

## **Xianjun Dong, Ph.D.**

### **WORK**

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### **PART I: GENERAL INFORMATION**

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#### **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: Drs. Boris Lenhard and Rein Aasland

#### **Postdoctoral Training**

2010 - 2013      Postdoctoral Associate, Program of Bioinformatics and Integrative Biology, University of Massachusetts Medical School (Dr. Zhiping Weng)

#### **Appointments at Hospitals/Affiliated Institutions**

2013 - present      Instructor, Department of Neurology, Harvard Medical School  
2013 - present      Assistant Scientist in Neurology, Brigham and Women's Hospital (Dr. Clemens Scherzer)

#### **Other Professional Positions**

2005 - 2005      Manager Trainee / Process Engineer, Procter & Gamble Co.

#### **Major Administrative Leadership Positions**

2013 - present      Leader of bioinformatics team in Neurogenomics Laboratory, Harvard Medical School  
2007 - 2007      Organizer of the "Ensembl in a Nutshell" Bioinformatics Workshop, University of Bergen, Norway  
2005 - 2007      President, Chinese Students and Scholars Association (CSSA) of Bergen, Norway

#### **Professional Societies**

2013 - present      American Society for Human Genetics (ASHG), Member  
2006 - present      International Society for Computational Biology (ISCB), Member

#### **Honors and Prizes**

2015      Reviewers' Choice – top 10% best posters in the American Society of Human Genetics (ASHG) meeting, US  
2010      Chinese Government Award for Outstanding Self-financed Students Abroad, Ministry of Education, China (1 of 500 annual awardees in the world wide)  
2009      Full Scholarship, "Chromatin Domains and Insulators" Workshop, Spain  
2009      Travel Fellowship, MCB Research School, University of Bergen, Norway  
2002      Distinguished Graduate Student Award, Southeast University, China  
2001      1<sup>st</sup> prize of 2001 "Sony Cup" National Undergraduate Electronic Design Contest, China (winning by designing a robot-controlled electronic car)  
2001      **Meritorious** winner (top 10%) in the international Mathematical Contest in Modeling (MCM) (winning by modeling the growth control of Zebra mussels in the Great Lakes)  
2001      Distinguished Student with 1<sup>st</sup> grade Scholarship, Southeast University, China  
2000      2<sup>nd</sup> prize of the National Undergraduate Mathematical Contest in Modeling  
2000      *Liu Yonglin* Fellowship Award, Southeast University, China  
2000      Distinguished Student with 1<sup>st</sup> grade Scholarship, Southeast University, China

## Service to Professional Publications

### - Ad hoc referee - (Total: 26 times for 15 journals)

2011 - present Ad hoc referee for *PLoS Computational Biology* (1 paper)  
 2011 - present Ad hoc referee for *Genome Research* (1 paper)  
 2012 - present Ad hoc referee for *Nature Biotechnology* (1 paper)  
 2013 - present Ad hoc referee for *PLoS ONE* (2 paper)  
 2013 - present Ad hoc referee for *Genome Biology* (2 paper)  
 2014 - present Ad hoc referee for *Bioinformatics* (5 paper)  
 2014 - present Ad hoc referee for *PLoS Genetics* (1 paper)  
 2014 - present Ad hoc referee for *Evolutionary Bioinformatics* (2 paper)  
 2014 - present Ad hoc referee for *International Journal of Biological Sciences* (3 paper)  
 2014 - present Ad hoc referee for *Journal of Biomedical Informatics* (2 paper)  
 2014 - present Ad hoc referee for *Movement Disorders* (1 paper)  
 2014 - present Ad hoc referee for *The Pharmacogenomics Journal* (1 paper)  
 2015 - present Ad hoc referee for *Current Bioinformatics* (2 paper)  
 2015 - present Ad hoc referee for *Neurogenetics* (1 paper)  
 2015 - present Ad hoc referee for *Journal of Bioinformatics and Computational Biologys* (1 paper)

### - Editor -

2014 - present Guest Editor for *Journal of Applied & Translational Genomics* (Elsevier)

