper Conference (GHC) Wrangler: 2020, 2021.
Computer Science Assessment Coordinator: 2017, 2019.
Computer Science OPT/CPT Coordinator: 2019 - 2021.
Bioinformatics Tenure Track Hiring Advisor (Biology): 2015.

Advising

Undergraduate Researchers Advised

Bryce Bernstein '26
Kendra Winhall '25
Thea Traw '25. **CRA Outstanding Undergraduate Researcher Honorable Mention.**
Matthew Smith-Erb '23 (additionally, a reading group participant).
Cathy Guang '23 (additionally, a reading group participant).
Quoc Nguyen '23 (additionally, a reading group participant).
Cecilia Erhlichman '24.
Conor Babcock O'Neill '24.
Maya Murphy '22.
Muyang Shi '21 (additionally, a reading group participant). **CRA Outstanding Undergraduate Researcher Honorable Mention.**
Minh Pham '22 (additionally, a reading group participant).
Qianzi Li '21 (additionally, a reading group participant).
Zach DiNardo '21.
Nobuaki Masaki '20 (reading group participant).
Chiraag Goel '20 (additionally, a reading group participant).
Rosa Zhou '20. **CRA Outstanding Undergraduate Researcher Honorable Mention.**
Thais Del Rosario Hernandez '20. Summer Science Fellow Program.
Kiran Tomlinson '19 **CRA Outstanding Undergraduate Researcher Honorable Mention.**
Kiya Govek '18. **CRA Outstanding Undergraduate Researcher Honorable Mention**.

Camden Sikes '18.
Vianne Gao '18.
Michael Hoffert '18.
Qimeng Yu '18.
Allie Warren '17.

Students advised at Brown University
Alex Ashery '16.
Hannah Acheson-Field '15.
Caleb Weinreb '15.
Max Song.
Stephanie Demane '13.
Ryan Drebin '12.

Research Educational Associates Advised

Quoc Nguyen '23: June 2023-September 2023.

Other Activities

Mathematics for Human Flourishing Book Discussion Group, LTC Reading group: 2024.
Carleton Advising Circle (Addressing the needs of BIPOC students): 2021.

Last updated: June 13, 2025