Anamaria Crisan, PhD

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I have over 10 years of experience translating machine learning (ML) research into products and policy-making within industry, government, and academia. My track record includes award-winning publications at top-tier conferences of the ACM (CHI, FAccT) and IEEE (TVCG, CG&A) in addition to biomedical journals (Nature, Oxford Bioinformatics, PLOS). I serve on the organizing and program committees of the IEEE Vis and ACM CHI conferences. My goals are to help people make informed and trustworthy decisions with data and in partnership with AI/ML systems. My research has been cited nearly 5,000 times, my h-index is 19 and my i-10 index is 27.

Current Position

Aug 2024 - **Assistant Professor**, University of Waterloo
Cheriton School of Computer Science

Education

2015 - 2019 **PhD Computer Science**, University of British Columbia
Thesis: Visualizing Heterogenous Data in Genomic Epidemiology
Supervisors: Dr. Tamara Munzner and Dr. Jennifer L. Gardy
Committee: Dr. Raymond Ng and Dr. Bonnie Henry
Notable Awards: Vanier CGS-D and UBC Public Scholar

2008 - 2010 **MSc Bioinformatics**, University of British Columbia
Thesis: Mutation Discovery in Regions of Segmental Cancer Genome Amplifications from Next Generation Sequencing of Tumours
Supervisors: Dr. Sohrab Shah and Dr. Samuel Aparicio
Notable Awards: CIHR-MSFHR Bioinformatics Trainee Award

2004 - 2008 **BSc Computer Science**, Queen's University at Kingston
Specialization: Biomedical Computing
Honours Thesis: Genomics of Autism
Honours Thesis Supervisor: Dr. Hagit Shatkay
Notable Awards: NSERC USRA, CRA-W Distributed Mentorship Trainee Award

Research Work Experience

2019 - 2024 **Lead Research Scientist, Tableau Research**
Seattle, Washington, USA

- I developed strategic research directions for human-ML/AI collaboration, including technical approaches and best practice toward responsible use of ML/AI
- I lead research projects in partnership with cross-functional engineering and product teams to inform, influence, and support ML/AI product strategy
- I contributed to the Tableau Main (`Overcoming Misinformation`, `Data Science Reflection`) and Engineering Blog Sites (`Interactive Machine Learning`, `AutoML and People`)

2013 - 2015 **Bioinformatician, British Columbia Centre for Disease Control**
Vancouver, British Columbia, CANADA

- Lead cutting edge research to integrate new genomic technology and machine learning into public health applications in British Columbia
- Collaborated with international partners to establish standards for clinical genomic reporting in infectious diseases

2010 - 2013 **Bioinformatician, Decipher Biosciences**
Vancouver, British Columbia, CANADA

- Start-up (then GenomeDx Biosciences) where I was employee 3, grew it up to 100 people, and which sold in 2021 $600 million valuation.
- I was the co-inventor of the flagship product : a genomic classifier that predicts metastatic prostate cancer post-surgery. This product is used in clinics today.
- Participated in early funding rounds to raise over $10 million

Awards

2024	IEEE Computer Graphics and Applications - Best Paper Runner-up
2024	ACM CHI'24 HEAL Workshop - Highlight Presentation
2023	ACM CHI'23 - Best Paper Honorable Mention
2021	ACM CHI'21 - Best Paper Honorable Mention
2021	Visualization in Data Science Symposium - Best Paper
2019	ABPHM Conference Software Prize
2018	Li Tze Fong Memorial Fellowship ($25,000)
2018	UBC Public Scholar Award ($5,000)
2015	UBC Four Year Fellowship ($72,000)
2015	Vanier CGS-D ($150,000)

Students

I currently supervise two graduate students. As an industrial researcher, I also independently supervised interns.

