**Lana X Garmire**

**Associate Professor of Translational Bioinformatics**

University of Michigan

1600 Huron Parkway, Ann Arbor, MI 48105

Phone: 734-615-0514

Email:lgarmire@med.umich.edu

**Education and Training**

**Education**

07/2001 BS, Food Science and Engineering, Ocean University of China, Qingdao, China

05/2005 MA, Statistics, UC Berkeley, Berkeley, CA

08/2001-12/2007 PhD, Comparative Biochemistry (Computational Biology focus), UC Berkeley, Berkeley, CA

**PostDoctoral Training**

03/2008-02/2011 Postdoctoral Fellow, Bioengineering Department, UC-San Diego, La Jolla, CA

**Academic, Administrative, Clinical and Military Appointments**

**Academic Appointments**

09/2001-09/2002 Graduate Student Researcher, Nutritional Science Department, University of \ California – Berkeley, Berkeley, CA

09/2002-09/2007 Graduate Student Researcher/Instructor, Comparative Biochemistry Program,

University of California – Berkeley, Berkeley, CA

12/2012-06/2017 Assistant Researcher/Professor (Tenure-track), Cancer Epidemiology Program,

University of Hawaii Cancer Center, Honolulu, HI

02/2013-08/2018 Graduate Cooperate Faculty, Program of Molecular Biosciences and

Bioengineering, College of Tropical Agriculture and Human Resources,

Honolulu, HI

07/2014-08/2018 Faculty Member, Institute of Biogenesis Research, John A. Burns School of

Medicine, University of Hawaii, Honolulu, HI

07/2014-08/2018 Adjunct Associate Professor, Department of Anatomy, Biochemistry and

Physiology, John A. Burns School of Medicine, University of Hawaii, Honolulu,

HI

01/2016-08/2018 Adjunct Faculty, Department of Obstetrics, Gynecology and Women’s Health,

John A. Burns School of Medicine, University of Hawaii, Honolulu, HI

07/2017-08/2018 Associate Professor (with tenure), Cancer Epidemiology Program, University of

Hawaii, Honolulu, HI

09/2018-present Associate Professor (with tenure), Department of Computational Medicine and Bioinformatics, University of Michigan, MI

09/2018-present Affiliated Faculty, Biomedical Engineering Department, University of Michigan, MI

09/2018-present Core member, Rogel Cancer Center, University of Michigan, MI

04/2019-present Faculty member, M-LEEAD Center, University of Michigan, MI

**Industrial Positions**

08/2005-12/2005 Computational Biology Intern, Berlex Research Lab, Schering AG. Richmond,

CA

04/2011-08/2012 Senior Scientist in Computational Biology, Asuragen Inc., Austin, TX

**Current Research Interests**

I have broad interests in biomedical data science research, leading to actionable transformation on human health from the bench to bedside. Current research focus areas include cutting edge single-cell sequencing informatics and genomics; precision medicine through integration of multi-modal biomedical data types (eg. electronic health record data, genomics data, imaging data, mobile health data, and geographic data); novel modeling and computational methods for biomarker research; public health genomics. I apply my biomedical informatics and analytical expertise to study diseases such as cancers, as well the impact of pregnancy/early life complications on later life diseases.

**Grants**

**Current**

02/2019-02/2020 Mcubed Project

Role: MPI $60,000

“New Methods for Study of Placental Health and Dysfunction”.

This Mcubed collaboration project among Drs Rita Loch-Caruso and Kelly Balkuski and me, is to identify the response of exo-transplant of placenta to toxicity.

07/2016-06/2021 R01/Grant #HD084633

Role: PI $3, 093,000

“An integrative omics approach to identify biomarkers related to preeclampsia

and breast cancer risks NICHD”

This R01 project is to identify biomarkers for preeclampsia using multi-omics (epigenetics, transcriptomics and proteomics) approach, and further study the impact of the biomarkers in relation to later life breast cancer risks.

09/2016-08/2020 R01/Grant # LM012373

Role: PI $1,388,611

“An integrative bioinformatics platform with application in single cancer cells

NLM”

This R01 project is to develop a one-stop bioinformatics suite to study heterogeneity of tumors at the single-cell resolution

10/2014-06/2022NIEHS 1 K01 ES025434-01

Role: PI $905,080

“An integrative bioinformatics approach to study single cancer cell heterogeneity”

This K01 career development project is to develop an integrated bioinformatics platform to study heterogeneity of tumors at the single-cell resolution

**Pending**

07/2019-06/2022 NLM R01

Role: PI $1,540,000

“Dr. EPS: Drug repurposing for extended patient survival”

It aims to develop an actionable prognosis model that improves cancer patients’ survival time

09/2019-08/2023 NIDCR R01 (PI: Darnell Kaigler) noticed for funding

Role: Co-I $2,278,541

“Redefining mesenchymal stem cells: using their cellular and molecular phenotypes to determine their regenerative and therapeutic properties”

09/2019-08/2024 K01

Role: Primary Mentor $470,398

“Data-driven computational approach to advance personalized medicine for Alzheimer’s disease”

07/2019-08/2020 Mi-kickstart

Role: PI $42,500

“In vivo validation of a drug for tamoxifen resistance”

**Past**

07/2014-08/2018 2 P20 GM103457-06A1

Role: Project Leader $1,336,140

(succeeded by Dr. Kelly Yamasato due to change of institute)

“Linking maternal obesity and offspring cancer risks through integration of transcriptome and methylome of the cord blood stem cells Institute for Biogenesis Research: COBRE NIGMS”

This P20 project is to identify newborn biomarkers associated with maternal obesity, and study how these biomarkers may have impacts on later life cancer risks.

04/2017-03/2018University of Hawaii Cancer Center Seed Grant #4503293

Role: PI $50,000

“Novel lincRNA as liver cancer biomarkers”

This pilot study investigates the clinical application of a panel of non-long coding RNAs as screening biomarkers for over ten types of cancers.

2014-201514ADVC-64566

Role: PI $38,000

Using next generation sequencing to detect circulating microRNAs as diagnostic

Biomarkers of liver cancer” Hawaii Community Foundation

2013-2014 NIGMS 5 P30 GM103341-02

Role: PI of the Pilot Project Program $45,500

“Investigating microRNA-targetome interaction in macrophage polarization”

2013-2014 RCMI Translational Research Network NIMHD/Charles R. Drew U.

Role: PI $10,000

“An integrative bioinformatics platform with application in single cancer cells”

2012-2014 NIH/SBIR R43 HG007140

Role: PI $242,940

“Integrated bioinformatics analysis suite for deep targeted amplicon sequencing”

(project succeeded by CO-PI Choudhary Ashish upon resignation from Asuragen)

**Honors and Awards**

**International**

2018 Guided graduated PhD student, Sijia Huang, to win Travel Fellowship to attend International Conference Intelligent Biology and Medicine (ICIBM) 2018

2017 Top Research Tools in 2017 (Ranked No. 3 for Granatum software)

2017 Faculty Travel Award of 12th International Conference on Pathways, Networks,

and Systems Medicine

2014 Conference Travel Award, ISBRA 2014

2007 Best Student Paper Award in International Conference of Computational Biology

(ICCB)

**National**

2019 **US Presidential Early Career Awards for Scientists and Engineers**

2019 Nominated for American Medical Informatics Association (AMIA) New Investigator Award

2019 Guided MS student Qianhui Huang (Biostat), to get Conference Travel Fellowship to attend Great Lakes Bioinformatics Conference 2019.

