Sang (Tony) Young Chun

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EDUCATION

2011-2017	Ph.D., Bioinformatics, University of Michigan, Ann Arbor, MI, USA
2009-2011	M.Sc., Bioinformatics, University of Michigan, Ann Arbor, MI, USA
2007	B.A., Biology, Kalamazoo College, Kalamazoo, MI, USA

RESEARCH TRAINING

2017-Current	Post-doctoral Research Fellow, University of Michigan, Ann Arbor, MI, USA (Principal Investigator: Ryan E. Mills, Ph.D.)
2012-2017	Graduate Student Research Assistant, University of Michigan, Ann Arbor, MI, USA (Thesis Advisor: Ryan E. Mills, Ph.D.)
2012	Graduate Student Research Assistant, University of Michigan, Ann Arbor, MI, USA (Rotation Advisor: Goncalo Abecasis, Ph.D.)
2011	Graduate Student Research Assistant, University of Michigan, Ann Arbor, MI, USA (Rotation Advisor: John K. Kim, Ph.D.)
2009-2011	Graduate Student Research Assistant, University of Michigan, Ann Arbor, MI, USA (Advisor: Arul M. Chinnaiyan, M.D., Ph.D.)

SKILLS

Software and algorithm development
- Applied supervised and unsupervised machine learning approaches to assess the efficiency of protein synthesis through integrative analysis of multi-scalar next-generation sequencing data
- Developed and implemented a weighted sampling methodology to simulate variable imperfections in sequence data

Data curation and integration
- Cultivated expertise in the aggregation, extraction, and integration of large data sets and databases including the 1000 Genomes Projects, TCGA, COSMIC, GEO, Ensembl, GENCODE, and NCBI
- Refined an approach to extract shared features from structured genomic, transcriptomic, and proteomic data
- Predicted novel gene architecture through integration of transcript annotation databases and semi-structured sequence records

Data visualization and presentation
- Procedurally generated spatially consistent and depth sensitive read coverage models over genes derived from multiple sequencing methods using ggplot in R
- Presented thesis research to Nobel laureates Phillip A. Sharp and Craig C. Mello at an inaugural research symposium on RNA biomedicine

Collaboration and mentorship
- As part of several intra- and inter-institutional multi-disciplinary research teams, authored several articles in peer-reviewed journals including Nature, Genes and Development, PLOS Genetics, and BMC Bioinformatics with over 960 citations since their publication
- Earned exemplary student evaluations as a Graduate Student Instructor for subject matter expertise and academic mentorship (4.9 out of 5.0 compared to the university-wide mean of 4.58)

QUALIFICATIONS

Programming and scripting languages
- Python, R, MySQL, AWK, Bash, Java, C++

Data integration and visualization
- ggplot, Plotly, matplotlib, Shiny, NumPy, SciPy, Pandas

Machine learning and feature extraction
- Signal processing, clustering (k-means, k-nn, DBSCAN), regression (linear, logistic, multivariate), PCA, SVM, random forest, Bayesian inference, Tensorflow, scikit-learn

Environments and version control
‣ Linux, OS X, Windows, Anaconda, GitHub, SVN, RStudio, Jupyter Notebooks, Jupyter Lab
Bioinformatics
‣ Next-generation sequencing analysis: whole genome, exome, RNA-Seq, ribosome profiling
‣ Sequence alignment: Bowtie/2, BWA, STAR, TopHat/2, Kallisto, Sailfish, BLAST, BLAT
‣ Data aggregation and manipulation: HTSeq, BEDtools, SAMtools, picard-tools
‣ Differential expression analysis: Cufflinks, DESeq/2, EdgeR, Riborex, RSEM
‣ Quality control: cutadapt, fastq-mcf, FASTQC, Trimmomatic
‣ Visualization: IGVtools, UCSC Genome Browser
‣ Annotation: GO, GSEA, GATK
‣ Mass spectrometry: crux/percolator, Trans-Proteomic Pipeline
Presentation and editing
‣ Microsoft (Excel, Powerpoint, Word), Adobe (Illustrator, Photoshop), GIMP
Languages
‣ English (native), Korean (conversational), French (basic)

EMPLOYMENT

2005-2009	Research Technician Associate, University of Michigan, Ann Arbor, MI, USA
	(Principal Investigator: Long H. Dang, M.D., Ph.D.)
2002-2005	Research Technician Associate, University of Michigan, Ann Arbor, MI, USA
	(Principal Investigator: Susan E. Lyons, M.D., Ph.D.)

TEACHING

2016	Graduate Student Instructor, University of Michigan, Ann Arbor, MI, USA
	BIOINF 527: Introduction to Bioinformatics

HONORS AND AWARDS

2017	Rackham Conference Travel Grant, University of Michigan, Ann Arbor, MI, USA
	(Awarded: $800)
2015	Rackham Conference Travel Grant, University of Michigan, Ann Arbor, MI, USA
	(Awarded: $800)
2013-2015	Proteome Informatics of Cancer Training Grant, NIH: T32GM070499
	(Principal Investigator: Alexey I. Nesvizhskii, Ph.D.)
2013	Rackham Graduate Student Research Grant, University of Michigan, Ann Arbor, MI, USA
	(Awarded: $1500)
2011-2013	Bioinformatics Training Grant, NIH: T32CA140044
	(Principal Investigator: Brian Athey, Ph.D.)

