

Travers H. Ching

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Education

University of Hawai'i at Mānoa <i>Ph.D. in Molecular Biosciences and Bioengineering</i> Research area: Non-coding RNA, bioinformatics, machine learning and cancer biology	Honolulu, HI 2013-2017
University of Hawai'i at Mānoa <i>M.S. in Microbiology</i> Research area: biological fuel contamination, mechanical corrosion and novel species identification	Honolulu, HI 2010-2012
Cornell University <i>B.S. in Applied Engineering Physics</i> Minor: Biomedical Engineering	Ithaca, NY 2004-2008

Skills

Machine learning and computational biology

Training in machine learning, computational biology and statistical analysis.

Programming

Extensive programming experience. Languages known include (in order of experience): R, Python, JavaScript, Perl.

Microbiology and molecular biology

Knowledge of proper molecular biology techniques and microbiology through laboratory research and laboratory teaching experience.

Analytical chemistry

Extensive Gas Chromatographic analysis using the Hewlett Packard GC-FID 5890.

Awards

<i>Weinman Symposium Presentation Award</i>	2014
<i>Roche/ARCS PhD student scholarship</i>	2015-2017

Experience

Epidemiology Program, University of Hawaii Cancer Center <i>Research Assistant</i> Research on DNA methylation platforms, next generation sequencing and non-coding RNAs and their role in cancer and other diseases. Collaborative research with Kapiolani Medical Center, Yale University and Shanghai Jiao Tong University.	Honolulu, HI 2013-2017
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Microsoft Research Summer Internship**Redmond, WA***Internship*

2015

Research on predicting drug response in acute myeloid leukemia patients based on RNA-Seq and exome sequencing data.

Hawaii Natural Energy Institute, University of Hawaii at Manoa**Honolulu, HI***Research Assistant*

2010-2013

Identified and cultured novel yeast species from biodiesel fuel contamination for publication. Determined the effects of microorganisms on metal corrosion and fuel degradation through Gas Chromatographic analysis.

Department of Microbiology, University of Hawaii at Manoa**Honolulu, HI***Teaching Assistant*

2012

Instructed the laboratory course for introductory Microbiology. Educated students on proper microscopy, culturing techniques and species nomenclature.

Department of MBBE, University of Hawaii at Manoa**Honolulu, HI***Teaching Assistant (Volunteer)*

2012

Developed protocols for students for statistical analysis of gas chromatograms using the R programming language. Helped students conduct chromatographic experiments and taught basic chromatographic principles.

Publications

Ph.D. dissertation

Ching T. Integrative transcriptomic analysis of long intergenic non-coding RNAs in cancer (2017).

Master's thesis

Ching T. Characterization of biocontaminants in biodiesel fuels and potential roles in the formation of microbially induced corrosion (2012).

Peer reviewed journal articles*Primary author publications*

1. **Ching, T. H.**, Yoza, B. A., Wang, R., Masutani, S., Donachie, S., Hihara, L., & Li, Q. X. (2016). Biodegradation of biodiesel and microbiologically induced corrosion of 1018 steel by *Moniliella wahieum* Y12. *International Biodeterioration & Biodegradation*, 108, 122–126.
2. **Ching, T.**, Masaki, J., Weirather, J., & Garmire, L. X. (2015). Non-coding yet non-trivial: a review on the computational genomics of lincRNAs. *BioData Mining*, 8(1), 1.
3. **Ching, T.**, Peplowska, K., Huang, S., Zhu, X., Shen, Y., Molnar, J., ... & Garmire, L. X. (2016). Pan-cancer analyses reveal long intergenic non-coding RNAs relevant to tumor diagnosis, subtyping and prognosis. *EBioMedicine*, 7, 62-72.
4. **Ching, T.***, Ha, J.* , Song, M.-A., Tiirikainen, M., Molnar, J., Berry, M. J., ... Garmire, L. X. (2015). Genome-scale hypomethylation in the cord blood DNAs associated with early onset preeclampsia. *Clinical Epigenetics*, 7(1), 1. *Contributed equally.

