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1 Academic Degrees

mm/yyyy	Degree	Field	Institution	Thesis Topic
04/2024	Ph.D. <i>Thesis accepted as-is</i>	Computing Science	Simon Fraser University	Computational reconstruction of multiscale interaction in multichannel superresolution microscopy
		Supervisors: Prof. Ghassan Hamarneh (SFU) Prof. Keval Vora (SFU) DOI: Under Preparation		
07/2017	M.Sc. <i>with greatest distinction</i>	Computer Science	University of Antwerp	Convergence of Symbolic Regression Using Metaheuristics
		Supervisor: Prof. Jan Broeckhove DOI: 10.5281/zenodo.11549519		
07/2015	B.Sc. <i>with great distinction</i>	Computer Science	University of Antwerp	A Parallel Discrete Event Simulator in C++
		Supervisors: Prof. Jan Broeckhove Dr. Kurt Vanmechelen		

2 Research Experience

2.1 Employment History at Academic Institutions

from-to (mm/yyyy)	Position	Department and Institution
10/2023-04/2024	Graduate Academic Assistant	Life Sciences Institute, University of British Columbia, Canada. (Host Prof. Ivan Robert Nabi)
09/2023-12/2023	Teaching Assistant	School of Computing Science, Simon Fraser University, Canada. (CMPT-340: Biomedical Computing, Prof. Ghassan Hamarneh)
09/2018-06/2019	Research Internship (NSERC)	Life Sciences Institute, University of British Columbia, Canada. (Host Prof. Ivan Robert Nabi)
09/2017-08/2023	Graduate Academic Assistant	School of Computing Science, Simon Fraser University, Canada (Host Prof. Ghassan Hamarneh)
09/2016-07/2017	Research Internship	MOSAIC Research Group, University of Antwerp, Belgium (Host Prof. Jan Broeckhove)

2.2 Academic Community Service

2.2.1 Independent Reviewer

In addition to supervised journal and conference reviewer duties, I have served as an independent reviewer for the following journals:

- IEEE Transactions In Medical Imaging ([IEEE-TMI](#))
- Simulation (SAGE)
- Journal of Open Source Software ([JOSS](#))

2.2.2 Supervision

Supervision Assistance During my Ph.D. I assisted/supervised the following students supervised by Prof. Ghassan Hamarneh.

- Kathleen Moriarty, MSc, XAI driven weakly supervised detection of Zika infected cell in Stimulated Emission Depletion (STED) [26] Super Resolution Microscopy (SRM) (Nat. Sci. Rep [11])
- Ashwin Samudre, MSc., Unsupervised equivariant reconstruction of Endoplasmic Reticulum (ER) tubules in microscopy. (Under review, Nat. Com.)
- Christian Hallgrimson, MSc., Adversarial symmetric MIL-driven detection of label-dependent protein conformation changes in Single Molecule Localization Microscopy (SMLM) [24]. Under preparation.

2.3 Inclusion, Equity and diversity contributions

I helped organize and presented an invited talk during the University of British Columbia, Vancouver, Canada (UBC) ‘Geering Up’ workshop for underrepresented students, where I invited other scholars, and provided extra material. The participants were shown what AI is in practice, and what its risks are in real life applications, including medical imaging. In my spare time, I have volunteered for Ride for Refuge, an organization that helps guide and support refugees through the Canadian asylum application process.

2.4 Professional Membership

- ISCB Student member
- UBC Vision Cluster student member
- ASCB Student member

2.5 Professional Development

In order to keep my academic, professional, and technical skillset up to date, I attend frequent workshops. These include but are not limited to: accelerated computing workshops, voice coaching for more effective presentation, cluster computing workshops on more effective hyperscale deployment of scientific computing, and writing consultations.

3 Teaching

3.1 Experience

While most of my Ph.D. was funded by graduate awards, scholarships or fellowships, I did serve during Fall 2023 I was a full time Teaching Assistant for Prof. Hamarneh’s CMPT340 ‘Biomedical Computing’ course. My duties were focused on helping students develop projects in teams of up to five students that apply or develop novel deep learning algorithms to open problems in biomedical computing. This assignment proved invaluable in understanding how students from different curricular and societal backgrounds require a different approach in guidance and mentoring to successfully complete the course. At the same time, as a graduate student I was thrilled to be able to introduce the undergraduate students to open research problems and remove some thresholds that prevent them from participating in real-world problem solving. This included showing them how to use LaTeX, how to organize code version management, how to define the research problem succinctly, identify related work and open datasets, and overcome challenges in implementing and designing novel solutions.

