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PART I: GENERAL INFORMATION

Education

1998 - 2002	B.Sc., Biomedical Engineering, Southeast University, China
2002 - 2005	M.Sc., Biomedical Engineering, Southeast University, China
2005 - 2010	Ph.D., Bioinformatics, University of Bergen, Norway (Advisor: Dr. Boris Lenhard)

Postdoctoral Training

09/10 - 09/13	Postdoctoral Associate, Program of Bioinformatics and Integrative Biology, University of Massachusetts Medical School (Supervisor: Dr. Zhiping Weng)

Appointments at Hospitals/Affiliated Institutions

12/16 - present	Director of Computational Neuroscience, Neurogenomics Lab and Parkinson Personalized Medicine (PPM), Harvard Medical School and Brigham & Women's Hospital
11/13 - present	Instructor, Department of Neurology, Harvard Medical School
09/13 - present	Faculty in Neurology, Brigham and Women's Hospital (Mentor: Dr. Clemens Scherzer)

Other Professional Positions

2005 - 2005	Manager Trainee / Process Engineer, P&G

Major Administrative Leadership Positions

2005 - 2007	President, Chinese Students and Scholars Association (CSSA) of Bergen, Norway
2007 - 2007	Organizer of the "EnsEMBL in a Nutshell" Bioinformatics Workshop, University of Bergen
2017 - present	Founder of the Bioinformatics Club in Brigham and Women's Hospital

Professional Societies

2006 - present	International Society for Computational Biology (ISCB), Member
2013 - present	American Society for Human Genetics (ASHG), Member
2015	The 10th Annual DNA Day Essay Contest, Judge
2016 - present	American Academy of Neurology (AAN), Member

Honors and Prizes

2000	*Liu Yonglin* Fellowship Award, Southeast University, China
2000	Distinguished Student with 1st grade Scholarship, Southeast University, China
2000	2nd prize of the National Undergraduate Mathematical Contest in Modeling
2001	1st prize of 2001 "Sony Cup" National Undergraduate Electronic Design Contest, China
2001	Meritorious winner (top 10%) in the International Mathematical Contest in Modeling (MCM)
2001	Distinguished Student with 1st grade Scholarship, Southeast University, China
2002	Distinguished Graduate Student Award, Southeast University, China
2009	Full Scholarship, "Chromatin Domains and Insulators" Workshop, Spain
2009	Travel Fellowship, MCB Research School, University of Bergen, Norway
2010	Chinese Government Award for Outstanding Self-financed Students Abroad, Ministry of Education, China (1 of 500 annual awardees in the world wide)
2015	Reviewers' Choice – best abstract in the American Society of Human Genetics (ASHG) meeting, US
2018	Finalist of the PacBio Structural Variant SMRT Grant program

Service to Professional Publications

- Ad hoc reviewer -

Nature Biotechnology, Bioinformatics, PLoS Computational Biology, Genome Research, PLoS ONE, Genome Biology, PLoS Genetics, Evolutionary Bioinformatics, International Journal of Biological Sciences, Journal of Biomedical Informatics, Movement Disorders, The Pharmacogenomics Journal, Current Bioinformatics, Neurogenetics, Journal of Bioinformatics and Computational Biology, Nucleic Acids Research

- Other editorial Roles -

2017 - present	*PeerJ* (Academic Editor)
2017 - present	*Evolutionary Bioinformatics* (Academic Editor)
2017 - present	*Personalized Medicine* (Editorial Board)
2018 - present	*Frontiers in Neuroscience - Neurogenomics* (Editorial Board)

Funding Information

- Past -

2011 - 2016	Epigenetic Markers in Huntington's Disease Brain NIH R01 NS073947 Key Personnel (PI: Richard H. Myers) The goal of this project is to map, genome-wide HD disease-related changes in histone methylation markings in prefrontal neurons.
2012 - 2016	EDAC: ENCODE Data Analysis Center NIH U41 HG007000 Key Personnel (PI: Zhiping Weng) The goal of this project is to perform integrative analysis on ChIP-Seq, CAGE, and RNA-Seq data as a part of the ENCODE data analysis center.