## Funding Information

### - Past -

2008 - 2012 Title: EDAC: ENCODE Data Analysis Center  
Grant number: U01 HG004695-04  
Goal: The goal of this project is to perform integrative analysis on ChIP-Seq, FAIRE-Seq and RNA-Seq data as a part of the ENCODE data analysis center.  
Role: Bioinformatics engineer

### - Current -

2013 - 2016 Title: A Next Generation of Biomarkers for Incipient Huntington's Disease  
Grant number: U01 NS082080  
Goal: The goal of this project is to establish a national RNA biobank resource and develop digital biofluid markers useful for tracking disease progression.  
Role: Co-investigator

2011 - 2016 Title: Epigenetic Markers in Huntington's Disease Brain  
Grant number: R01 NS073947  
Goal: The goal of this project is to map, genome-wide HD disease-related changes in histone methylation markings in prefrontal neurons.  
Role: Bioinformatics analyst

### - Pending -

2015-2016 Title: Discovery of a new microcosm of circular RNAs in neurons of human brain  
Grant: BWH Institute for the Neurosciences – Neuroscience Seed Grants  
Goal: The goal of this project is to define circular RNAs and validate its function in human dopamine neurons.  
Role: PI

**PART II: PUBLICATIONS****Original Articles:**

1. **Dong X**, Tsuji J, Labadorf A, Roussos P, Chen JF, Myers RH, Akbarian S, Weng Z: The role of H3K4me3 in transcription initiation is altered in Huntington's disease. *PLoS ONE* 2015 (in press)
2. Locascio JJ, Eberly S, Liao Z, Liu G, Hoising AN, Duong K, Trisini-Lipsanopoulos A, Dhima K, Hung AY, Flaherty AW, Schwarzschild MA, Hayes MT, Wills AM, Shivraj Sohur U, Mejia NI, Selkoe DJ, Oakes D, Shoulson I, **Dong X**, Marek K, Zheng B, Iverson A, Hyman BT, Growdon JH, Sudarsky LR, Schlossmacher MG, Ravina B, Scherzer CR: Association between  $\alpha$ -synuclein blood transcripts and early, neuroimaging-supported Parkinson's disease. *Brain*. 2015,138(Pt 9):2659-71.
3. Bai G, Cheung I, Shulha HP, Coelho JE, Li P, **Dong X**, Jakovcevski M, Wang Y, Grigorenko A, Jiang Y, Hoss A, Patel K, Zheng M, Rogaev E, Myers RH, Weng Z, Akbarian S, Chen JF: Epigenetic dysregulation of hairy and enhancer of split 4 (HES4) is associated with striatal degeneration in postmortem Huntington brains. *Hum Mol Genet*. 2014, pii: ddu561.
4. Hoss AG, Kartha VK, **Dong X**, Latourelle JC, Dumitriu A, Hadzi TC, Macdonald ME, Gusella JF, Akbarian S, Chen JF, Weng Z, Myers RH: MicroRNAs located in the Hox gene clusters are implicated in huntington's disease pathogenesis. *PLoS Genet*. 2014, 10(2):e1004188.
5. Haberle V, Li N, Hadzhiev Y, Plessy C, Previti C, Nepal C, Gehrig J, **Dong X**, Akalin A, Suzuki AM, van IJcken WFJ, Armant O, Ferg M, Strähle U, Carninci P, Müller F, Lenhard B: Two independent transcription initiation codes overlap on vertebrate core promoters. *Nature* 2014, 507:381–385