3.2 Teaching Vision

To fill the current gap in interdisciplinary course offerings, I aim to develop a curriculum that teaches students how state-of-the-art computational algorithms can help real world problems in biomedical computing, including but not limited modalities such as diffuse optical tomography (DOT), SMLM, and confocal microscopy. Specifically, my focus will be on accurate, reproducible quantification in a weakly supervised setting, aligned with my expertise. During my bachelor, master, and doctorate I found the courses that split between theory and project the most effective, I intend to structure my curriculum therefore in this way. The outcome of the course would be to offer each student, independent of their background, an equal opportunity to improve their skillset both as a critical thinker and an application specialist. Given that in my research teamwork across disciplines and cultures has been critical to publications, I will favor and reward teamwork across backgrounds and skillsets of students to encourage students to mentor each other, while improving their soft skills, critical to any further career in industry or academia.

4 Research Profile

4.1 Executive Summary

I focus on the design of scalable, robust, and interpretable interaction analysis algorithms in biomedical computing, with a specific application focus on state of the art [SRM](#) modalities such as 3D [STED](#) and [SMLM](#). These algorithms are deployed by cellular biologists with the objective of discovering novel functional mechanisms in cellular biology up to the nanometer scale. Given the absence of ground truth, implied by discovery, I focus on self- and weakly supervised learning paradigms. My background in the design of optimized parallel discrete event simulation ([DEVS](#)) ([PDEVS](#)) engines allows me to augment existing sparsely annotated data with tractable simulations to verify, validate, and train more complex models. Given that cellular health is determined by a complex network of organelles and protein structures in equilibria, a significant part of my research is framed extreme value analysis or imbalanced regression to ensure minute genomic or pathologic driven differences that cause major symptoms are captured accurately.

4.2 Research Trajectory

4.2.1 Parallel Discrete Event Simulation with Runtime Switchable Execution Policies

[DEVS](#) is a paradigm that enables computational modelling of very large-scale simulations of discrete ‘agents’, with a arbitrarily complex state. Agents interact by exchanging messages across dynamic topologies. In this context I developed a C++ state of the art parallel [DEVS](#) simulation engine with thread local memory management [19]. Parallel [DEVS](#) can be executed using an optimistic or conservative scheduling policy. Under an optimistic policy agents do not wait until all messages have been delivered, requiring occasional roll backs (‘speculative execution’). Excessive rollbacks under heavy bursts of messaging can negate an otherwise marked speedup in runtime. In conservative execution messaging constraints are strict, at a cost of reduced performance. Given that the topology of interaction is not known in the general case, it is impossible to determine which policy will be optimal ahead of time for the practitioner. In a subsequent work [17], we extended our engine to switch ‘at runtime’ between parallel execution policies. This required exceptional care in engine and synchronization design as automatic memory management was shown to be too slow with up to 2 orders of magnitude difference. The end result offered practitioners a simulation engine that could switch, conditional on tracing triggers, between parallel execution policies, ensuring optimal performance for each new use case.

4.2.2 Distributed Hyperheuristics Models for Epidemiology Simulations

Nation scale agent based simulation can help model the spread and impact of disease in large populations. Specifically, interventions and ‘what if’ scenarios can be evaluated ‘in silico’, giving stakeholders at agency and state level key insights into the most effective policy. Such simulations are emburdened by a very large parameter space, and can in themselves become intractable, even when executed on clusters. In order to address this one can learn, in supervised setting, a ‘surrogate model’ that encodes the relation between the use case, parameters, and the outcome of the simulation, without having to run the simulation in the first place. Interpretability of the model enables higher-level reasoning on the impact of interventions in epidemics. Therefore, this problem statement is one of ‘symbolic regression’, where the output and input are mapped onto each other by a closed form mathematical equation that is derived by supervised learning. In this project I improved the convergence of existing approaches using genetic programming (hyperheuristics) by combining them with swarm-based optimization algorithms (metaheuristics). In addition, I showed that a distributed (MPI) set of solvers could improve convergence, and tested which topologies gave best convergence [16].