POSTER PRESENTATIONS AND INVITED TALKS

2017	"Regulation of differentiation in SH-SY5Y neuroblastoma cells by translation of upstream open read frames". Poster presentation. RECOMB, Hong Kong, China
2017	"Spectral profiling of uORF translation in non-differentiated and differentiated neuroblastoma cells". Poster presentation. The Keystone Symposia Conference Series: Omic Strategies to Study the Proteome (A8), Breckenridge, CO, USA
2016	"SPECtre: a spectral coherence-based classification of actively translated transcripts from ribosome profiling sequence data." Oral presentation. Center for RNA Biomedicine Inaugural Symposium, University of Michigan, Ann Arbor, MI, USA
2015	"Spectral coherence classification of uORF translation in a neuroblastoma cell model of differentiation". Poster presentation. RECOMB/ISCB Conference on Regulatory and Systems Genomics with DREAM Challenges, Philadelphia, PA, USA

PUBLICATIONS

1. Rodriguez CM, **Chun SY**, Mills RE, Todd PK. Conditional translation of upstream open reading frames limits protein translation in neuronal differentiation. *eLife*. In review.
2. **Chun SY**, Rodriguez CM, Todd PK, Mills RE. SPECtre: a spectral coherence-based classifier of actively translated transcripts from ribosome profiling sequence data. *BMC Bioinformatics*. 17(482), 2016.
3. Chen F, Zhou Y, Qi YB, Khivansara V, Li H, **Chun SY**, Kim JK, Fu XD, Jin Y. Context-dependent modulation of Pol II CTD phosphatase SSUP-72 regulates alternative polyadenylation in neuronal development. *Genes Dev*. 29(22), 2015.
4. Billi AC, Freeberg MA, Day AM, **Chun SY**, Khivansara V, Kim JK. A conserved upstream motif orchestrates autonomous, germline-enriched expression of Caenorhabditis elegans piRNAs. *PLoS Genetics*. 9(3), 2013.
5. Grasso CS, Wu YM, Robinson DR, Cao X, Dhanasekaran SM, Khan AP, Quist MJ, Jin X, Lonigro RJ, Brenner JC, Asangani IA, Ateeq B, **Chun SY**, Siddiqui J, Sam L, Anstett M, Mehra R, Prensner JR, Palanisamy N, Ryslik GA, Vandin F, Raphael BJ, Kunju LP, Rhodes DR, Pienta KJ, Chinnaiyan AM, Tomlins SA. The mutational landscape of lethal castration-resistant prostate cancer. *Nature*. 487(7406), 2012.
6. **Chun SY**, Johnson C, Washburn JG, Cruz-Correa MR, Dang DT, Dang LH. Oncogenic KRAS modulates mitochondrial metabolism in human colon cancer cells by inducing HIF-1a and HIF-2a target genes. *Mol Cancer*. 9(293), 2010.
7. Wenger JB, **Chun SY**, Dang DT, Luesch H, Dang LH. Combination therapy targeting cancer metabolism. *Med Hyoptheses*. 76(2), 2011.
8. Burkitt K, **Chun SY**, Dang DT, Dang LH. Targeting both HIF-1 and HIF-2 in human colon cancer cells Improves tumor response to sunitinib treatment. *Mol Cancer Ther*. 8(5), 2009.
9. Dang DT, **Chun SY**, Burkitt K, Abe M, Chen S, Havre P, Mabjeesh NJ, Heath EI, Vogelzang NJ, Cruz-Correia MR, Blayney DW, Ensminger WD, St Croix B, Dang DH, Dang LH. Hypoxia-inducible factor-1 target gets as Indicators of tumor vessel response to vascular endothelial growth factor inhibition. *Cancer Res*. 68(6), 2008.
10. **Chun SY**, Chen F, Washburn JG, MacDonald JW, Innes KL, Zhar R, Cruz-Correia MR, Dang LH, Dang DT. CDX2 promotes anchorage-independent growth by transcriptional repression of IGFBP-3. *Oncogene*. 26(32), 2007.
11. Dang LH, Chen F, Ying C, **Chun SY**, Knock Sa, Appelman HD, Dang DT. CDX2 has tumorigenic potential in the human colon cancer cell lines LOVO and SW48. *Oncogene*., 25(15), 2006.
12. Juarez MA, Su F, **Chun SY**, Kiel MJ, Lyons SE. Distinct roles for SCL in erythroid specification and maturation zebrafish. *J Biol Chem*, 280(50), 2005.
13. Lin L, Prescott MS, Zhu Z, Singh P, **Chun SY**, Kuick RD, Hanash SM, Orringer MB, Glover TW, Beer DG. Identification and characterization of a 19q12 amplicon in esophageal adenocarcinomas reveals cyclin E as the best candidate for this amplicon. *Cancer Res*. 60(24), 2000.