CURRICULUM VITAE

Contact

Name:	Gang Peng
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Education

2009 – 2015	The University of Texas Graduate School of Biomedical Sciences	Houston, TX
	PhD, Biostatistics and Bioinformatics	
2001 – 2005	Fudan University	Shanghai, China
	BS, Physics	

Professional Experience

7/2018 – present	*Associate Research Scientist*
	Department of Biostatistics, School of Public Health, Yale University
11/2015 – 6/2018	*Postdoctoral Associate*
	Department of Biostatistics, School of Public Health, Yale University
1/2011 – 8/2015	*Graduate Research Assistant*
	Bioinformatics and Computational Biology, University of Texas MD Anderson Cancer Center
9/2009 – 12/2010	*Graduate Research Assistant*
	Biostatistics, School of Public Health, University of Texas
8/2005 – 7/2009	*Statistical Analyst*
	Laboratory of Theoretical Systems Biology and Center for Evolutionary Biology, School of Life Science, Fudan University, China

Honors and Awards

2017	Top Rated Abstract (ACMG Annual Clinical Genetics Meeting)
2015	GSBS student travel award (ENAR 2015 Spring Meeting)
2014	AAAS/Science Program for Excellence in Science
2012	Top-cited Article of 2012, European Journal of Human Genetics
2008	Second Place Award of Research Day Post, The University of Texas School of Public Health
2005	Excellent Graduate Student of Shanghai

Teaching

Teaching assistant: Introduction to Bioinformatics (GS0011062)

Professional Activities

Membership: ENAR/International Biometric Society, American Association for the Advancement of Science

Journal referee for: Computers in Biology and Medicine, PLOS One, BioData Mining, Journal of Computational Biology, Interdisciplinary Sciences: Computational Life Sciences, IEEE/ACM Transactions on Computational Biology and Bioinformatics

Areas of Interest:

Risk Prediction, Statistical Learning, Newborn Screening, Next Generation Sequencing, Proteomics, Metabolomics

Completed Grants

Co-Investigator

Development of a Proteomics Data Analysis and Visualization Tool

The Yale/NIDA Neuroproteomics Center

PI – Hongyu Zhao, 4/2016-5/2017

Publications

Papers in Refereed Journals

1. **Peng G**, Wilson R, Tang Y, Lam T, Nairn A, Williams K, Zhao H. ProteomicsBrowser: MS/Proteomics Data Visualization and Investigation. *Bioinformatics*, 35 (13), 2313-2314
2. **Peng G**, Fontnouvellea C, Enns G, Cowan T, Zhao H, Scharfe C. Elevated methylmalonic acidemia (MMA) screening markers in Hispanic and preterm newborns. *Molecular Genetics and Metabolism*. 126 (1), 39-42
3. Zhang X, Hu Y, Aouizerat B, **Peng G**, Marconi V, Corley M, Hulgan T, Bryant K, Zhao H, Krystal J, Justice A, Xu K. Machine learning selected smoking-associated DNA methylation signatures that predict HIV prognosis and mortality. *Clinical Epigenetics*, 10 (1), 155.
4. Xie Y, Ostriker A, Jin Y, Hu H, Sizer A, **Peng G**, Morris A, Ryu C, Herzog E, Kyriakides T, Zhao H, Dardik A, Yu J, Hwa J, Martin K. LMO7 is a negative feedback regulator of TGF-β signaling and fibrosis. *Circulation*, 139 (5), 679-693
5. **Peng G***, Shen P*, Gandotra N*, Le A, Fung E, Jelliffe-Pawlowski L, Davis R, Enns G, Zhao H, Cowan T, Scharfe C. Combining newborn metabolic and DNA analysis for second-tier testing of methylmalonic acidemia. *Genet Med*. 2018 Sep 13. doi: 10.1038. *authors contributed equally
6. Madsen T, Braun D, **Peng G**, Parmigiani G, Trippa L. Efficient computation of the joint probability of multiple germline mutations from pedigree data. *Genet Epidemiol*. 2018 Sep;42(6):528-538. doi: 10.1002.

