Vita **LANA XIA GARMIRE** Aug. 2017

Associate Professor 701 Ilalo Street, Honolulu, HI 96813

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**EDUCATION**

**Postdoc (Mar. 2008-Feb. 2011)** Bioengineering Department, UC-San Diego, La Jolla, CA. (Advisors: Shankar Subramaniam and Christopher K Glass)

**Ph.D. (Aug.2001-Dec. 2007)** Comparative Biochemistry (Computational Biology focus). UC Berkeley, Berkeley, CA, (Advisor: Anthony C. Hunt)

**M.A. (May 2005)** Statistics, UC Berkeley, Berkeley, CA.

**B.S. (July 2001)** Food Science and Engineering, Ocean University of China, Qingdao, China

**EXPERIENCE**

**4/2011-8/2012**: Senior scientist in computational biology, Asuragen Inc. (a spin-off from Ambion, the RNA company), Austin, TX

**8/2005-12/2005**: Computational Biology Intern, Berlex Research Lab, Schering AG. Richmond, CA.

**9/2002-9/2007**: Graduate Student Researcher/Instructor, Comparative Biochemistry Program, University of California – Berkeley, Berkeley, CA

**9/2001-9/2002**: Graduate Student Researcher, Nutritional Science Department, University of California – Berkeley, Berkeley, CA

**PRIMARY FACULTY APPOINTMENT**

**06/2017-present**: Associate Professor (with tenure)

Cancer Epidemiology Program

University of Hawaii Cancer Center

**03/2017-present**: Director

Computational Science Core

University of Hawaii Cancer Center

**09/2012-06/2017**: Assistant Researcher/Professor (Tenure-track)

Cancer Epidemiology Program

University of Hawaii Cancer Center

**AFFILIATED FACULTY APPOINTMENT**

**07/2014-present**: Adjunct Assistant Professor

Department of Anatomy, Biochemistry and Physiology

John A. Burns School of Medicine University of Hawaii

**07/2014-present**: Faculty member

Institute of Biogenesis Research

John A. Burns School of Medicine University of Hawaii

**02/2013-present**: Graduate Cooperate Faculty

Program of Molecular Biosciences and Bioengineering

College of Tropical Agriculture and Human Resources

**01/2016-present**: Adjunct Faculty

Department of Obstetrics, Gynecology and Women’s Health

John A. Burns School of Medicine University of Hawaii

**HONORS AND AWARDS**

1. Faculty Travel Award of 12th International conference on pathways, networks and systems medicine.
2. Finalist, University of Hawaii Board of Reagent’s Excellence in Research Award, 2016.
3. Guided undergraduate student Austin Tasato to win Undergraduate Opportunity Program Scholarship, April 2016.
4. Elected as Early Career Reviewer (ECR) by NIH, since Jan. 12th 2016.
5. Guided PhD student Sijia Huang to win Giving Tree Graduate Student Scholarship at University of Hawaii, 2015
6. Guided PhD student Travers Ching to win the three-year Roche Scholar Award in Life Sciences from Roche and ARCS Foundation, 2015
7. Guided PhD student Runmin Wei to win Giving Tree Graduate Student Scholarship at University of Hawaii, 2014
8. Guided undergraduate student Nicole Chong to win Undergraduate Research Opportunity Program Scholarship at University of Hawaii, 2014
9. Best Scientific Paper Award, University of Hawaii Cancer Center, Nov. 2014
10. Conference Travel Award, ISBRA 2014, 2014
11. Guided PhD student Travers Ching to win the “Best Poster Award” at Weinman Symposium 2014, judged by Nobel Laureates Dr. Bruce Beutler and Dr. Jules Hoffmann
12. NSR Physiome Project Training Award, 2007
13. Conference Travel Fellowship, University of California, 2007
14. Best Student Paper Award in International Conference on Computational Biology (ICCB), 2007
15. Excellent Student Award of Shandong Province, China, 1998
16. Jing Sui Fellowship, Ocean University of China, 1997
17. Top-ten Excellent College Student at Ocean University of China, 1997 (Ranked No. #2)

**PROFESSIONAL AFFILIATIONS**

International Society of Computational Biology (ISCB) member (since 2014)