2018 Guided PhD student Xun Zhu, to win NIGMS Fellowship to attend Cold Spring Harbor Single Cell Analysis Course 2018.

2017 Nominated for United States Presidents’ Early Career Award for Scientists and Engineers (PECASE), the highest award in the nation (nominated, currently still under evaluation).

2016 Elected as Early Career Reviewer (ECR) by NIH

2015 Guided PhD Student, Travers Ching, to win the Three-Year Roche Scholar Award in Life Sciences from Roche and ARCS Foundation

2007 NSR Physiome Project Training Award

**Institutional**

2019 Guided MS student Qianhui Huang (Biostatistics), to get Rackham Graduate School Travel Fellowship to attend Great Lakes Bioinformatics Conference 2019.

2019 Guided MS student Noshad Hosseini (DCMB), to get Rackham Graduate School Conference Travel Fellowship to attend Great Lakes Bioinformatics Conference 2019.

2016 Finalist, University of Hawaii Board of Reagent’s Excellence in Research Award

2016 Guided Undergraduate Student, Austin Tasato, to win Undergraduate Opportunity

Program Scholarship

2015 Finalist, University of Hawaii Board of Reagent’s Excellence in Research Award

2015 Guided PhD Student, Sijia Huang, to win Giving Tree Graduate Student

Scholarship at University of Hawaii

2014 Guided Undergraduate Student, Nichole Chong, to win Undergraduate Research

Opportunity Program Scholarship at University of Hawaii

2014 Guided Graduate Student, Runmin Wei, to win Giving Tree Graduate Student

Scholarship at University of Hawaii

2014 Best Scientific Paper Award, University of Hawaii Cancer Center

2014 Best Scientific Poster Award, University of Hawaii Cancer Center, Weinman

Symposium, judged by Nobel Laureates Dr. Bruce Beutler and Dr. Jules

Hoffmann

2007 Conference Travel Fellowship, University of California

1997 Top-ten Excellent College Student at Ocean University of China, Ranked No. #2

1997 Jing Sui Fellowship, Ocean University of China

1998 Excellent Student Award of Shandong Province, China

**Memberships in Professional Societies**

1. International Society of Computational Biology (ISCB)
2. American Medical Informatics Association (AMIA)
3. American Chemistry Society (ACS)

**Editorial Positions, Boards, and Peer-Review Service**

**Study Sections/Advisory Panels**

1. NLM BILDS study section, June 2019
2. University of Ghent, Belgium, “University Research Professor” reviewer, April 2019
3. NIGMS MIRA study section, March 2019
4. NICHD P50 study section, Nov 2018
5. University of Tennessee at Chattanooga Internal Grant Competition, 2018
6. NIH GCAT study section, June 2017
7. NLM T15 study section, August 2016
8. NIH BDMA study section, September 2016
9. Germany, Kom Op Tegen Kanker Foundation, Collaborator biomedical researcher grants, 2015
10. Mentorship on grant proposal, Faculty mentor: T32 cardiovascular disease training grant (PI: Ralph Shohet)
11. Mentorship on grant proposal, co-mentor: mentored career development award (K01) for Dr. Michael Coley (now Assistant Researcher at University of Hawaii).
12. Mentorship on grant proposal, faculty mentor: R25 National Cancer Institute Youth Enjoy Science Research Education Program (PIs: Marskarinec, Ramos, Nigg)
13. Peer mentor for junior-faculty, Dr. Junming Yin, Assistant Professor, Department of Management Information Systems, University of Arizona
14. Peer mentor for junior-faculty, Dr. Quyenh Nguyen, Assistant Professor, Department of Health Promotion and Education, University of Utah (now Assistant Professor at University of Maryland)
15. Peer mentor for junior-faculty, Dr. Ruogu Rachel Fang, Assistant Professor, School or Computing and Information Sciences, Florida International University (now Assistant Professor at University of Florida)

**Editorial Boards**

01/2016-present Associate Editor, BMC Bioinformatics

01/2016-present Guest Editor, PLOS Computational Biology

**Journal/Abstract Reviewer**

1. 2016, Reviewer, RNA journal
2. 2015-present, Reviewer, PLoS Computational Biology journal
3. 2015, Reviewer, AACR: Cancer Epidemiology, Biomarkers and Prevention
4. 2012- present, Reviewer, PLoS One journal
5. 2014-present, Reviewer, Genome Medicine journal
6. 2014-present, Reviewer, BMC Bioinformatics journal
7. 2015, Reviewer, Clinical Epigenetics journal
8. 2015-present, Reviewer, Scientific Reports journal
9. 2016, Reviewer, IEEE Transactions on NanoBioscience conference proceedings
10. 2015, Reviewer, AJP – Heart and Circulatory Physiology journal
11. 2014, Reviewer, Molecular Human Reproduction journal
12. 2016, Reviewer, Nucleic Acid Research journal
13. 2016, Reviewer, Genetics journal
14. 2017, Reviewer, Frontiers in Genetics journal
15. 2017-present, Reviewer, Nature Communications journal
16. 2017, Reviewer, PLoS Genetics journal
17. 2016-present, Reviewer, Bioinformatics journal
18. 2017, Reviewer, Pacific Scientific Biocomputing conference proceedings
19. 2017, Reviewer, IEEE/ACM Transactions on Computational Biology and Bioinformatics conference proceedings
20. 2017-present, Reviewer, Genome Biology journal
21. 2018-present, Reviewer, PeerJ journal
22. 2019, Reviewer, Nature Methods journal

**Teaching Activities**

**Institutional**

08/2003-12/2003 General Biology

08/2005-12/2005 Introduction to Protein Bioinformatics

01/2006-05/2006 Introduction to Human Nutrition

05/2006-08/2006 Introduction to Biostatistics

01/2007-05/2007 Survey of Principles in Biochemistry & Molecular Biology

05/2007-08/2007 Introduction to Biostatistics

04/2013-07/2013 Postdoc Researcher, Jason Weirather, PhD, Currently postdoc at University of Iowa

06/2013-08/2013 Mentor, Cameron Yee, 3rd year undergraduate intern from University of Washington at

Seattle, currently software engineer at Nomic

08/2013-12/2013 MBBE 699 (CRN#: 80146): Directed Research

08/2013-05/2017 Thesis advisor, Travers Ching, PhD student, currently Computational Biologist, Adaptive

Biotechnologies, Seattle, WA

08/2013-12/2017 Thesis advisor, Sijia Huang, PhD student, currently postdoc fellow in U Penn, Dr. Jason Moore’s group

01/2014-05/2014 MBBE 699 (CRN#: 89838): Directed Research

01/2014-05/2016 Thesis advisor, Liangqun Lu, MS student, currently PhD student in Univ. Memphis

02/2014-09/2014 Research volunteer, Jayson Masaki, MD, currently resident at Chicago Medical School

05/2014 Mentor, Mark Menor, PhD, currently junior researcher in John A Burns Medical School of Hawaii

06/2014-present Thesis advisor, Xun Zhu, PhD Student

06/2014-08/2014 Mentor, James Ha, 2nd year undergraduate intern from California Institute of Technology,

currently medical student at University of Hawaii

06/2014-08/2014 Mentor, Jeffrey Li, 2nd year undergraduate summer research assistant from Johns

Hopkins University, currently product management associate at Athena Health

06/2014-12/2014 Mentor, Nichole Chong, 3rd year student in Biology major

08/2014-12/2014 MBBE 699 (CRN#: 78735): Directed Research

08/2014-12/2014 Mentor, Jonathan Uiebe, senior year student in Electrical Engineering

