

Résumé

Pradipta R. Ray

School of Behavioral and Brain Sciences
The University of Texas at Dallas
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Richardson, TX 75080
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www.pradiptaray.com

LinkedIn: www.linkedin.com/in/pradiptaray/
Google Scholar: scholar.google.com/citations?user=1Uynk5gAAAAJ
Github: <https://github.com/pradiptaray>

Signed:



Professional experience

The University of Texas at Dallas, Richardson, TX
Research Scientist (Postdoctoral Research Scientist / Research Associate)
October 2010 – present

Primary duty: Perform research, write research papers and research grants

Service to school: teach graduate level courses, advise and mentor graduate and undergraduate students in research projects

Service to community: peer review research papers, journal peer review editorial duties, conference program committee, high school outreach

Education

☞ **Carnegie Mellon University**, Pittsburgh, PA

Fall 2004 - Summer 2010 (thesis defense: 2012, awarded: 2013)

Ph.D., School of Computer Science (full scholarship as research assistant)

Thesis: Computational Methods for Analyzing the Architecture & Evolution of the Regulatory Genome (Co-advisors: Eric P. Xing and Veronica Hinman)

☞ **Carnegie Mellon University**, Pittsburgh, PA

Fall 2004 - Fall 2007 (awarded: 2008) (full scholarship as research assistant)

M.S., Language Technologies Institute (parallel to Ph.D.)

☞ **IIT Kharagpur**, Kharagpur, India

Fall 2002 - Summer 2004 in M.S. program, Computer Science & Engg., (transferred to CMU Ph.D.) (full scholarship as research assistant)

☞ **Jadavpur University**, Kolkata, India

Fall 1998 - Summer 2002 (awarded: 2002)

B.Engg., Computer Science & Engineering (high honors)

Teaching

Previous teaching experience:

Co-instructor (UT Dallas): Computational Biology (Ph.D.), BIOL 6385

<https://personal.utdallas.edu/~prr105020/biol6385/2017/index.html>

Teaching materials: <https://personal.utdallas.edu/~pradiptaray/teach.html>

Previously co-taught with Michael Q. Zhang. Comprehensive Ph. D. level course providing a solid background of statistical and computational framework for solving classical computational genomics and systems biology problems.

Helped develop syllabus, taught comparative genomics unit (as well as other units as required), held office hours, mentored TAs, maintained website, set and graded exams

Teaching Assistant (CMU): Computational Biology (Ph.D.), and Machine Learning (Ph. D.)

<https://web.archive.org/web/20171118183333/http://www.cs.cmu.edu:80/~epxing/Class/10810/index.html>

<https://web.archive.org/web/20111018144205/http://www.cs.cmu.edu:80/~zivbj/class/10701/index.html>

Comprehensive Ph. D. level courses where teaching assistants were required to teach a few classes, hold recitations and office hours, set and grade homework and exams.

Service and Professional Memberships

Scientific peer review and advising

Thesis committee and advising

Ph D, Biological Sciences: Milos Pavlovic (thesis committee, defended: Oct 2017)

M S, Bioengineering: Aaron Kotamarti (thesis co-advisor, thesis committee, defended: Aug 2013)

Conference reviewer: International Conference on Research in Computational Molecular Biology (RECOMB), International Conference in Intelligent Systems in Molecular Biology (ISMB), IEEE International Conference on Bioinformatics and Bioengineering (BIBE), Asia Pacific Bioinformatics Conference (APBC)

Journal reviewer: PAIN Reports, OUP Bioinformatics, BMC Bioinformatics, BMC Biology, PLoS One, IEEE/ACM Transactions on Computational Biology and Bioinformatics, European Journal of Pain, Neurobiology of Pain, Frontiers in Pain Research, European Journal of Physiology, PAIN, Frontiers in Pain Research, Frontiers in Human Neuroscience, Frontiers in Molecular Neuroscience

Conference program committee: ISMB 2011, ISMB 2013

Organizing committee: 1st Symposium on Indian Morphology, Phonology and Language Engineering (SIMPLE'04), Kharagpur, 2004

Journal editorial duties

Guest editor: Frontiers in Cellular and Infection Microbiology (2022) (managing peer review)
Associate editor: Frontiers in Pain Research (Aug 2022 – current) (managing peer review)