6. Hoss AG, Kartha VK, **Dong X**, Latourelle JC, Dumitriu A, Hadzi TC, Macdonald ME, Gusella JF, Akbarian S, Chen J-F, Weng Z, Myers RH: MicroRNAs located in the Hox gene clusters are implicated in huntington's disease pathogenesis. *PLoS Genet* 2014, 10:e1004188
7. Li XZ, Roy CK, **Dong X**, Bolcun-Filas E, Wang J, Han BW, Xu J, Moore MJ, Schimenti JC, Weng Z, Zamore PD: An ancient transcription factor initiates the burst of piRNA production during early meiosis in mouse testes. *Mol Cell* 2013, 50:67–81.
8. Wang J, Zhuang J, Iyer S, Lin X-Y, Greven MC, Kim B-H, Moore J, Pierce BG, **Dong X**, Virgil D, Birney E, Hung J-H, Weng Z: Factorbook.org: a Wiki-based database for transcription factor-binding data generated by the ENCODE consortium. *Nucleic Acids Res* 2013, 41:D171–6.
9. Wang J, Zhuang J, Iyer S, Lin X, Whitfield TW, Greven MC, Pierce BG, **Dong X**, Kundaje A, Cheng Y, Rando OJ, Birney E, Myers RM, Noble WS, Snyder M, Weng Z: Sequence features and chromatin structure around the genomic regions bound by 119 human transcription factors. *Genome research* 2012, 22:1798–1812.
10. Cheng C, Alexander R, Min R, Leng J, Yip KY, Rozowsky J, Yan K-K, **Dong X**, Djebali S, Ruan Y, Davis CA, Carninci P, Lassman T, Gingeras TR, Guigó R, Birney E, Weng Z, Snyder M, Gerstein M: Understanding transcriptional regulation by integrative analysis of transcription factor binding data. *Genome research* 2012, 22:1658–1667.
11. ENCODE Project Consortium, Dunham I, Kundaje A, Aldred SF, Collins PJ, Davis CA, Doyle F, Epstein CB, Frietze S, Harrow J, Kaul R, Khatun J, Lajoie BR, Landt SG, Lee B-K, Pauli F, Rosenbloom KR, Sabo P, Safi A, Sanyal A, Shores N, Simon JM, Song L, Trinklein ND, Altshuler RC, Birney E, Brown JB, Cheng C, Djebali S, **Dong X**, et al.: An integrated encyclopedia of DNA elements in the human genome. *Nature* 2012, 489:57–74.
12. **Dong X**, Greven MC, Kundaje A, Djebali S, Brown JB, Cheng C, Gingeras TR, Gerstein M, Guigó R, Birney E, Weng Z: Modeling gene expression using chromatin features in various cellular contexts. *Genome Biol* 2012, 13:R53.
13. Yildirim O, Li R, Hung J-H, Chen PB, **Dong X**, Ee L-S, Weng Z, Rando OJ, Fazio TG: Mbd3/NURD complex regulates expression of 5-hydroxymethylcytosine marked genes in embryonic stem cells. *Cell* 2011, 147:1498–1510
14. ENCODE Project Consortium: A user's guide to the encyclopedia of DNA elements (ENCODE). *PLoS Biol* 2011, 9:e1001046.
15. **Dong X**, Navratilova P, Fredman D, Drivenes Ø, Becker ST, and Lenhard B. Exonic remnants after whole-genome duplication reveal *cis*-regulatory function of coding exons. *Nuclear Acids Research*. 2009 Dec 6