08/2014-08/2015 Mentor, Reimin Wei, MS student, currently PhD student in Dr. Wei Jia lab, University of

Hawaii

11/2014 Developmental and Reproductive Biology Graduate-level Seminar Course (DRB 613)

Fall 2014. Topic: Introduction to Next Generation Sequencing. Nov 26th 2014. Received

90/100 scores from attending graduate students

11/2014-present Postdoc Researcher, Karolina Peplowska, PhD (joint with Dr. Maarit Tiirikainen,

Director of Genomics Shared Resources), since Nov 2014

01/2015-05/2015 MBBE 699 (CRN#: 88461): Directed Research

05/2015-05/2016 Mentor, Austin Tasato, 2nd year student in Electrical Engineering major

08/2015-12/2015 MBBE 699 (CRN#: 77457): Directed Research

10/2015-12/2015 Mentor, rotational student, Hsin-Yi Chen, PhD

01/2016-05/2016 MBBE 699 (CRN#: 87125): Directed Research

01/2016-05/2016 MBBE 700 (CRN#: 90061): Thesis Research

01/2016-present OB/GYN fellow, Ryan Schlueter, MD

01/2016-2017 Postdoc Researcher, Kelly Yamasato, MD, OB/GYN fellow, currently Assistant Clinical Faculty at University of Hawaii

02/2016-06/2018 Postdoc Researcher, Olivier Poirion, PhD

03/2016-12/2017 Postdoc Researcher, Kumardeep Chaudhary, PhD

06/2016 University of Hawaii Cancer Center CURE summer internship seminar. Topic:

Translational Bioinformatics

08/2016-12/2016 MBBE 699 (CRN#: 76802): Directed Research

06/2016-08/2016 Mentor, Jack Fennick, PhD, currently PhD student in Math Department at University of

Hawaii Manoa

06/2016-06/2016 Mentor, Shaw Chun, pre-med undergraduate student, University of Hawaii Manoa

06/2016-08/2016 Mentor, Jordan Fernandez, 2nd year undergraduate summer research assistant from

Washington State University

09/2016-12/2016 Mentor, Joshua Chen, MS, currently MS student in EE Department at University of

Hawaii Manoa

11/2016-present Postdoc Researcher, Paula-Beth Angelica Tiqui Benny, PhD

11/2016-present Postdoc Researcher, Fadhl Al-Akwaa, PhD

11/2016-08/2018 Postdoc Researcher, Thomas Wulfguber, PhD

01/2017-05/2017 MBBE 699 (CRN#: 76101): Directed Research

01/2017-05/2017 MBBE 700 (CRN#: 78377): Thesis Research

01/2017-09/2017 Postdoc Researcher, Michael Ortega, PhD

08/2017-12/2017 MBBE 699 (CRN#: 85722): Directed Research

08/2017-12/2017 MBBE 700 (CRN#: 87268): Thesis Research

03/2017 Mock grant reviewer/mentor for grant writing course, John A Burns Medical School, University of Hawaii. Proposal title: Genetic disposition in addition to BAP1 mutation contributes to the increased lifetime risk of cancer. Graduate student: Jiaming Xue

08/2017-05/2018 Mentor, Cedric Arisdakessian, PhD student

06/2017-08/2017 Mentor, Dylan Combs, 2nd year student in Sociology Major, Harvard University

01/2018-08/31/2018 Ingrid Chern, OB/GYN research assistant (admitted as MD fellow, OB/GYN Dept at University of Hawaii)

01/2018-08/31/2018 Mentor, Biyu Wu, MS graduate research assistant

05/2018-08/31/2018 Postdoc Researcher, Cedric Badowski, PhD

09/2018-10/2018 Rotational graduate student, Kelly Sovacool (PIBS)

09/2018-10/2018 Rotational graduate student, Gabrielle Dotson (DCMB)

09/2018-present Graduate Researcher, Noshad Hosseini, MS (DCMB)

11/2018-present Graduate Researcher, Qianhui Huang, MS (Biostat)

12/2018-present Graduate Researcher, Yuheng Du, MS (Biostat)

09/2018-present K01 Co-mentor, Assistant Professor, Michael Corley, PhD. University of Hawaii

02/2019-present Visiting graduate student, Elorri Cervera-Marzal, MS (France)

06/2019-present Graduate student, Yibo Wang, MS (Biostat)

05/2019-present Undergraduate student, Zhijie Ren (EECS)

03/2019-present Co-mentor K99 proposal, Postdoc Researcher, Sean Harris (Environmental Science)

10/2018-present Co-mentor, Assistant Professor, Vincent Chen (Hepatology Program)

**Dissertation Committees**

2012-2014 PhD thesis committee, member, Min-Ae Song

2014-2016 Chair, MS thesis committee, Liangqun Lu

2013-2017 Chair, PhD thesis committee, Travers Ching

2013-2017 Chair, PhD thesis committee, Sijia Huang

2014-2018 Chair, PhD thesis committee, Xun Zhu

**Committee, Organizational, and Volunteer Service**

**Committees/Boards**

2008 Session Chair of ISCA 21st International Conference on Computer Applications in Industry and Engineering, (CAINE 2008).

2012-present Multi-time Faculty Candidate Interviewer at UH Cancer Center

1. Organization committee member for UH Cancer Center faculty retreat

2016-present University of Hawaii Cyberinfrastructure Faculty Advisory Committee

1. Poster award review committee for ISMB, July 8-12th, Orlando, FL
2. Chair, workshop “the making of next generation data scientists in biomedicine”, Pacific Symposium on Biocomputing

2017 Program Committee for “Applications to Microbes and Imaging Genetics” session, ACM BCB

2017-2019 Parasite Award Committee member, Pacific Symposium on Biocomputing

1. Publicity Committee Chair, International Conference on Intelligent Biology and Medicine (ICIBM), 2018

2018 Poster Award Committee Chair, DCMB department retreat

2018 *Ad hoc* tenure and promotion review committee, DCMB department

2019 Session Chair, “Single Cell Analysis- what is in the future”, Pacific Symposium on Biocomputing, 2019

2019 Session Chair, “Machine learning and precision medicine”, Great Lakes Bioinformatics Meeting, 2019

**Volunteering Services**

05/2014 Host for Professor Jason Moore, Director of the Institute for Quantitative Biomedical Sciences of Dartmouth College, to visit University of Hawaii Cancer Center

03/2015 Host for Dr. Kjie Zhao, Director of Systems Biology Center of National Heart, Lung, and Blood Institute, to visit the University of Hawaii

07/2015 Host for Dr. Jianhua Ruan, Associate Professor of Biomedical Informatics Department, University of Pittsburgh, to visit the University of Hawaii

02/2016 Host for Dr. Russ Altman, Professor of Biomedical Informatics, Stanford University, to visit the University of Hawaii

02/2016 Host for Dr. Casey Greene, Assistant Professor of Pathology Department, University of Pennsylvania, to visit the University of Hawaii

05/2016 Host for Dr. Derek Radisky, Associate Professor from Mayo Clinic, Jacksonville FL, to visit the University of Hawaii

03/2017 Host for Dr. Kin Fa, Au, Assistant Professor from University of Iowa, to visit the University of Hawaii

08-12/2017 Sabbatical Host for Dr. John Hu, Professor of Plant Pathology, [Department of Plant and Environmental Protection Sciences](http://www.ctahr.hawaii.edu/peps), University of Hawaii

08/2018 Host for Dr. Sheng Zhong, University of California at San Diego, to visit University of Hawaii

09/2018 Introduction of the BRCF Bioinformatics Core, Associate Chairs of Research meeting, Medical School

09/2018 Presentation “Machine learning methods in multi-omics data integration”, Mathias Kretzler Group, Department of Internal Medicine.