- Current -

2016 – 2019	Parkinson Disease: Predicting the Future NIH U01 NS095736 Key Personnel (PI: Clemens Scherzer) The goal of this project is to identify genetic variants in susceptibility loci and familial genes that predict cognitive or motor progression, and replicate and verify forwarded genetic variants in independent populations.
2017 - 2018	Cracking the code of chr17q21 for Parkinson: From GWAS to novel drug targets American Parkinson Disease Association (APDA) Research Grant PI ($50,000) The goal of this project is to discover the causal variants in chr17q21 locus and validate them in iPSC-derived neurons.
2017 - 2022	Integrative Multi-Omic Discovery of Proximal Mechanisms Driving Age-Dependent Neurodegeneration NIA RF1AG057331 Key Personnel (PI: Mel Feany, Ernest Fraenkel, Clemens Scherzer) The goals of this study are to perform genome-scale genetic analysis of neurodegeneration in *Drosophila*, to decode gene-regulatory mechanisms of Alzheimer's disease risk loci specifically in human pyramidal neurons, and discover genes and networks driving neurodegeneration.

PART II: Report of Teaching, Training, and Presentations

Teaching of Students in Courses

2007	"EnsEMBL in a Nutshell" workshop, University of Bergen, Norway
	Role: Lecturer
	National-wide bioinformatics students / researchers, 8-hr sessions per day for 5 days
2017 - present	Lecturer in the weekly "Bioinformatics Club" in Brigham and Women's Hospital

Formally Supervised Trainees / Students

2009 - 2012	Yogita Sharma (graduate student in University of Bergen, Norway)
	Mentor, co-supervisor for her research project & thesis, and co-author of one article in *BMC Bioinformatics*
2013 - 2014	Carmen Portenkirchner (medical student in Paracelsus Medical University, Austria)
	Thesis co-advisor, research advisor
2013 - 2014	Dr. Shuilin Jin (visiting research scholar from Harbin Institute of Technology, China)
	Co-supervisor, Bioinformatics trainer
2014 - 2015	Alyssa Ehrlich (medical student in Harvard Medical School)
	Supervisor, research advisor for her proposal and her internship in the laboratory
2014 - 2015	Ruoting Wang (undergraduate in University of Massachusetts)
	Supervisor, research advisor for his summer internship in the neurogenomics laboratory
2014 - 2016	David Gritsch (postdoc in BWH Neurogenomics laboratory)
	Research advisor for his research in the laboratory
2015 - 2015	Will Nemirovsky (junior high school student in BB&N)
	Supervisor, research advisor for his summer bioinformatics training in Harvard
2015 - 2016	Dr. Yunfei Bai (visiting scholar from Southeast University, China)
	Co-supervisor, Bioinformatics trainer
2015 - 2018	Tao Wang (PhD Joint Training Program student, Harbin Institute of Technology, China)
	Supervisor, research advisor for his two-year bioinformatics training in Harvard
2016 -2016	Ellen DeGennaro (graduate student in Harvard-MIT HST PhD program)
	Supervisor, research advisor for her proposal and her internship in the laboratory
2016 - 2018	Zhuo Wang (PhD Joint Training Program student, Harbin Institute of Technology, China)
	Supervisor, research advisor for her two-year bioinformatics training in Harvard

Invited Presentations

- Local -

2011	Correlate histone modifications and gene expression / BIB seminar (UMass Medical School)
2012	Redefining the piRNA-producing loci of the mouse testis as genes / Invited Bioinformatics talk (UMass Medical School)
2014	From ENCODE to PD Brain Map: Bioinformatics in Big Data Research / The Center for Neurologic Diseases' ADPD seminar series (Harvard Institute of Medicine, BWH)
2015	The BRAINCODE consortium: Decoding neuronal genome function in human brain / The Center for Neurologic Diseases' ADPD seminar series (Harvard Institute of Medicine)

- Regional -

2007	Remnants of lost bystander genes under non-coding selection pressure in human-zebrafish synteny blocks (BREW 2007, Norway)
2012	Modeling gene expression with chromatin features (ENCODE conference, MIT)
2013	Studying gene regulation using comparative genomics and epigenomics (DFCI / HMS)

- National -

2011	Modeling gene expression with chromatin features / Invited talk (ENCODE conference, Stanford University)
2013	Long-range gene regulation in vertebrates genome (Berkeley Lawrence Laboratory)
2017	From the known world to an expanding universe of genomic dark matter (NIH)

- International -

2010	Translog, a web browser for studying the expression divergence of homologous genes (The 8th Asia Pacific Bioinformatics Conference, India)
2010	Web resources to study the expression divergence of homologous genes (Huazhong Agricultural University, China)
2010	Evolutionary mechanisms of developmental long-range gene regulation in vertebrate genomes (GIS, Singapore)
2013	Studying gene regulation using comparative genomics and epigenomics (Southeast University / Huazhong Agricultural University / Tongji University, China)
2015	NGS and its application in translational medicine (Tongji Hospital, China)