16. **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.
17. **Dong X**, Fredman D, Lenhard B. Synorth: exploring the evolution of synteny and long-range regulatory interactions in vertebrate genomes. *Genome Biol.* 2009 Aug 21;10(8):R86.
18. Akalin A, Fredman D, Arner E, **Dong X**, Bryne JC, Suzuki H, Daub CO, Hayashizaki Y, Lenhard B. Transcriptional features of genomic regulatory blocks. *Genome Biol.* 2009; 10(4):R38.
19. Mungpakdee S, Seo HC, Angotzi AR, **Dong X**, Akalin A, Chourrout D. Differential evolution of the 13 Atlantic salmon Hox clusters. *Molecular Biology Evolution.* 2008 Jul; 25(7):1333-43.

#### Reviews:

20. **Dong X**, Weng Z: The correlation between histone modifications and gene expression. *Epigenomics* 2013, 5:113-116.
21. Fredman D, **Dong X**, Lenhard B: Making enhancers from spare parts of the genome. *Genome Biol* 2011, 12:138.

#### 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.

#### Poster Presentations Presented at Professional conference:

1. **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. BRAINCORE: How does the Human Genome Function in Specific Brain Neurons? *The American Society of Human Genetics (ASHG)*, Baltimore, 2015.
2. 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.
3. **Dong X**. Modeling gene expression with chromatin features. ENCODE Conference, MIT, 2012. **(Oral)**
4. **Dong X**. Correlating histone modifications and gene expression. *Systems Biology: Global Regulation of Gene Expression*, CSHL, 2012.
5. **Dong X**. Predicting gene expression using histone modifications. ENCODE Conference, Stanford, 2011.
6. **Dong X**. Translog, a web browser for studying the expression divergence of homologous genes. *The 8<sup>th</sup> Asia Pacific Bioinformatics Conference (APBC)*, Bangalore, India, 2010. **(Oral)**
7. **Dong X**, Akalin A, Fredman D, Lenhard B. Evolutionary dynamics of genomic regulatory blocks: HCNEs and HARs, the content and the boundaries. *The 7<sup>th</sup> Asia Pacific Bioinformatics Conference (APBC)*, China, 2009.
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**, Sheng Y, Gupta P, Lenhard B. Computational prediction of ncRNAs as target genes in genomic regulatory blocks. *The 6<sup>th</sup> Asia Pacific Bioinformatics Conference (APBC)*, Japan, 2008.
10. **Dong X**, Akalin A, Fredman D, Lenhard B. Distribution of highly conserved non-coding elements in *Danio rerio*. *The 5<sup>th</sup> Asia Pacific Bioinformatics Conference (APBC)*, Hong Kong, 2007.
11. **Dong X**, Fredman D, Engström P, Lenhard B. Reconstructing the Evolutionary History of Genomic Regulatory Blocks in Vertebrates. *The 15<sup>th</sup> Annual International Conference on Intelligent Systems for Molecular Biology (ISMB)*, Austria, 2007.
12. **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)**
13. 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.

14. **Dong X**, Zhang L. 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.
15. **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.

**PART III: REPORT OF TEACHING, TRAINING, AND PRESENTATIONS**

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**Teaching of Students in Courses**

2007                      EnsEMBL in a Nutshell, Bergen Center of Computational Science, University of Bergen, Norway  
                                 Role: Lecturer  
                                 Bioinformatics students / researchers, 24 hours

**Laboratory and Other Research Supervisory and Training Responsibilities**

2015 - 2016              Bioinformatics training for the visiting scholar Dr. Yunfei Bai  
                                 Role: co-supervisor  
 2013 - 2014              Bioinformatics training for the visiting research scholar Dr. Shuilin Jin  
                                 Role: co-supervisor  
 2013 - present           Bioinformatics training and supervision of the bioinformatics staff, students, engineers  
                                 Role: co-leader, bioinformatics group, The Neurogenomics Laboratory, BWH

**Formally Supervised Trainees / Students**

2015 - 2017              Tao Wang (PhD Joint Training Program student, Harbin Institute of Technology, China)  
                                 Supervisor, research advisor for his two-year bioinformatics training in Harvard  
 2015 - 2015              Will Nemirovsky (junior high school student in BB&N)  
                                 Supervisor, research advisor for his summer bioinformatics training in Harvard  
 2015 - 2015              Ruoting Wang (3<sup>rd</sup> year undergraduate in University of Massachusetts)  
                                 Supervisor, research advisor for his summer intern in the neurogenomics laboratory  
 2014 - 2015              Alyssa Ehrlich (1<sup>st</sup> year graduate student in Harvard University)  
                                 Research advisor for her proposal and her internship in the laboratory  
 2014 - 2014              Ruoting Wang (2<sup>nd</sup> year undergraduate in University of Massachusetts)  
                                 Supervisor, research advisor for his summer internship in the neurogenomics laboratory  
 2013 - 2014              Carmen Portenkirchner (MD candidate in Paracelsus Medical University, Austria)  
                                 Thesis co-advisor, research advisor  
 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*

**Invited Talks****- Local talks -**

2015                      NGS and its application in translational medicine (Tongji Hospital, China)  
 2013                      Studying gene regulation using comparative genomics and epigenomics (Southeast University / Huazhong Agricultural University / Tongji University, China)  
 2013                      Long-range gene regulation in vertebrates genome (Berkeley Lawrence Laboratory)  
 2013                      Studying gene regulation using comparative genomics and epigenomics (DFCI / HMS)  
 2013                      Studying gene regulation using comparative genomics and epigenomics (BWH / HMS)  
 2012                      Redefining the piRNA-producing loci of the mouse testis as genes (UMass Medical School)  
 2011                      Correlate histone modifications and gene expression (UMass Medical School)  
 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)