Doctoral

2024 - Li (Felicia) Feng
co-supervised with Dr. Jian Zhao (75:25 supervisory split; I have the majority)
Project: Multidirectional Human-AI Collaboration in Data Science
🏆***Nominated by UWaterloo for NSERC Vanier CGS-D***

2023 Matt-Heun Hong [Industrial Research Intern]
Project: Data has Entered the Chat: How Data Workers Conduct Visual Analytic Conversations with GenAI

2023 Sneha Gathani [Industrial Research Intern]
Project: Groot: A System for Editing and Configuring Automated Data Insights

2022 Camelia Brumar [Industrial Research Intern]
Project: Visualizing, Contextualizing, and Evaluating Recommendations Generating Using Graph Neural Networks

2021 Jennifer Rogers [Industrial Research Intern]
Project: Tracing and Visualizing Human-AI Collaborative Processes through Artifacts of Data Work
🏆***ACM CHI'23 - Best Paper Honorable Mention***

Masters

2024 -	Xinxin Yu *Project:* Human-Centered Evaluation and Optimization of LLM-generated Code for Data Science

Undergraduate

2025	Austing Dong *Project:* Leveraging Digital Cognitive Personas to Generate Textual Explanations of Data Visualizations

Funding

Awarded

2024 - 2029	Start-up Grant *Value:* $150,000

Applied

2024	NSERC Discovery Grant *Value:* $496,775

Publications

I primarily publish in competitive top-tier venues of Human Computer Interaction (HCI) and Information Visualizations (Vis), with acceptance rates around 25% and stringent two rounds of peer review. These include, the ACM Conference on Human Factors in Computing Systems (CHI), ACM Conference on Fairness, Accountability, and Transparency (FAccT), and IEEE Trans. on Visualization and Computer Graphs (TVCG, also associated with the IEEE Vis conference). I also submit my research to competitive workshops, with at least one peer-review round, appearing at top-tier conferences (e.g., VIS, CHI, NeurIPs). Earlier in my career (prior to 2019) I published predominately in bioinformatics and medical science journals with high impact factors (e.g., Nature, Oxford Bioinformatics).

A full publication list with updated citation counts are available my Google Scholar profile

Note that below: § indicates joint authorship; † indicates senior author position; underline indicates work students are clickable links

VIS'24	Gathani, S.,Crisan A., Setlur, V, Srinivasan A.,*GROOT: A System for Editing and Configuring Automated Data Insights.* IEEE Visualization Conference (Short Paper) 10.1109/VIS55277.2024.00015
TVCG 2024	Srinivasan A.,Purich J., Correll M., Battle L., Setlur V., **Crisan A.**†,*From Dashboard Zoo to Census: A Case Study with Tableau Public.*IEEE Transactions on Visualization and Computer Graphics 10.1109/TVCG.2024.3490259
TVCG 2023	**Crisan A.**, Shang M., Brochu ER., *Eliciting Model Steering Interactions from Users via Data and Visual Design Probes.* IEEE Transactions on Visualization and Computer Graphics 10.1109/TVCG.2023.3322898

CHI 2023

Rogers J., **Crisan A.** *Tracing and Visualizing Human-ML/AI Collaborative Processes through Artifacts of Data Work.* Proc. of CHI'23

10.1145/3544548.358081

Best Paper Honorable Mention - CHI'23

CG&A 2023

Tory M., Bartram L., Fiore-Gartland B., **Crisan, A.**, *Finding Their Data Voice: Practices and Challenges of Dashboard Users.* IEEE Computer Graphics and Applications

10.1109/MCG.2021.3136545 GC&A Preview Tableau Engineering Blog

Best Paper Runner Up

AJPH 2022

Crisan A. *The Importance of Data Visualization in Combating a Pandemic.* The American Journal of Public Health

10.2105/AJPH.2022.306857

FAccT 2022

Crisan A.§, Drouhard M.§, Vig J, Ranjani, N., *Interactive Model Cards: Human Centered Approach to Model Documentation.* Proc. FAccT'22

10.1145/3531146.3533108 FAccT'22 Video Streamlit Application

TVCG 2021

Crisan A, Fisher, S, Gardy, JL, Munzner T., *GEViTRec: Data reconnaissance through recommendation using a domain-specific visualization prevalence design space.* IEEE Transaction on Visualization and Computer Graphics

10.1109/TVCG.2021.3107749 VIS'22 Video Tableau Engineering Blog

Winner - ABPHM'19 Software Prize

CHI 2021

Crisan A, Fiore-Gartland, B., *Fits and Starts: Enterprise use of AutoML and the role of humans in the loop.* Proc. of CHI'21

