Ren-Hua Chung, PhD
Associate Investigator
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Education

- 2000
  B.S. in Computer Science,
  National Chiao-Tung University, Taiwan
- 2003
  M.S. in Computer Science,
  University of California at Davis, U.S.A.
- 2006
  Ph.D. in Bioinformatics, minor in Statistics
  North Carolina State University, U.S.A.

Professional Experiences

- 2012/02-present
  Institute of Population Health Sciences, National Health Research Institutes, Taiwan
  Associate Investigator
- 2008/4-2011/12
  John P. Hussman Institute of Human Genomics, University of Miami Miller School of Medicine, USA
  Assistant Professor
- 2007/1-2008/3
  Center for Human Genetics, Duke University Medical Center, USA
  Postdoctoral Fellow
- 2003/7-2006/12
  Center for Human Genetics, Duke University Medical Center, USA
  Internship

Research Interests

Statistical genetics, bioinformatics and computational biology.

Research Activities & Accomplishment

Development of powerful statistical association tests for case-control and family data, design and implementation of efficient computational tools for genetic studies, and performing large-scale genetic association studies for metabolic-related traits.
National Health Research Institutes-Institutional Repository:
http://ir.nhri.org.tw/handle/3990099045/6395

Selected Publications

Chung RH*, Kang CY. A powerful gene-based test accommodating common and low-frequency variants to detect main effects and gene-gene interaction effects in case-control studies. Frontiers in genetics. 2018. 8:228.

	Chung RH, Chiu YF, Hung YJ, Lee WJ, Wu KD, Chen HL, Lin MW, Chen YDI, Quertermous T, Hsiung CA. Genome-wide copy number variation analysis identified deletions in SFMBT1 associated with fasting plasma glucose in a Han Chinese population. BMC Genomics. 2017. 18:591. Ehret GB,…,**Chung RH**,…,et al. The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. Nature Genetics. 2016. 48:1171-1184. Sung PY, Wang YT, Hsiung CA, **Chung RH***. GCORE-sib: An efficient gene-gene interaction tool for genome-wide association studies based on discordant sib pairs. BMC Bioinformatics. 2016. 17:273. **Chung RH***, Tsai WY, Kang CY, Yao PJ, Tsai HJ, Chen CH. FamPipe: An automatic analysis pipeline for analyzing sequencing data in families for disease studies. PLOS Computational Biology. 2016. 12(6):e1004980. Yao PJ, **Chung RH***. GESDB: A platform of simulation resources for genetic epidemiology studies. Database. 2016. May 30. pii:baw082. Sung PY, Wang YT, Yu YW, **Chung RH***. An efficient gene-gene interaction test for genome-wide association studies in trio families. Bioinformatics. 2016. 32(12):1848-1855. Yao PJ, **Chung RH***. SeqSIMLA2_extact: simulate multiple disease sites in large pedigrees with given disease status for diseases with low prevalence. Bioinformatics. 2016. 32(4):557-562. Hsieh CH, **Chung RH**, Lee WJ, Lin MW, Chuang LM, Quertermous T, Assimes T, Hung YJ, Yu YW. Effect of common genetic variants of growth arrest-specific 6 gene on insulin resistance, obesity and type 2 diabetes in an Asian population. PLOS One. 2015. 10(8):e0135681. Wang YT, Sung PY, Lin PL, Yu YW, **Chung RH***. A multi-SNP association test for complex diseases incorporating an optimal p-value threshold algorithm in nuclear families. BMC Genomics. 2015. 16: 381. **Chung RH***, Tsai WY, Hsieh CH, Hung KY, Hsiung CA, Hauser ER. SeqSIMLA2: Simulating Correlated Quantitative Traits Accounting for Shared Environmental Effects in User-Specified Pedigree Structure. Genetic Epidemiology. 2015. 39(1):20-24. **Chung RH***, Tsai WY, Martin ER. Family-based association test using both common and rare variants and accounting for directions of effects for sequencing data. PLOS ONE. 2014. 9(9):e107800. Wang SC, Tsou HH, **Chung RH**, Chang YS, Fang CP, Chen CH, Ho IK, Kuo HW, Liu SC, Shih YH, Wu HY, Huang BH, Lin KM, Chen AC, Hsiao CF, Liu YL. The association of genetic polymorphisms in the κ-opioid receptor 1 gene with body weight, alcohol use, and withdrawal

symptoms in patients with methadone maintenance. J Clin Psychopharmacol. 2014. 34(2):205-211.

Park YS, Schmidt MA, Martin ER, Pericak-Vance MA, **Chung RH***. Pathway-PDT: a flexible pathway analysis tool for nuclear families. *BMC Bioinformatics*. 2013. 14:267.

Chung RH*, Shih CC. SeqSIMLA: a sequence and phenotype simulation tool for complex disease studies. *BMC Bioinformatics*. 2013. 14:199.

Patent