**- International talks -**

2012                      Modeling gene expression with chromatin features (ENCODE conference, MIT)  
 2010                      Translog, a web browser for studying the expression divergence of homologous genes (The 8<sup>th</sup> Asia Pacific Bioinformatics Conference, India)  
 2007                      Remnants of lost bystander genes under non-coding selection pressure in human-zebrafish synteny blocks (BREW 2007, Norway)

**PART IV: REPORT OF ACTIVITIES AND INNOVATIONS**

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**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: <a href="http://synorth.genereg.net">http://synorth.genereg.net</a> Published as first author on <i>Genome Biology</i> (Impact factor: 10.30), 13 citations
Translog	A website designed to study the expression divergence of homologous genes URL: <a href="http://translog.genereg.net">http://translog.genereg.net</a> Published as first author on <i>BMC Bioinformatics</i> (Impact factor: 3.02)
Factorbook	A Wiki-based database for transcription factor-binding data generated by the ENCODE consortium URL: <a href="http://factorbook.org">http://factorbook.org</a> Published as co-author on <i>Nucleic Acid Research</i> (Impact factor: 8.28), 4 citations

**Educational Activities to the Community**

Teaching science at elementary school in 2012	As part of the STEM program organized by UMass Medical School, I was teaching kids at local elementary schools in Worcester basic hands-on science experiments, such as how to extract DNA from an onion—a simple yet elegant technique that connects everyday objects to scientific discovery and makes something seemingly abstract real. News detail: <a href="http://www.umassmed.edu/news/2012/education/gpbs-students-take-science-on-road.aspx">http://www.umassmed.edu/news/2012/education/gpbs-students-take-science-on-road.aspx</a>
Bioinformatics blog	My bioinformatics tips blog, “One Tip Per Day” ( <a href="http://onetipperday.blogspot.com/">http://onetipperday.blogspot.com/</a> ) has 300 visit per day on average and more than 400,000 visits in total.

**Media Coverage**

ENCODE consortium, Dong et al. <i>Nature</i> , 2012	CNN: <a href="http://www.cnn.com/2012/09/05/health/encode-human-genome/">http://www.cnn.com/2012/09/05/health/encode-human-genome/</a> BBC: <a href="http://www.bbc.com/news/health-19202141">http://www.bbc.com/news/health-19202141</a> Scientific American: <a href="http://www.scientificamerican.com/article/junk-dna-encode/">http://www.scientificamerican.com/article/junk-dna-encode/</a> Evolution News: <a href="http://www.evolutionnews.org/2012/09/junk_no_more_en_1064001.html">http://www.evolutionnews.org/2012/09/junk_no_more_en_1064001.html</a> New York Times: <a href="http://www.nytimes.com/2012/09/06/science/far-from-junk-dna-dark-matter-proves-crucial-to-health.html">http://www.nytimes.com/2012/09/06/science/far-from-junk-dna-dark-matter-proves-crucial-to-health.html</a> LA Times: <a href="http://articles.latimes.com/2012/sep/05/science/la-sci-dna-encode-20120906">http://articles.latimes.com/2012/sep/05/science/la-sci-dna-encode-20120906</a> The Guardian: <a href="http://www.theguardian.com/science/2012/sep/05/genes-genome-junk-dna-encode">http://www.theguardian.com/science/2012/sep/05/genes-genome-junk-dna-encode</a> Washington Post: <a href="http://www.washingtonpost.com/national/health-science/junk-dna-concept-debunked-by-new-analysis-of-human-genome/2012/09/05/cf296720-f772-11e1-8398-0327ab83ab91_story.html">http://www.washingtonpost.com/national/health-science/junk-dna-concept-debunked-by-new-analysis-of-human-genome/2012/09/05/cf296720-f772-11e1-8398-0327ab83ab91_story.html</a>
Dong et al. <i>Genome Biology</i> , 2012	Genomeweb: <a href="http://www.genomeweb.com/blog/week-genome-biology-59">http://www.genomeweb.com/blog/week-genome-biology-59</a> Biomed Central: <a href="http://blogs.biomedcentral.com/bmcblog/2012/09/07/human-genomics-comes-of-age-encode-open-access-and-biomed-central/">http://blogs.biomedcentral.com/bmcblog/2012/09/07/human-genomics-comes-of-age-encode-open-access-and-biomed-central/</a> Umassmed News: <a href="http://www.umassmed.edu/news/news-archives/2012/09/umms-faculty-integral-to-consortium-decoding-human-genome/">http://www.umassmed.edu/news/news-archives/2012/09/umms-faculty-integral-to-consortium-decoding-human-genome/</a>