10.1145/3411764.3445775 CHI'21 Video Tablaeu Engineering Blog

Best Paper Honorable Mention - CHI'21

CHI 2021

Crisan A, Correll M.,*User ex Machina: Simulation as a design probe in human in the loop text analytics.* Proc. of CHI'21

10.1145/3411764.3445425 CHI'21 Video Tableau Engineering Blog

TVCG 2021

Crisan A., Fiore-Gartland, B., Tory, M. *Passing the data baton: A retrospective analysis on Data Science work and workers.* IEEE Transactions on Visualization and Computer Graphics

10.1109/TVCG.2020.3030340 VDS'21 Video Tableau Main Blog

Best Paper at the Visualization in Data Science Symposium

CHI 2020

McNutt, A. **Crisan A**, Correll, M. *Divining insights: Visual analytics through cartomancy* Proc. ACM CHI'20 – alt.CHI

10.1145/3334480.3381814

VIS 2019

Crisan A., Munzner T. *Uncovering data landscapes through data reconnaissance and task wrangling* IEEE Visualization Conference (Short Paper)

10.1109/VISUAL.2019.8933542

Bioinf. 2018

Crisan A., Gardy JL., Munzner T. *A systematic method for surveying data visualizations and its resulting Genomic Epidemiology Visualization Typology: GEViT* Oxford Bioinformatics

10.1093/bioinformatics/bty832

Bioinf. 2018

Crisan A., Munzner T., Gardy JL., *Adjutant: an R-based tool to support topic discovery for systematic and literature reviews* Oxford Bioinformatics

10.1093/bioinformatics/bty722 R Package

PeerJ 2018

Crisan A., McKee G., Munzner T., Gardy JL. *Evidence-based design and evaluation of a whole genome sequencing clinical report for the reference microbiology laboratory.* PeerJ

10.7717/peerj.4218

IDMM 2016 Miller RR., Langille MG., Montoya V., **Crisan A.**, Stefanovic A., Martin I., Hoang L., Patrick DM., Romney M., Tyrrell G., Jones SJ., Brinkman FS., Tang P., McKee G., Munzner T., Gardy JL. *Genomic analysis of a serotype 5 streptococcus pneumoniae outbreak in British Columbia, Canada, 2005 - 2009.* Canadian Journal of Infectious Diseases and Medical Microbiology
10.1155/2016/5381871

MGen 2016 Hatherell H., Didelot X., Pollock SL., Tang P., **Crisan A.**, Johnston JC., Colijn C., Gardy JL. *Declaring a tuberculosis outbreak over with genomic epidemiology.* Microbial Genomics
10.1099/mgen.0.000060

IJTLD 2015 **Crisan A.**, Wong HY., Johnston JC., Tang P., Colijn C., Otterstatter M., Hiscoe L., Parker R., Pollock SL., Gardy JL. *Spatio-temporal analysis of tuberculous infection risk among clients of a homeless shelter during an outbreak.* International Journal of Tuberculosis and Lung Disease
10.5588/ijtld.14.0957

Eur Urol. 2015 Cooperberg MR., Davicioni E., **Crisan A.**, Jenkins RB., Ghadessi M., Karnes RJ. *Combined value of validated clinical and genomic risk stratification tools for predicting prostate cancer mortality in a high-risk prostatectomy cohort.* European Urology
10.1016/j.eururo.2014.05.039

BJUI 2014 **Crisan A.**§, Alshalalfa M.§ , Vergara IA., Ghadessi M., Buerki C., Erho N., Yousefi K., Sierocinski T., Haddad Z., Black PC., Karnes RJ., Jenkins RB., Davicioni E. *Clinical and genomic analysis of metastatic prostate cancer progression with a background of postoperative biochemical recurrence.* British Journal of Urology International
10.1111/bju.13013

PCPD 2016 Ross AE., Feng FY., Ghadessi M., Erho N., **Crisan A.**, Buerki C., Sundi D., Mitra AP., Vergara IA., Thompson DJ., Triche TJ., Davicioni E., Bergstralh EJ., Jenkins RB., Karnes RJ., Schaeffer EM. *A genomic classifier predicting metastatic disease progression in men with biochemical recurrence after prostatectomy.* Prostate Cancer and Prostatic Diseases
110.1038/pcan.2013.49

