

Education

- 2006—2012 Doctor of Philosophy, Department of Computer Science, University of British Columbia, Vancouver, Canada, GPA – 4.0/4
Advisors: Ján Maňuch, Cedric Chauve and Arvind Gupta
Thesis title: “Variants of the consecutive-ones property motivated by the reconstruction of ancestral species”
- 2004—2006 Master of Science, School of Computing Science, Simon Fraser University, Burnaby, British Columbia, Canada, GPA – 3.9/4
Advisors: Eugenia Ternovska and Arvind Gupta
Thesis title: “Grounding for model expansion in k -guarded formulas”
- 1999—2003 Bachelor of Computer Science (Honours), Jodrey School of Computer Science, Acadia University, Wolfville, Nova Scotia, Canada, GPA – 3.8/4 (top 5%)
Advisors: Raymond J. Spiteri and Jim Diamond
Thesis title: “Implementing Runge-Kutta solvers in Java”

Work Experience

- 2020— Assistant Professor, Department of Computer Science, Georgia State University, Atlanta, Georgia, USA
Teaching both undergraduate and graduate courses in computer science, as well as carrying out my research program in bioinformatics
- 2019—2020 Visiting Assistant Professor, Department of Computer Science and Engineering, Fairfield University, Fairfield, Connecticut, USA
Teaching both undergraduate and graduate courses in computer science, as well as carrying out my research program in bioinformatics
- 2016—2019 Postdoctoral Researcher, Experimental Algorithmics Lab (AlgoLab), Informatics Department, Università degli Studi di Milano-Bicocca, Milano, Italy
Advisors: Gianluca Della Vedova and Paola Bonizzoni
Performing research on haplotype assembly, cancer phylogenetics and their application
- 2014—2016 Postdoctoral Researcher, Laboratoire de Biométrie et Biologie Évolutive (LBBE), Université Claude Bernard Lyon 1, Villeurbanne, France
Advisors: Daniel Kahn and Vincent Daubin
Studying the co-evolution of (metabolic) function, and how it can be used to help the construction of phylogenetic trees

- 2013—2014 ERCIM Postdoctoral Research Fellow, Life Sciences Group, Centrum Wiskunde Informatica (CWI), Amsterdam, The Netherlands
 Advisors: Alexander Schönhuth and Gunnar W. Klau
 Improving the state-of-the-art haplotype assembly methods for next-generation genome sequencing data
 Research funded by ERCIM Marie Curie ABCDE Postdoctoral Fellowship
- 2012—2013 ERCIM Postdoctoral Research Fellow, INRIA Rhône-Alpes and the Laboratoire de Biométrie et Biologie Évolutive, Université Claude Bernard Lyon 1, Villeurbanne, France
 Advisor: Eric Tannier
 Performing a study of the co-evolution of genes, and how it can be used to help the construction of phylogenetic trees
 Research funded by ERCIM Marie Curie ABCDE Postdoctoral Fellowship

Contracts

- 2018 Project Collaboration, Experimental Algorithmics Lab, Informatics Department, Università degli Studi di Milano-Bicocca, Milano, Italy, Amount: 5,000 € (2 months)
 Advisor: Raffaella Rizzi
 The development of efficient algorithms for comparing evolutionary histories of cancerous tumours as inferred by the latest methods
- 2017 Project Collaboration, Experimental Algorithmics Lab, Informatics Department, Università degli Studi di Milano-Bicocca, Milano, Italy, Amount: 5,000 € (2 months)
 Advisor: Gianluca Della Vedova
 Studying phylogenetic models and how they can be used to model the evolution of tumours. This project resulted in a publication at CiE 2017

