

Murray Patterson

Curriculum Vitae

Education

- 2006—2011 **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

- 2016— **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
- 2018 **Project Collaborator**, *Experimental Algorithmics Lab, Informatics Department, Università degli Studi di Milano-Bicocca, Milano, Italy.*
Advisor: Raffaella Rizzi
The development of efficient algorithms for comparing evolutionary histories of cancerous tumours as inferred by the latest methods
- 2017 **Project Collaborator**, *Experimental Algorithmics Lab, Informatics Department, Università degli Studi di Milano-Bicocca, Milano, Italy.*
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
- 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

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- 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
- 2004 **Systems Administrator**, *Department of Mathematics, Acadia University*, Wolfville, Nova Scotia, Canada.
 Directors: Richard Karsten and Holger Teismann
 Leading the installation and maintenance of computers and software for doing numerical simulations of large-scale systems of differential equations
- 2003 **Research Assistant**, *Department of Mathematics, Acadia University*, Wolfville, Nova Scotia, Canada.
 Advisor: Franklin Mendivil
 Performing the development in C/C++ of methods for image compression using wavelets
- 2002 **Undergraduate Research Assistant**, *Department of Computer Science, Dalhousie University*, Halifax, Nova Scotia, Canada.
 Advisor: Raymond J. Spiteri
 Developing of a suite of ordinary differential equation solvers in Java. This would become the subject of my Undergraduate Honors Thesis
 Research was funded by an Undergraduate Student Research Award (USRA) of the Natural Sciences and Engineering Research Council (NSERC) of Canada

Teaching Experience

- 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
- 2004—2005 **Teaching Assistant**, *Department of Computing Science, Simon Fraser University*, Burnaby, British Columbia, Canada.
 Advisor: F. Warren Burton
 Giving tutorials, holding office hours and marking papers for a course on functional and logic programming (Prolog and Haskell). Occasionally I gave a course lecture

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Volunteer Experience

- 2017— **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.

Awards

- 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	<i>7+ years experience</i>
intermediate	Java, Unix tools, Shell programming	<i>4+ years experience</i>
basic	Matlab, R, Prolog, Haskell	<i>2+ years experience</i>

Languages

English	maternal language	
French	second language	<i>conversational and technical fluency</i>
Italian	intermediate	<i>comprehension and basic conversational skills</i>
中文	basic	<i>basic words and phrases</i>

Publications

Current Preprints

1. Simone Ciccolella*, Murray Patterson*, Paola Bonizzoni and Gianluca Della Vedova. **Effective clustering for single cell sequencing cancer data**. *bioRxiv*, 586545 (2019).

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2. Simone Ciccolella, Mauricio Soto Gomez, Murray Patterson, Gianluca Della Vedova, Iman Hajirasouliha and Paola Bonizzoni. **Inferring Cancer Progression from Single Cell Sequencing while allowing loss of mutations.** *bioRxiv*, 268243 (2018).
3. Marcel Martin*, Murray Patterson*, Shilpa Garg, Sarah O. Fischer, Nadia Pisanti, Gunnar W. Klau, Alexander Schönhuth and Tobias Marschall. **WhatsHap: fast and accurate read-based phasing.** *bioRxiv*, 085050 (2016).
4. Murray Patterson, Thomas Bernard and Daniel Kahn. **Correlated Evolution of Metabolic Functions over the Tree of Life.** *bioRxiv*, 093591 (2016).

Journal Articles

1. 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).
2. Wandrille Duchemin, Yoann Anselmetti, Murray Patterson, Yann Ponty, S everine B erard, Cedric Chauve, Celine Scornavacca, Vincent Daubin, Eric Tannier. **DeCoSTAR: Reconstructing the ancestral organization of genes or genomes using reconciled phylogenies.** *Genome Biology and Evolution*, **9**(5):1312–1319 (2017).
3. 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).
4. Murray Patterson*, Tobias Marschall*, Nadia Pisanti, Leo van Iersel, Leen Stougie, Gunnar W. Klau[†] and Alexander Schonhuth[†]. **WhatsHap: Weighted haplotype assembly for future-generation sequencing reads.** *Journal of Computational Biology*, **22**(6):498–509 (2015).
5. Murray Patterson, Gergely Sz oll osi, Vincent Daubin and Eric Tannier. **Lateral Gene Transfer, Rearrangement, Reconciliation.** *BMC Bioinformatics*, **14**(15):S4 (2013).
6. Mohammed El-Kebir*, Tobias Marschall*, Inken Wohlers*, Murray Patterson, Jaap Heringa, Alexander Sch onhuth and Gunnar W. Klau. **Mapping proteins in the presence of paralogs using units of coevolution.** *BMC Bioinformatics*, **14**(15):S18 (2013).
7. J an Ma uch*, Murray Patterson*, Roland Wittler*, Cedric Chauve and Eric Tannier. **Linearization of ancestral multichromosomal genomes.** *BMC Bioinformatics*, **13**(19):S11 (2012).
8. J an Ma uch*, Murray Patterson* and Cedric Chauve. **Hardness results on the gapped consecutive-ones property problem.** *Discrete Applied Mathematics*, **160**(18):2760–2768 (2012).
9. J an Ma uch* 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).