5. Li, J.* **Ching, T.***, Huang, S., & Garmire, L. X. (2015). Using epigenomics data to predict gene expression in lung cancer. *BMC Bioinformatics*, 16(Suppl 5), S10. **Contributed equally.*
6. Menor, M.* **Ching, T.***, Zhu, X., Garmire, D., & Garmire, L. X. (2014). mirMark: a site-level and UTR-level classifier for miRNA target prediction. *Genome Biology*, 15(10), 1–16. **Contributed equally.*
7. **Ching, T.**, Song, M.-A., Tiirikainen, M., Molnar, J., Berry, M., Towner, D., & Garmire, L. X. (2014). Genome-wide hypermethylation coupled with promoter hypomethylation in the chorioamniotic membranes of early onset pre-eclampsia. *Molecular Human Reproduction*, 20(9), 885–904.
8. **Ching, T.**, Huang, S., & Garmire, L. X. (2014). Power analysis and sample size estimation for RNA-Seq differential expression. *Rna*, 20(11), 1684–1696.
9. **Ching, T. H.**, Yoza, B. A., & Li, Q. X. (2014). Quartet Analysis of Putative Horizontal Gene Transfer in Crenarchaeota. *Journal of Molecular Evolution*, 78(2), 163–170.

Co-author publications

10. Wang B.D., Ceniccola K., Hwang S., Andrawis R., Horvath A., Freeman J.A., Knapp S., **Ching T.**, Garmire L.X., Pate I.V., Garcia-Blanco M.A., Patierno S.R., Lee N.H., Aberrant Alternative Splicing in African American Prostate Cancer: novel driver of tumor aggressiveness and drug resistance. *Nature Communications (accepted/pre-print).*
11. Han B., Park H.K., **Ching T.**, Panneerselvam J., Wang H., Shen Y., Zhang J., Li L., Che R., Garmire L., & Fei P. (2017). Human DBR1 Modulates the Recycling of snRNPs to Affect RNA Alternative Splicing and Contributes to the Suppression of Cancer Development. *Oncogene (accepted/preprint).*
12. Zhu X., **Ching T.**, Pan X., Weissman S., Garmire L.X. (2016). Detecting heterogeneity in single-cell RNA-Seq data by non-negative matrix factorization, *PeerJ* 5:e2888
13. Poirion, O. B., Zhu, X., **Ching, T.**, & Garmire, L. (2016). Single-Cell Transcriptomics Bioinformatics and Computational Challenges. *Frontiers in Genetics*, 7.
14. 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 L.X., 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* 6. **Contributed equally.*
15. Baker, M. R., Tabb, D. L., **Ching, T.**, Zimmerman, L. J., Sakharov, I. Y., & Li, Q. X. (2016). Site-specific N-glycosylation characterization of windmill palm tree peroxidase using novel tools for analysis of plant glycopeptide mass spectrometry data. *Journal of Proteome Research*.
16. Gagliani, N., Vesely, M. C. A., Iseppon, A., Brockmann, L., Xu, H., Palm, N. W., ... **Ching, T.**, (2015). Th17 cells transdifferentiate into regulatory T cells during resolution of inflammation. *Nature*, 523(7559), 221–225.
17. Huang, S., Yee, C., **Ching, T.**, Yu, H., & Garmire, L. X. (2014). A novel model to combine clinical and pathway-based transcriptomic information for the prognosis prediction of breast cancer. *PLoS Comput Biol*, 10(9), e1003851.

Conference abstracts/posters

1. Pan-cancer analyses reveal lincRNAs relevant to tumour diagnosis, subtyping and prognosis. Stanford Big Data in Biomedicine 2016.
2. Neural network survival applied to pancancer lincRNA data. Pacific Symposium on Biocomputing 2016.
3. Pan-cancer analysis of lincRNAs reveals robust diagnostic biomarkers. Pacific Symposium on Biocomputing 2015.
4. Differential methylation in cord blood in early-onset preeclampsia in a predominantly Asian cohort. ISPD 18th International Conference on Prenatal Diagnosis and Therapy.
5. Differential methylation in the chorioamnion membranes in early-onset preeclampsia in a predominantly Asian cohort. ISPD 18th International Conference on Prenatal Diagnosis and Therapy.

Journal articles under submission

1. **Ching T.**, Garmire L.X. Pan-cancer analysis of expressed single nucleotide variants in long intergenic non-coding RNA (*in preparation*).
2. **Ching T.**, Zhu X., Garmire L.X. Cox-nnet: an artificial neural network Cox regression for prognosis prediction. Submitted to PLoS Comp Biol (*in revision*).
3. Yamasato K., **Ching T.**, Garmire L.X., Berry M., Towner D., Evaluation of a maternal cardiovascular gene array in early on-set preeclampsia in a dominantly Asian cohort. Submitted to Pregnancy and hypertension (*under review*).