4.2.3 Multichannel interaction analysis in [SRM](#)

In my Ph. D. (Thesis defended April 2024, Simon Fraser University, accepted ‘as-is’) I focus on reconstructing interaction between subcellular organelles and proteins where, technically, they cannot be observed.

Improving unbiased acquisition in SMLM A first project tackled the bias that exists in multichannel SMLM reconstructions where the localization algorithm can be disrupted by high density emissions. In ERGO [10] we use an LSTM [hochreiter1997long] and graph heuristic to predict emission density, thus enabling accurate and unbiased localization across channels. This in turn is a key requirement for interaction analysis. Our contribution outperformed existing approaches in accuracy and balance of prediction.

Robust and unbiased weakly supervised object detection and localization In order to detect interaction, robust and noise-invariant detection and localization of objects is critical. In SPECHT [8] we developed an weakly supervised object detection (WSOD) algorithm that uses a self-tuning object detection stage to negate variable signal to noise ratio (SNR), common in STED. Second, our contrastive learning stage then learns which objects are unique, conditional on the genomic or treatment label of the cell. Uniquely, our approach has provable lower and upper boundaries for each object, and can be applied in hierachical label settings.

Unsupervised subprecision interaction detection SRM does not always have the precision to observe the changes cellular biologists are interested in, even though it dramatically increases the precision of object detection compared to diffraction limited microscopy. Computing science fills in the hole by ‘reconstructing’ what can only be partially seen. In other words, the objective is to detect objects below the precision of the system, e.g. ‘subprecision’. In practice this means most of my algorithms take in multiple ‘channels’ of data, each captures a specific protein or organelle. The outcome then is the spatio-temporal ‘interaction’ by proximity and state change between the identified objects. This requires highly robust, fair, and balanced algorithms, ideally with provable upper and lower limits to their performance. In the MCS-DETECT project we designed [4] an unsupervised reconstruction of subprecision ER-mitochondria contacts that is able to detect such variable width (20-80 nm) contacts in 3D STED volume of 2000x2000x70 voxels. Such spatial interactions are shown to be at the forefront of their associated dysfunction in neurodegenerative, metabolic, and psychiatric disease [13, 23, 21, 20, 22, 18, 15, 14, 12].

Reproducibility meets scalability: ‘recipe’ driven pipelines Critically, to ensure reproducible work, I developed a package ‘DataCurator’ [3] that is able to compose complex pipelines, without code, and execute them on clusters with arbitrary parallelism. Given the large scale of the data, designing scalable algorithms is key, as is parallelizing them. Most of my more recent algorithms are implemented in Julia, which allows for JIT or precompiled code near C/C++ speeds, while offering high level language features. Where possible I parallelize the algorithms, leveraging the knowledge from earlier work on C++ discrete event simulators.

Imbalance meets extreme value theory: towards stable detection of equilibrium perturbations Finally, cellular function is a carefully evolved equilibrium, where only small changes can have major effects (e.g. ‘disease’). In machine learning or statistical terms, this means I am typically focusing on minute differences between datasets, e.g. ‘severe imbalance’ or ‘extreme value’ problems. At the same time, discovery in this setting requires reconstructing those equilibria, often from image data alone, in an self-, unsupervised, or weakly supervised setting. In this aspect of my projects I discovered that under conditions that we ended up describing in closed form, one can inadvertently trigger a paradoxical reversal of research conclusions [5].

Parallel research trajectories: deep learning based multifrequency reconstruction During my research on the above topics I collaborated on a number of papers with the same themes of extreme imbalance, reconstruction in sparsely annotated weakly supervised data, and spatio-temporal reconstruction in different modalities. These projects enriched my own work, apart from being fun problems to solve, because they taught me to abstract problems away from the imaging modality and into abstract mathematical problem formulation, before selecting the most optimal closed form solution or approximate learned model.