10/2018 Faculty Interviewer, DNA Sequencing Core Managing Director candidate

11/2018 Presentation “Overview of Research in Garmire Group”. Rogel Cancer Center Cancer Epidemiology and Prevention Program.

12/2018 Presentation “Recent research work in liver cancer”, Clinical Hepatology Program, Medical School

12/2018 Presentation “Multi-omics integration from population to single cell resolution”, Nephrology Program, Internal Medicine. Medical School

12/2018 Presentation “Introduction of BRCF Bioinformatics Core”, Single Cell Retreat, Internal Medicine. Medical School, University of Michigan

12/2018 Presentation “Introduction of the BRCF Bioinformatics Core”, Department of Internal Medicine. Medical School, University of Michigan

02/2019 Faculty interviewer for PIBS graduate student candidate

02/2019 Faculty interviewer for DCMB graduate student candidates

02/2019 Faculty interviewer for Biostatistics Department faculty candidate

04/2019 Presentation “Deep learning applications in genomics research”, Biomedical Engineering Department Seminar 500 series, University of Michigan

04/2019 Presentation “Deep learning applications in genomics research”, Biostatistics Department seminar series, School of Public Health, University of Michigan

**Visiting Professorships and Extramural Invited Presentations**

**Extramural Invited Presentations**

1. Systems biology and personalized medicine—Promises from ultra-high throughput data analysis. Pathology Department, University of Alabama at Birmingham, April 1-2nd, 2012.

2014 The challenges of Big Data integration. Genetics Department, Yale University, June 20th, 2014.

1. The challenges of Big Data integration. Shanghai JiaoTong University, School of Public Health, Shanghai, China. July 2nd, 2014.
2. Towards solving the challenges of big cancer data integration. CAS-MPG Partner Institute for Computational Biology. Shanghai, China July 4th, 2014.

1. Integration of Big Data with applications in cancer research. Computational Biology Institute, George Washington University, Feb 25th, 2015.

2015 Big Data integration: from population to single cells. Stem Cell Center, Yale University,

Feb 28th, 2015.

2015 Big Data integration: from population to single cells. Biomedical Engineering Department, Columbia University, Mar 2nd, 2015.

2015 Big Data integration: from population to single cells. Webinar to the RCMI Translational Research Network (RTRN), a consortium supported by NIH on Minority Health and Health Disparities through Grant U54MD008149, April 2nd, 2015.

2015 Big Data integration: from population to single cells. Systems Biology Center, National Heart, Lung and Blood Institute, NIH. April 21st, 2015.

2015 Big Data integration: from population to single cells. Biomedical Engineering Department, University of Florida. April 22nd, 2015.

2015 Big Data integration: from population to single cells. Department of Biomedical Informatics, Ohio State University. April 24th, 2015.

2015 Big Data integration: from population to single cells. Biomedical Informatics Department, UC-San Diego. May 22nd, 2015.

2015 Big Data integration: from population to single cells. Institute of Biomedical Informatics, Perelman School of Medicine, University of Pennsylvania, July 21st, 2015.

2015 Big Data integration for precision medicine: from population to single cells. Department of Biomedical Informatics, School of Medicine, University of Pittsburgh. July 23rd, 2015.

2015 Integration of Big Data in Cancer Research. Development of Modern Methods for Linear Algebra Workshop (DMML). UC-Berkeley, Oct 23-24th, 2015.

2015 Big Data integration: from population to single cells. Biomedical Engineering Department, George Washington University, Nov 11th, 2015.

2015 Pathway-based metabolomics classification models reveal key metabolic pathways for breast cancer diagnosis and progression, Big Data in Cancer, a joint meeting between Cold Spring Harbor Asia and AACR. SuZhou, China. Dec. 6th, 2015.

1. Big Data integration: from population to single cells. Department of Biomedical Informatics and Medical Education, University of Washington. Feb. 21st, 2016.

2016 Enable Precision Medicine with Big Data Analytics. Sanford-Burnham Institute, San Diego, May 27th, 2016.

2016 Knowledge-driven Big Data Analytics Approach for Cancer Biomarker Discovery. University of Florida, July 7th 2016.

2016 Cancer Prognosis and Diagnosis Using Personalized Pathway-based Modeling. Mayo Clinic, Florida, July 13th, 2016.

2016 Big Data Analytics for Precision Medicine, Center for Biomedical Informatics, Brown University, July 25th, 2016.

2016 Scalable Meta-dimensional and Multi-dimensional Data Integration for Clinical and Biological Insights, University of Pennsylvania, Dec. 1st, 2016.

2017 Machine-learning and deep-learning based genomics data integration on cancer biomarker discoveries, Bioengineering Department, University of Illinois at Chicago, March 20th, 2017

2017 Machine-learning and deep-learning based genomics data integration for biomarker research, Department of Biochemistry and Molecular Genetics, University of Virginia, June 1st, 2017

2017 Machine-learning and deep-learning based genomics data integration for biomarker studies, Department of Computational Medicine and Bioinformatics, University of Michigan, June 5th, 2017

2017 Genomics data integration for population based prognostic and diagnostic biomarker research, Department of Genetics and Genomic Sciences, Icahn School of Medicine at Mount Sinai, June 9th, 2017

2017 Biomarker research using machine-learning and deep-learning based multi-omics integration, Department of Biomedical Informatics, University of Pittsburgh, June 16th, 2017

2017 Machine-learning and deep-learning based genomics data integration for biomarker studies, Department of Biomedical Informatics, Vanderbilt University, June 20th, 2017

2017 New Computational methods in cancer biomarker research using multi-omics data integration, Institute of Computational Health Sciences, UC-San Francisco, July 17th, 2017.

2017 Leveraging population science with machine learning and deep learning methods, Epidemiology Department, Columbia University, Sept 7th, 2017.

2018 Single Cell Data Analysis, from imputation, subpopulation identification to data portals. University of Michigan 2nd Annual Symposium on Single-Cell Genomic Data Analytics. Aug 6th, 2018.