Teaching Experience

- Fall 2024 Georgia State University
 ○ CSC 4520 / 6520 — a senior year / masters-level course on the design and analysis of algorithms, and
 ○ CSC 8540 — a grad-level course on advanced algorithms in bioinformatics
- Spring 2024 Georgia State University
 ○ CSC 4330 / 6330 — a senior year / masters-level programming language concepts course
- Fall 2023 Georgia State University
 ○ CSC 4330 / 6330 — a senior year / masters-level programming language concepts course
- Spring 2023 Georgia State University
 ○ CSC / DSCI 4810 / 6810 — a senior year / master-level course on artificial intelligence
- Fall 2022 Georgia State University
 ○ CSC 4330 / 6330 — a senior year / masters-level programming language concepts course
- Spring 2022 Georgia State University
 ○ CSC 4330 / 6330 — a senior year / masters-level programming language concepts course
- Fall 2021 Georgia State University
 ○ CSC 4710 / 6710 — a senior year / masters-level course on database systems

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- Spring 2021 Georgia State University
- CSC 4330 / 6330 — a senior year / masters-level programming language concepts course
- Fall 2020 Georgia State University
- CSC 4330 / 6330 — a senior year / masters-level programming language concepts course
- Spring 2020 Fairfield University
- CS 131 — an introductory programming course in Java, and
 - CS 354 — a junior year theory of programming languages course using Haskell and Prolog
- Fall 2019 Fairfield University
- CS 131 — an introductory programming course in Java
 - CS 231 — an intermediate (sophomore year) programming course, focusing on the object-oriented features of Java, and
 - SW 402 — a senior-year / masters-level course on database management systems
- 2015 Instructor, Department of Mathematics, Université Claude Bernard Lyon 1, Villeurbanne, France
- Section head: Raymond Lobry
- Teaching a section of mathematics for the life sciences to first-year university students

Advising

- Fall 2024 I supervised PhD students Sarwan Ali, Prakash Chourasia, Avais Jan, Ayotomiwa Ezekiel Adeniyi and Mansoor Ahmed, Master's student Sai Roopesh Mandava, and Undergraduate student Ramita Rathore
- Sai Roopesh Mandava successfully completed his Master's project titled: "Kickstarting football skills: A reinforcement learning approach".
 - Sarwan Ali successfully defended his PhD dissertation titled: "Designing representation learning methods for molecular sequences analysis".
 - Sarwan Ali received a Georgia State dissertation grant award.
- Spring 2024 I supervised PhD students Zahra Tayebi, Sarwan Ali, Prakash Chourasia, Taslim Murad, Avais Jan and Ayotomiwa Ezekiel Adeniyi, Master's students Raghuveer Gummadi and Sai Roopesh Mandava, and Undergraduate students Ramita Rathore and Anderson Hernandez
- Taslim Murad successfully defended her PhD dissertation titled: "Designing methods for representation learning of molecular sequences and its application in analysis tasks".
 - Zahra Tayebi successfully defended her PhD dissertation titled: "Clustering, classification, and simulation of evolutionarily related sequences in the context of cancer and viral spread".
 - Sarwan Ali received the 2024 Graduate Research Award in the Department of Computer Science.
 - Ramita Rathore won a 1st Place Novice Research Award at the 2024 GSU Summer Undergraduate Research Symposium.

