

## CURRICULUM VITAE

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## Research Interests

I'm interested in the theoretical population genetics and specialized in computational biology and mathematical modelling. My PhD's work is focused on the integration of theoretical population genetics and computation models with genomic data of cancer and normal tissues. I'm interested in exploring how mutation, selection, migration and other evolutionary driving forces to affect tumorigenesis, cancer metastasis, tumor heterogeneity and aging.

In addition to somatic evolution, I'm interested in theoretical aspects of traditional evolutionary processes, including the evolution of sex, how recombination and beneficial mutations affect the fitness dynamics of a population, rigorous characterization of Hill-Robertson effect. Recently, I'm studying the origin and early evolution of COVID-19, the founder effect in COVID-19 outbreaks.

## Education

Year/Period	Degree	Thesis	Institution
09/2015 - 08/2020	Ph.D. in Biochemistry and Molecular Biology	Theoretical Study on Evolution of Mutation Rate in Soma and Germline Cell	School of Life Sciences, Sun Yat-sen University Mentor: Prof. Chung-I Wu
09/2011 - 07/2015	B.S. in Biotechnology	Heat shock impact on the development of <i>dcr-1</i> <sup>RNAi</sup> <i>Drosophila Melanogaster</i>	School of Life Sciences, Sun Yat-sen University

## Professional History

Year/Period	Position	Institution
10/2020 - date	Postdoctoral Research Fellow	School of Life Science, Sun Yat-sen University

## Awards and Other Honors

05/2021	National Postdoctoral Innovative Talents Supporting Program (博士后创新人才支持计划)
12/2017	Third prize of the 14 <sup>th</sup> China Post-Graduate Mathematical Contest in Modeling
08/2012	Outstanding student scholarship, Sun Yat-sen University

## Grants

Year/Period	Project
2021 - 2023	The origin tracing of SARS-CoV-2 and evaluation of epidemic prevention and control strategies based on adaptive evolution theory, National Postdoctoral Innovative Talents Supporting Program (博士后创新人才支持计划), 630K RMB

## Publications <sup>1-9</sup>

- 1 **Ruan, Y.**, Hou, M., Li, J., Song, Y., Wang, H.-Y., He, X., Zeng, H., Lu, J., Wen, H., Chen, C. & Wu, C.-I. One viral sequence for each host? – The neglected within-host diversity as the main stage of SARS-CoV-2 evolution. *bioRxiv*, 2021.2006.2021.449205, doi:10.1101/2021.06.21.449205 (2021).
- 2 **Ruan, Y.**, Luo, Z., Tang, X., Li, G., Wen, H., He, X., Lu, X., Lu, J. & Wu, C.-I. On the founder effect in COVID-19 outbreaks: how many infected travelers may have started them all? *Natl. Sci. Rev.* **8**, nwaa246, doi:10.1093/nsr/nwaa246 (2021).
- 3 **Ruan, Y.**, Wen, H., He, X. & Wu, C.-I. A theoretical exploration of the origin and early evolution of a pandemic. *Sci. Bull.* **66**, 1022-1029, doi:<https://doi.org/10.1016/j.scib.2020.12.020> (2021).
- 4 Wu, C. I., Wen, H., Lu, J., Su, X. D., Hughes, A. C., Zhai, W., Chen, C., Chen, H., Li, M., Song, S., Qian, Z., Wang, Q., Chen, B., Guo, Z., **Ruan, Y.**, Lu, X., Wei, F., Jin, L., Kang, L., Xue, Y., Zhao, G. & Zhang, Y. P. On the origin of SARS-CoV-2-The blind watchmaker argument. *Sci China Life Sci* **64**, 1560-1563, doi:10.1007/s11427-021-1972-1 (2021).
- 5 Zhang, L., Qin, Z., Huang, T., Tam, B., **Ruan, Y.**, Guo, M., Wu, X., Li, J., Zhao, B., Chian, J. S., Wang, X., Wang, L. & Wang, S. M. Prevalence and spectrum of DNA mismatch repair gene variation in the general Chinese population. *J. Med. Genet.*, jmedgenet-2021-107886, doi:10.1136/jmedgenet-2021-107886 (2021).
- 6 Chen, B., Wu, X., **Ruan, Y.**, Zhang, Y., Wen, H. J., Lan, P. & Wu, C.-I. Many are called but few are chosen – Multiple clonal origins greatly elevate the functional heterogeneity of tumors. *bioRxiv*, 2020.2009.2001.277848, doi:10.1101/2020.09.01.277848 (2020).
- 7 Ma, F. Q., Lu, G. A., Chen, Q. J., **Ruan, Y. S.**, Li, X., Lu, X. M. & Li, C. Y. Dynamic global analysis of transcription reveals the role of miRNAs in synergistic stabilization of gene expression. *Sci. Bull.* **65**, 2130-2140, doi:10.1016/j.scib.2020.08.011 (2020).
- 8 **Ruan, Y.**, Wang, H., Chen, B., Wen, H. & Wu, C. I. Mutations Beget More Mutations-Rapid Evolution of Mutation Rate in Response to the Risk of Runaway Accumulation. *Mol. Biol. Evol.* **37**, 1007-1019, doi:10.1093/molbev/msz283 (2020).
- 9 **Ruan, Y.**, Wang, H., Zhang, L., Wen, H. & Wu, C.-I. Sex, fitness decline and recombination – Muller's ratchet vs. Ohta's ratchet. *bioRxiv*, 2020.2008.2006.240713, doi:10.1101/2020.08.06.240713 (2020).

## Academic Presentations

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| 2019-7-22  | <b>Yongsen Ruan</b> , Chung-I Wu. <i>Mutations beget more mutations – The evolution of mutation rate and the runaway accumulation</i> . Oral presentation (OR-051) at the Annual Meeting of the Society for Molecular Biology and Evolution, Manchester, England.                          |
| 2018-07-11 | <b>Yongsen Ruan</b> , Ao Lan, Chung-I Wu. <i>Different types of cell migration during tumor growing process lead to spatial patterns of genetic variation</i> . Poster (POB-086) presentation at the Annual Meeting of the Society for Molecular Biology and Evolution, Pacifico Yokohama, |

Yokohama, Japan.