American Medical Informatics Association (AMIA) member (since 2017)

**AWARDED GRANTS AND CONTRACTS (DIRECT COST)**

**1) University of Hawaii Cancer Center Seed Grant (Garmire)**

$40,000

04/01/2017-03/31/2018

Role: PI

Project: Novel lincRNA as liver cancer biomarkers

**2) NICHD R01 (Garmire)**

$1,980,918

7/1/2016 – 6/30/21

Role: PI (sole)

Project: An Integrative Omics Approach to Identify Biomarkers Related to Preeclampsia and Breast Cancer Risks

**3) NLM R01 (Garmire)**

$900,800

9/1/2016 – 8/30/20

Role: PI (sole)

Project: An Integrative Bioinformatics Platform with Application in Single Cancer Cells

**4) NIGMS 2 P20 GM103457-06A1 (Ward)**

$875,000 for Garmire’s Project

7/1/2014 – 6/30/19

Role: Project Leader

Institute for Biogenesis Research: COBRE

Project: Linking Maternal Obesity and Offspring Cancer Risks through Integration of transcriptome and methylome of the cord blood stem cells

**5) NIEHS 1 K01 ES025434-01 (Garmire)**

$865,000

10/1/14 –9/30/19

Role: PI

Project: An Integrative Bioinformatics Approach to Study Single Cancer Cell Heterogeneity

**6) Hawaii Community Foundation 14ADVC-64566 (Garmire)**

$38,000

7/1/14 – 12/31/15

Role: PI

Project: Using Next Generation Sequencing to Detect Circulating microRNAs as Diagnostic Biomarkers of Liver Cancer

**7) NIGMS 5 P30 GM103341-02 (Shohet)**

9/24/2013-6/30//2014

$48,500

Role: PI of the Pilot Project Program

COBRE III: Center for Cardiovascular Research – Pilot Project Program

Project: Investigating microRNA-targetome Interaction in Macrophage Polarization

This pilot study will establish a comprehensive map to uncover the global roles of microRNA in macrophage polarization.

**8) NIMHD/Charles R. Drew U. (Bazargan)**

$10,000

12/16/2013-6/30/2014

Role: PI

RCMI Translational Research Network

Collaborative Award: An Integrative Bioinformatics Platform with Application in Single Cancer Cells

**9) NIH/SBIR R43 HG007140 (Garmire and Choudhary)**

$242,940

Role: PI, succeeded by CO-PI Choudhary Ashish upon resignation from Asuragen

Project: Integrated Bioinformatics Analysis Suite for Deep Targeted Amplicon Sequencing