Professional memberships

Society memberships: International Society for Computational Biology (2007 – present), Society for Neuroscience (2017 – present), International Association for the Study of Pain (2018 – present)

Honors and invited talks

(No in-person conferences attended in 2020 and 2021)

Selected podium talk, Peripheral Nerve Society (2022) Annual Meeting, Miami FL 2022

Invited talk, Texas Pain Research Consortium Conference, San Antonio TX 2019

Invited talk, Human DRG Consortium Conference, Richardson TX 2019

Invited talk, School of Life Sciences, University of Nottingham, Nottingham UK 2019

Best research abstract and invited podium talk, 7th International Congress on Neuropathic Pain, London UK, 2019

Distinguished trainee talk, Gulf Coast Consortium Translational Pain Research 8th Annual Symposium, Houston TX, 2018

Invited talk, Texas Pain Research Consortium Conference, Richardson TX 2015

Invited talk, Epigenomics 2013: A roadmap to the living genome, Boston MA 2013

Selected podium talk, ISMB 2009

Graduate student research travel fellowship: ISMB 2009

Selected podium talk, RECOMB 2008

Graduate student research travel fellowship: RECOMB 2008

Language Technologies Institute Research Fellowship, Carnegie Mellon University, 2004

Media Lab Asia Research Fellowship, Indian Institute of Technology Kharagpur, 2002

Showcase undergraduate research project, Kolkata Undergraduate Entrepreneurship Competition, The Indus Entrepreneurs (TiE), 2000

Research output

Relevant research publications, reviews, and thesis

First, co-first, corresponding and co-corresponding authorships for Pradipta Ray in italics

Complete and updated list at: scholar.google.com/citations?user=1Uynk5gAAAAJ

► RNA Profiling of Neuropathic Pain-Associated Human DRGs Reveal Sex-differences in Neuro-immune Interactions Promoting Pain

Pradipta R. Ray, Stephanie Shiers, Diana Tavares-Ferreira, Ishwarya Sankaranarayanan, Megan L. Uhelski, Yan Li, Robert Y. North, Claudio Tatsui, Gregory Dussor, Michael D. Burton, Patrick M. Dougherty, Theodore J. Price

Brain, In Press, 07/22/2022, awac266 [first author]

RNA sequencing on muscle biopsy from a 5-week bed rest study reveals the effect of exercise and potential interactions with dorsal root ganglion neurons

Amelia J McFarland, Pradipta R Ray, Salman Bhai, Benjamin D Levine, Theodore J Price

Physiological Reports, 10(3), e15176, 2022

Transcriptomic analysis of human sensory neurons in painful diabetic neuropathy reveals inflammation and neuronal loss

Bradford E Hall, Emma Macdonald, Margaret Cassidy, Sijung Yun, Matthew R Sapio, Pradipta Ray, Megan Doty, Pranavi Nara, Michael D Burton, Stephanie Shiers, Abhik Ray-Chaudhury, Andrew J Mannes, Theodore J Price, Michael J Iadarola, Ashok B Kulkarni

Scientific Reports 12 (4729): 1-16, 2022

Spatial transcriptomics reveals unique molecular fingerprints of human nociceptors

Diana Tavares-Ferreira, Stephanie Shiers, Pradipta Ray, Andi Wangzhou, Vivekanand Jeevakumar, Ishwarya Sankaranarayanan, Alexander Chamessian, Bryan Copits, Patrick M Dougherty, Robert Gereau, Michael D Burton, Gregory Dussor, Theodore J Price

Science Translational Medicine 14 (632): eabj8186, 2022

Studying human nociceptors: from fundamentals to clinic

Steven J Middleton, Allison M Barry, Maddalena Comini, Yan Li, Pradipta R Ray, Stephanie Shiers, Andreas C Themistocleous, Megan L Uhelski, Xun Yang, Patrick M Dougherty, Theodore J Price, David L Bennett

Brain 144 (5), 1312-1335, 2021

► A ligand-receptor interactome platform for discovery of pain mechanisms and therapeutic targets

Andi Wangzhou, Candler Paige, Sanjay V Neerukonda, Dhananjay K Naik, Moeno Kume, Eric T David, Gregory Dussor, Pradipta R Ray, Theodore J Price

Science Signaling 14 (674), 2021 [co-corresponding author]

Sex-stratified genome-wide association study of multisite chronic pain in UK Biobank