PART III: REPORT OF ACTIVITIES AND INNOVATIONS

Technological and Other Scientific Innovations

Synorth	A website designed for genome research, allowing to explore the evolution of synteny and long-range regulatory interactions between vertebrate genomes URL: http://synorth.genereg.net Published as first author on *Genome Biology* (Impact factor: 10.30), 13 citations
Translog	A website designed to study the expression divergence of homologous genes URL: http://translog.genereg.net Published as first author on *BMC Bioinformatics* (Impact factor: 3.02)
Factorbook	A Wiki-based database for transcription factor-binding data generated by ENCODE URL: http://factorbook.org Published as co-author on *Nucleic Acid Research* (Impact factor: 8.28), 4 citations
BRAINcode	A web resource allowing users to query the gene expression profile and eQTL result in human dopamine neurons. URL: http://humanbraincode.org

Educational Activities to the Community

2012	Innovation Month in the Worcester Public Schools: How to extract DNA from an onion Claremont Academy, Worcester http://www.umassmed.edu/news/2012/education/gsbs-students-take-science-on-road.aspx
2008 – present	Founder of bioinformatics blog, "**One Tip Per Day**" (http://onetipperday.sterding.com/), which has 200 visit per day on average and more than 520,000 visits in total
2017 – present	Founder of the "**Bioinformatics Club**" (http://bioinformatics.bwh.harvard.edu), which is a weekly forum for learning and sharing bioinformatics in the whole BWH level. To date, we have already scheduled 27 talks, serving more than 300 persons.

Media Coverage

ENCODE consortium et al. *Nature*, 2012	CNN: http://www.cnn.com/2012/09/05/health/encode-human-genome/ BBC: http://www.bbc.com/news/health-19202141 Scientific American: http://www.scientificamerican.com/article/junk-dna-encode/ Evolution News: http://www.evolutionnews.org/2012/09/junk_no_more_en_1064001.html New York Times: http://www.nytimes.com/2012/09/06/science/far-from-junk-dna-dark-matter-proves-crucial-to-health.html LA Times: http://articles.latimes.com/2012/sep/05/science/la-sci-dna-encode-20120906 The Guardian: http://www.theguardian.com/science/2012/sep/05/genes-genome-junk-dna-encode
Dong et al. *Genome Biology*, 2012	Genomeweb: http://www.genomeweb.com/blog/week-genome-biology-59 Biomed Central: http://blogs.biomedcentral.com/bmcblog/2012/09/07/human-genomics-comes-of-age-encode-open-access-and-biomed-central/ Umassmed News: http://www.umassmed.edu/news/news-archives/2012/09/umms-faculty-integral-to-consortium-decoding-human-genome/

PART IV: PUBLICATIONS

Original Articles:

1. Mungpakdee S, Seo HC, Angotzi AR, **Dong X**, Akalin A, et al. Differential evolution of the 13 Atlantic salmon Hox clusters. *Molecular biology and evolution*. 2008; 25(7):1333-43. PMID: 18424774
2. **Dong X**, Fredman D, Lenhard B. Synorth: exploring the evolution of synteny and long-range regulatory interactions in vertebrate genomes. *Genome biology*. 2009; 10(8):R86. PMID: 19698106, PMCID: PMC2745767
3. Akalin A, Fredman D, Arner E, **Dong X**, Bryne JC, et al. Transcriptional features of genomic regulatory blocks. *Genome biology*. 2009; 10(4):R38. PMID: 19374772, PMCID: PMC2688929
4. **Dong X**, Akalin A, Sharma Y, Lenhard B. Translog, a web browser for studying the expression divergence of homologous genes. *BMC bioinformatics*. 2010; 11 Suppl 1:S59. PMID: 20122234, PMCID: PMC3009532
5. **Dong X**, Navratilova P, Fredman D, Drivenes Ø, Becker TS, et al. Exonic remnants of whole-genome duplication reveal cis-regulatory function of coding exons. *Nucleic acids research*. 2010; 38(4):1071-85. PMID: 19969543, PMCID: PMC2831330
6. A user's guide to the encyclopedia of DNA elements (ENCODE). *PLoS biology*. 2011; 9(4):e1001046. PMID: 21526222, PMCID: PMC3079585
7. Yildirim O, Li R, Hung JH, Chen PB, **Dong X**, et al. Mbd3/NURD complex regulates expression of 5-hydroxymethylcytosine marked genes in embryonic stem cells. *Cell*. 2011; 147(7):1498-510. NIHMSID: NIHMS343144 PMID: 22196727, PMCID: PMC3252821
8. **Dong X**, Greven MC, Kundaje A, Djebali S, Brown JB, et al. Modeling gene expression using chromatin features in various cellular contexts. *Genome biology*. 2012; 13(9):R53. PMID: 22950368, PMCID: PMC3491397
9. Wang J, Zhuang J, Iyer S, Lin X, Whitfield TW, et al. Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. *Genome research*. 2012; 22(9):1798-812. PMID: 22955990, PMCID: PMC3431495
10. Cheng C, Alexander R, Min R, Leng J, Yip KY, et al. Understanding transcriptional regulation by integrative analysis of transcription factor binding data. *Genome research*. 2012; 22(9):1658-67. PMID: 22955978, PMCID: PMC3431483
11. An integrated encyclopedia of DNA elements in the human genome. *Nature*. 2012; 489(7414):57-74. NIHMSID: NIHMS381381, PMID: 22955616, PMCID: PMC3439153
12. Wang J, Zhuang J, Iyer S, Lin XY, Greven MC, et al. Factorbook.org: a Wiki-based database for transcription factor-binding data generated by the ENCODE consortium. *Nucleic acids research*. 2013; 41(Database issue):D171-6. PMID: 23203885, PMCID: PMC3531197
13. Li XZ, Roy CK, **Dong X**, Bolcun-Filas E, Wang J, et al. An ancient transcription factor initiates the burst of piRNA production during early meiosis in mouse testes. *Molecular cell*. 2013; 50(1):67-81. NIHMSID: HHMIMS469552 PMID: 23523368, PMCID: PMC3671569
14. Hoss AG, Kartha VK, **Dong X**, Latourelle JC, Dumitriu A, et al. MicroRNAs located in the Hox gene clusters are implicated in huntington's disease pathogenesis. *PLoS genetics*. 2014; 10(2):e1004188. PMID: 24586208, PMCID: PMC3937267
15. Haberle V, Li N, Hadzhiev Y, Plessy C, Previti C, et al. Two independent transcription initiation codes overlap on vertebrate core promoters. *Nature*. 2014; 507(7492):381-5. PMID: 24531765
16. **Dong X**, Tsuji J, Labadorf A, Roussos P, Chen JF, et al. The Role of H3K4me3 in Transcriptional Regulation Is Altered in Huntington's Disease. *PLoS ONE*. 2015; 10(12):e0144398. PMID: 26636336, PMCID: PMC4670094
17. Bai G, Cheung I, Shulha HP, Coelho JE, Li P, et al. Epigenetic dysregulation of hairy and enhancer of split 4 (HES4) is associated with striatal degeneration in postmortem Huntington brains. *Human molecular genetics*. 2015; 24(5):1441-56. PMID: 25480889, PMCID: PMC4321450
18. Locascio JJ, Eberly S, Liao Z, Liu G, Hoesing AN, et al. Association between α-synuclein blood transcripts and early, neuroimaging-supported Parkinson's disease. *Brain*. 2015; 138(Pt 9):2659-71. PMID: 26220939, PMCID: PMC4643625

19. Liu G, Boot B, Locascio JJ, Jansen IE, Winder-Rhodes S, et al. Specifically neuropathic Gaucher's mutations accelerate cognitive decline in Parkinson's. *Ann Neurol*. 2016 Nov;80(5):674-685. PMID: 27717005; PMCID: PMC5244667.
20. Mittal S, Bjornevik K, Im DS, Flierl A, **Dong X**, Abo KM, Long E, Jin M, Xu B, Xiang YK, Rochet JC, Engeland A, Rizzu P, Heutink P, Bartels T, Selkoe DJ, Caldarone BJ, Glicksman MA, Khurana V, Schüle B, Park DS, Riise T, and Scherzer CR. β2-adrenoreceptor is a regulator of the α-synuclein gene driving risk of Parkinson's disease. *Science*. 2017; 357 (6354), 891-898
21. **Dong X**, Liao Z, Gritsch D, Hadzhiev Y, Bai Y, Locascio J, Guennewig B, Liu G, Blauwendraat C, Wang T, Adler CH, Frosch MP, Nelson PT, Rizzu P, Cooper AA, Heutink P, Beach TG, Mattick JS, Mueller F, Scherzer CR. Enhancers active in dopamine neurons are a primary link between genetic variation and neuropsychiatric disease. *Nature Neuroscience*. (Under revision)

Reviews:

1. Fredman D, **Dong X**, Lenhard B. Making enhancers from spare parts of the genome. *Genome biology*. 2011; 12(12):138. PMID: 22206586, PMCID: PMC3334608
2. **Dong X**, Weng Z. The correlation between histone modifications and gene expression. *Epigenomics*. 2013; 5(2):113-6. NIHMSID: NIHMS598474, PMID: 23566087, PMCID: PMC4230708

Public Science:

1. **Dong X**. The brainstorm. *IEEE Potential*. 2009 Vol. 28, No.1.

