CURRICULUM VITAE

Contact

Name: Gang Peng
Mailing address: MS 502, 635 Barnhill Dr, Indianapolis, IN 46202
E-mail: gangpeng@iu.edu

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

9/2022 – present	*Assistant Professor* Department of Medical and Molecular Genetics, Indiana University School of Medicine
9/2022 – present	*Director of Bioinformatics* Indiana Center for Musculoskeletal Health (ICMH), Indiana University School of Medicine
9/2022 – present	*Associate Faculty Member* Center for Computational Biology and Bioinformatics (CCBB), Indiana University School of Medicine
7/2018 – 8/2022	*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

2022	Lecturer of "Quantitative Biomedical Science" (IUSM Q581), Indiana University School of Medicine, Indianapolis, IN USA

Professional Activities

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, Annals of Biometrics and Biostatistics, Egyptian Journal of Medical Human Genetics, Journal of Personalized Medicine, Genome Medicine, Human Genomics, Genes, PeerJ, International Journal of Environmental Research and Public Health, Childrend

Areas of Interest:

High Throughput Sequencing, Proteomics, Metabolomics, Epigenomics, Omics Data Integration, Newborn Screening, Cancer Risk Prediction, Statistical Learning

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**, Pakstis AJ, Gandotra N, Cowan TM, Zhao H, Kidd KK, Scharfe C., 2022, Metabolic diversity in human populations and correlation with genetic and ancestral geographic distances. *Molecular Genetics and Metabolism.*
2. **Peng G***, Xi Y*, Bellini C, Kien P, Zhuang Z, Yan Q, Jia M, Wang G, Krishnan-Sarin S, Tang M, Zhao H, Wang H., 2022, Nicotine Dose-Dependent Epigenomic-Wide DNA Methylation changes in the mice with long-term electronic cigarette exposure. *American Journal of Cancer Research.* 12(8):3679-92. *authors contributed equally

3. **Peng G**, Zhang Y, Zhao H, Scharfe C., 2022, dbRUSP: a database of investigating influence of clinical variables to metabolic levels in newborn screening. *International Journal of Neonatal Screening*. 8(3):48.
4. AlOlaby RR, Zafarullah M, Barboza M, **Peng G**, Varian BJ, Erdman SE, Lebrilla C, Tassone F., 2022, Differential Methylation Profile in Fragile X Syndrome-Prone Offspring Mice after in Utero Exposure to Lactobacillus Reuteri. *Genes*. 13(8):1300.
5. **Peng, G.**, Chai, H., Ji, W., Lu, Y., Wu, S., Zhao, H., Li, P., Hu, Q., 2021, Correlating genomic copy number alterations with clinicopathologic findings in 75 cases of hepatocellular carcinoma. *BMC Medical Genomics*, 14.1 (2021): 1-9.
6. Xiao, C., Beitler, J., **Peng, G.**, Levine, M., Conneely, K., Zhao, H., Felger, J., Wommack, E., Chico, C., Jeon, S., Higgins, K., Shin, D., Saba, N., Burtnes, B., Bruner, D., Miller, A., 2021, Epigenetic age acceleration, inflammation, and fatigue in patients undergoing radiation therapy for head and neck cancer: a longitudinal study. *Cancer*, 127(18):3361-3371.
7. **Peng, G.**, Tang, Y., Cowan, T.M., Zhao, H. and Scharfe, C., 2021. Timing of newborn blood collection alters metabolic disease screening performance. *Frontiers in Pediatrics*, 8.
8. Xiao, C., Miller, A.H., **Peng, G.**, Levine, M.E., Conneely, K.N., Zhao, H., Eldridge, R.C., Wommack, E.C., Jeon, S., Higgins, K.A. and Shin, D.M., 2021. Association of epigenetic age acceleration with risk factors, survival, and quality of life in patients with head and neck cancer. *International Journal of Radiation Oncology* Biology* Physics.*
9. Xiao, C., Fedirko, V., Beitler, J., Bai, J., **Peng, G.**, Zhou, C., Gu, J., Zhao, H., Lin, I.H., Chico, C.E. and Jeon, S., 2020. The role of the gut microbiome in cancer-related fatigue: pilot study on epigenetic mechanisms. *Supportive Care in Cancer*, pp.1-10.
10. Zerjav, M., DiAdamo, A., Grommisch, B., Katherine, A., Chai, H., **Peng, G.** and Li, P., 2020. Cytogenomic Abnormalities in 19 Cases of Salivary Gland Tumors of Parotid Gland Origin. *Case reports in genetics*, 2020.
11. Mansuri, M.S., **Peng, G.**, Wilson, R.S., Lam, T.T., Zhao, H., Williams, K.R. and Nairn, A.C., 2020. Differential Protein Expression in Striatal D1-and D2-Dopamine Receptor-Expressing Medium Spiny Neurons. *Proteomes*, 8(4), p.27.
12. Simpson, S., Kaislasuo, J., **Peng, G.**, Aldo, P., Paidas, M., Guller, S., Mor, G. and Pal, L., 2020. Peri-implantation cytokine profile differs between singleton and twin IVF pregnancies. *American Journal of Reproductive Immunology*, p.e13348.
13. Johnson, R.M., Olivares-Strank, N. and **Peng, G.**, 2020. A Class II-Restricted CD8γ13 T-Cell Clone Protects During Chlamydia muridarum Genital Tract Infection. *The Journal of Infectious Diseases*, 221(11), pp.1895-1906.
14. Zhang, Y.H., Aldo, P., You, Y., Ding, J., Kaislasuo, J., Petersen, J.F., Lokkegaard, E., **Peng, G.**, Paidas, M.J., Simpson, S. and Pal, L., 2020. Trophoblast ‐ secreted soluble ‐ PD ‐ L1 modulates macrophage polarization and function. *Journal of Leukocyte Biology*.
15. Ordulu, Z., Chai, H., **Peng, G.**, McDonald, A.G., De Nictolis, M., Garcia-Fernandez, E., Hardisson, D., Prat, J., Li, P., Hui, P. and Oliva, E., 2020. Molecular and clinicopathologic characterization of intravenous leiomyomatosis. *Modern Pathology*, pp.1-17.
16. Silasi, M., You, Y., Simpson, S., Kaislasuo, J., Pal, L., Guller, S., **Peng, G.**, Ramhorst, R., Grasso, E., Etemad, S. and Durosier, S., 2020. Human chorionic Gonadotropin modulates CXCL10 Expression through Histone Methylation in human decidua. *Scientific Reports*, 10(1), pp.1-17.