Keira JA Johnston, Joey Ward, Pradipta R Ray, Mark J Adams, Andrew M McIntosh, Blair H

Smith, Rona J Strawbridge, Theodore J Price, Daniel J Smith, Barbara I Nicholl, Mark ES Bailey

PLoS Genetics 17 (4), e1009428, 2021

Nasal administration of mitochondria reverses chemotherapy-induced cognitive deficits

Jenolyn F Alexander, Alexandre V Seua, Luis D Arroyo, **Pradipta R Ray**, Andi Wangzhou, Laura Heiß-Lückemann, Manfred Schedlowski, Theodore J Price, Annemieke Kavelaars, Cobi J Heijnen

Theranostics 11 (7), 3109, 2021

ACE2 and SCARF expression in human dorsal root ganglion nociceptors: implications for SARS-CoV-2 virus neurological effects

Stephanie Shiers, Pradipta R Ray, Andi Wangzhou, Ishwarya Sankaranarayanan, Claudio Esteves Tatsui, Laurence Rhines, Yan Li, Megan Uhelski, Patrick Dougherty, Theodore Price

Pain 161 (11), 2494-2501, 2020

Sex differences in nociceptor translatomes contribute to divergent prostaglandin signaling in male and female mice

Diana Tavares-Ferreira, Pradipta R Ray, Ishwarya Sankaranarayanan, Galo L Mejia, Andi Wangzhou, Stephanie Shiers, Ruta Uttarkar, Salim Megat, Paulino Barragan-Iglesias, Gregory Dussor, Armen N Akopian, Theodore J Price

Biological Psychiatry, 91(1), 129 – 140, 2022

A role for protease activated receptor type 3 (PAR3) in nociception demonstrated through development of a novel peptide agonist

Juliet Mwirigi, Moeno Kume, Shayne N Hassler, Ayesha Ahmad, **Pradipta R Ray**, Changyu Jiang, Alexander Chamessian, Nakleh Mseeh, Brea P Ludwig, Benjamin D Rivera, Marvin T Nieman, Thomas Van de Ven, Ru-Rong Ji, Gregory Dussor, Scott Boitano, Josef Vagner, Theodore J Price

The Journal of Pain, 22 (6): 692-706, 2021

Diversity of receptor expression in central and peripheral mouse neurons estimated from single cell RNA sequencing

Andi Wangzhou, Candler Paige, Pradipta R Ray, Gregory Dussor, Theodore J Price

Neuroscience 463: 86-96, 2021

Intercellular Arc Signaling Regulates Vasodilation

June Bryan de la Peña, Paulino Barragan-Iglesias, Tzu-Fang Lou, Nikesh Kunder, Sarah Loerch, Tarjani Shukla, Lokesh Basavarajappa, Jane Song, Dominique N James, Salim Megat, Jamie K Moy, Andi Wangzhou, Pradipta R Ray, Kenneth Hoyt, Oswald Steward,

Theodore J Price, Jason Shepherd, Zachary T Campbell
Journal of Neuroscience 41 (37), 7712-7726, 2021

A peptide encoded within a 5' untranslated region promotes pain sensitization in mice

Paulino Barragan-Iglesias, Nikesh Kunder, Andi Wangzhou, Bryan Black, Pradipta R Ray, Tzu-Fang Lou, June Bryan de la Peña, Rahul Atmaramani, Tarjani Shukla, Joseph J Pancrazio, Theodore J Price, Zachary T Campbell

PAIN 162 (6), 1864-1875, 2021

Sex-stratified genome-wide association study of multisite chronic pain in UK Biobank

Keira JA Johnston, Joey Ward, Pradipta R Ray, Mark J Adams, Andrew M McIntosh, Blair H Smith, Rona J Strawbridge, Theodore J Price, Daniel J Smith, Barbara I Nicholl, Mark ES Bailey

PLoS Genetics 17 (4), e1009428, 2021

A role for protease activated receptor type 3 (PAR3) in nociception demonstrated through development of a novel peptide agonist

Juliet Mwirigi, Moeno Kume, Shayne N Hassler, Ayesha Ahmad, Pradipta R Ray, Changyu Jiang, Alexander Chamessian, Nakleh Mseeh, Brea P Ludwig, Benjamin D Rivera, Marvin T Nieman, Thomas Van de Ven, Ru-Rong Ji, Gregory Dussor, Scott Boitano, Josef Vagner, Theodore J Price