Thesis:

1. **Dong X**. Evolutionary mechanisms of developmental long-range gene regulation in vertebrate genomes. 2010.

Abstracts, Poster Presentations Presented at Professional Meetings:

1. **Dong X**, Xie J, Lu Z. PatternExplorer2.0: a tool to explore related genes with random pattern sequence in genome. *The International Forum on Biochip Technologies (IFBT2004)*, Beijing, China, 2004.
2. **Dong X**, Zhang L, Lu Z. Why SARS virus only infects the lung of human? A model to analyze the association of virus attachment proteins and cell receptors. *The 2nd International Forum on Post-Genome Technologies (2'IFPT)*, Nanjing, 2004.
3. Xie J, Sun X, Lu Z, Xue W, **Dong X**, Lu Z. gWord: A Tool for Genome-Wide Word Search and Count. *Proceeding of Bioinformatics and Biomedical Engineering*, 2007. ICBBE 2007.
4. **Dong X.** Remnants of lost bystander genes under non-coding selection pressure in human-zebrafish synteny blocks. *Bioinformatics Research and Education Workshops (BREW)*, Bergen, Norway, 2007. **(Oral)**
5. **Dong X**, Fredman D, Engström P, Lenhard B. Reconstructing the Evolutionary History of Genomic Regulatory Blocks in Vertebrates. *The 15th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB)*, Austria, 2007.
6. **Dong X**, Akalin A, Fredman D, Lenhard B. Distribution of highly conserved non-coding elements in *Danio rerio*. *The 5th Asia Pacific Bioinformatics Conference (APBC)*, Hong Kong, 2007.
7. **Dong X**, Sheng Y, Gupta P, Lenhard B. Computational prediction of ncRNAs as target genes in genomic regulatory blocks. *The 6th Asia Pacific Bioinformatics Conference (APBC)*, Japan, 2008.
8. **Dong X**, Fredman D, Lenhard B. GRB Evolution Browser: a web resource for exploring evolutionary behaviours of vertebrate genomic regulatory blocks. *The 4th EMBO Conference: From Functional Genomics to Systems Biology*, Germany, 2008.
9. **Dong X**, Akalin A, Fredman D, Lenhard B. Evolutionary dynamics of genomic regulatory blocks: HCNEs and HARs, the content and the boundaries. *The 7th Asia Pacific Bioinformatics Conference (APBC)*, China, 2009.
10. **Dong X.** Translog, a web browser for studying the expression divergence of homologous genes. *The 8th Asia Pacific Bioinformatics Conference (APBC)*, Bangalore, India, 2010. **(Oral)**
11. **Dong X**. Predicting gene expression using histone modifications. ENCODE Conference, Stanford, 2011.

12. **Dong X**. Correlating histone modifications and gene expression. *Systems Biology: Global Regulation of Gene Expression*, CSHL*, 2012.*

13. **Dong X**. Modeling gene expression with chromatin features. ENCODE Conference, MIT, 2012. **(Oral)**

14. Liao Z, Zheng B, **Dong X**, Vanderburg CR, Locascio JJ, Pochet N, Regev A, Portenkirchner C, Altmann P, Jin S, Beach TG, Adler CH and Scherzer CR. The PD Brain Map: Mapping the Transcriptional Architecture of Dopamine Neurons in Human Brain. *The American Society of Human Genetics (ASHG)*, Boston, 2013.

15. **Dong X**, Liao Z, Gritsch D, Guennewig B, Hadzhiev Y, Bai Y, Liu G, Zheng B, Blauwendraat C, Hu Q, Adler CH, Hedreen JC, Frosch MP, Faull R, Nelson PT, Locascio J, Vanderburg C, Rizzu P, Cooper AA, Heutink P, Beach TG, Mueller F, Mattick JS, Scherzer CR. BRAINCODE: How does the Human Genome Function in Specific Brain Neurons? *The American Society of Human Genetics (ASHG)*, Baltimore, 2015.