2018 “Machine learning and deep learning methods for multi-omics integration”. VIB training program, University of Ghent, Belgium, Nov 19th, 2018

2018 The training of next generation data scientists, Data Science and Training Workshop, NIEHS, NC, Aug 2018

2019 Genetically explainable non coding RNA expression by SNVs, “Reading between genes” workshop, Pacific Biocomputing Symposium, HI, Jan 2019

2019 Applications of deep-learning in genomics research, 4th Ann Arbor Deep Learning event (A2-dlearn4), Feb 23rd, 2019

2019 Single Cell Analysis, the usual and the unusual. Workshop: The Promise of Single Cell and Single Molecule Analysis Tools to Advance Environmental Health Research, National Academy of Sciences, Washington DC, March 7-8, 2019

2019 Novel methods to improve single cell analysis. UCLA Bioinformatics Graduate Program April 8th, 2019

2019 Using Single nucleotide variants to detect subpopulation heterogeneity and link genotype-phenotype, 5th Annual Single Cell Analysis USA Congress, May 14th, Boston, 2019

2019 Application of Deep Learning on Genomics Research across Scales, Bioengineering Department, Michigan State University, July 10th

2019 TBD, Mid-Atlantic Bioinformatics Conference, “Multi-omics Data Integration for Biomedical Discovery: Statistical and Machine Learning Approaches to Big Data”, Philadelphia, PA, Oct 11, 2019. (Scheduled)

**Other**

1. A novel class of in-silico devices to study drug transport through intestinal barriers. University of Hawaii Cancer Center. Nov 27, 2007.
2. ISCA 21st International Conference on Computer Applications in Industry and Engineering, (CAINE 2008). Peak-Finding Refinement in the Chip-SEQ Experiment. Honolulu, Hawaii Nov. 12-14, 2008.
3. UCSD Next-Gen Sequencing Symposium. Genomic association study (CHIP-Seq) of Liver X receptors beta in combination with gene expression analysis. La Jolla, Nov 9-10th, 2008.
4. 10th Annual UC Systemwide Bioengineering Symposium. Using CHIP-Seq to Identify Intergenic Non-coding RNA in Mouse Macrophages, June 19-21st, 2009. Merced, CA.
5. IEEE International Conference on Bioinformatics & Bioengineering (BIBE). A Clustering Approach to Identify Intergenic Non-coding RNA in Mouse Macrophages, May 31 – June 4, 2010. Philadelphia, PA.
6. 32nd Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC 2010). Regulatory network of microRNAs in RAW 264.7 macrophage cells. Buenos Aires, Argentina. Sept 30-Oct 4th, 2010.
7. Biomedical Engineering Society Annual Meeting (BMES 2011). Evaluation of normalization methods for microRNA-Sequencing. Hartford, Oct 12-15th, 2011.
8. Cold Spring Harbor Asian Conferences: Frontiers in Bioinformatics and Computational Biology. Power Analysis and Sample Size Estimation for RNA-Seq. Suzhou, China, Sept. 23-27th. 2013.
9. Personalized medicine and systems biology: promise from ultra-high throughput data analysis. University of Hawaii Cancer Center. June 19th, 2012.
10. What can systems biology do for you. Hawaii Institute of Marine Biology, Feb 6th, 2013.

1. 10th International Symposium on Bioinformatics Research and Applications (ISBRA2014). Integration of methylation, long noncoding RNA and mRNA expression data in Lung Cancer. Zhangiajie, China, June 28-30th, 2014.
2. 10th International Symposium on Bioinformatics Research and Applications (ISBRA 2014). The roles of microRNA and targetsome in macrophage polarization Zhangiajie, China, June 28-30th, 2014.
3. Differential methylation of the chorioamnion membranes in early-onset preeclampsia in a predominantly Asian cohort, 18th International Conference on Prenatal Diagnosis and Therapy, Brisbane, Australia, July 20-23rd, 2014.
4. Epigenomics and beyond in pregnancy adversities. Grand Rounds talk, Department of Ob/Gyn and Women’s Health, JABSOM, University of Hawaii. June 24th. 2015.
5. Big data for precision medicine: from population to single cells. Institute of Biogenesis Research. University of Hawaii. Dec. 11th, 2015.
6. Applying Big Data Analytics to Cancer Precision Medicine, The Queen’s multidisciplinary oncology all-sites tumor conference, Queen’s Medical Center, Honolulu, May 4th 2016.
7. Detecting tumor heterogeneity at the single cell level. Nov 28th. BD2K All Hands Meeting K01 awardee symposium, 2016.
8. How to turn secondary data analysis into primary funding, workshop “the making of next generation data scientists in biomedicine”, Pacific Scientific Biocomputing, Jan 3rd, Big Island, HI 2017 (chair of the workshop).
9. How to turn secondary data analysis into primary funding, Jan 5th, BD2K Training Working Group webinar meetings, 2017.
10. Deep learning predicts estrogen receptor status in breast cancer metabolomics data, Translational Bioinformatics Conference, 2017

**PhD Thesis**

Garmire, L, “A novel class of in silico devices to study drug transport through intestinal barriers.” UC

Berkeley Thesis.

**Patent and Disclosure**

**Patent**

1. Patent, Ching T and Garmire LX, “panel of long intergenic noncoding RNA as pan-cancer biomarkers,”

Filed by OTTED of UH. Application #62120310. US patent pending.