The Journal of Pain, 22 (6): 692-706, 2021

Nasal administration of mitochondria reverses chemotherapy-induced cognitive deficits

Jenolyn F Alexander, Alexandre V Seua, Luis D Arroyo, Pradipta R Ray, Andi Wangzhou, Laura Heiß-Lückemann, Manfred Schedlowski, Theodore J Price, Annemieke Kavelaars, Cobi J Heijnen

Theranostics 11 (7), 3109, 2021

Sex differences in nociceptor translatomes contribute to divergent prostaglandin signaling in male and female mice

Diana Tavares-Ferreira, Pradipta R Ray, Ishwarya Sankaranarayanan, Galo L Mejia, Andi Wangzhou, Stephanie Shiers, Ruta Uttarkar, Salim Megat, Paulino Barragan-Iglesias, Gregory Dussor, Armen N Akopian, Theodore J Price

Biological psychiatry, S0006-3223(20)31952-1, 2020

► A pharmacological interactome between COVID-19 patient samples and human sensory neurons reveals potential drivers of neurogenic pulmonary dysfunction

Pradipta Ray, Andi Wangzhou, Nizar Ghneim, Muhammad Yousuf, Candler Paige, Diana Tavares-Ferreira, Juliet Mwirigi, Stephanie Shiers, Ishwarya Sankaranarayanan, Amelia

McFarland, Sanjay Neerukonda, Steve Davidson, Gregory Dussor, Michael Burton, Theodore Price

Brain, Behavior, and Immunity, 89, October 2020: 559-568, 2020 [first and co-corresponding author]

► Pharmacological target-focused transcriptomic analysis of native vs cultured human and mouse dorsal root ganglia

Andi Wangzhou, Lisa A McIlvried, Candler Paige, Paulino Barragan-Iglesias, Stephanie Shiers, Ayesha Ahmad, Carolyn A Guzman, Gregory Dussor, Pradipta R Ray, Robert W Gereau IV, Theodore J Price

PAIN, 161(7): 1497-1517, 2020 [corresponding author]

The cellular basis of protease-activated receptor 2–evoked mechanical and affective pain

Shayne N Hassler, Moeno Kume, Juliet M Mwirigi, Ayesha Ahmad, Stephanie Shiers, Andi Wangzhou, Pradipta R Ray, Serge N Belugin, Dhananjay K Naik, Michael D Burton, Josef Vagner, Scott Boitano, Armen N Akopian, Gregory Dussor, Theodore J Price

JCI insight, 5(11): e137393, 2020

Differences between dorsal root and trigeminal ganglion nociceptors in mice revealed by translational profiling

Salim Megat, Pradipta R Ray, Diana Tavares-Ferreira, Jamie K Moy, Ishwarya Sankaranarayanan, Andi Wangzhou, Tzu Fang Lou, Paulino Barragan-Iglesias, Zachary T Campbell, Gregory Dussor, Theodore J Price

Journal of Neuroscience, Jun 2019, 2663-18, 2019

Recent advances toward understanding the mysteries of the acute to chronic pain transition

Theodore J Price, Pradipta R Ray

Current Opinion in Physiology, 11 (Oct 2019): 42-50, 2019

► Transcriptome Analysis of the Human Tibial Nerve Identifies Sexually Dimorphic Expression of Genes Involved in Pain, Inflammation, and Neuro-Immunity

Pradipta R Ray, Jawad Khan, Andi Wangzhou, Diana Tavares-Ferreira, Armen N. Akopian, Gregory Dussor and Theodore J. Price

Frontiers in Molecular Neuroscience 12 (37), 1-15, 2019 [first and corresponding author]

► Electrophysiological and transcriptomic correlates of neuropathic pain in human dorsal root ganglion neurons

Robert Y North, Yan Li, Pradipta Ray, Laurence D Rhines, Claudio Esteves Tatsui, Ganesh Rao, Caj A Johansson, Hongmei Zhang, Yeun Hee Kim, Bo Zhang, Gregory Dussor, Tae Hoon Kim, Theodore J Price, Patrick M Dougherty

Brain 142 (5), 1215-1226, 2019 [co-first author]

Nociceptor translational profiling reveals the RagA-mTORC1 network as a critical generator of neuropathic pain