**PUBLICATIONS**

**PhD Thesis**

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

**Journal Publications**

*Primary/Senior Author Publications*

1. Al-alkwaa F, Chaudhary K, **Garmire LX**, Deep learning predicts estrogen receptor status in breast cancer metabolomics data, accepted by Translational Bioinformatics Conference 2017, will appear in one of the designated partnering journals.
2. 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
3. Huang SJ, Chaudhary K, **Garmire LX**, More is better: recent progress in multi-omics integration methods, *Frontiers in Genetics*. 8:84. doi: 10.3389/fgene.2017.00084. eCollection 2017
4. **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.
5. 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#. Integrated Analysis of DNA Methylation, LncRNA and Gene Expression in Non-Small Cell Lung Cancer, 2016, 6:37233. doi: 10.1038/srep37233. *Scientific Reports* (. #: co-corresponding authors)
6. 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.*
7. Poirion O, Zhu X, Ching T, **Garmire LX**, Single-cell transcriptomic bioinformatics and computational challenges, 2016, 7:163 *Frontiers in Genetics*
8. Wei R, De Vivo I, Huang S, Risch, H, Moore JH, Yu H, **Garmire LX,** meta-dimensional data integration identifies critical pathways for endometrial cancer susceptibility, tumorigenesis and progression, *Oncotarget.* Jul 9. doi: 10.18632/oncotarget.10509. [Epub ahead of print]
9. 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 lincRNAs relevant to tumour diagnosis, subtyping and prognosis, *EBioMedicine,* 2016, 7:62-72.
10. Huang S, Chong N, Lewis NE, Jia W, Xie G, **Garmire LX**. Novel pathway-based metabolomics classification models reveal key metabolic pathways for breast cancer diagnosis, *Genome Medicine*. 8(1):34. 2016.
11. Ching T, Masaki J, Weirather J, Subramaniam S, **Garmire LX**. Non-coding yet non-trivial: a review on the genomics of long intergenic non-coding RNAs, *BioData Mining.* Dec 22;8:44. 2015.
12. 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
13. 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.
14. 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.
15. Ching T, Huang S, **Garmire LX**. Power analysis and sample size estimation for RNA-Seq differential expression. *RNA*. 20(11): 1684-96. 2014
16. 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.
17. Ching T,Song MA, Tiirikainen M, Berry M, Towner D, **Garmire LX**. Global hypermethylation coupled with promoter hypomethylation in the chorioamniotic membranes of early onset preeclampsia, *Mol Hum Reprod*. 20(9): 885-904, 2014.
18. **Garmire LX**, Subramaniam S. The poor performance of TMM on microRNA-Seq. *RNA* 2013,19(6), 735-6
19. 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)
20. **Garmire LX**, Subramaniam S. Evaluation of microRNA-Seq normalization methods, *RNA*, 18(6):1279-1288, 2012
21. **Garmire LX**, Garmire DG, Huang W, Yao J, Glass CK, Subramaniam S. A global clustering approach to identify intergenic non-coding RNA, with application in mouse macrophages, *PLoS ONE,* 6(9):e24051, 2011
22. **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.*
23. **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
24. **Garmire LX**, Garmire DG, Hunt CA. An in silico transwell device for drug transport and drug-drug interaction studies, *Pharmaceutical Research*, **Featured Article**, 24(12): 2171-86, 2007
25. **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

*Collaborative Co-author Publications*

1. 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 tumor aggressiveness and drug resistance, *Nature Communications,* 8:15921, 2017
2. Greene CS, **Garmire LX**, Gilbert JA, Ritchie MD, Hunt L, Celebrate parasites, *Nature Genetics.* 49(4):483-484, 2017
3. 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,* doi: 10.1038/onc.2017.150. [Epub ahead of print]
4. 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].
5. Yang J, Tanaka Y, Seay M, Li Z, Jin JQ, **Garmire L**, Zhu X, Euskirchen 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.* Dec 20. pii: gkw1214. doi: 10.1093/nar/gkw1214. [Epub ahead of print]. 2016.
6. 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
7. 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
8. 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.
9. 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
10. 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
11. 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
12. 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
13. 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
14. 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)
15. Fan T, **Xia L**\*, Han Y. Mitochondrion and apoptosis. Acta Biochica et Biophysica Sinica 2001, 33(1): 7-12 (\*: Maiden name)

**Manuscripts under Review or Revision**

*Senior/Primary Author Manuscripts*

1. Ching T, Zhu X, **Garmire LX**. Cox-nnet: artificial neural network Cox regression for prognosis prediction, revision submitted, *PLoS Computational Biology.*
2. Chaudhary K, Lu L, Ching T, Huang S, **Garmire LX**, Clinical and transcriptomics associations of putative driver gene mutations in liver hepatocellular carcinoma, submitted, *eLife*
3. 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, in revision,*Nature Communications*
4. Chaudhary K, Poirion O, Lu L, **Garmire LX**, Deep Learning based multi-omics integration robustly predicts survivals in liver cancer, revision submitted, *Clinical Cancer Research.*
5. Zhu X, Wolfgruber T, Tasato A, **Garmire LX,** Granatum: A web server for single cell RNA-Seq analysis, in revision, *Genome Medicine.*
6. Ortega M, Poirion O, Zhu X, Huang SJ, Sebra R, **Garmire LX**, Using Single-Cell Multiple Omics Approaches to Resolve Tumor Heterogeneity. Submitted.