7. Rauniyar R*, **Peng G***, Lam T, Zhao H, Mor G, Williams, K. Data-independent acquisition (DIA) and parallel reaction monitoring (PRM) mass spectrometry identification of serum biomarkers for ovarian cancer. *Biomark Insights*. 2017; doi: 10.1177/1177271917710948. *authors contributed equally
8. Goffredo M, Santoro N, Tricò D, Giannini C, D'Adamo E, Zhao H, **Peng G**, Yu X, Lam TT, Pierpont B, Caprio S, Herzog RI. A branched-chain amino acid-related metabolic signature characterizes obese adolescents with non-alcoholic fatty liver disease. *Nutrients*. 2017; 9(7). pii: E642. doi: 10.3390/nu9070642.
9. **Peng G**, Bojadzieva J, Ballinger ML, Li J, Blackford AL, Mai PL, Savage SA, Thomas DM, Strong LC, Wang W. Estimating TP53 mutation carrier probability in families with Li-Fraumeni syndrome using LFSPRO. *Cancer Epidemiol Biomarkers Prev*. 2017; 26(6):837-844.
10. Lefterova MI, Shen P, Odegaard JI, Fung E, Chiang T, **Peng G**, Davis RW, Wang W, Kharrazi M, Schrijver I, Scharfe C. Next-generation molecular testing of newborn dried blood spots for cystic fibrosis. *J Mol Diagn.* 2016 Mar;18(2):267-82.
11. **Peng G**, Fan Y, Wang W. FamSeq: A Variant Calling Program for Family-Based Sequencing Data Using Graphics Processing Units. *PLoS Computational Biology*. 2014; 10(10), e1003880
12. Yuan X, Song H, **Peng G**, Hua X, Tang X. Prevalence of corneal astigmatism in patients before cataract surgery in northern China. Journal of Ophthalmology. 2014; 2014:536412. doi: 10.1155/2014/536412.
13. **Peng G**, Fan Y, Palculict TB, Shen P, Ruteshouser EC, Chi A, Davis RW, Huff V, Scharfe C, Wang W. Rare variant detection using family-based sequencing analysis. *Proc Natl Acad Sci U S A.* 2013 Mar 5;110(10):3985-90.
14. Wu X, Dong H, Luo L, Zhu Y, **Peng G**, Reveille JD, Xiong M. A novel statistic for genome-wide interaction analysis. *PLoS Genet*. 2010 Sep 23;6(9).
15. Luo L, **Peng G**, Zhu Y, Dong H, Amos CI, Xiong M. Genome-wide gene and pathway analysis. *Eur J Hum Genet*. 2010 Sep;18(9):1045-53.
16. **Peng G**, Luo L, Siu H, Zhu Y, Hu P, Hong S, Zhao J, Zhou X, Reveille JD, Jin L, Amos CI, Xiong M. Gene and pathway-based second-wave analysis of genome-wide association studies. *Eur J Hum Genet*. 2010 Jan;18(1):111-7.
17. Seitsonen SP, Onkamo P, **Peng G**, Xiong M, Tommila PV, Ranta PH, Holopainen JM, Moilanen JA, Palosaari T, Kaarniranta K, Meri S, Immonen IR, Järvelä IE. Multifactor effects and evidence of potential interaction between complement factor H Y402H and LOC387715 A69S in age-related macular degeneration. *PLoS One.* 2008;3(12):e3833.

Papers in Peer Reviewed Conference Proceedings

1. Xiong MM, Dong H, Siu, H, **Peng G**, Wang Y, Jin L (2010). Genome-Wide Association Studies of Copy Number Variation in Glioblastoma. 2010 4th International Conference on Bioinformatics and Biomedical Engineering (iCBBE), Digital Object Identifier: 10.1109/ICBBE.2010.5516437, PP. 1-4.
2. Zhou Q, **Peng G**, Jin L, Xiong M. (2009). The Results on the Stability of Glycolytic Metabolic Networks in Different Cells. Complex Sciences: Springer; 2009. p. 536-40.