Salim Megat, Pradipta Ray, Jamie Moy, Tzu-Fang Lou, Paulino Barragan-Iglesias, Yan Li, Grishma Pradhan, Andi Wangzhou, Ayesha Ahmad, Robert North, Patrick Dougherty, Arkady Khoutorsky, Nahum Sonenberg, Kevin Webster, Gregory Dussor, Zachary Campbell, Theodore Price

Journal of Neuroscience 39 (3), 393-411, 2019

► Comparative transcriptome profiling of the human and mouse dorsal root ganglia: an RNA-seq-based resource for pain and sensory neuroscience research

Pradipta Ray, Andrew Torck, Lilyana Quigley, Andi Wangzhou, Matthew Neiman, Chandranshu Rao, Tiffany Lam, Ji-Young Kim, Tae Hoon Kim, Michael Q Zhang, Gregory Dussor, Theodore J Price

PAIN, 159 (7), 1325-1345, 2018 [first author]

Angiotensin II triggers peripheral macrophage-to-sensory neuron redox crosstalk to elicit pain

Andrew J Shepherd, Bryan A Copits, Aaron D Mickle, Páll Karlsson, Suraj Kadunganattil, Simon Haroutounian, Satya M Tadinada, Annette D de Kloet, Manouela V Valtcheva, Lisa A McIlvried, Tayler D Sheahan, Sanjay Jain, **Pradipta R Ray**, Yuriy M Usachev, Gregory Dussor, Eric G Krause, Theodore J Price, Robert W Gereau, Durga P Mohapatra

Journal of Neuroscience, 3542-17, 2018

Sigma 2 receptor / Tmem97 agonists produce long lasting anti-neuropathic pain effects in mice

James J Sahn, Galo L Mejia, **Pradipta R Ray**, Stephen F Martin, Theodore J Price

ACS Chemical Neuroscience 8 (8), 1801-1811, 2017

► DIRECTION: a machine learning framework for predicting and characterizing DNA methylation and hydroxymethylation in mammalian genomes

Milos Pavlovic, Pradipta Ray, Kristina Pavlovic, A Kotamarti, Min Chen, Michael Zhang

Bioinformatics 33 (19), 2986-2994, 2017 [co-first and co-corresponding author]

Integrative analysis of haplotype-resolved epigenomes across human tissues

Danny Leung, Inkyung Jung, Nisha Rajagopal, Anthony Schmitt, Siddarth Selvaraj, Ah Young Lee, Chia-An Yen, Shin Lin, Ying Lin, Yunjiang Qiu, Wei Xie, Feng Yue, Manoj Hariharan, Pradipta Ray, Samantha Kuan, Lee Edsall, Hongbo Yang, Neil Chi, Michael Zhang, Joseph Ecker, Bing Ren

Nature 518 (7539), 350-354, 2015

Epigenomic analysis of multilineage differentiation of human embryonic stem cells

Wei Xie, Matthew Schultz, Ryan Lister, Zhonggang Hou, Nisha Rajagopal, Pradipta Ray, John Whitaker, Shulan Tian, R David Hawkins, Danny Leung, Hongbo Yang, Tao Wang, Ah Young Lee, Scott Swanson, Jiuchun Zhang, Yun Zhu, Audrey Kim, Joseph Nery, Mark Urich, Samantha Kuan, Chia-an Yen, Sarit Klugman, Pengzhi Yu, Kran Suknuntha, Nicholas Propson, Huaming Chen, Lee Edsall, Ulrich Wagner, Yan Li, Zhen Ye, Ashwinikumar Kulkarni, Zhenyu Xuan, Wen-Yu Chung, Neil Chi, Jessica Antosiewicz-Bourget, Igor Slukvin, Ron Stewart, Michael Zhang, Wei Wang, James Thomson, Joseph Ecker, Bing Ren

Cell 153 (5), 1134-1148, 2013

► Computational Methods for Analyzing the Architecture and Evolution of the Regulatory Genome

Pradipta Ray, Ph.D. thesis (advisors: Eric P. Xing, Veronica Hinman)

Carnegie Mellon University technical report (CMU-LTI-12-018), submitted: 2012, awarded: 2013 [*thesis author*]

► DISCOVER: a feature-based discriminative method for motif search in complex genomes

Wenjie Fu, Pradipta Ray, Eric P Xing

OUP Bioinformatics 25 (12), i321-i329, 2009 [*co-first author*]