*Collaborative Co-author Manuscripts*

1. 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, submitted, *Pregnancy Hypertension*

**INVITED SEMINARS**

*National and international institutes*

1. New computational methods in cancer biomarker research using multi-omics data integration, Institute of Computational Health Sciences, UC-San Francisco, July 17-18th, 2017.
2. Machine-learning and deep-learning based genomics data integration on cancer biomarker discoveries, Bioengineering Department, University of Illinois at Chicago, March 20th, 2017.
3. Scalable Meta-dimensional and Multi-dimensional Data Integration for Clinical and Biological Insights, University of Pennsylvania, Dec. 1st, 2016.
4. Big Data Analytics for Precision Medicine, Center for Biomedical Informatics, Brown University, July 25th, 2016.
5. Cancer Prognosis and Diagnosis Using Personalized Pathway-based Modeling. Mayo Clinic, Florida, July 13th , 2016.
6. Knowledge-driven Big Data Analytics Approach for Cancer Biomarker Discovery. University of Florida, July 7th 2016.
7. Enable Precision Medicine with Big Data Analytics. Sanford-Burnham Institute, San Diego, May 27th, 2016.
8. Big Data integration: from population to single cells. Department of Biomedical Informatics and Medical Education, University of Washington. Feb. 21st, 2016.
9. 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.
10. Big Data integration: from population to single cells. Biomedical Engineering Department, George Washington University, Nov 11th, 2015
11. Integration of Big Data in Cancer Research. Development of Modern Methods for Linear Algebra Workshop (DMML). UC-Berkeley, Oct 23-24th, 2015
12. Big Data integration for precision medicine: from population to single cells. Department of Biomedical Informatics, School of Medicine, University of Pittsburgh. July 23rd, 2015.
13. Big Data integration: from population to single cells. Institute of Biomedical Informatics, Perelman School of Medicine, University of Pennsylvania, July 21st, 2015.
14. Big Data integration: from population to single cells. Biomedical Informatics Department, UC-San Diego. May 22nd, 2015.
15. Big Data integration: from population to single cells. Department of Biomedical Informatics, Ohio State University. April 24th, 2015.
16. Big Data integration: from population to single cells. Biomedical Engineering Department, University of Florida. April 22nd, 2015.
17. Big Data integration: from population to single cells. Systems Biology Center, National Heart, Lung and Blood Institute, NIH. April 21st, 2015.
18. 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
19. Big Data integration: from population to single cells. Biomedical Engineering Department, Columbia University, Mar 2nd, 2015
20. Big Data integration: from population to single cells. Stem Cell Center, Yale University, Feb 28th, 2015
21. Integration of Big Data with applications in cancer research. Computational Biology Institute, George Washington University, Feb 25th, 2015
22. Towards solving the challenges of big cancer data integration. CAS-MPG Partner Institute for Computational Biology. Shanghai, China July 4th, 2014
23. The challenges of Big Data integration. Shanghai JiaoTong University, School of Public Health, Shanghai, China. July 2nd, 2014
24. The challenges of Big Data integration. Genetics Department, Yale University, June 20th, 2014
25. Systems biology and personalized medicine—Promises from ultra-high throughput data analysis. Pathology Department, University of Alabama at Birmingham, April 1-2nd, 2012.

*Hawaii communities*

1. 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.
2. Big data for precision medicine: from population to single cells. Institute of Biogenesis Research. University of Hawaii. Dec. 11th, 2015.
3. Epigenomics and beyond in pregnancy adversities. Grand Rounds talk, Department of Ob/Gyn and Women’s Health, JABSOM, University of Hawaii. June 24th. 2015
4. What can systems biology do for you. Hawaii Institute of Marine Biology, Feb 6th, 2013.
5. Personalized medicine and systems biology: promise from ultra-high throughput data analysis. University of Hawaii Cancer Center. June 19th, 2012
6. A novel class of in-silico devices to study drug transport through intestinal barriers. University of Hawaii Cancer Center. Nov 27, 2007.

