HARIANTO TJONG

<p style="text-align:center">Computer Scientist
The Jackson Laboratory</p>

EDUCATION

Florida State University
Degree: PhD in Physics (Computational Biophysics)   *December 2008*
Degree: MS in Physics   *December 2004*

University of Indonesia
Degree: BS in Physics   *August 2000*

WORK EXPERIENCE

The Jackson Laboratory, Dept. of Genome Technologies, Farmington, CT
Computational Scientist   *Nov 7, 2016 – present*
- Develop computational tools and pipelines for NGS data QC & analysis.
- Design & implement methods and problem-solving strategies for scientific research.
- Perform QC & troubleshooting in support for scientific service role under Dept. of Genome Technologies.

University of Southern California, Computational and Molecular Biology, Los Angeles, CA
Senior Research Associate   *July 1, 2013 – Oct 31, 2016*
- Generated human genome models and proposed new insight about the major drivers of chromosome-chromosome interactions through high-throughput sequencing.
- Improved the capability of modeling method to integrate diverse experiment data (high-throughput sequencing, FISH microscopy and DamID) into higher resolution 3D models.
- Provided the informatics platform to investigate inter-chromosomal interaction in both health and disease settings.

University of Southern California, Computational and Molecular Biology, Los Angeles, CA
Postdoctoral Research Associate   *July 1, 2009 – June 30, 2013*
- Generated the first putative 3-D models of the budding yeast genome structures in nuclear and proposed the governing principles of the genome packing.
- Developed the first population of human 3D genome structures using high-throughputs DNA-DNA interaction data (highlighted in the cover art and News & View by a high profile scientist in Nature Biotech 2012).

Institute of Molecular Biophysics, Florida State University, Tallahassee, FL
Postdoctoral Fellow   *December 1, 2008 - June 30, 2009*
- Developed fast and accurate computational biophysics methods and Molecular Dynamics simulation techniques to study protein folding and protein-protein interactions.
- Improved computational methods predicting mutational effects on protein solubility and protein folding stability.
- Designed, developed, and maintained bioinformatics web servers: DISPLAR http://pipe.scs.fsu.edu/displar.html, cons-PPISP http://pipe.scs.fsu.edu/ppisp.html, and WESA http://pipe.scs.fsu.edu/wesa.html. These servers have been visited 100,000 times by over 48,000 unique visitors indicating the large impact to scientific community.

SELECTED PUBLICATIONS

[1] Y. Zhu, A.D. Gujar, C.H. Wong, **H.Tjong**, et.al (2021). Oncogenic extrachromosomal DNA functions as mobile enhancers to globally amplify chromosomal transcription. *Cancer Cell* 39:694.

[2] C.Y. Ngan, C.H. Wong, **H. Tjong**, et. al (2020). Chromatin interaction analyses elucidate the roles of PRC2-bount silencers in mouse development. *Nat. Genet.* 52:264.

[3] J.A. Bertolini, R. Favaro, Y. Zhu, M. Pagin, C.Y. Ngan, C.H. Wong, **H. Tjong,** et. al (2019). Mapping the global connectivity network for Sox2 function in neural stem cell maintenance. *Cell Stem Cell* 24:462.

[4] L. Gong, C.H. Wong, W.C. Cheng, **H. Tjong**, F. Menghi, C.Y. Ngan, E.T. Liu, and C.L. Wei (2018). Picky comprehensively detects high-resolution structural variants in nanopore long reads. *Nat. Methods* 15:455.

[5] N. Hua, **H. Tjong**, H. Shin, K. Gong, X.J. Zhou, and F. Alber (2018). Producing genome structure population with the dynamic and automated PGS software. *Nat. Protoc.* 13:915.

[6] Q. Li, **H. Tjong**, X. Li, K. Gong, X.J. Zhou, I. Chiolo, and F. Alber (2017). The three-dimensional genome organization of drosophila melanogaster through data integration. *Genome Biol.* 18:145.

[7] C. Dai, W. Li, **H. Tjong**, S. Hao, B. Zhu, L. Chen, F. Alber, and X. Zhou (2016). Mining 3D genome structure populations identifies major factors governing the stability of regulatory communities. *Nature Communications* 7:11549.

[8] **H. Tjong**, W. Li, C. Dai, R. Kalhor, S. Hao, K. Gong, H. Li, C. Larabell, M. LeGros, L. Chen, X. Zhou, and F. Alber (2016). Population-based 3D genome structure analysis reveals driving forces in spatial genome organization. *PNAS* 113:E1663-E1672.

[9] H. Shin, Y. Shi, C. Dai, **H. Tjong**, K. Gong, F. Alber, and X. Zhou (2015). TopDom: An Efficient and deterministic method for identifying topological domains in genomes. *Nucleic Acids Research*, doi: 10.1093/nar/gkv1505.

[10] E. Dultz, **H. Tjong**, E. Weider, M. Herzog, B. Young, C. Brune, D. Mullner, C. Loewen, F. Alber, and K. Weis (2015). Global reorganization of budding yeast chromosome conformation in different physiological conditions. *The Journal of Cell Biology* 212:321-334..

[11] K. Gong , **H. Tjong**, X. Zhou, and F. Alber (2015). Comparative 3D genome structure analysis of the fission and the budding yeast. Plos One 10(3):e0119672.

[12] **Tjong, H.**, K. Gong, L. Chen, and F. Alber (2012). Physical tethering and volume exclusion determine higher order genome organization in budding yeast. *Genome Research* 22:1295–1305.

[13] R. Kalhor, **H. Tjong**, N. Jayathilaka, L. Chen, and F. Alber (2012). Genome architectures revealed by tethered chromosome conformation capture and population-based modeling. *Nature Biotechnology* 30:90–98. *A high profile scientist wrote a highlight for the paper on the same issue.*

[14] M. Beck, M. Topf, Z. Frazier, **H. Tjong**, M. Xu, S. Zhang, and F. Alber (2011). Exploring the spatial and temporal organization of a cell's proteome. *Journal of Structural Biology* 173:483–496.

[15] **H. Tjong**, S. Qin, and H.-X. Zhou (2007). PI2PE: protein interface/interior prediction engine. *Nucleic Acids Research* 35:W357–W362.

[16] **H. Tjong** and H.-X. Zhou (2007). GBr6: a parameterization-free, accurate, analytical generalized Born method. *The Journal of Physical Chemistry B* 111:3055–3061.

[17] **H. Tjong** and H.-X. Zhou (2007). DISPLAR: an accurate method for predicting DNA-binding sites on protein surfaces. *Nucleic Acids Research* 35:1465–1477.