

贾耿介

研究员，食品科学中心，
农业基因组所，中国农业科学院

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研究方向

领域包括生物医学信息学、个性化营养、健康大数据（如电子病历）挖掘、自然语言处理、多组学数据分析、生物分子网络建模。

通过开发分析多维度健康大数据的新算法：

- 发掘复杂疾病的亚型，解析其遗传学基础，设计亚型特异的个性化营养干预方案；
- 阐释食品营养，人体消化等系统，和其间微生物群落三方的相互作用关系。

职业履历

中国农业科学院农业基因组所，食品科学中心	2021–
职位：研究员	
芝加哥大学，遗传医学系和基因组与系统生物学研究所	2016–2020
职位：博士后	
合作导师：Andrey Rzhetsky	
Compagnie Générale de Géophysique (CGG) 公司，数据处理和建模分部	2013–2016
职位：地球物理学家	
苏黎世联邦理工学院 (ETH Zurich)，化学与生物工程研究所	2011
职位：访问学者	

教育背景

新加坡国立大学和麻省理工学院联合培养博士项目 (Singapore-MIT Alliance)	2008–2013
学位：化学与制药工程博士	
导师：Rudiyanto Gunawan, Gregory N. Stephanopoulos	
中国科学技术大学	2004–2008
学位：生物科学学士，	学分绩 3.71/4.3,
导师：田志刚	排名 4/86

学术论文

1. **G. Jia**, Y. Li, H. Zhang, I. Chattopadhyay, A. B. Jensen, D. R. Blair, L. Davis, P. N. Robinson, T. Dahlén, S. Brunak, M. Benson, G. Edgren, N. J. Cox, X. Gao, A. Rzhetsky*, Estimating Heritability

and Genetic Correlations from Large Health Datasets in the Absence of Genetic Data, **Nature Communications**, 10, 5508 (2019). (*corresponding authors)

2. **G. Jia**, G. Stephanopoulos, R. Gunawan*, Ensemble Kinetic Modeling of Metabolic Networks from Dynamic Metabolic Profiles, **Metabolites**, 2 (4), 891–912 (2012).
3. **G. Jia**, G. Stephanopoulos, R. Gunawan*, Incremental Parameter Estimation of Kinetic Metabolic Network Models, **BMC Systems Biology**, 6, 142 (2012).
4. **G. Jia**, G. Stephanopoulos, R. Gunawan*, Parameter Estimation of Kinetic Models from Metabolic Profiles: Two-phase Dynamic Decoupling Method, **Bioinformatics**, 27 (14), 1964–1970 (2011).
5. B. Chicoine, A. Rivelli, V. Fitzpatrick*, L. Chicoine, **G. Jia**, A. Rzhetsky, Prevalence of Common Disease Conditions in a Large Cohort of Individuals with Down Syndrome in the United States, **Journal of Patient-Centered Research and Reviews**, 2021, 8(2): 86-97.
6. X. Zhong*, Z. Yin, **G. Jia**, D. Zhou, Q. Wei, A. Faucon, P. Evans, E. R. Gamazon, B. Li, R. Tao, A. Rzhetsky, L. Bastarache, N. J. Cox*, Electronic Health Record Phenotypes Associated with Genetically Regulated Expression of CFTR and Application to Cystic Fibrosis, **Genetics in Medicine**, 22, 1191–1200 (2020).
7. C. Zhang, H. Tu, **G. Jia**, T. Mukhtar, V. Taylor, A. Rzhetsky, S. Tay*, Ultra-multiplexed Analysis of Single-cell Dynamics Reveals Logic Rules in Differentiation, **Science Advances**, 5 (2019).