- Fall 2023 I supervised PhD students Zahra Tayebi, Sarwan Ali, Prakash Chourasia, Taslim Murad, Avais Jain and Ayotomiwa Ezekiel Adeniyi, and Master's students Raghuveer Gummadi and Eunice Olorunshola.
- Prakash Chourasia won an MBD fellowship, funding the remainder of his study.
 - Zahra Tayebi successfully completed her dissertation proposal titled: "Efficient clustering and classification of protein sequences".
 - Sarwan Ali successfully completed his dissertation proposal titled: "Designing representation learning methods for molecular sequences analysis".
 - Eunice Olorunshola successfully defended her Master's thesis titled: "Classifying different cancer types based on transcriptomics data using machine learning algorithms".
- Spring 2023 I supervised PhD students Zahra Tayebi, Sarwan Ali, Prakash Chourasia, Taslim Murad and Avais Jain, and Master's students Raghuveer Gummadi, Eunice Olorunshola, Sai Venkata Sumanth Gaddam, Kushal Khatri, Surya Subrahmanya Sai Chandra Sekhar Kolli, Samvidha Reddy Mannem, Fatma Noor, Ashwin Pilgaonkar, Ria C. Thazhe Punathil, Sainikhila Vemulapalli and Karishma Mahendra Wadhe.
- Taslim Murad successfully completed her dissertation proposal titled: "Designing methods for representation learning of biological sequences and its application in analysis tasks".
- The following Master's projects were graduated:
- Sai Gaddam: "Diabetic retinopathy detection using deep learning".
 - Kushal Khatri: "A stratified subsampler for hierarchically structured data".
 - Surya Kolli: "Recommendations using graph databases".
 - Fatma Noor: "Can community detection build a good phylogeny?".
 - Ashwin Pilgaonkar: "Robinson Country Intelligence Index (RCII) – A country risk analysis tool".
 - Ria Punathil: "CoVScan – A tool for viral host specification from coronavirus spike sequences".
 - Sainikhila Vemulapalli: "Vehicle image classification and damage analysis using deep learning model".
 - Karishma Wadhe: "Drive safe – A driver drowsiness alert system".
- Fall 2022 I supervised PhD students Zahra Tayebi, Sarwan Ali, Prakash Chourasia and Taslim Murad, and Master's students Supriya Arun, Kaustubh Khandai, Kushal Khatri, Prashanth Annam, Babitha Reddy Devireddy, Indu Munnangi, Venkata Krishna Chaitanya Nuthalapati, Dhruval Patel, Shraddha Sharma and Atharv Utkarsh Yeolekar.
- Zahra Tayebi won a B&B fellowship, funding the remainder of her study.
- The following Master's projects were graduated:
- Supriya Arun: "Comparative analysis of Covid classifiers".
 - Kaustubh Khandai: "Determining significant correlation between pairs of extant characters in a small parsimony framework".

- Prashanth Annam: “Neobook: A social medial application using Flutter and Fire-base”.
 - Babitha Reddy Devireddy: “Chaos engineering using Gremlin and GC analyzer”.
 - Indu Munnangi: “My recipe book: A MERN stack web application”.
 - Venkata Krishna Chaitanya Nuthalapati: “Tsuba: Web security scanner”.
 - Dhruval Patel: “Best actor detection”.
 - Shraddha Sharma: “Sunsetting customer identification service”.
 - Atharv Utkarsh Yeolekar: “Data condensation using generative adversarial networks”.
- Spring 2022 I supervised PhD students Zahra Tayebi, Sarwan Ali, Prakash Chourasia and Taslim Murad, and Master’s students Babatunde Bello, Supriya Arun and Kaustubh Khandai.
- Babatunde Bello graduated with Master’s thesis titled: “Functional enrichment analysis of transcriptomics data of breast cancer RNA-seq”.
- Fall 2021 PhD students Zahra Tayebi, Sarwan Ali and Prakash Chourasia, Master’s students Babatunde Bello and Kaustubh Khandai, and Honors student Yijing Zhou.
- Sarwan Ali won an MBD fellowship, funding the remainder of his study.
 - Yijing Zhou graduated with honors thesis titled: “Towards a complete workflow for inferring tumor phylogeny from raw single-cell sequencing reads”
- Spring 2021 I supervised PhD students Zahra Tayebi and Sarwan Ali
- Fall 2020 I supervised PhD student Zahra Tayebi

Volunteer Experience

- 2017—2019 Research Advisor, Lycée Stendhal, Milan, Italy
Advising and guiding students on an after-school mathematics project which is part of the larger European program: Math en Jeans. There is an annual conference where the students go to present their work on the year's project.