► CSMET: comparative genomic motif detection via multi-resolution phylogenetic shadowing

Pradipta Ray, Suyash Shringarpure, Mladen Kolar, Eric P Xing

PLoS Computational Biology 4 (6), e1000090, 2008 [*co-first author*]

► Baycis: a bayesian hierarchical hmm for cis-regulatory module decoding in metazoan genomes

Tien-ho Lin, Pradipta Ray, Geir K Sandve, Selen Uguroglu, Eric P Xing

Proceedings of the 12th Annual International Conference on Research in Computational Biology Singapore, Springer (LNCS, volume 4955) 2008 [*co-first author*]

Selected publications on Natural Language Processing (pre-2005):

Isolated-word Error Correction for Partially Phonemic Languages using Phonetic Cues

Bhupesh Bansal, Monojit Choudhury, Pradipta Ray, Sudeshna Sarkar, Anupam Basu

Proceedings of Fifth International Conference on Knowledge based Computer Systems (KBCS 2004), 2004

Part of speech tagging and local word grouping techniques for natural language parsing in Hindi

Pradipta Ray, V Harish, Sudeshna Sarkar, Anupam Basu

Proceedings of the 1st International Conference on Natural Language Processing (ICON 2003), 2003 [first author]

Research Funding

Instrumental in setting up computational genomics unit of the UT Dallas Pain Neurobiology research group to help obtain funding:

<https://bbs.utdallas.edu/painneurosciencelab/sensoryomics/>

Lead computational biology researcher, dedicated effort for following grants:

Current:

As Co-investigator: Identifying novel therapeutic targets for chronic neck pain: RNA-sequencing in human painful atlanto-axial arthropathy, NIH R01AR078192, (Total Fiscal Year 2021: \$595,549)

As Other Key Personnel: Translational control of pain plasticity, NIH R01NS065926, (Total Fiscal Year 2021: \$537,341)
Anatomic, Physiologic and Transcriptomic Mechanisms of Neuropathic Pain in Human DRG, NIH R01NS111929, (Total Fiscal Year 2021 funding: \$652,350)

Pending:

As Multi-Principal Investigator: Human Nociceptor and Spinal Cord Molecular Signature Center, National Institute of Neurological Disorders and Stroke Special Emphasis Panel Discovery and Functional Evaluation of Human Pain-associated Genes and Cells (U19)

Scientific Software, Scripts and Databases

Software and scripts

Ray, P.R.

AESTHESIS: Algorithmic Elucidation of Sensory Transcriptomic landscapes for rapid hypotHESIS testing, Scripts for post-processing of human tissue transcriptome data

<https://github.com/pradiptaray/aesthesis>

Ray, P.R., Wangzhou, A. and Chandy, L.

TITAN: Toolkit for bioInformatic Translation Assay aNalysis, Tool for analyzing ribosomal footprinting assays

<https://bbs.utdallas.edu/painneurosciencelab/sensoryomics/titan/>

Song, L and Ray, P.R.

ASD – Admixture of Stochastic Dictionaries for eukaryotic regulatory sequences

<https://github.com/pradiptaray/asd>

Ray, P. R., and Fu, Wenjie

DISCOVER - a discriminative model of conditional random field for motif finding in

eukaryotic genomes

<https://web.archive.org/web/20151207002626/http://www.sailing.cs.cmu.edu/main/discover/index.html> (archived)

Ray, P. R., Shringarpure, S., and Kolar, M.

CSMET - a mixture of phylogeny based Hidden Markov Model for motif finding in aligned eukaryotic sequences <https://github.com/pradiptaray/csmet>

Kolar, M., **Ray, P. R.** and Lin, T.-H.