17. **Peng, G.**, Tang, Y., Gandotra, N., Enns, G.M., Cowan, T.M., Zhao, H. and Scharfe, C., 2020. Ethnic variability in newborn metabolic screening markers associated with false‐positive outcomes. *Journal of Inherited Metabolic Disease*.
18. **Peng, G.**, Tang, Y., Cowan, T.M., Enns, G.M., Zhao, H. and Scharfe, C., 2020. Reducing False-Positive Results in Newborn Screening Using Machine Learning. *International Journal of Neonatal Screening*, 6(1), p.16.
19. Shin, S.J., Dodd-Eaton, E.B., **Peng, G.**, Bojadzieva, J., Chen, J., Amos, C.I., Frone, M.N., Khincha, P.P., Mai, P.L., Savage, S.A. and Ballinger, M.L., 2020. Penetrance of different cancer types in families with Li-Fraumeni syndrome: A validation study using multicenter cohorts. *Cancer Research*, 80(2), pp.354-360.
20. Kaislasuo, J., Simpson, S., Petersen, J.F., **Peng, G.**, Aldo, P., Lokkegaard, E., Paidas, M., Pal, L., Guller, S. and Mor, G., 2020. IL‐10 to TNF α ratios throughout early first trimester can discriminate healthy pregnancies from pregnancy losses. *American Journal of Reproductive Immunology,* 83(1), p.e13195.
21. **Peng, G.**, Wilson, R., Tang, Y., Lam, T.T., Nairn, A.C., Williams, K. and Zhao, H., 2019. ProteomicsBrowser: MS/proteomics data visualization and investigation. *Bioinformatics*, 35(13), pp.2313-2314.
22. **Peng, G.***, Shen, P.*, Gandotra, N.*, Le, A., Fung, E., Jelliffe-Pawlowski, L., Davis, R.W., Enns, G.M., Zhao, H., Cowan, T.M. and Scharfe, C., 2019. Combining newborn metabolic and DNA analysis for second-tier testing of methylmalonic acidemia. *Genetics in Medicine*, 21(4), pp.896-903. *authors contributed equally
23. Xie, Y., Ostriker, A.C., Jin, Y., Hu, H., Sizer, A.J., **Peng, G.**, Morris, A.H., Ryu, C., Herzog, E.L., Kyriakides, T. and Zhao, H., 2019. LMO7 is a negative feedback regulator of transforming growth factor β signaling and fibrosis. *Circulation*, 139(5), pp.679-693.
24. **Peng, G.**, de Fontnouvelle, C.A., Enns, G.M., Cowan, T.M., Zhao, H. and Scharfe, C., 2019. Elevated methylmalonic acidemia (MMA) screening markers in Hispanic and preterm newborns. *Molecular genetics and metabolism*, 126(1), pp.39-42.
25. Zhang, X., Hu, Y., Aouizerat, B.E., **Peng, G.**, Marconi, V.C., Corley, M.J., Hulgan, T., Bryant, K.J., Zhao, H., Krystal, J.H. and Justice, A.C., 2018. Machine learning selected smoking-associated DNA methylation signatures that predict HIV prognosis and mortality. *Clinical epigenetics*, 10(1), p.155.
26. Madsen, T., Braun, D., **Peng, G.**, Parmigiani, G. and Trippa, L., 2018. Efficient computation of the joint probability of multiple inherited risk alleles from pedigree data. *Genetic epidemiology*, 42(6), pp.528-538.
27. Goffredo, M., Santoro, N., Tricò, D., Giannini, C., D'Adamo, E., Zhao, H., **Peng, G.**, Yu, X., Lam, T.T., Pierpont, B. and Caprio, S., 2017. A branched-chain amino acid-related metabolic signature characterizes obese adolescents with non-alcoholic fatty liver disease. *Nutrients,* 9(7), p.642.
28. Rauniyar, N.*, **Peng, G.***, Lam, T.T., Zhao, H., Mor, G. and Williams, K.R., 2017. Data-independent acquisition and parallel reaction monitoring mass spectrometry identification of serum biomarkers for ovarian cancer. *Biomarker insights*, 12, p.1177271917710948. *authors contributed equally
29. **Peng, G.**, Bojadzieva, J., Ballinger, M.L., Li, J., Blackford, A.L., Mai, P.L., Savage, S.A., Thomas, D.M., Strong, L.C. and Wang, W., 2017. Estimating TP53 mutation carrier probability in families with Li–Fraumeni syndrome using LFSPRO. *Cancer Epidemiology and Prevention Biomarkers*, 26(6), pp.837-844.
30. Lefterova, M.I., Shen, P., Odegaard, J.I., Fung, E., Chiang, T., **Peng, G.**, Davis, R.W., Wang, W., Kharrazi, M., Schrijver, I. and Scharfe, C., 2016. Next-generation molecular testing of newborn dried blood spots for cystic fibrosis. *The Journal of Molecular Diagnostics*, 18(2), pp.267-282.