J Urol 2013 Karnes RJ., Bergstralh EJ., Davicioni E., Ghadessi M., Buerki C., Mitra AP., **Crisan A.**, Erho N., Vergara IA., Lam LL., Carlson R., Thompson DJ., Haddad Z., Zimmermann B., Sierocinski T., Triche TJ., Kollmeyer T., Ballman KV., Black PC., Klee GG., Jenkins RB. *Validation of a genomic classifier that predicts metastasis following radical prostatectomy in an at risk patient population.* Journal of Urology
10.1016/j.juro.2013.06.017

IJRO 2013 Feng FY., Ghadessi M., Davicioni E., **Crisan A.**, Erho N., Mitra AP., Triche TJ., Jenkins RB., Ross AE., Schaeffer EM. *Validation of a Genomic Classifier That Predicts Metastatic Disease Progression in Men With Biochemical Recurrence Post-Radical Prostatectomy.* International Journal of Radiation Oncology
10.1038/pcan.2013.49

PLOS 2013 **Crisan A.**§, Erho N.§, Vergara IA., Mitra AP., Ghadessi M., Buerki C., Bergstralh EJ., Kollmeyer T., Fink S., Haddad Z., Zimmermann B., Sierocinski T., Ballman KV., Triche TJ., Black PC., Karnes RJ., Klee G., Davicioni E., Jenkins RB., *Discovery and validation of a prostate cancer genomic classifier that predicts early metastasis following radical prostatectomy.* PLOS ONE
10.1371/journal.pone.0066855

Nature 2012 — Shah SP., Roth A., Goya R., Oloumi A., Ha G., Zhao Y., Turashvili G., Ding J., .., **Crisan A.**, ... Marra MA., Aparicio S., *The clonal and mutational evolution spectrum of primary triple-negative breast cancers* Nature
10.1038/nature10933
I engineered a distributed analytic pipeline for this research

Bioinf. 2012 — Roth A., Ding J., Morin R., **Crisan A.**, Ha G., Giuliany R., Bashashati A., Hirst M., Turashvili G., Oloumi A., Marra MA., Aparicio S., Shah SP. *JointSNVMix: a probabilistic model for accurate detection of somatic mutations in normal/tumour paired next-generation sequencing data.* Oxford Bioinformatics
10.1093/bioinformatics/bts053

Frontiers 2012 — Vergara I., Erho N., Triche T., Ghadessi M., **Crisan A.**, Sierocinski T., Black PC., Buerki C., Davicioni E.. *Genomic dark matter in prostate cancer: exploring the clinical utility of ncRNA as biomarkers.* Frontiers in Genetics
10.3389/fgene.2012.00023

Bioinf. 2012 — **Crisan A.**, Goya R., Ha G., Ding J., Prentice LM., Oloumi A., Senz J., Zeng T., Tse K., Delaney A., Marra MA., Huntsman DG., Hirst M., Aparicio S., Shah SP. *Mutation discovery in regions of segmental cancer genome amplifications with CoNAn-SNV: a mixture model for next generation sequencing of tumors.* PLOS ONE
10.1371/journal.pone.0041551

Bioinf. 2010 — Goya R., Sun MG., Morin RD., Leung G., Ha G., Wiegand KC., Senz J., **Crisan A.**, Marra MA., Hirst M., Huntsman D., Murphy KP., Aparicio S., Shah SP. *SNVMix: predicting single nucleotide variants from next-generation sequencing of tumors.* Oxford Bioinformatics
bioinformatics/btq040

Workshop Publications

IEEE VIS 2024 — **Crisan A.***We Don't Know how to Assess LLM Contributions in VIS/HCI.* BELIV'24
10.1109/BELIV64461.2024.00018

IEEE VIS 2024 — **Crisan A.**, Butters N., Zoe., *Exploring Subjective Notions of Explainability through Counterfactual Visualization of Sentiment Analysis.* BELIV'24
10.1109/BELIV64461.2024.00007

ACM CHI 2024 — **Crisan A.**, Hoque, EP., *Towards a Holistic Evaluation of LLM Generated Code for Exploratory Visual Analysis.* HEAL'24

NeurIPs 2022 — **Crisan, A.**, Kotthoff, L., Streit, M., Xu, K. *Towards a Human-Centered Approach for Automation in Data Science.* HCAI @ NeurIPs'22
https://tinyurl.com/3yv8y7vs