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10. Roland Wittler, Ján Maňuch*, Murray Patterson* and Jens Stoye. **Consistency of sequence-based gene clusters**. *Journal of Computational Biology*, **18**(9):1023–1039 (2011).

Refereed Conference Proceedings

1. Giulia Bernardini*, Paola Bonizzoni*, Gianluca Della Vedova* and Murray Patterson*. **A rearrangement distance for fully-labelled trees**. In proceedings of the 30th Annual *Symposium on Combinatorial Pattern Matching* (CPM, Pisa, Italy, 2019), to appear.
2. Simone Ciccolella, Mauricio Soto, Murray 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**. In proceedings of the 8th IEEE *International Conference on Computational Advances in Bio and Medical Sciences* (ICCABS, Las Vegas, USA, 2018), 1–1 (2018). *Invited for publication in special issue of BMC Bioinformatics*.
3. Gianluca Della Vedova*, Murray Patterson*, Raffaella Rizzi* and Mauricio Soto*. **Character-based Phylogeny Construction and its Application to Tumor Evolution**. In Proceedings of the 13th Conference on *Computability in Europe* (CiE, Turku, Finland, 2017), LNCS **10307**:3–13 (2017).
4. Marco Aldinucci, Andrea Bracciali, Tobias Marschall, Murray Patterson, Nadia Pisanti and Massimo Torquati. **High-Performance Haplotype Assembly**. In Post Conference Proceedings of the 11th *International Meeting on Computational Intelligence Methods for Bioinformatics and Biostatistics* (CIBB, Cambridge, UK, 2014), LNCS **8623**:245–258 (2015).
5. Murray Patterson*, Tobias Marschall*, Nadia Pisanti, Leo van Iersel, Leen Stougie, Gunnar W. Klau[†] and Alexander Schönhuth[†]. **WhatsHap: Haplotype assembly for future-generation sequencing reads**. In Proceedings of the 18th Annual *International Conference on Research in Computational Molecular Biology* (RECOMB, Pittsburgh PA, USA, 2014), LNCS **8394**:237–249 (2014).
6. Cedric Chauve*, Murray Patterson* and Ashok Rajaraman*. **Hypergraph covering problems motivated by genome assembly questions**. In Proceedings of the *International Workshop on Combinatorial Algorithms* (IWOCA, Rouen, France, 2013), LNCS **8288**:428–432 (2013).
7. Ján Maňuch*, Murray Patterson*, Roland Wittler*, Cedric Chauve and Eric Tannier. **Linearization of ancestral multichromosomal genomes**. In Proceedings of the 12th Annual *Cologne-Twente Workshop on Graphs and Combinatorial Optimization* (CTW, Enschede, The Netherlands, 2013), 169–173 (2013).
8. Cedric Chauve*, Ján Maňuch*, Murray Patterson* and Roland Wittler*. **Tractability results for the consecutive-ones property with multiplicity**. In Proceedings of the 22nd Annual *Symposium on Combinatorial Pattern Matching* (CPM, Palermo, Italy, 2011), LNCS **6661**:90–103 (2011).

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9. Ján Maňuch*, Murray Patterson* and Arvind Gupta. **Towards a characterization of the generalized cladistic character compatibility problem for non-branching character trees.** In Proceedings of the 7th *International Symposium on Bioinformatics Research and Applications* (ISBRA, Changsha, China, 2011), LNCS **6674**:440–451 (2011).
10. Ján Maňuch* and Murray Patterson*. **The complexity of the gapped consecutive-ones property problem for matrices of bounded maximum degree.** In Proceedings of the 8th Annual *RECOMB Comparative Genomics* (Ottawa, Canada, 2010), LNBI **6398**:278–289 (2010).
11. Ján Maňuch*, Murray Patterson*, Sheung-Hung Poon* and Chris Thachuk*. **Complexity of finding non-planar rectilinear drawings of graphs.** In Proceedings of the 18th *International Symposium on Graph Drawing* (GD, Konstanz, Germany, 2010), LNCS **6502**:305–316 (2011).
12. Cedric Chauve*, Ján Maňuch* and Murray Patterson*. **On the gapped consecutive-ones property.** In Proceedings of the *European Conference on Combinatorics, Graph Theory and Applications* (EuroComb, Bordeaux, France, 2009), ENDM **34**:121–125 (2009).
13. Ján Maňuch*, Murray Patterson* and Arvind Gupta. **On the generalised character compatibility problem for non-branching character trees.** In Proceedings of the 15th Annual *International Computing and Combinatorics Conference* (COCOON, Niagara Falls, USA, 2009), LNCS **5609**:268–276 (2009).
14. Murray Patterson, Yongmei Liu, Eugenia Ternovska and Arvind Gupta. **Grounding for model expansion in k -guarded formulas with inductive definitions.** In Proceedings of the 20th *International Joint Conferences on Artificial Intelligence* (IJCAI, Hyderabad, India, 2007), 161–166 (2007).