4.3 Future work

In current and future projects I am exploring algorithms that solve problems at the intersection of implicit equilibria detection using implicitly learned continuous time Markov Chain (CTMC) [9]. Parallel to this I am exploring more robust, yet more sparse neural models such as differential neural networks, to tackle extreme imbalance defined problems in multichannel SRM interaction analysis. Specifically, I am exploring methods that only reconstruction interaction that is causally related to a genomic label. Finally, I intend to extend my work on symbolic regression to the complex nanometer scale physics of interaction in SRM. In parallel to these trajectories I am extending my work on distributed PDEVS to augment data required for validation, hypothesis testing, and learning more complex models. If you wish to collaborate on these topics, feel free to reach out.

4.4 Keywords

Computer Vision; Superresolution Microscopy; Imbalanced Regression, Interaction Analysis, Weakly-Supervised Learning, Machine Learning, Reconstruction, Statistics, Uncertainty, Vectorfields, Counting, Restoration, Denoising

ACM Classification Codes: I.: Computing Methodologies; I.2: Artificial Intelligence; I.2.6: Learning; I.2.10: Vision and Scene Understanding; I.4: Image Processing and

Computer Vision; I.4.3: Enhancement; I.4.6: Segmentation; I.4.9: Applications; J.: Computer Applications; J.3: Life and

Medical Sciences.

NSERC Research Subject Codes: 2603 Computer vision; 2708 Image and video processing; 1901 Biomedical technology; 1211 Medical and health sciences.

5 Research Awards, Scholarships and Recognitions

5.1 Scholarships

- Fall 2017 Graduate Fellowship
- Spring 2018 Computing Science Fellowship
- 2018-2019 NSERC-Create Bioinformatics PhD Scholarship
- Spring 2019 SFU CMPT Graduate Fellowship
- Fall 2019 SFU Big Data Fellowship
- Fall 2019 SFU Big Data Fellowship
- Spring 2020 SFU Faculty of Applied Sciences Graduate Fellowship
- Spring 2021 SFU Computing Science Graduate Fellowship
- Spring 2023 Helmut and Eppo Eppich Family Graduate Fellowship
- Spring 2024 Helmut and Eppo Eppich Family Graduate Fellowship

5.2 Thesis Awards

- (2024) Doctor in Philosophy in Computing Science, thesis defence accepted *as is* (CGPA 4.17), Simon Fraser University, Burnaby, Canada.
- (2017) Master of Science in Computer Science, *with greatest distinction, first of of class*, University of Antwerp, Belgium.
- (2015) Bachelor of Science in Computer Science, *with great distinction*, University of Antwerp, Belgium.

5.3 Publication Recognitions

- MCS-DETECT [4] was highlighted as a newsitem by [UBC](#) and [SFU](#), as well as selected as cover publication by Journal of Cell Biology ([JCB](#))

6 Publications

The following papers are *selected* papers, a full publication record is available on my ORCID page [0000-0001-6871-1165](#). Presentations and technical reports can be found on my website [vsert.com](#), including PDF links to all publications. Please do not hesitate to contact me if you are interested in author copies.