**Bibliography**

**Peer-Reviewed Journals and Publications**

1. Fan T, **Xia L**\*, Han Y. Mitochondrion and apoptosis. *Acta Biochica et Biophysica Sinica* 2001, 33(1):7-12 (\*: Maiden name)
2. **Garmire LX**. Mechanistic study of enzyme-efflux transporter relations using in silico devices, *Lecture Notes in Engineering and Computer Science*, 2167 (1): 34-39, 2007.
3. **Garmire LX**, Garmire DG, Hunt CA. An in silico transwell device for the study of drug transport and drug-drug interactions, *Pharmaceutical Research*, **Featured Article**, 24(12): 2171-86, 2007. PMID: 17703347
4. **Garmire LX**, Hunt CA. In silico methods for unraveling the mechanistic complexities of intestinal absorption: metabolism-efflux transport interactions. *Drug Metab Dispos*. 36(7):1414-24, 2008. PMID: 18436618.
5. Wang KC, **Garmire LX**, Young A, Nguyen P, Trinh A, Subramaniam S, Wang NP, Shyy J, Li J, Chien S. Role of miR-23b in flow-regulation of microRNA signature and cell growth in endothelial Cells, *Proc Natl Acad Sci U S A*, 107(7): 3234-9, 2010. PMID: 20133741.
6. **Garmire LX**, Shen ZX, Briggs S, Yeo G, Glass CK, Subramaniam S. Regulatory Network of microRNAs in RAW 264.7 Macrophage Cells, *Proceedings of 32nd International Conference of the IEEE Eng Med Biol Soc, 2010:6198-201.* PMID: 21097158.
7. **Garmire LX**, Garmire DG, Huang W, Yao J, Glass CK, Subramaniam S. A global clustering algorithm to identify long intergenic non-coding RNA--with applications in mouse macrophages, *PLoS ONE,* 6(9):e24051, 2011. PMID: 21980340.
8. **Garmire LX**, Subramaniam S. Evaluation of normalization methods in mammalian micoRNA-Seq data, *RNA*, 18(6):1279-1288, 2012. PMID: 22532701.
9. Wu Y, **Garmire LX**, Fan R. Dynamic analysis of intercellular signaling reveals a mechanistic transition in tumor microenvironment, *Integrative Biology*, 4(12):1478-86, 2012. PMID: 23080410.
10. Colas A, McKeithan W, Cunningham T, Bushway P, **Garmire LX**, Duester G, Subramaniam S, Mercola M. Whole genome microRNA screening identifies let-7 and mir-18 as regulators of germ layer formation during early embryogenesis, *Genes & Development,* 26(23):2567-79, 2012
11. Nathan S\*, **Garmire LX\***, McDonald J, Norihito S, Reichart D, Heudobler D, Raetz CR, Murphy RC, Merril AH, Brown A, Dennis EA, Li AC, Fahy E, Subramaniam S, Quehenberger O, Russell DW, and Glass CK. [Regulated accumulation of desmosterol integrates macrophage lipid metabolism and inflammatory responses.](http://www.ncbi.nlm.nih.gov/pubmed/23021221), *Cell*, 151(1): 138-52, 2012 (\*: equal contributions). PMID: 23021221.
12. Hadd AG, Houghton J, Choudhary A, Sah S, Chen L, Marko AC, Sanford T, Buddavarapu K, Krosting J, **Garmire L**, Wylie D, Shinde R, Beaudenon S, Alexander EK, Mambo E, Adai AT, Latham GJ. Ultra-deep, targeted next generation sequencing of cancer genes in formalin-fixed, paraffin-embedded and fine-needle aspirate tumor specimens, *J Mol Diagn*. 15(2):234-47, 2013. PMID: 23321017.
13. **Garmire LX**, Subramaniam S. The poor performance of TMM on microRNA-Seq. *RNA* 2013,19(6), 735-6. PMID: 23616641.
14. Huang S, Yee C, Ching T, Yu H, **Garmire LX**. A novel model to combine clinical and pathway-based transcriptomic information for the prognosis prediction of breast cancer, *PLOS Comput Biol.* 20(9): e1003851, 2014. PMID: 25233347.
15. Ching T, Huang S, **Garmire LX**. Power analysis and sample size estimation for RNA-Seq differential expression. *RNA*. 20(11): 1684-96. 2014. PMID: 25246651.
16. Menor M, Ching T, Garmire D, Zhu X, **Garmire LX**. mirMark: a site-level and UTR-level classifier for miRNA target prediction. *Genome Biology*. 15(10):50. 2014. PMID: 25344330.
17. Han L, Zi XY, **Garmire LX**, Pan XH, Weissman SM, Fan R. Co-detection and sequencing of genes and transcripts from the same single cells enabled by a microfluidics platform, *Sci Rep*. Sep 26; 4:6485, 2014. PMID: 25255798.
18. Ching T,Song MA, Tiirikainen M, Molnar J, Berry M, Towner D, **Garmire LX**. Genome-wide hypermethylation coupled with promoter hypomethylation in the chorioamniotic membranes of early onset pre-eclampsia, *Mol Hum Reprod*. 20(9): 885-904, 2014. PMID: 24944161.
19. Gagliani N, Iseppon A, Vesely CA, Brockmann L, Palm NW, Zeote MR, Licona-Limon P, Paiva R, Ching T, Zi X, Fan R, **Garmire LX**, Geginat J, Stockinger B, Esplugues E, Huber S, Flavell R. Th17 cells transdifferentiate into regulatory T cells during resolution of inflammation, *Nature*. 523(7559):221-5, 2015. PMID: 25924064.
20. Ching T, Ha J, Song MA, Tiirikainen M, Molnar J, Berry M, Towner D, **Garmire LX**. Global hypomethylation in the cord blood cells associated with early onset preeclampsia, *Clin Epigenetics.* 13;7(1):21. 2015. PMID: 25806090.
21. Li J, Ching T, Huang S, **Garmire LX**. Using Epigenomics Data to Predict Differential Gene Expression in Lung Cancer, *BMC Bioinformatics*.16 Suppl 5:S10. 2015. PMID: 25861082.
22. Ching T, Masaki J, Weirather J, Subramaniam S, **Garmire LX**. Non-coding yet non-trivial: a review on the computational genomics of lincRNAs, *BioData Mining.* Dec 22;8:44. 2015. PMID: 26697116.
23. Xie G, Zhou B, Zhao Y, Qiu Y, Zhao X, **Garmire LX**, Yu H, Yen Y, Jia W Lowered circulating aspartate is a metabolic feature of human breast cancer, *Oncotarget.* 6(32):33369-81, 2015. PMID: 26452258.
24. Huang S, Yu C, Furuya H, Kattan M, Goodison S, **Garmire LX**, Rosser CJ.A nomogram derived by combination of molecular and clinical data improves the non-invasive evaluation of patients at risk for bladder cancer, *Cancer Epidemiology, Biomarkers and Prevention*. 25(9):1361-6, 2016. PMID: 27383773.
25. Huang S, Chong N, Lewis NE, Jia W, Xie G, **Garmire LX**. Novel personalized pathway-based metabolomics models reveal key metabolic pathways for breast cancer diagnosis, *Genome Medicine*. 8(1):34. 2016. PMID: 27036109.
26. Ching T, Peplowska K, Huang S, Zhu X, Shen Y, Molnar J, Yu H, Tiirikainen M, Fogelgren B, Fan R, **Garmire LX**. Pan-cancer analyses reveal long intergenic non-coding RNAs relevant to tmor diagnosis, subtyping and prognosis, *EBioMedicine,* 2016, 7:62-72. PMID: 27322459
27. Wei R, De Vivo I, Huang S, Risch, H, Moore JH, Yu H, **Garmire LX,** Meta-dimensional data integration identifies critical pathways for susceptibility, tumorigenesis and progression of endometrial cancer, *Oncotarget.* 2016. 7(34):55249-55263. PMID: 27409342.
28. Yang J, Tanaka Y, Seay M, Li Z, Jin JQ, **Garmire L**, Zhu X, Euskichen G, Synder M, Li W, Park IH, Pan X, Weissman SM. [Single cell transcriptomics reveals unanticipated features of early hematopoietic precursors.](https://www.ncbi.nlm.nih.gov/pubmed/28003475) *Nucleic Acids Research.* 2017, 45(3): 1281-1296. PMID: 28003475.
29. Poirion O, Zhu X, Ching T, **Garmire LX**, Single-cell transcriptomic bioinformatics and computational challenges, 2016, 7:163 *Frontiers in Genetics.* PMID: 27708664.
30. Lu L, McCurdy S, Huang S, Zhu X, Peplowska K, Tiirikainen M, Boisvert WA, **Garmire LX**, Time Series miRNA-mRNA integrated analysis reveals critical miRNAs and targets in macrophage polarization, 2016, 6:37446, *Scientific Reports.* PMID: 27981970.
31. Feng N, Ching T**,** Wang Y, Liu B, Lin H,Shi O,Zhang X, Yao Y, Hua L, Zheng X, Gao M, Yu H#, **Garmire LX** #, Qian B#. Analysis of microarray data on gene expression and methylation to identify long non-coding RNAs in Non-Small Cell Lung Cancer, *Scientific Reports*, 2016, 6:37233. (. #: co-corresponding authors). PMID: 27849024.
32. Huang SJ, Chaudhary K, **Garmire LX**, More is better: recent progress in multi-omics integration methods, *Frontiers in Genetics*. 2017. 8:84. doi: 10.3389/fgene.2017.00084. eCollection. PMID: 28670325.
33. Zhu X, Ching T, Pan X, Weissman S, **Garmire LX.** Detecting heterogeneity in single-cell RNA-Seq data by non-negative matrix factorization, *PeerJ.* 2017. 5(11):e2888. PMID: 28133571.
34. Alakwaa FM, Chaudhary K, **Garmire LX**, Deep learning accurately predicts estrogen receptor status in breast cancer metabolomics data, *Journal of Proteome Research*, 2018. 17(1): 337-347. PMID: 29110491.
35. Chaudhary K#, Poirion O#, Lu L, **Garmire LX**, Deep Learning based multi-omics integration robustly predicts survivals in liver cancer, *Clinical Cancer Research*. 2018. 24(6): 1248-1259. PMID: 28982688.
36. Feng N, Wang Y, Zheng M, Yu X, Lin H, Ma RN, Shi O, Zheng X, Gao M, Yu H, **Garmire L**, Qian B. Genome-wide analysis of DNA methylation and their associations with long noncoding RNA/mRNA expression in non-small-cell lung cancer. *Epigenomics*, 2017, Jan 23rd. doi: 10.2217/epi-2016-0120 [Epub ahead of print]. PMID: 28111977.
37. Han B, Park HK, Wang H, PanneerselvamJ, ShenY, ZhangJ, Li L, Lee YH, Su M, Ching T, **Garmire LX**, Jia W, Yu H, Fei P, HDBR1 Modulates U2 snRNP Function to Maintain RNA Populations, Contributing to the Suppression of Human Cancer Development, *Oncogene,* 2017, 36(38):5382-5391. PMID: 28504715.
38. Greene CS, **Garmire LX**, Gilbert JA, Ritchie MD, Hunt L, Celebrate parasites, *Nature Genetics.* 2017. 49(4):483-484. PMID: 28358134.
39. Wang BD, Ceniccola K, Hwang S, Andrawis R, Horvath A, Freeman JA, Knapp S, Ching T, **Garmire LX**, Patel V, Garcia-Blanco MA, Patierno SR, Lee NH, Aberrant Alternative Splicing in African American Prostate Cancer: novel driver of tumo r aggressiveness and drug resistance, *Nature Communications,* 2017. 8:15921. PMID: 28665395.
40. Zhu X, Wolfgruber T, Tasato A, Garmire DG, **Garmire LX,** Granatum: A graphical single cell RNA-Seq analysis, *Genome Medicine. 2017.* 9(1):108. PMID: 29202807.
41. Ortega M, Poirion O, Zhu X, Huang SJ, Wolfgruber T, Sebra R, **Garmire LX**, Using Single-Cell Multiple Omics Approaches to Resolve Tumor Heterogeneity. *Clinical Translational Medicine*. 2017. 6(1):46. PMID: 29285690.
42. Ching T, Zhu X, **Garmire LX**. Cox-nnet: artificial neural network Cox regression for prognosis prediction, *PLoS Computational Biology.* 2018. 14(4):e1006076. PMID: 29634719.
43. Stein-Obrien GL, Arora R, Culane AC, Favorov AV, **Garmire LX**, Greene CS, Goff LA, Li Y, Ngom A, Ochs MF, Xu Y, Fertig EJ. Enter the matrix: factorization uncovers knowledge from omics, *Trends in Genetics.* 2018 Oct;34(10):790-805
44. Chaudhary K, Lu L, Ching T, Huang S, **Garmire LX**, Multi-modal meta-analysis of 1494 hepatocellular carcinoma samples reveals vast impacts of consensus driver genes on phenotypes, *Clinical Cancer Research.* 2019 .25(2):463-472 doi: 10.1158/1078-0432.CCR-18-0088.
45. Poirion O, Zhu X, Ching T, **Garmire LX**, Using single nucleotide variations in single-cell RNA-Seq to identify tumor subpopulations and genotype-phenotype linkage,*Nature Communications*. 2018. 9(1):4892. doi: 10.1038/s41467-018-07170-5.
46. Alakwaa F, Huang S, **Garmire LX**. Lilikoi: an R package for personalized pathway-based classification modeling using metabolomics data, *GigaScience.* 2018. 7(12). doi: 10.1093/gigascience/giy136.
47. Taylor DM, Aronow BJ, Tan K, Bernt K, Salomonis N, Greene CS, Frolova A, Henrickson SE, Wells A, Pei L, Jaiswal JK, Whitsett J, Hamilton KE, MacParland SA, Kelsen J, Heuckeroth RO, Potter SS, Vella LA, Terry NA, Ghanem LR, Kennedy BC, Helbig I, Sullivan KE, Castelo-Soccio L, Kreigstein A, Herse F, Nawijn MC, Koppelman GH, Haendel M, Harris NL, Rokita JL, Zhang Y, Regev A, Rozenblatt-Rosen O, Rood JE, Tickle TL, Vento-Tormo R, Alimohamed S, Lek M, Mar JC, Loomes KM, Barrett DM, Uapinyoying P, Beggs AH, Agrawal PB, Chen YW, Muir AB, **Garmire LX,** Snapper SB, Nazarian J, Seeholzer SH, Fazelinia H, Singh LN, Faryabi RB, Raman P, Dawany N, Xie HM, Devkota B, Diskin SJ, Anderson SA, Rappaport EF, Peranteau W, Wikenheiser-Brokamp KA, Teichmann S, Wallace D, Peng T, Ding YY, Kim MS, Xing Y, Kong SW, Bönnemann CG, Mandl KD, White PS. The Pediatric Cell Atlas: Defining the Growth Phase of Human Development at Single-Cell Resolution. 2019. *Dev Cell*. 49(1):10-29
48. Chen B, **Garmire LX** , Calvisi BF, Chen X, Discovery of novel therapeutics for hepatocellular carcinoma using big omics data and artificial intelligence, 2019. Accepted, *Nature Reviews Gastroenterology & Hepatology.*
49. J Olender, BD Wang, T Ching, **L Garmire**, C Samtal, Y JI, J Rim,P Latham, K Nguyen, NH Lee, Identification and cloning of a novel FGF3 splice variant involved in Arfican American prostate cancer disparities, accepted, *Molecular Cancer Research.*