Baycis - a generalized hierarchical Hidden Markov Model for motif finding in Eukaryotes <https://github.com/pradiptaray/baycis>

Databases

Gene co-expression patterns in DRG along with 12 other reference tissue transcriptomes, for both human and mouse tissues

<https://paincenter.utdallas.edu/sensoryomics/>

TRAP-seq gene expression profiles in mouse models of chemotherapy induced neuropathy

<https://www.utdallas.edu/bbs/painneurosciencelab/sensoryomics/cipntrap/>

Gene expression profiles of human DRG clinical cohorts with and without associated neuropathic pain, in both males and females

<https://www.utdallas.edu/bbs/painneurosciencelab/sensoryomics/hdrgclinical/>

Sex differential gene expression patterns, correlation with age, in the human tibial nerve

<https://www.utdallas.edu/bbs/painneurosciencelab/sensoryomics/sexdiffnerve/>

Gene expression differences between acutely dissected and cultured human DRGs

<https://bbs.utdallas.edu/painneurosciencelab/sensoryomics/culturetxome/>

Transcriptome-wide association study for neuropathic pain, pain-associated co-expression

http://www.pradiptaray.com/pain_twas.html

Current research projects

Research Scientist, UT Dallas (primary mentor: Theodore J. Price)

☞ Computational analysis of **TWAS and pain-associated gene co-expression modules in human Dorsal Root Ganglia** RNA-seq in chronic pain patients

☞ Computational **identification of regulatory and signaling pathways in human Dorsal Root Ganglia**, and whether they are **evolutionarily conserved** between primates, rodents and more distantly related species

☞ Modelling **molecular sex differences in the human peripheral nervous system**

☞ Computational analysis of sensory neuronal transcriptomes **to identify candidate therapeutic targets for pain neuropathies** in sensory tissues (peripheral nerves, dorsal root ganglia, trigeminal ganglia, dura mater)

☞ Computational modelling of **alternative promoter usage, alternative splicing and polyadenylation in sensory neurons** to identify gene transcript variants specific to sensory versus central nervous system (brain and spinal cord) neurons

☞ Integrative analysis of single cell and single nucleus RNA-seq, **spatial RNA-seq and single cell epigenomic assays** (ATAC-seq) in human and rodent sensory tissues

Past research projects

Research Scientist, UT Dallas

☞ Computational modelling and analysis of active transcriptome in mouse sensory neurons using **Translating Ribosome Affinity Purification** (TRAP pulldown) and **ribosomal footprinting assays**, and corresponding motif analysis of untranslated regions

☞ Developing **machine learning models of predicting pain state** based on transcriptome

☞ Identification of **human and mouse Dorsal Root Ganglia specific gene expression** and evolutionary conservation, identification of sensory neuronal genes in human Tibial Nerve RNA-seq

☞ Analysis of transcriptomic data and integrative analysis with **histone, methylation and DNase-I HS sites in H1 ES cells and derived lineages** as part of the UCSD mapping center and NIH Roadmap Epigenome Consortium project

☞ **Computational prediction of epigenetic marks** (DNA methylation and hydroxymethylation) from correlated genomic and other epigenomic features

Graduate Research Assistant, Carnegie Mellon University

Fall 2004 – Summer 2010

Advised by Eric P. Xing, School of Computer Science, Carnegie Mellon

☞ **Phylogenetic shadowing algorithm for comparative genomic motif finding** under functional turnover (using novel graphical models)

☞ Discriminative (Conditional Random Field) and generative (generalized hierarchical HMM) **predictive models for regulatory regions and motifs** in single species by modelling sequence composition, genetic/epigenetic factors correlated with regulatory modules

☞ Evolutionary and co-evolutionary analysis and detection of positive and negative selection in eukaryotic regulatory regions using admixture models over k-mers in eukaryotes

Advised by Veronica F. Hinman, Biological Sciences, Carnegie Mellon

☞ Selectional analyses of the sea urchin *Strongylocentrotus purpuratus* regulatory genome and ChIP-seq analysis of transcription factors in the sea star *Patiria miniata*

Graduate Research Assistant, IIT Kharagpur

Co-advised by Anupam Basu and Sudeshna Sarkar, Media Lab Asia, IIT Kharagpur

Natural language processing tools for Indian languages: the first grapheme to phoneme mapper, morphological analyzer, and phoneme-space spellchecker for Bengali, and one of the earliest word chunkers for Hindi. Corpus-based statistical analyses of Indian languages

Undergraduate Research Assistant, Jadavpur University

Advised by Chandan Mazumdar, Distributed Systems Lab, Jadavpur University

Image matching using wavelet-based image analysis, texture analysis, topological features

Podium talks: conference, institute, departmental

Discovery of pain-associated neuroimmune protein interaction networks from sex differential neuronal and immune gene expression profiles in human DRGs

Peripheral Nerve Society Annual Meeting (PNS 2022), Miami FL, May 2022. Abstract published in conference proceedings.