6.1 Journal

- Ivan Robert Nabi, **Ben Cardoen**, Khater, Guang Gao, Timothy H. Wong, and Ghassan Hamarneh. *AI-based analysis of super-resolution microscopy: Biological discovery in the absence of ground truth*. **The Journal Of Cell Biology (JCB)**, <https://doi.org/10.1083/jcb.202311073>, 2024
- Hanene Ben Yedder, **Ben Cardoen**, Majid Shokoufi, Farid Golnaraghi, and Ghassan Hamarneh. *Deep Orthogonal Multi-Wavelength Fusion for Tomogram-Free Diagnosis in Diffuse Optical Imaging*. **Computers in Biology and Medicine (CIBM)**, <https://doi.org/10.1016/j.compbiomed.2024.108676000:000>, 2024
- **Ben Cardoen**, Kurt Vandevoorde, Guang Gao, Milene Ortiz-Silva, Parsa Alan, Ellie Tiliakou, William Liu, A. Wayne Vogl, Ghassan Hamarneh, and Ivan Robert Nabi. *Membrane contact site detection (MCS-DETECT) reveals dual control of rough mitochondria-ER contacts* (Cardoen, Vandevoorde, Gao, and Ortiz: Joint first authors; Hamarneh and Nabi: Joint senior authors). **The Journal Of Cell Biology (JCB)**, <https://doi.org/10.1083/jcb.202206109>, 11 2023.
- **Ben Cardoen**, Hanene Ben Yedder, Sieun Lee, Ivan Robert Nabi, and Ghassan Hamarneh. *DataCurator.jl: Efficient, portable, and reproducible validation, curation, and transformation of large heterogeneous datasets using human-readable recipes compiled into machine verifiable templates*. **Bioinformatics Advances**, 3(1-5): <http://dx.doi.org/10.1093/bioadv/vbad068>, 2023.
- Parsa Alan, Bharat Joshi, **Ben Cardoen**, Kurt Vandevoorde, Guang Gao, Peter Overby, James D. Johnson, Ghassan Hamarneh, and Ivan Robert Nabi. *Basal Gp78-dependent mitophagy promotes mitochondrial health and limits mitochondrial ROS* (Alan, Joshi, Cardoen, and Vandevoorde: Joint first authors; Hamarneh and Nabi: Joint senior authors). **Cellular and Molecular Life Sciences (CMLS)**, 79(565):1-20, 2022. <http://dx.doi.org/10.1007/s00018-022-04585-8>, 2023.
- **Ben Cardoen**, Timothy H. Wong, Parsa Alan, Sieun Lee, Joanne Aiko Matsubara, Ivan Robert Nabi, and Ghassan Hamarneh. *SPECHT: Self-tuning Plausibility Based Object Detection Enables Quantification of Conflict in Heterogeneous Multi-scale Microscopy* (Nabi and Hamarneh: Joint senior authors). **PLOS ONE**, <http://dx.doi.org/10.1371/journal.pone.0276726> 2022.
- Hanene Ben Yedder, **Ben Cardoen**, and Ghassan Hamarneh. *Deep Learning for Biomedical Image Reconstruction: A Survey*. **Artificial Intelligence Review (AIRE)**, 54(1):215-251, <http://dx.doi.org/10.1007/s10462-020-09861-2> 2021.
- Hanene Ben Yedder, **Ben Cardoen**, Majid Shokoufi, Farid Golnaraghi, and Ghassan Hamarneh. *Multitask Deep Learning Reconstruction and Localization of Lesions in Limited Angle Diffuse Optical Tomography*. **IEEE Transactions on Medical Imaging (IEEE TMI)**, 41(3):515-530 <https://doi.org/10.1109/TMI.2021.3117276>, 2021.
- **Ben Cardoen**, Hanene Ben Yedder, Anmol Sharma, Keng C. Chou, Ivan Robert Nabi, and Ghassan Hamarneh. *ERGO: Efficient Recurrent Graph Optimized Emitter Density Estimation in Single Molecule Localization Microscopy*. **IEEE Transactions on Medical Imaging (IEEE TMI)**, 39(6):1942-1956, <http://dx.doi.org/10.1038/s41598-020-77170-3> 2020.

- Rory Long, Kathleen Moriarty, **Ben Cardoen**, Guang Gao, A. Wayne Vogl, François Jean, Ghassan Hamarneh, and Ivan Robert Nabi. *Super Resolution Microscopy and Deep Learning Identify Zika Virus Reorganization of the Endoplasmic Reticulum* (Long and Moriarty: Joint first authors; Hamarneh and Nabi: Joint senior authors). **Nature - Scientific reports**, 10(20937):1-18, <https://www.nature.com/articles/s41598-020-77170-3> 2020.
- **Cardoen Ben**, Manhaeve S, Van Tendeloo Y, Broeckhove J. *A PDEVS simulator supporting multiple synchronization protocols: implementation and performance analysis*. **SIMULATION**. 2018;94(4):281-300. <https://journals.sagepub.com/doi/full/10.1177/0037549717690826>, 2018

6.2 Conference

Author copies of presentations can be found at <https://vsert.com/page/publications/>