31. **Peng, G.**, Fan, Y. and Wang, W., 2014. FamSeq: a variant calling program for family-based sequencing data using graphics processing units. *PLoS Comput Biol*, 10(10), p.e1003880.
32. Yuan, X., Song, H., **Peng, G.**, Hua, X. and Tang, X., 2014. Prevalence of corneal astigmatism in patients before cataract surgery in Northern China. *Journal of Ophthalmology*, 2014.
33. **Peng, G.**, Fan, Y., Palculict, T.B., Shen, P., Ruteshouser, E.C., Chi, A.K., Davis, R.W., Huff, V., Scharfe, C. and Wang, W., 2013. Rare variant detection using family-based sequencing analysis. *Proceedings of the National Academy of Sciences*, 110(10), pp.3985-3990.
34. Wu, X., Dong, H., Luo, L., Zhu, Y., **Peng, G.**, Reveille, J.D. and Xiong, M., 2010. A novel statistic for genome-wide interaction analysis. *PLoS Genet*, 6(9), p.e1001131.
35. Luo, L., **Peng, G.**, Zhu, Y., Dong, H., Amos, C.I. and Xiong, M., 2010. Genome-wide gene and pathway analysis. *European Journal of Human Genetics*, 18(9), pp.1045-1053.
36. **Peng, G.**, Luo, L., Siu, H., Zhu, Y., Hu, P., Hong, S., Zhao, J., Zhou, X., Reveille, J.D., Jin, L. and Amos, C.I., 2010. Gene and pathway-based second-wave analysis of genome-wide association studies. *European Journal of Human Genetics*, 18(1), pp.111-117.
37. Seitsonen, S.P., Onkamo, P., **Peng, G.**, Xiong, M., Tommila, P.V., Ranta, P.H., Holopainen, J.M., Moilanen, J.A., Palosaari, T., Kaarniranta, K. and Meri, S., 2008. Multifactor effects and evidence of potential interaction between complement factor H Y402H and LOC387715 A69S in age-related macular degeneration. *PloS one*, 3(12), p.e3833.

Papers in Peer Reviewed Conference Proceedings

1. Xiong, M., Dong, H., Siu, H., **Peng, G.**, Wang, Y. and Jin, L., 2010, June. Genome-Wide Association Studies of Copy Number Variation in Glioblastoma. *In 2010 4th International Conference on Bioinformatics and Biomedical Engineering* (pp. 1-4). IEEE.
2. Zhou, Q., **Peng, G.**, Jin, L. and Xiong, M., 2009, February. The Results on the Stability of Glycolytic Metabolic Networks in Different Cells. *In International Conference on Complex Sciences* (pp. 536-540). Springer, Berlin, Heidelberg.

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

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 cancer 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. Target Sequence Analysis Pipeline (R), https://github.com/peng-gang/TGPipeline
8. Newborn Screening with Random Forest (R), https://rusptools.shinyapps.io/RandomForest/
9. RUSPtools: Relation between Metabolite Levels and Age at Blood Collection (R), http://rusptools.shinyapps.io/AaBC/
10. Other Biostatistics and Bioinformatics tools, https://github.com/peng-gang