**CONFERENCE PRESENTATIONS**

*Oral presentations*

1. How to turn secondary data analysis into primary funding, Jan 5th, BD2K Training Working Group webnar meetings, 2017.
2. 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.
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. 10th International International Symposium on Bioinformatics Research and Applications (ISBRA 2014). The roles of microRNA and targetsome in macrophage polarization. Zhangjiajie, China, June 28-30th, 2014
5. 10th International Symposium on Bioinformatics Research and Applications (ISBRA2014). Integration of methylation, long noncoding RNA and mRNA expression data in Lung Cancer. Zhangjiajie, China, June 28-30th, 2014.
6. 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.
7. Biomedical Engineering Society Annual Meeting (BMES 2011). Evaluation of normalization methods for microRNA-Sequencing. Hartford, Oct 12-15th, 2011.
8. 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](http://ieeexplore.ieee.org/xpls/abs_all.jsp?arnumber=5627742). Buenos Aires, Argentina. Sept 30-Oct 4th, 2010
9. 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
10. 10th Annual UC Systemwide Bioengineering Symposium. Using CHIP-Seq to Identify Intergenic Non-coding RNA in Mouse Macrophages, June 19-21st, 2009. Merced, CA
11. 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.
12. World Congress on Engineering and Computer Science 2007. [Study of Metabolic Enzyme-Efflux Transporter Relations with in Silico Devices](http://citeseerx.ist.psu.edu/viewdoc/summary?doi=10.1.1.148.4356). San Francisco. Oct 24-26th, 2007. (**Best Paper Award).**
13. 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.

*Poster presentations*

1. Pathway-based metabolomics classification models reveal key metabolic pathways for breast cancer diagnosis and progression, ISMB, FL, July 2016.
2. Pan-cancer analyses reveal lincRNAs relevant to tumour diagnosis, subtyping and prognosis. Big Data in Biomedicine Conference, Stanford, CA May 2016.
3. Pan-cancer analyses reveal lincRNAs relevant to tumour diagnosis, subtyping and prognosis. NIH IdeA meeting, Washington DC, June 2016.
4. Novel personalized pathway-based modeling approach reveals key pathways in predicting breast cancer diagnosis and prognosis, NIH IdeA meeting, Washington DC, June 2016.
5. Application of non-negative matrix factorization to single cell RNA-Seq analysis, BD2K Annual All Hands Grantee Meeting, Bethesda, NIH, Nov 12th 2015.
6. 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.
7. Neural network survival applied to pan-cancer lincRNA data. Pacific Symposium on Biocomputing, Big Island, HI Jan 2016.
8. Association analysis of driver genes of hepatocellular carcinoma with cancer hallmarks. 13th Rocky Mountain Bioinformatics Conference, Aspen, Dec.10-13. 2015.
9. 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
10. Pan-cancer analysis of lincRNAs reveals robust diagnostic biomarkers. Pacific Symposium on Biocomputing, Big island, Jan 2015.
11. 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
12. 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
13. 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

**COURSES & GUEST LECTURES**

1. 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.
2. MBBE 699 (CRN#: 80146): Directed Research. Fall 2013.
3. MBBE 699 (CRN#: 89838): Directed Research. Spring 2014.
4. MBBE 699 (CRN#: 78735): Directed Research. Fall 2014.
5. MBBE 699 (CRN#: 88461): Directed Research. Spring 2015.
6. MBBE 699 (CRN#: 77457): Directed Research. Fall 2015.
7. MBBE 699 (CRN#: 87125): Directed Research. Spring 2016.
8. MBBE 700 (CRN#: 90061): Thesis Research, Spring 2016.
9. University of Hawaii Cancer Center CURE summer internship seminar. Topic: Translational Bioinformatics.
10. General Biology (Fall 2003)
11. Introduction to Protein Bioinformatics (Fall 2005)
12. Introduction to Human Nutrition (Spring 2006)
13. Introduction to Biostatistics (Summer 2006)
14. Introduction to Biostatistics (Summer 2007)
15. Survey of Principles in Biochemistry & Molecular Biology (Spring 2007)

**INVENTIONS**

**Provisional Patents**

1. Huang S and **Garmire LX**. “A novel pathway-based genomic model and signatures for breast cancer prognosis prediction,” Filed by OTTED of UH. Application # 61952769.