Papers in Preparation

1. Peng G, Tang Y, Gandotra N, Enns G, Cowan T, Zhao H, Scharfe C. Race/ethnicity-associated differences in newborn screening markers for inborn metabolic disorders. (Submitted)
2. Kaislasuo J, Simpson S, Peng G, Petersen JF, Aldo P, Lokkegaard E, Paidas M, Pal L, Guller S, Mor G. IL-10 to TNFα ratios throughout the first trimester of pregnancy: potential predictive value for pregnancy losses. (Submitted)

3. Seung Jun Shin, Elissa Dodd, Gang Peng, Jasmina Bojadzieva, Jingxiao Chen, Chris Amos, Phuong L Mai, Sharon A Savage, Mandy L Ballinger, David M Thomas, Louise C Strong, Wenyi Wang. Risk of differential cancer types over age in families with Li-Fraumeni syndrome: a validation study using multi-center cohorts. (Submitted)
4. Yonghong Zhang, Paulomi Aldo, Yuan You, Jiahui Ding, Jannina Kaislasuo, Samantha Simpson, Jesper F Petersen, Gang Peng, Ellen Lokkegaard, Michael Paidas, Lubna Pal, Seth Guller, Hong Liu, Aihua Liao, Gil Mor. Trophoblast Derived soluble-PD-L1 modulates macrophage polarization and function. (Submitted)
5. Peng G, Tang Y, Zhao H, Scharfe C. Second-tier newborn screening test with random forest and an online tool application.
6. Peng G, Cai H, Zhao H, Li P. Survival prediction for hepatocellular carcinoma using copy number variation data.

Peer Reviewed Presentations

1. ENAR 2015 Spring Meeting, Miami, FL, "Estimating TP53 Mutation Carrier Probability in Families with Li-Fraumeni Syndrome Using LFSpro."
2. Annual Meeting, Texas Genetics Society, Houston, TX, "Genome-wide Association Studies of Copy Number Variation in Glioblastoma."

Google Scholar

https://scholar.google.com/citations?user=YuHfhPQAAAAJ&hl=en

Website

https://gangpeng.org

News Report

1. GenomWeb, “This Week in PNAS”, February 19, 2013.
2. Stanford Medicine, “Fast, accurate cystic fibrosis test developed at Stanford”, February 1, 2016.
3. KQED Science, “New Low-Cost Test for Cystic Fibrosis”, February 1, 2016
4. Kaiser Health News (KHN), “Cutting Edge DNA Technology Could Boost Cystic Fibrosis Screening for Newborns”, February 4, 2016
5. Genetic Engineering & Biotechnology News, “Breathing New Life into Cystic Fibrosis Genetic Testing”, July 6, 2016
6. YaleNews, “New approach improves detection of diseases at birth”, September 12, 2018
7. UPI, “New methods speed up disease diagnoses in newborns”, September 13, 2018
8. Technology Networks, “New Approach Improves Detection of Diseases at Birth”, September 14, 2018

Software

1. ProteomicsBrowser (Java), https://medicine.yale.edu/keck/nida/proteomicsbrowser.aspx
2. PTNorm: Proteomics data normalization and batch effect correction, https://proteomicstools.shinyapps.io/PTNormShiny/

3. FamSeq: Analysis of family-based sequencing data (C++), http://bioinformatics.mdanderson.org/main/FamSeq
4. LFSPRO: Personalized risk assessment for families with Li-Fraumeni syndromes (C++ and R, co-author), http://bioinformatics.mdanderson.org/main/LFSPRO
5. LFSPRO online, https://gangpeng.shinyapps.io/LFSPRO/
6. BayesMendel (C++ and R, co-author), http://bcb.dfci.harvard.edu/bayesmendel/software.php
7. Other Bioinformatics tools, https://github.com/peng-gang