**Conference Proceedings**

* + - 1. **Garmire XL**, Fan R, Yeo G, Yuan GC, Quackenbush J. Single cell analysis, what is in the future? *Pac Symp Biocomput*. 2019; 24, 332-337
      2. Grant MR, Hunt CA, **Xia L**\*, Fata JM, Bissell MJ. Modeling mammary gland morphogenesis as a reaction-diffusion process, *Proceedings of the 26th Annual International Conference of the IEEE EMBS*, San Francisco, CA, USA September 1-5, 2004 (\*: Maiden name)
      3. **Garmire L**, Gliske S, Nguyen QC, Chen JH, Nemati S, Van Horn JD, Moore JH, Shreffler C, Dunn M. The making of next generation data scientists in biomedicine. *Pac Symp Biocomput*. 2016; 22:640-645. PMID: 27897014
      4. Poirion O, Chaudhary K, **Garmire LX**, Deep Learning data integration for better risk stratification models of bladder cancer. *AMIA joint summit meeting*, 2018.
      5. Ching T, **Garmire LX**, Pan-cancer analysis of expressed single nucleotide variants in long inter-genic non-coding RNA, *Pac Symp Biocomput*. 2018; 23:512-523. PMID: 29218910.

**In Review/Revision**

1. Schlueter, RJ, Al-Akwaa FM, Benny PA, Gurary A, Xie G, Jia W, Chun X, Chern I, **Garmire LX**, Metabolomics profile of cord blood is associated with maternal pre-pregnant obesity in a prospective multi-ethnic cohort, in revision. *Journal of Proteome Research*
2. Yamasato K, Ching T, **Garmire LX,** Berry M, Towner D, Evaluation of a maternal cardiovascular gene array in early on-set preeclampsia in a dominantly Asian cohort, in revision, *BMC Pregnancy and childbirth.*
3. Benny P, Al-akwaa, FM, Schleuter, R, Lassiter C, **Garmire LX**, A review and meta-analysis of genomics approaches to study preeclampsia. Under review. *Placenta*
4. Paula A Benny, Fadhl M. Al-akwaa , Corbin Dirkx, Ryan J. Schlueter, Thomas K. Wolfgruber, Ingrid Y. Chern , Suzie Hoops, Dan Knights, **Lana X. Garmire** . Placenta microbiome diversity is associated with maternal pre-pregnancy obesity and placenta biogeography, Submitted, *mBio*
5. Arisdakessian C, Poirion O, Yunits B, Zhu X, **Garmire LX** . DeepImpute: an accurate, fast and scalable deep neural network method to impute single-cell RNA-Seq data. in revision. *Genome Biology*