## PART V: NARRATIVE REPORT

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I feel extremely lucky to be a young scientist in this exciting era of biomedical research. Ten years ago, it took more than a decade and over \$3 billion to get a human genome sequence draft. Today, it takes less than one week and under \$3000 to sequence a personal genome, and the speed is increasing. In light of the next-generation sequencing (NGS) techniques such as ChIP-Seq and RNA-Seq, a tremendous volume of data is constantly being generated, covering various aspects of biomedicine, such as genomics, transcriptomics, gene regulation, epigenomics, proteomics, and metabolomics. This deluge of data is challenging both in the way we analyze it and the way we interpret it. This challenge is exactly what I plan to tackle in my research as a computational biologist.

Three fourths of my time is spent in academic research in the Neurogenomics Laboratory; for most of that time I have leaded at least two projects. The remainder of my time is divided between administrative duties and training the fellows in the bioinformatics team as an Instructor.

**My goal is to understand the molecular mechanisms and biological processes that underlie development and disease by developing and applying computational methods to integrate and interpret big data.** My current research focuses mainly on the neurodegenerative diseases, including Parkinson's disease (PD) and Huntington's disease (HD), to delineate their genetic architecture using various NGS techniques and integrative bioinformatics methods. With Dr. Clemens Scherzer at BWH, I have started two projects -- one is to create a national RNA biobank resource and develop digital biofluid markers useful for tracking HD progression (funded by NIH); the other is to provide a high-definition view of gene activity in PD dopamine neurons via ultra-deep sequencing of the transcriptome of PD hallmark genes, including the  $\alpha$ -synuclein locus. My long-term goal is to understand the complexity of both the human genome and the human brain, both in healthy people and people with neuronal disorders.

My publication record reflects my growing national and international standing in the field. I have six publications as first author and twelve as co-author, including articles in *Nature*, *Cell*, *Molecular Cell*, *Genome Research*, *Genome Biology*, *Nucleic Acids Research*, and *BMC Bioinformatics*, with total citations of >5000 times. One of my main contributions to the field was the discovery of regulatory elements (e.g., enhancers) coupled in the coding exons, which has largely expanded the sequence space people usually looking for enhancers. The work has been highly cited by other researchers exploring the unknown space for regulatory elements.

During my postdoc, I was an active member of the ENCODE consortium (ENCyclopedia Of DNA Elements) and am a co-author of the corresponding landmark article in *Nature* as well as first or co-author of five related publications (in journals such as *PLoS Biology*, *Genome Biology*, *Genome Research*, and *Nucleic Acids Research*) on various aspects of this milestone "roadmap" of human genome functions, which has been compared to the Human Genome Project. I also developed and made publicly available three web-based tools useful for studying gene regulation, Synorth, Translog, and Factorbook.org.

I also love teaching and communicating with people. I have served as mentor and co-advisor for junior PhD students since my last year of PhD study. I also now co-supervise the bioinformatics students in Dr. Scherzer's lab, and have trained/supervised eight (8) students after I joined in Dr. Scherzer's lab. Moreover, I like to share knowledge; my blog on bioinformatics tips (<http://onetipperday.blogspot.com>) has been viewed >300 times per day.

In 2007, I organized a bioinformatics workshop in Norway with over 50 national participants. It was the introduction of the Ensembl (<http://www.ensembl.org>) outreach to Norway and was considered extremely useful by local researchers. I am also enthusiastic in supporting educational activities in my local community, for example, by teaching hands-on science experiments in local elementary schools.

In summary, with a demonstrated record of accomplished and productive research in the area of genomics, I believe that my expertise and experience in bioinformatics have prepared me to the new role as an Assistant Professor in neurogenomics.