Grants

- 2021 Global education online module design, Hanyang University ERICA, Amount: \$24,255 USD (3 years)
PI: Zhipeng Cai, Co-I: Armin Mikler, Rajshekhar Sunderraman, Pavel Skums, Murray Patterson, Rolando Estrada, Yingshu Li, Jennifer Sherer, Geoffrey Graybeal
○ For the development of online modules in data science and business intelligence, which could be offered as a course or training program.
- 2024 REU site: Multidisciplinary graph data analytics, National Science Foundation, Amount: \$372,720 USD (3 years)
PI: Esra Akbas, Mehmet Emin Aktas
○ To establish Georgia State University as a Research Experiences for Undergraduates (REU) site by hiring paid undergraduate summer interns to work together with faculty and graduate students on their research projects.
- 2024 Using AI techniques to uncover transmission dynamics and hotspots from HIV big data, Research Internal Grant (RIG), GSU, Amount: \$20,000 USD (1 year)
PI: Alexander Kirpich
○ To collect HIV incidence data and numerically encode it for analysis for trends in transmission with machine learning algorithms

Contracts

- 2021 AI Learning Alliance: Broadening participation, Meta, Inc., Amount: \$50,000 USD (2 years)
PI: Anu Bourgeois, Co-I: Murray Patterson
○ To support work related to providing education at the frontier of R&D and to increase the representation of historically marginalized researchers and engineers by preparing them for jobs in the artificial intelligence field.

Under Review

- 2024 A methodology for reconciling incompatible spatial boundaries for reliably linking cancer rates to social and environmental data, National Cancer Institute, Amount: \$427,680.00 USD (2 years)

PI: Murray Patterson, Co-I: Chetan Tiwari and Armin Mikler

○ This project seeks to develop methods for harmonizing geospatial data to improve the linkages between place-based characteristics and cancer outcomes. Such data are typically available as geographic layers, each representing a distinct attribute such as driving time distance to cancer screening centers or language vulnerability. However, since these layers are constructed independently of each other, their boundaries are likely to be spatially incongruent. Such misalignments create spatial inconsistencies that challenge data integration and introduce bias, potentially concealing true geographic associations or relationships. The proposed work will develop an algorithmic approach to align such layers, aiming to minimize distortion while preserving spatial integrity.

Not Funded

- 2023 Unveiling large-scale trends in diet and disease from gut microbiome sequencing data, National Institutes of Health, Amount: \$429,000 USD (2 years)

PI: Murray Patterson, Co-I: Alexander Kirpich

○ The objective of this project is to develop a universal analysis framework for large-scale studies on gut microbiome shotgun metagenomics sequencing data. The application of such a framework to the rapidly growing collections of such data will unveil links to diseases and disorders that previous smaller datasets could not reveal.

- 2023 Tracing seeding metastasis histories from CRISPR-Cas9 sc-seq, National Cancer Institute, Amount: \$383,844 USD (2 years)

PI: Murray Patterson, Co-I: Pavel Skums, External: Sagi Snir (Univ. Haifa, Israel)

○ This project aims to develop a computationally efficient methodology, and resulting toolkit, for phylogenetic and phylodynamic inference from CRISPR-Cas9 single-cell lineage tracing data, with a special emphasis on scalability and accuracy. Such a tool will then need to be extensively and comprehensively benchmarked using the available lineage tracing data.

- 2023 Data-driven support system for computer-aided antibody design, National Institutes of Health, Amount: \$348,948 USD (2 years)

PI: Murray Patterson, External: Muhammad Shoaib (PI), Imdad Ullah Khan, Khurram Bashir (LUMS, Pakistan)