- **Ben Cardoen**, Kurt Vandevorde, Guang Gao, Milene Ortiz-Silva, Parsa Alan, Ellie Tiliakou, William Liu, A. Wayne Vogl, Ghassan Hamarneh, and Ivan Robert Nabi. *Membrane contact site detection (MCS-DETECT) reveals dual control of rough mitochondria-ER contacts* (Cardoen, Vandevorde, Gao, and Ortiz: Joint first authors; Hamarneh and Nabi: Joint senior authors). In **Keystone Symposia on Molecular and Cellular Biology - Organelle Membrane Contact Sites in Health and Disease** (Joint with: Mitochondria Signaling and Disease), pages 1, 2024.
- Jieyi Zheng, **Ben Cardoen**, Ghassan Hamarneh, and Ivan Robert Nabi. *Comparison of Specificity of Confocal and Super-Resolution Approaches to Detecting Mitochondria-ER Contact Sites* (Hamarneh and Nabi: Joint senior authors). In **Keystone Symposia on Molecular and Cellular Biology - Organelle Membrane Contact Sites in Health and Disease** (Joint with: Mitochondria Signaling and Disease), pages 1, 2024.
- Parsa Alan, Bharat Joshi, **Ben Cardoen**, Kurt Vandevorde, Guang Gao, Peter Overby, James D. Johnson, Ghassan Hamarneh, and Ivan Robert Nabi. *Basal Gp78-dependent mitophagy promotes mitochondrial health and limits mitochondrial ROS* (Alan, Joshi, Cardoen, and Vandevorde: Joint first authors; Hamarneh and Nabi: Joint senior authors). In **American Society of Cell Biology (ASCB) - Cell Bio**, 2022.
- Parsa Alan, Kurt Vandevorde, Bharat Joshi, **Ben Cardoen**, Guang Goa, Ghassan Hamarneh, and Ivan Robert Nabi. *Basal Gp78-dependent mitophagy promotes mitochondrial health and limits mitochondrial ROS*. In **UBC SBME 2022**.
- **Ben Cardoen**, Kurt Vandevorde, Guang Gao, Parsa Alan, Ellie Tiliakou, William Liu, A. Wayne Vogl, Ghassan Hamarneh, and Ivan Robert Nabi. *A novel sub-precision detection method (MCS-DETECT) identifies shape complexity of mitochondria-ER contacts (MERCs) in 3D STED super-resolution microscopy* (Cardoen, Vandevorde, and Gao: Joint first authors; Hamarneh and Nabi: Joint senior authors). In **American Society of Cell Biology (ASCB) - Cell Bio**, 2022.
- **Ben Cardoen** and Ghassan Hamarneh. *Learning to look beyond what we can see: Leveraging statistical learning to improve scientific discovery from fluorescence microscopy*. In **Biomedical Imaging and Artificial Intelligence (BMIAI) cluster Fall Research Showcase**, Vancouver, Canada, pages 1, 2021.
- **Ben Cardoen**, Timothy H. Wong, Parsa Alan, Sieun Lee, Joanne Aiko Matsubara, Ivan Robert Nabi, and Ghassan Hamarneh. *Self-tuning Weakly Supervised Object Detection (SPECHT) of Sub-Diffraction Limited Caveolae and Scaffold and Amyloid-Beta Deposits*. In **American Society of Cell Biology – Cell Bio 2021**, 2021.
- **Ben Cardoen**, Timothy H. Wong, Ivan Robert Nabi, and Ghassan Hamarneh. *Belief theory enables detection of Caveolae in superresolution microscopy*. In **Microscopy Societies Symposium - Advanced Imaging and Analysis at Nanoscale**, November 2021.
- **Ben Cardoen**, Timothy H. Wong, Parsa Alan, Sieun Lee, Joanne Aiko Matsubara, Ivan Robert Nabi, and Ghassan Hamarneh. *Automatic identification of protein complexes in multi-scale microscopy with applications to metastasis and Alzheimer disease*. In **The 2nd Annual Tri-Cluster Research Day**, Canada, pages 1, 2020.
- **Ben Cardoen**, Timothy H. Wong, Parsa Alan, Sieun Lee, Joanne Aiko Matsubara, Ivan Robert Nabi, and Ghassan Hamarneh. *Belief theory enables identification of protein complexes in multi-scale microscopy with applications to metastasis and Alzheimer disease*. In **Centre for Artificial Intelligence Decision-making and Action (CAIDA), BC's AI Showcase**, Canada, pages 1, 2020.