KDD 2021 — **Crisan, A.**, Setlur V. *Natto: Rapid and Visual Iteration of Analytic Data Models with Intelligent Assistance.* VDS @ KDD'21
https://tinyurl.com/mr25p23c

IEEE VIS 2018 — **Crisan A.**, Elliott M.*How to evaluate an evaluation study? Comparing and contrasting practices in vis with those of other disciplines.* BELIV'18
10.1109/BELIV.2018.8634420

IEEE VIS 2016 — **Crisan A.**, Gardy JL., Munzner T., *On regulatory and organizational constraints in visualization design and evaluation.* BELIV'16
10.1145/2993901.2993911

Reports

2024 **Crisan A.**, Kotthoff L., Streit M., Xu, K. *Human-Centered Approaches for Provenance in Automated Data Science.* Dagstuhl Seminar 23372
10.4230/DagRep.13.9.116

Under Review

2024 Hong M., **Crisan A.**, *Data has Entered the Chat: How Data Workers Conduct Exploratory Visual Analytic Conversations with GenAI Agents.*
Conditionally Accepted - ACM Transactions on Interactive Intelligent Systems

Selected Presentations

Over the past six years I gave 7 invited talks, one of them as a keynote

Shonan 2024 Translating Visualization Research into Practice
Location: Shonan Village, Japan
Invited Talk

SCI 2024 Scaling Data Driven Decision-Making through Human-AI interaction
Location: Salt Lake City, USA
Invited Talk

HILDA 2023 Scaling Data Driven Decision-Making through Human-AI interaction
Location: Seattle, USA
Invited Talk & Keynote

FAccT 2022 Interactive Model Cards : a Human-Centered Approach to Model Documentation
Location: Seoul, Korea

CHIL 2022 Are Log Scales Endemic Yet? Strategies for Visualizing Biomedical and Public Health Data
Location: Virtual (due to COVID-19)
Invited Talk

VIZBI 2022 Visualization in Public Health
Location: Virtual (due to COVID-19)
Invited Talk

CHI 2021 Fits and Starts: Enterprise Use of AutoML and the Role of Humans in the Loop
Vis ex Machina: Simulation as a Design Probe in Human in the Loop Text Analytics
Location: Virtual (due to COVID-19)

ABPHM 2019 Automated Visualization Recommendations for Genomic Epidemiology
Location: Hinxton, UK
Winner - ABPHM'19 Software Prize

Dagstuhl 2019 Dagstuhl Seminar 18161 – BioVis Crossroads
Location: Schloss Dagstuhl, Germany
Organized by: Jan Aerts (KU Leuven, BEL); Nils Gehlenborg (Harvard University, USA);Elisabeta Marai (University of Illinois,USA); and Kay Nieselt (Uni. Tübingen, DEU)
Invited Talk

DBMI 2018 Creating Explorable Visualization Design Spaces: An Example from Infectious Disease Genomic Epidemiology
Location: Boston, USA
Invited Talk

Service

Program Committees

2023 - 2024	NeurIPs AI4Science Workshop, Area Chair
2023	ACM CHI - Paper Awards Committee
2022 -	ACM CHI - Associate Chair, Visualization Subcommittee
2022	ISVC - Visualization Area Chair
2021 -	IEEE VIS - Program Committee
2021 - 2023	VADA (Visual and Automated Disease Analytics) - Steering Committee
2020 - 2023	Frontiers in Bioinformatics- Review Editor
2017 - 2019	Bioinformatics Open Source Conference - Program Committee

Organizing Committees

2024	IEEE VIS - Workshops Chair
2023 - 2024	IEEE VIS - Application Spotlights Chair
2021 - 2024	Visualization in Data Science Symposium - Papers co-chair
2021 - 2022	IEEE VIS - Vis in Practice co-chair
2018 - 2020	Biovis@IEEEVIS Chair
2016 - 2018	Biovis Website chair

Reviewing

2020- 2023	Frontiers in Bioinformatics
2019-	IEEE VIS
2019	ACM CHI
2018-	IEEE TVCG
2017-	Bioinformatics Open Source Conference

Leaves

Dec'22 - June'23	Parental Leave