- Disease diagnosis, therapeutics, and biological research rely heavily on antibodies, however, antibody development is a time-consuming, expensive, and labor-intensive process requiring specialized infrastructure, trained personnel, and animal immunizations. The proposed research aims to develop an end-to-end pipeline with a user-friendly graphical interface that utilizes cutting-edge machine learning algorithms and data analysis techniques for the computer-aided design of antibodies, which will significantly reduce costs and time while ensuring high binding affinity and specificity. This advancement has the potential to accelerate the development of antibodies, leading to improved diagnostics, efficient therapies, enhanced understanding of biological systems, and ultimately better health outcomes for individuals and society as a whole.
- 2023 Reconciling geographic resolution and statistical robustness in cancer mapping using a novel partitioning algorithm, National Cancer Institute, Amount: \$429,000 USD (2 years)
PI: Murray Patterson, Co-I: Chetan Tiwari, Armin Mikler
 - Disease mapping methods developed in this project will provide more accurate and reliable representations of cancer incidence, prevalence, and mortality across communities. This improvement is crucial for identifying high-risk areas and deploying targeted prevention and treatment strategies more effectively. Ultimately, our work aims to contribute significantly to cancer control efforts, potentially leading to earlier detection, better resource allocation, and improved health outcomes in populations.
- 2023 Benchmarking tumor phylogeny reconstruction from scDNA-seq data, Chan Zuckerberg Initiative, Amount: \$199,777 USD (18 months)
PI: Murray Patterson, Co-I: Eric Gaucher, External: Simone Ciccolella (PI), Gianluca Della Vedova
 - To develop benchmarks and standards for existing and future tools which reconstruct tumor phylogenies from sc-DNA-seq data.
- 2024 A methodology for reconciling incompatible spatial boundaries for reliably linking cancer rates to social and environmental data, NCI, Amount: \$427,680 USD (2 years)
PI: Murray Patterson, Co-I: Chetan Tiwari, Armin Mikler
 - We develop methods to reconcile misaligned boundaries, enabling the integration of data from different geographic regions for cancer risk analysis. This makes it possible to link neighborhood characteristics to cancer outcomes and to make resource allocation decisions.

Awards and Honors

- 2023 Nomination for membership to Sigma Xi, the scientific research honor society
- 2011 The Marie Curie Alain Bensoussan (ABCDE) Postdoctoral Fellowship of the European Research Consortium for Informatics and Mathematics (ERCIM)
Award of 60,300 € and 5000 € for travel, in order to fully fund 2 years of postdoctoral study in the European ERCIM member countries

- 2006 The Postgraduate Scholarship (PGS) of the Natural Sciences and Engineering Research Council (NSERC) of Canada
Award of \$63,000 CAD in order to fully fund 3 years of postgraduate (PhD) research
- 2006 Simon Fraser University Computing Science Graduate Fellowship
Award of \$3000 CAD towards funding postgraduate research
- 2005 Simon Fraser University Computing Science Graduate Fellowship
Award of \$3000 CAD towards funding postgraduate research
- 2002 The Undergraduate Student Research Award (USRA) of the Natural Sciences and Engineering Research Council (NSERC) of Canada
Award of \$6400 CAD in order to fully fund a summer of undergraduate research

Technical Skills

advanced	C/C++, Python, \LaTeX	7+ years experience
intermediate	Java, Unix tools, Shell programming	4+ years experience
basic	Matlab, R, Prolog, Haskell	2+ years experience

Languages

English	maternal language	
French	second language	conversational and technical fluency
Italian	intermediate	comprehension and basic conversational skills
Spanish	intermediate	comprehension and basic conversational skills
中文	basic	basic words and phrases