**In Preparation for submission with set deadlines**

1. Poirion O, Chaudhary K, Huang SJ, **Garmire LX**, Predicting pan-cancer survival using deepProg, a deep-learning based ensemble method. *Nature Methods (plan to submit June 2019)*
2. Huang Q, Liu Y, **Garmire LX,** Evaluation of computational methods to deconvolute cell types in single cell RNA-seq data, *Briefings in Bioinformatics (plan to submit July 2019)*
3. Du Y, **Garmire LX**, Comparing two popular aligners for single cell RNA-seq application. *Nucleic Acid Research (plan to submit July 2019)*
4. Cervera-Marzal E, Al-Kawaa F, Liu Y, He K, **Garmire LX**, clinical covariates associated with telomere length in a preeclampsia case control cohort. *Pediatric Research (plan to submit in July 2019)*
5. Zhu X, Yunits B, Faust E, Wolfgruber T, Poirion O, Liu Y, Huang Q, Arisdakessian C, **Garmire LX**. GranatumX: A community engaging and flexible software environment for single-cell analysis. *Nature methods (plan to submit June 2019)*
6. Hosseini N, Al-kawaa, Piorion, O, Westerhoff M, Choi K, **Garmire LX**. Using histopathology whole-slide images to predict liver cancer patient survival. *Clinical Cancer Resarch (plan to submit Aug 2019)*
7. Liu Y, Lassiter C, Al-Akwaa F, Benny P, …., **Garmire LX**, Comprehensive analysis of DNA methylation in a large preeclampsia case control cohort. *Nature Genetics (plan to submit in Aug 2019)*

**Book chapter**

X Zhu, **LX Garmire**. Chapter 19: Data analysis in Single Cell Omics. Single-cell Omics, Vol. 1 (Elsevier)

**Abstracts/Posters**

**US and international conferences**

1. Differential methylation on cord blood in early-onset preeclampsia in a predominantly asian cohort, 18th International Conference on Prenatal Diagnosis and Therapy, Brisbane, Australia, July 20-23rd, 2014.
2. Using Epigenomics Data to Predict Differential Gene Expression in Lung Cancer. Seventh Annual RECOMB/ISCB Conference on Regulatory and Systems Genomics, San Diego, Nov 9-14th 2014
3. A novel model to combine clinical and pathway-based transcriptomic information for the prognosis prediction of breast cancer, Seventh Annual RECOMB/ISCB Conference on Regulatory and Systems Genomics, San Diego, Nov 9-14th 2014
4. Pan-cancer analysis of lincRNAs reveals robust diagnostic biomarkers. Pacific Symposium on Biocomputing, Big island, Jan 2015
5. Pathway-based metabolomics classification models reveal key metabolic pathways for breast cancer diagnosis and progression, Big Data in Biomedicine Conference, Stanford, CA, May 21st, 2015
6. Association analysis of driver genes of hepatocellular carcinoma with cancer hallmarks. 13th Rocky Mountain Bioinformatics Conference, Aspen, Dec.10-13. 2015
7. Application of non-negative matrix factorization to single cell RNA-Seq analysis, BD2K Annual All Hands Grantee Meeting, Bethesda, NIH, Nov 12th 2015
8. Detecting heterogeneity in single-cell RNA-Seq (scRNA-Seq) data by non-negative matrix factorization. NIH Single Cell Analysis Program Investigators Meeting, Nov 2015.
9. Neural network survival applied to pan-cancer lincRNA data. Pacific Symposium on Biocomputing, Big Island, HI Jan 2016
10. Pan-cancer analyses reveal lincRNAs relevant to tumour diagnosis, subtyping and prognosis. Big Data in Biomedicine Conference, Stanford, CA May 2016
11. Novel personalized pathway-based modeling approach reveals key pathways in predicting breast cancer diagnosis and prognosis, Big Data in Biomedicine Conference, Stanford, CA May 2016
12. Novel personalized pathway-based modeling approach reveals key pathways in predicting breast cancer diagnosis and prognosis, NIH IdeA meeting, Washington DC, June 2016
13. Pan-cancer analyses reveal lincRNAs relevant to tumour diagnosis, subtyping and prognosis. NIH IDeA meeting, Washington DC, June 2016
14. Pathway-based metabolomics classification models reveal key metabolic pathways for breast cancer diagnosis and progression, ISMB, FL, July 2016
15. Using genetic features to identify subpopulations in single-cell RNA-Seq data. Frontiers in Single Cell Genomics meeting, Cold Spring Harbor Asia, Suzhou, China. Nov 2016
16. Granatum: a graphical single-cell RNA-seq analysis pipeline for genomics scientists, Visualization Biological Data Conference. Sydney, Australia. June 2017.
17. DeepProg: Multi-omics integration to predict cancer survival subtypes", RECOMB Satellite Meeting Barcelona, Spain. Oct. 2017
18. Pan-cancer analysis of expressed somatic nucleotide variants in long intergenic non-coding RNA.Pacific Symposium on Biocomputing, Big Island, HI. Jan 2018
19. Metabolomics analysis of umbilical cord blood associated with maternal obesity, Annual SMFM Meeting, Dallas, TX. 2018
20. Metabolomics analysis identifies subtypes of breast cancers, Great Lakes Bioinformatics meeting, WI, 2019
21. Evaluation of Computational methods to de-convolute cell types in single cell RNA-Seq data, Great Lakes Bioinformatics meeting, WI, 2019
22. Using histopathology whole-slide image quantitative features to predict liver cancer patient survival, Great Lakes Bioinformatics meeting, WI, 2019

**University of Michigan conferences**

**University of Hawaii conferences**

1. Integration of methylation, long non-coding RNA and mRNA expression data in lung Cancer, Weinman Symposium. May 2014 (Best Poster Award)
2. Combining clinic and pathway-based transcriptomic information improves the prognosis prediction of breast cancers. University of Hawaii Cancer Center, Weinman Symposium. May 2014
3. Application of non-negative matrix factorization method to single-cell RNA-Seq analysis, John A. Burns School of Medicine, Biomedical Science and Health Disparities Symposium, April. 2015.
4. Pathway-based metabolomics classification models reveal key metabolic pathways for breast cancer diagnosis and progression. John A. Burns School of Medicine, Biomedical Science and Health Disparities Symposium, April. 2015.
5. Differential epigenetic profile analysis in cord blood stem cells from offspring of obese and normal weight mothers in a multi-ethnic cohort. John A. Burns School of Medicine, Biomedical Science and Health Disparities Symposium, April. 2017.
6. Granatum: a graphical single-cell RNA-seq analysis pipeline for genomics scientists, John A. Burns School of Medicine, Biomedical Science and Health Disparities Symposium, April. 2017.
7. Novel personalized pathway-based approach reveals key pathways in predicting breast cancer diagnosis and prognosis. John A. Burns School of Medicine, Biomedical Science and Health Disparities Symposium, April. 2017.
8. Metabolomics analysis of umbilical cord blood in maternal obesity: pilot results. John A. Burns School of Medicine, Biomedical Science and Health Disparities Symposium, April. 2017.
9. Optimizing a machine learning algorithm to classify GSE samples, CURE Summer undergraduate internship presentations, University of Hawaii Cancer Center, Aug 2017