Theses

- PhD Murray Patterson. **Variants of the consecutive-ones property motivated by the reconstruction of ancestral species.** PhD Thesis, Department of Computer Science, University of British Columbia, Canada, 2012.
- MSc Murray Patterson. **Grounding for model expansion in k -guarded formulas.** Masters Thesis, Department of Computing Science, Simon Fraser University, Canada, 2006.
- BSc Murray Patterson. **Implementing Runge-Kutta solvers in Java.** Bachelor of Science Honours Thesis, Department of Computer Science, Acadia University, Canada, 2003.

Conference Contributions

1. Murray Patterson, Thomas Bernard and Daniel Kahn. **Correlated evolutionary scenarios of metabolic functions.** *Lyon Systems Biology* (LyonSysBio, Villeurbanne, France, 2015).

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2. Murray Patterson, Thomas Bernard and Daniel Kahn. **Correlated evolutionary scenarios of metabolic functions.** The annual meeting of the *Society for Molecular Biology and Evolution* (SMBE, Vienna, Austria, 2015).
3. Murray Patterson, Thomas Bernard and Daniel Kahn. **Correlated evolutionary scenarios of metabolic functions.** *Mathematical and Computational Evolutionary Biology* (MCEB, Porquerolles, France, 2015).
4. Murray Patterson, Thomas Bernard and Daniel Kahn. **Correlated evolutionary scenarios of metabolic functions.** *Advanced Lecture Course on Computational Systems Biology* (CompSysBio, Aussois, France, 2015).
5. Murray Patterson, Gergely Szöllösi, Vincent Daubin and Eric Tannier. **Lateral gene transfer, rearrangement, reconciliation.** *Mathematical and Computational Evolutionary Biology* (MCEB, Hérault, France, 2014).
6. Cedric Chauve*, Murray Patterson* and Ashok Rajaraman*. **Hypergraph covering problems motivated by genome assembly questions.** *Netherlands Consortium for Systems Biology* (NCSB, Egmond aan Zee, Netherlands, 2013).
7. Murray Patterson. **The reconstruction of ancestral genome organization in bacteria.** *Netherlands Bioinformatics Conference* (NBIC, Lunteren, Netherlands, 2013).
8. Cedric Chauve*, Murray Patterson* and Ashok Rajaraman*. **Hypergraph covering problems motivated by genome assembly questions.** *Models and Algorithms for Genome Evolution* (MAGE: honoring 50 years of research by David Sankoff, Montreal, Canada, 2013).
9. Ján Maňuch*, Murray Patterson*, Roland Wittler*, Cedric Chauve and Eric Tannier. **Linearization of ancestral multichromosomal genomes.** *Journées du Groupe de Travail sur la Génomique Comparative* (Journées GTGC, Lille, France, 2012).
10. Cedric Chauve*, Ján Maňuch* and Murray Patterson*. **The gapped consecutive-ones property.** The 3rd Biennial *Canadian Discrete and Algorithmic Mathematics Conference* (CanaDAM, Victoria, Canada, 2011).
11. Cedric Chauve*, Ján Maňuch* and Murray Patterson*. **The gapped consecutive-ones property.** The 15th Annual *International Conference on Research in Computational Molecular Biology* (RECOMB, Vancouver, Canada, 2011).
12. Cedric Chauve*, Ján Maňuch* and Murray Patterson*. **Hardness results for the gapped consecutive-ones property.** The 5th *Latin-American Algorithms, Graphs and Optimization Symposium* (LAGOS, Gramado, Brazil, 2009).
13. Murray Patterson, Yongmei Liu, Eugenia Ternovska and Arvind Gupta. **Grounding for model expansion in k -guarded formulas.** The 21st Annual *IEEE Symposium on Logic in Computer Science* (LICS, Seattle, USA, 2006).
14. Murray Patterson, Yongmei Liu, Eugenia Ternovska and Arvind Gupta. **Grounding for model expansion in k -guarded formulas.** *Search and Logic: Answer Set Programming and SAT* (LaSh, Seattle, USA, 2006).

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15. Murray Patterson and Raymond J. Spiteri. **odeToJava: A Java package of ordinary differential equation solvers**. *Atlantic Provinces Council on the Sciences Conference* (APICS, Sackville, Canada, 2002).

note In any publication listing containing a *, this indicates that all authors whose names are followed by a * have contributed equally to this publication. In order to be consistent, this means that for papers that list the names of authors alphabetically (which is a common practice amongst computer science and theoretical bioinformatics papers), there is a * following every name.

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