Publications

Journal Articles

1. Simone Ciccolella, Murray Patterson, Iman Hajirasouliha, and Gianluca Della Vedova. Cancer progression inference using a finite-state model to allow recurrences and losses of mutations. *Neural Computing and Applications*, 2025. doi:10.1007/s00521-025-11474-1.
2. Sarwan Ali, Tamkanat E. Ali, and Murray Patterson. Hash-binding: DNA-protein binding prediction using hashing-based embedding. *Neural Computing and Applications*, 2025. doi:10.1007/s00521-025-11349-5.
3. Sarwan Ali, Tamkanat E. Ali, Haris Mansoor, Prakash Chourasia, and Murray Patterson. Hist2Vec: a histogram and kernel-based embedding method for molecular sequence analysis. *Expert Systems with Applications*, 273:126859, 2025. doi:10.1016/j.eswa.2025.126859.
4. Sarwan Ali, Madiha Shabbir, Haris Mansoor, Prakash Chourasia, and Murray Patterson. Elliptic geometry-based kernel matrix for improved biological sequence classification. *Knowledge-Based Systems*, 304:112479, 2024. doi:10.1016/j.knsys.2024.112479.
5. Zahra Tayebi, Sarwan Ali, and Murray Patterson. TCellR2Vec: Efficient feature selection for TCR sequences for cancer classification. *PeerJ Computer Science*, 10:e2239, 2024. doi:10.7717/peerj-cs.2239.
6. Sarwan Ali, Tamkanat E. Ali, Taslim Murad, Haris Mansoor, and Murray Patterson. Molecular sequence classification using efficient kernel based embedding. *Information Sciences*, 679:121100, 2024. doi:10.1016/j.ins.2024.121100.
7. Sarwan Ali, Prakash Chourasia, and Murray Patterson. From PDB files to protein features: a comparative analysis of PDB bind and STCRDAB datasets. *Medical & Biological Engineering & Computing*, 62:2449–2483, 2024. doi:10.1007/s11517-024-03074-3.
8. Zahra Tayebi, Sarwan Ali, Taslim Murad, Imdad Ullah Khan, and Murray Patterson. PseAAC2Vec protein encoding for TCR protein sequence classification. *Computers in Biology and Medicine*, 170:107956, 2024. doi:10.1016/j.combiomed.2024.107956.
9. Sarwan Ali, Prakash Chourasia, and Murray Patterson. When protein structure embedding meets large language models. *MDPI Genes*, 15(1):25, 2023. doi:10.3390/genes15010025.
10. Sarwan Ali and Murray Patterson. Improving IOSOMAP efficiency with RKS: a comparative study with t-distributed neighbor embedding on protein sequences. *MDPI J — Multidisciplinary Scientific Journal*, 6(4):579–591, 2023. doi:10.3390/j6040038.
11. Taslim Murad*, Sarwan Ali*, Imdad Ullah Khan, and Murray Patterson. Spike2CGR: an efficient method for spike sequence classification using chaos game representation. *Machine Learning*, 112:3633–3658, 2023. doi:10.1007/s10994-023-06371-4.