学术会议

1. “Computational Model of Melanoma Cancer”, In the 18th International Conference on Systems Biology, Blacksburg, Virginia, USA, *Aug. 6-12, 2017*.
2. “Metabolic Network Model Identification – Parameter Estimation and Ensemble Modeling”, Department of Systems Biology, Harvard Medical School, Boston, USA, *Jan. 11-12, 2016*.
3. “Cable Sensitivity Correction for Time-series Measurement”, CGG Geophysical Meeting Series on Data Processing and Modeling, Calgary, Canada, *Jun. 3, 2015*.
4. “A new 3-D approach for signal decay compensation”, CGG Asia-Pacific Subsurface Imaging Technical Symposium, Singapore, *Jan. 23, 2014*.
5. “Please mind the degrees of freedom”, In Frontiers in Systems and Synthetic Biology, Atlanta, USA, *Mar. 20-24, 2013*.
6. “Incremental Parameter Estimation and Ensemble Kinetic Modeling of Metabolic Networks”, In the 12th AIChE Annual Meeting, Pittsburgh, USA, *Oct. 28 – Nov. 2, 2012*.
7. “Construction of Kinetic Model Library of Metabolic Networks”, In the 8th IFAC International Symposium on Advanced Control of Chemical Processes, Singapore, *Jul. 10-13, 2012*.
8. “Estimating Kinetic Parameters of Large Scale Metabolic Models”, In the 14th Asia Pacific Confederation of Chemical Engineering Congress, Singapore, *Feb. 21-24, 2012*.
9. “Construction of Kinetic Model Library of Metabolic Networks from Dynamic Profiles”, In the 12th International Conference on Systems Biology, Heidelberg/Mannheim, Germany, *Aug. 28 – Sep. 1, 2011*. (poster)
10. “Estimating Kinetic Parameters of Metabolic Networks within Flux-defined Subspace”, In the 8th International Workshop on Computational Systems Biology, Zurich, Switzerland, *Jun., 2011*. (poster)
11. “Parameter Estimation of Kinetic Models from Metabolic Profiles: Two-phase Dynamic Decoupling Method”, In the 13th International Conference on Molecular Systems Biology, Lleida, Spain, *May 2011*. (poster)
12. “Parameter Estimation of Kinetic Models from Time-series Profiles”, In the 11th International Conference on Systems Biology, Edinburgh, UK, *Oct. 10 - 15, 2010*. (poster)

13. “Metabolic Network Identification - Parameter Estimation of Kinetic Models”, In the 5th International Symposium on Design, Operation and Control of Chemical Processes, Singapore, *Jul. 25 - 28, 2010*.

教学经历

关于课程设计和大学教学的教育学训练课程，芝加哥大学	2016
培训讲师，CGG 公司	2013
教学助理，新加坡国立大学	2010–2011

荣誉奖项

新加坡国立大学-麻省理工学院联盟学生奖学金	2008–2012
麻省理工学院颁发的制药工业结晶学科技培训证书	2010
新加坡 A*STAR 高性能计算研究所颁发的高性能计算培训的认证书	2010
大学期间连续四年获得优秀学生奖学金 (奖励给学院学分绩排名前 10% 的学生)	2004–2008
松下电子人才培养基金会奖学金	2005–2006
中科大优秀学生干部 (当选时为院学生会主席)	2007
杰出大学生研究计划奖	2006

学术服务和会员

Peer-reviewed journals (PLOS Computational Biology, Scientific Reports, PLOS ONE, FOSBE)	
审稿人	2017–至今
American Association for the Advancement of Science	2016–至今
International Society for Computational Biology	2011–至今

科研基金支持

1R01HL122712-01A1 (NIH/NIHBL)	
Mendelian Disease – Asthma Comorbidity to Find Subgroup-Specific Asthma Genes	
Julian Solway, Carole Ober, Andrey Rzhetsky (PI)	2016–2019
该项目的主要目标是通过分析并发症来发现新哮喘亚型的致病基因 (主要参与)。	
W911NF-14-1-0333 (DARPA)	
Big Machine Science	
Andrey Rzhetsky (PI)	2016–2019
该项目的主要目标是将机器自动读取与概率推理和癌症生物学实验相结合 (主要参与)。	
苏黎世联邦理工学院 (瑞士国家科学基金委), Rudiyanto Gunawan (PI)	2011
项目课题：代谢网络动力学模型群体的构建 (主要参与)	
新加坡国立大学-麻省理工学院联盟奖学金 (新加坡国家科学研究基金会),	2008–2012
项目课题：代谢网络模型的构建 – 参数估计和群体建模 (主持)	