Genomics and Bioinformatics Hub

An integrative hub of genomic services, data science, and bioinformatics training in Brigham and Harvard

Director: Xianjun Dong, PhD (Assistant Professor, Harvard Medical School) | Web: http://bioinformatics.bwh.harvard.edu

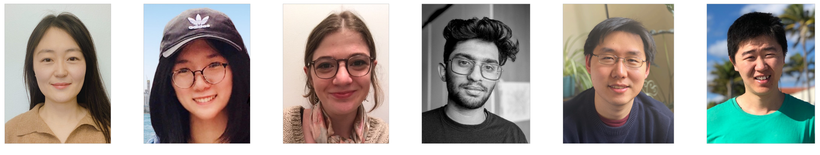
Our Goal: *To power your research with big data and computation*

Your Research	Support we can provide
Ideas	Grant writing, e.g., letter of support
Experiment design	Sample size, NGS kit recommendation
Data generation	Onsite sequencing and single-cell service (Illumina NextSeq, 10x Genomics)
Data analysis	NGS data analysis service: bulk and single-cell RNA-seq, ATAC-seq, WES, WGS, ChIP-seq, Hi-C, CAGE, genotyping etc.
Publication	External data access for replication
	Result report with publication-ready figures, tables, and periodic meetings
	Data management (storage/backup, GEO/dbGap submission)

Our Team: *Unique intersection of computation, genomics, and biology*

Xianjun Dong, PhD
Director

- Assistant Professor in Neurology, BWH and HMS
- PhD in genomics and bioinformatics
- Specialized in transcriptional regulation of eukaryotic genome
- A lead data analyst in ENCODE consortium
- Leading a bioinformatics team in Precision Neurology Program since 2013
- 40+ publications, 17,000+ citations and H-index 21
- Currently funded by APDA, ASAP, and NIH



Our Customers: *From basic scientists to physician scientists*

Our Publications: *Discoveries with medical impact*

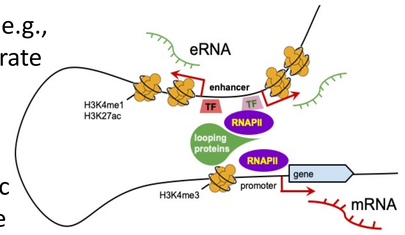
Our Expertise

Next-generation sequencing (NGS) data analysis

- Single-cell omics analysis (scRNA-seq, scATAC-seq, etc.);
- Spatial transcriptomics(10x Visium, MERFISH etc.);
- RNA-seq analysis (from raw sequencing data to QC, to normalized gene expression table, group comparison, pathway analysis, and interactive reporting and visualization of the results);
- Small RNA-seq analysis (e.g., miRNAs, circRNAs, eRNAs, etc.);
- ChIP-seq analysis (e.g., QC, peak calling, differential binding);
- Variant calling from genotyping/WGS/WES data;
- Other NGS data analysis (CAGE, ChIA-PET, Hi-C, Methyl-seq, etc.);
- Seamless NGS analysis on cloud computing environment.

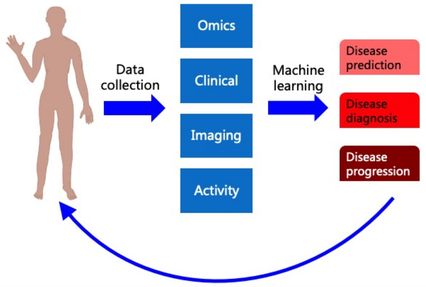
Transcriptional regulation of eukaryotic genome

- Discovery of regulatory elements (e.g., promoter, enhancer) in the vertebrate genome;
- Epigenetic regulation of gene expression;
- *Cis*- and *trans*-regulation of genetic variants (both SNP and SV) to gene expression, e.g., xQTL;
- Non-coding RNAs, e.g., eRNA, circRNA



Dong et al. *Nature Neuroscience*, 2018

Applying AI/machine learning to disease prediction



- Integration of multi-dimensional multi-source data (e.g., omics, clinical, imaging, and wearable device);
- Applying the latest machine learning methods to predict disease diagnosis and progression.

Tools and Data Resources

BRAINcode www.humanbraincode.org

powereQTL bwhbioinfo.shinyapps.io/powerEQTL

Data service we host

biobank uk · PARTNERS HEALTHCARE BIOBANK · All of Us RESEARCH PROGRAM · AMP-AD · AMP PD · GWAS Catalog · GENCODE · GTEx · ENCODE · FANTOM · BRAINcode · PsychENCODE

Training: *the Bioinformatics Club in BWH*

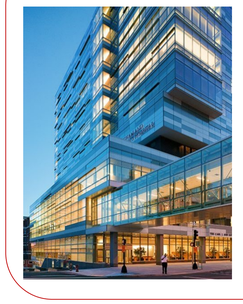
- Bioinformatics Club since 2017, with 350 members;
- 50 speakers, 75 talks, 3000+ participants so far;
- Winner of 2018 BRI NextGen Award;
- http://bioinformatics.bwh.harvard.edu/trainings

How to work with us

Email Us → Schedule a Meeting → Make a Plan → Get Work Done → Done

Flat price: $150/hr for all BWH/MGH/DFCI labs
New customer discount: 20% off for the first 30 hours

Contact us for your next project



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