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12. Sarwan Ali, Prakash Chourasia, Zahra Tayebi, Babatunde Bello, and Murray Patterson. ViralVectors: compact and scalable alignment-free virome feature generation. *Medical & Biological Engineering & Computing*, 2023. doi:10.1007/s11517-023-02837-8.
13. Taslim Murad, Sarwan Ali, and Murray Patterson. Exploring the potential of GANs in biological sequence analysis. *MDPI Biology*, 12(6):854, 2023. doi:10.3390/biology12060854.
14. Bikram Sahoo*, Sarwan Ali, Pin-Yu Chen, Murray Patterson, and Alexander Zelikovskiy*. Assessing the resilience of machine learning classification algorithms on SARS-CoV-2 genome sequences generated with long-read specific errors. *Biomolecules*, 13(6):934, 2023. doi:10.3390/biom13060934.
15. Danushka Bandara, Karen Exantus, Cristian Navarro-Martinez, Murray Patterson, and Ashley Byun. Identifying distinguishing acoustic features in felid vocalizations based on call type and species classification. *Acoustics Australia*, 2023. doi:10.1007/s40857-023-00298-5.
16. Sarwan Ali, Babatunde Bello, and Murray Patterson. Solvent accessibility of coronaviridae spike proteins through the lens of information gain. *MDPI J — Multidisciplinary Scientific Journal*, 6(2):236–247, 2023. doi:10.3390/j6020018.
17. Sarwan Ali, Bikram Sahoo, Alexander Zelikovskiy, Pin-Yu Chen, and Murray Patterson. Benchmarking machine learning robustness in covid-19 genome sequence classification. *Scientific Reports*, 13(1):4154, 2023. doi:10.1038/s41598-023-31368-3.
18. Prakash Chourasia, Sarwan Ali, Simone Ciccolella, Gianluca Della Vedova, and Murray Patterson. Reads2Vec: Efficient embedding of raw high-throughput sequencing reads data. *Journal of Computational Biology*, 2022. doi:10.1089/cmb.2022.0424.
19. Sarwan Ali, Babatunde Bello, Zahra Tayebi, and Murray Patterson. Characterizing SARS-CoV-2 spike sequences based on geographical location. *Journal of Computational Biology*, 2022. doi:10.1089/cmb.2022.0391.
20. Sarwan Ali, Bikram Sahoo, Muhammad Asad Khan, Alexander Zelikovskiy, Imdad Ullah Khan*, and Murray Patterson*. Efficient approximate kernel based spike sequence classification. *Transactions on Computational Biology and Bioinformatics*, 2022. doi:10.1109/TCBB.2022.3206284.
21. Kaustubh Khandai, Cristian Navarro-Martinez, Brendan Smith, Rebecca Buonopane, S. Ashley Byun*, and Murray Patterson*. Determining significant correlation between pairs of extant characters in a small parsimony framework. *Journal of Computational Biology*, 29(10):1132–1154, 2022. doi:10.1089/cmb.2022.0141.
22. Sarwan Ali, Babatunde Bello, Prakash Chourasia, Ria Thazhe Punathil, Yijing Zhou, and Murray Patterson. PWM2Vec: An efficient embedding approach for viral host specification from coronavirus spike sequences. *MDPI Biology*, 11(3):418, 2022. doi:10.3390/biology11030418.
23. Sarwan Ali, Yijing Zhou, and Murray Patterson. Efficient analysis of COVID-19 clinical data using machine learning models. *Medical & Biological Engineering & Computing*, 60(7):1881–1896, 2021. doi:10.1007/s11517-022-02570-8.

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24. Zahra Tayebi, Sarwan Ali, and Murray Patterson. Robust representation and efficient feature selection allows for effective clustering of SARS-CoV-2 variants. *Algorithms*, 14(12):348, 2021. doi:10.3390/a14120348.
25. Sarwan Ali, Simone Ciccolella, Lorenzo Lucarella, Gianluca Della Vedova, and Murray Patterson. Simpler and faster development of tumor phylogeny pipelines. *Journal of Computational Biology*, 28(11):1142–1155, 2021. doi:10.1089/cmb.2021.0271.
26. Andrew Melnyk, Fatemeh Mohebbi, Sergey Knyazev, Bikram Sahoo, Roya Hosseini, Pavel Skums, Alex Zelikovsky*, and Murray Patterson*. From alpha to zeta: Identifying variants and subtypes of SARS-CoV-2 via clustering. *Journal of Computational Biology*, 28(11):1113–1129, 2021. doi:10.1089/cmb.2021.0302.
27. Simone Ciccolella*, Murray Patterson*, Paola Bonizzoni, and Gianluca Della Vedova. Effective clustering for single cell sequencing cancer data. *IEEE Journal of Biomedical and Health Informatics*, 25(11):4068–4078, 2021. doi:10.1109/JBHI.2021.3081380.
28. Simone Ciccolella, Mauricio Soto, Murray D. Patterson, Gianluca Della Vedova, Iman Hajirasouliha, and Paola Bonizzoni. Gpps: An ILP-based approach for inferring cancer progression with mutation losses from single cell data. *BMC Bioinformatics*, 21(1):413, 2020. doi:10.1186/s12859-020-03736-7.
29. Simone Ciccolella, Camir Ricketts, Mauricio Soto Gomez, Murray Patterson, Dana Silverbush, Paola Bonizzoni, Iman Hajirasouliha, and Gianluca Della Vedova. Inferring cancer progression from single-cell sequencing while allowing mutation losses. *Bioinformatics*, 37(3):326–333, 2020. doi:10.1093/bioinformatics/btaa722.
30. Raffaella Rizzi, Stefano Beretta, Murray Patterson, Yuri Pirola, Marco Previtali, Gianluca Della Vedova, and Paola Bonizzoni. Overlap graphs and de Bruijn graphs: data structures for de novo genome assembly in the big data era. *Quantitative Biology*, 7(4):278–292, 2019. doi:10.1007/s40484-019-0181-x.
31. Stefano Beretta*, Murray Patterson*, Simone Zaccaria, Gianluca Della Vedova, and Paola Bonizzoni. HapCHAT: Adaptive haplotype assembly for efficiently leveraging high coverage in long reads. *BMC Bioinformatics*, 19(1):252, 2018. doi:10.1186/s12859-018-2253-8.
32. Wandrille Duchemin, Yoann Anselmetti, Murray Patterson, Yann Ponty, S  verine B  rard, Cedric Chauve, Celine Scornavacca, Vincent Daubin, and Eric Tannier. DeCoSTAR: Reconstructing the ancestral organization of genes or genomes using reconciled phylogenies. *Genome Biology and Evolution*, 9(5):1312–1319, 2017. doi:10.1093/gbe/evx069.
33. Andrea Bracciali, Marco Aldinucci, Murray Patterson, Tobias Marschall, Nadia Pisanti, Ivan Merelli, and Massimo Torquati. PWhatsHap: Efficient haplotyping for future generation sequencing. *BMC Bioinformatics*, 17(11):342, 2016. doi:10.1186/s12859-016-1170-y.
34. Murray Patterson*, Tobias Marschall*, Nadia Pisanti, Leo van Iersel, Leen Stougie, Gunnar W. Klau[†], and Alexander Schoenhuth[†]. WhatsHap: Weighted haplotype assembly for future-generation sequencing reads. *Journal of Computational Biology*, 22(6):498–509, 2015. doi:10.1089/cmb.2014.0157.