- **Ben Cardoen**, Fiona Dickson, Ismail M. Khater, Ivan Robert Nabi, and Ghassan Hamarneh. *Interaction zone analysis of CAV1 - CAVIN1 in breast cancer cells*. In **European Molecular Biology Organization EMBO Workshop Caveolae and nanodomains: Translating structural principles and dynamics into function**, Le Pouliguen, France, pages 1, 2019.
- Hanene Ben Yedder, **Ben Cardoen**, Majid Shokoufi, Farid Golnaraghi, and Ghassan Hamarneh. *Limited-Angle Diffuse Optical Tomography Image Reconstruction using Deep Learning*. In **Lecture Notes in Computer Science, Medical Image Computing and Computer-Assisted Intervention (MICCAI)**, volume 11764, pages 66-74, 2019.
- **Ben Cardoen**, Stijn Manhaeve, Tim Tuijn, Yentl Van Tendeloo, Kurt Vanmechelen, Hans Vangheluwe, Jan Broeckhove. *Performance analysis of a PDEVs simulator supporting multiple synchronization protocols* In **2016 Symposium on Theory of Modeling and Simulation (TMS-DEVS)**

6.3 Invited talks

- Adversarial AI in medical imaging: risks and opportunities: UBC Geering Up at UBC Biomedical Imaging and Artificial Intelligence Cluster (2021)
- Introduction to Causality: [SFU Vision, Computing, and Robotics Cluster](#) (2020)

7 Open Source Software

Without exception, all my articles that involve source code are published as open source repositories. Where possible, I provide container images to maximize reproducibility. In addition, I developed software packages for colocalization in 2/3D [SRM](#) [2], [SRM](#) registration [6], simple linux utility for resource management ([SLURM](#)) [25]/high performance computing ([HPC](#)) monitoring [7], and [SRM](#) visualization of point clouds [1]. A full listing of my source code can be found on my Github profile <https://github.com/bencardoen>.

8 Skills

8.1 Languages

- Dutch: native speaker
- English: professional proficiency
- French: elementary proficiency (reading)

8.2 Technical

8.2.1 Programming Languages

- Julia: proficient (2024)
- Python: proficient (2023)
- C++: proficient (2017)
- R, Rust: Exploratory experiments

8.2.2 Frameworks and key technologies

- SLURM based HPC/Cluster processing and administration (local cluster admin team)
- Linux administration (lab admin): bash, zsh, Linux profiling
- Visualization: 3D Slicer, Paraview
- PyTorch
- Singularity/Docker/AppTainer for virtualization

9 Referees

The following are faculty that have either supervised me, or who have worked closely with me during the last five years of research I published. Please inform me when you contact the referees.

Name	University	ORCID	Role	Email
Prof. Ghassan Hamarneh	SFU	0000-0001-5040-7448	Ph.D. Supervisor	hamarneh@sfu.ca
Prof. Keval Vora	SFU	0000-0002-5462-5116	Ph.D. Co- Supervisor	keval@sfu.ca
Prof. Ivan Robert Nabi	UBC	0000-0002-0670-0513	Collaborator	ivan.robert.nabi@ubc.ca
Prof. Joanne Aiko Matsubara	UBC	0000-0002-6236-9191	Collaborator	joanne.matsubara@ubc.ca

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- [2] Ben Cardoen. *Colocalization.jl A Julia reference implementation of image colocalization metrics* (<https://zenodo.org/record/7552357>). Jan. 2023. DOI: [10.5281/ZENODO.7552357](https://doi.org/10.5281/ZENODO.7552357). URL: <https://zenodo.org/record/7552357> (visited on 07/07/2023).
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List of Acronyms

ASCB American Society of Cell Biology	3
CMPT SFU Computing Science	7
CTMC continuous time Markov Chain	6
DEVS discrete event simulation	5
DOT diffuse optical tomography	3
ER Endoplasmic Reticulum	3
HPC high performance computing	10
IEEE-TMI IEEE Transactions In Medical Imaging	2
ISCB International Society for Computational Biology	3
JCB Journal of Cell Biology	7
JOSS Journal of Open Source Software	2
LSTM long term short term memory	5
PDEVS parallel DEVS	5
SFU Simon Fraser University, Burnaby, Canada	7
SLURM simple linux utility for resource management	10
SMLM Single Molecule Localization Microscopy	3
SNR signal to noise ratio	6
SRM Super Resolution Microscopy	3
STED Stimulated Emission Depletion	3
UBC University of British Columbia, Vancouver, Canada	3
WSOD weakly supervised object detection	6