Drug target identification in the human dorsal root ganglia using high throughput sequencing assays and machine learning

Functional Genomics section, National Institutes of Health, Bethesda MD, Dec 2019.

Decoding gene co-expression networks in the human peripheral nervous system

3rd Texas Pain Research Consortium Conference, San Antonio TX, Sept 2019. Abstract published digitally.

Investigating the molecular make-up of human DRGs: what genomics and machine learning can tell us

Human DRG Consortium meeting, Richardson TX, August 2019.

Deciphering human chronic pain and baseline transcriptomes in the peripheral nervous system

School of Pharmacy and School of Medicine, University of Nottingham, Nottingham UK, May 2019.

Predictive models for jointly inferring pain state and sex from human dorsal root ganglia RNA abundance profiles of autosomal genes yield insights into functions of gene co-expression modules

7th International Congress on Neuropathic Pain (NeuPSIG), London UK, 2019. Abstract published digitally.

Key overlapping pathways are upregulated in human DRG transcriptomes with neuropathic pain-associated dermatomes, with putative sex-differential gene expression

Gulf Coast Consortium Translational Pain Research 8th Annual Symposium, Houston TX, 2018. Abstract published digitally.

Analyzing human and mouse dorsal root ganglia transcriptomes: uncovering the molecular biology of pain and putative therapeutic targets using information theory

1st Texas Pain Research Consortium Conference, Richardson TX, 2015. Abstract published

digitally.

DIRECTION: An integrative toolkit for classification of epigenetic marks - a study on DNA 5-hmC + 5-mC marks in H1 and derived lineages

Epigenomics 2013: A roadmap to the living genome, Boston, 2013. Extended abstract published in Proceedings of Epigenomics 2013: A roadmap to the living genome.

DISCOVER: a feature-based discriminative method for motif search in complex genomes

17th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2009), Stockholm Sweden, 2009. Full paper published in OUP Bioinformatics.

Baycis: a bayesian hierarchical hmm for cis-regulatory module decoding in metazoan genomes

12th annual international conference on Research in Computational Biology (RECOMB 2008), Singapore, 2008. Full paper published in Springer Lecture Notes in Computer Science / Bioinformatics.

Research focus

Machine learning + biostatistics

Application of cutting-edge machine learning / machine intelligence / statistical techniques and development of novel algorithms (deep learning, discriminative models, Bayesian frameworks, and non-parametric approaches) to solve biological / biomedical problems

Broader interests: Estimation and inference algorithms for machine learning methods in the natural and social sciences

Computational biology + genomics

Transcriptome-wide and genome-wide association studies of diseases from human tissue and organ donors with joint analysis of clinical, imaging and electrophysiological datasets

Integrative modeling of transcriptome assays (bulk RNA-seq, scRNA-seq, spatial RNA-seq), and high-throughput immunoprecipitation, DNase/RNase and epigenome assays to identify regulatory and signaling networks in cell types and tissues, especially in the context of human disease

Identification of evolutionary conservation / divergence of gene expression in cell types and tissues between humans and other species, and between human diseases and model systems

Broader interests: Regulatory + comparative genomics, selectional + evolutionary analysis

Neuroscience + molecular biology:

Characterization of the molecular landscape (e.g., gene expression, promoter usage, alternative splicing) of human and animal sensory tissues (e.g., dorsal root and trigeminal

ganglia) and cell types, evolutionary comparison of expression profiles in cell types / tissues

Profiling of human neuropathic pain using molecular profile changes in the DRG, and / or correlated molecular changes in the CNS, periphery (e.g. skin biopsies), and blood to build predictive models of subtyping, prognosis and treatment strategies for neuropathic pain

Estimation of molecular changes in sensory neuropathies (like chronic pain), and inference of implicated regulatory and signaling pathways (especially neuro-immune signaling), and immune and sensory neuronal cell types involved, in the context of non-opioid drug target discovery

Identification of sex differences in molecular landscapes of healthy and diseased human sensory tissues, and identification of druggable genome and putative drug targets based on sex, disease subtype, molecular changes in disease, and pharmacological properties of targets

Keywords

machine learning in medicine, AI in medicine, regulatory genomics, comparative genomics, molecular evolution, transcriptome wide association studies, human disease transcriptomics, integrative neurogenomics, sensory neurobiology, pain transcriptomics, neuroimmunology