35. Murray Patterson, Gergely Szöllősi, Vincent Daubin, and Eric Tannier. Lateral gene transfer, rearrangement, reconciliation. *BMC Bioinformatics*, 14(15):S4, 2013. doi:10.1186/1471-2105-14-S15-S4.
36. Mohammed El-Kebir*, Tobias Marschall*, Inken Wohlers*, Murray Patterson, Jaap Heringa, Alexander Schoenhuth, and Gunnar W. Klau. Mapping proteins in the presence of paralogs using units of coevolution. *BMC Bioinformatics*, 14(15):S18, 2013. doi:10.1186/1471-2105-14-S15-S18.
37. Ján Maňuch*, Murray Patterson*, Roland Wittler*, Cedric Chauve, and Eric Tannier. Linearization of ancestral multichromosomal genomes. *BMC Bioinformatics*, 13(19):S11, 2012. doi:10.1186/1471-2105-13-S19-S11.
38. Ján Maňuch*, Murray Patterson*, and Cedric Chauve. Hardness results on the gapped consecutive-ones property problem. *Discrete Applied Mathematics*, 160(18):2760–2768, 2012. doi:10.1016/j.dam.2012.03.019.
39. Ján Maňuch* and Murray Patterson*. The complexity of the gapped consecutive-ones property problem for matrices of bounded maximum degree. *Journal of Computational Biology*, 18(9):1243–1253, 2011. doi:10.1089/cmb.2011.0128.
40. Roland Wittler, Ján Maňuch*, Murray Patterson*, and Jens Stoye. Consistency of sequence-based gene clusters. *Journal of Computational Biology*, 18(9):1023–1039, 2011. doi:10.1089/cmb.2011.0083.

Conference Proceedings

41. Sarwan Ali, Taslim Murad, Prakash Chourasia, Haris Mansoor, Imdad Ullah Khan, Pin-Yu Chen, and Murray Patterson. Position specific scoring is all you need? Revisiting protein sequence classification tasks. In the 22nd RECOMB Conference on Comparative Genomics (RECOMB-CG, Seoul, South Korea, 2025). 2025. to appear.
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