**Patents**

1. Ching T and **Garmire LX**, “panel of long intergenic noncoding RNA as pan-cancer biomarkers”, Filed by OTTED of UH. Application #62120310. **Full patent pending.**

**STUDENTS & POSTDOCS MENTORING**

**Postdoc and junior researcher**

1. Jason Weirather, PhD, Apr-July 2013. Currently postdoc at University of Iowa.
2. Karolina Peplowska, PhD (joint with Dr. Maarit Tiirikainen, Director of Genomics Shared Resources), since Nov 2014.
3. Kumardeep Chaudhary, PhD, since Mar. 2016.
4. Olivier Poirion, PhD, since Feb 2016.
5. Paula-Beth Angelica Tiqui Benny, PhD, since Nov 2016
6. Fadhl Al-Akwaa, PhD, since Nov 2016.
7. Thomas Wulfgruber, PhD, since Nov 2016
8. Ryan Schlueter, MD, OB/GYN fellow, since Jan 2016.
9. Kelly Yamasato, MD, OB/GYN fellow, since Jan 2016. Currently faculty at University of Hawaii.
10. Micheal Ortega, PhD, since Jan 2017.

**Graduate (Ph.D. students are in bold,** *graduated students are in italic***)**

1. **Cedric Arisdakessian**, PhD, since Aug. 2017 (thesis advisor)
2. **Abdelrahman Mohamed,** PhD, since Aug. 2017 (thesis advisor)
3. *Joshua Chen, MS, Sept -Dec2016. Currently MS student in EE Dept. UH Manoa*
4. ***Jack Fennick,*** *Ph.D. June-Aug 2016. Currently PhD student in Math Dept. UH Manoa*
5. ***Mark Menor***, Ph.D., graduated May, 2014. Currently data scientist in Contix.
6. ***Travers Ching****, Ph.D. student, Aug 2013-May 2017 (thesis advisor), currently Computational Biologist, Adaptive Biotechnologies, Seattle, WA*
7. **Sijia Huang,** Ph.D. student, since Aug, 2013 (thesis advisor)
8. **Xun Zhu**, Ph.D. student, since June, 2014 (thesis advisor)
9. *Liangqun Lu, MS. student, 2014-2016 (thesis advisor). Currently PhD student in Univ. Memphis.*
10. *Hsin-Yi Chen, Ph.D rotational student, Oct- Dec. 2015.*
11. *Reimin Wei, MS. student, Aug, 2014-Aug, 2015. Currently PhD student in Dr. Wei Jia lab, University of Hawaii.*
12. *Jayson Masaki, MD, volunteer, Feb, 2014-Sept, 2014, currently resident at Chicago medical school.*

**Undergraduates** (*past undergraduate students are in italic*)

1. Dylan Combs, 2nd year student in Sociology Major, Harvard University, Summer 2017.
2. Shaw Chun, pre-med undergraduate student, UH Manoa, since June 2016.
3. Austin Tasato, 2nd year student in Electrical Engineering major, May 2015 –May 2016.
4. *Jordan Fernandez*, 2nd year Undergraduate Summer Research Assistant from Washington State University, June 2016 –Aug 2016.
5. *Nicole Chong*, 3rd year student in Biology major, June 2014-Dec 2014.
6. *Jonathan Ujebe*, senior year student in Electrical Engineering, Aug 2014-Dec 2014.
7. *James Ha*, 2nd year Undergraduate Intern from California Institute of Technology. June 2014-Aug 2014. Currently medical student at University of Hawaii.
8. *Jeffrey Li*, 2nd year Undergraduate Summer Research Assistant from Johns Hopkins University. June 2014-Aug 2014. Currently product management associate at Athena Health.
9. *Cameron Yee*, 3rd year Undergraduate Intern from University of Washington at Seattle. June 2013-Aug 2013. Currently software engineer at Nomic.

**PROFESSIONAL SERVICE**

1. Reviewer for journals:

* RNA
* PLoS Computational Biology
* AACR: Cancer Epidemiology, Biomarkers and Prevention
* PloS One
* Genome Medicine
* BMC Bioinformatics
* Clinical Epigenetics
* Scientific Reports
* IEEE Transactions on NanoBioscience
* AJP- Heart and Circulatory Physiology
* Molecular Human Reproduction
* Nucleic Acid Research
* Genetics
* Frontiers in Genetics
* Nature Communications
* PLoS Genetiecs
* Bioinformatics
* Pacific Scientific Biocomputing Conference
* IEEE/ACM Transcations on Computational Biology and Bioinformatics

1. Grant reviewer for:

United States

NLM T15 study section, August 2016.

NIH BDMA study section, Sept. 2016.

NIH GCAT stuty section, June 2017.

Other countries

Germany: Kom Op Tegen Kanker Foundation, Collaborator biomedical research grants.

1. Editorial Services:

*Associate Editor* BMC Bioinformatics (since 2016)

*Guest Editor* PLOS Computational Biology (since 2016)

1. Mentorship on grant proposals:

Faculty mentor: T32 cardiovascular disease training grant (PI: Ralph Shohet)

Co-mentor: Mentored Career Development Award (K01) for Dr. Michael Coley

Faculty mentor: R25 National Cancer Institute Youth Enjoy Science Research Education

Program (PIs: Marskarinec, Ramos, Nigg)

1. Peer mentor for junior-faculty:

* Dr. Junming Yin, Assistant Professor, Department of Management Information Systems, University of Arizona.
* Dr. Quyenh Nguyen, Assistant Professor, Department of Health Promotion And Education, University of Utah.
* Dr. Ruogu Rachel Fang, Assistant Professor, School of Computing and Information Sciences, Florida International University.

1. Host for guest/visiting faculty:

* Professor Jason Moore, Director of the Institute for Quantitative Biomedical Sciences of Dartmouth College, to visit University of Hawaii Cancer Center, May 14th, 2014.
* Dr. Kejie Zhao, Director of Systems Biology Center of National Heart, Lung and Blood Institute, to visit the University of Hawaii. March 19-21st, 2015.
* Dr. Jianhua Ruan, Associate Professor of Computer Science, UT-San Antonio, to visit the University of Hawaii. July 17th, 2015.
* Dr. Xinghua Lu, Associate Professor of Biomedical Informatics Department, University of Pittsburgh, to visit the University of Hawaii. October 18-20th. 2015.
* Dr. James Foster, Professor of Bioinformatics, University of Idaho, to visit the University of Hawaii, Jan 11-12th, 2016.
* Dr. Russ Altman, Professor of Biomedical Informatics, Stanford University, to visit the University of Hawaii, Feb. 19, 2016.
* Dr. Casey Greene, Assistant Professor of Pathology Department, University of Pennsylvania, to visit the University of Hawaii, Feb. 19, 2016.
* Dr. Derek Radisky, Associate Professor from Mayo Clinic, Jacksonville FL, to visit the University of Hawaii, May 12th, 2016.
* Dr. Kin Fai, Au, Assistant Professor from University of Iowa, to visit the University of Hawaii, March 17th, 2017.
* Dr. John Quackenbush, Harvard University, to visit my group and the University of Hawaii, Aug 9-10th, 2017.

1. Conference/workshop/award organization activities:

* Session Chair of ISCA 21st International Conference on Computer Applications in Industry and Engineering, (CAINE 2008).
* Poster award review committee for ISMB 2016, July 8-12th, Orlando, FL.
* Chair of workshop “the making of next generation data scientists in biomedicine” at PSB 2017.
* Award Committee member for “Parasite Awards” at PSB 2017.
* Program Committee for “Applications to Microbes and Imaging Genetics” session, ACM BCB 2017
* Chair of Steering Committee, International Conference on Intelligent Biology and Medicine (ICIBM), Dec 2017.

1. Thesis committees:

Chair, PhD thesis committee, Travers Ching (graduated May 2017).

Chair, PhD thesis committee chair, Sijia Huang (expected to graduate Aug. 2017).

Chair, MS thesis committee chair, Liangqun Lu (graduated July 2016)

Committee member: PhD thesis committee member, Min-Ae Song (graduated 2014).

1. Organization committee member for UH Cancer Center faculty retreat, 2015.
2. Multi-time Faculty Candidate Interviewer at UH Cancer Center.
3. University of Hawaii Cyberinfrastructure Faculty Advisory Committee.
4. Mentoring postdoc from Atul Butte Group at Stanford for K01 award application.
5. Mentored postdoc Carrie Wright from Daniel Weinberger’s lab in Johns Hopkins University on the K01 application.
6. Peer mentor/leader for NIH/BD2K K01 awardees.