Rong Ma

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EDUCATION

Ph.D. student in Human Genetics September 2021 – Present
McGill University / Kyoto University

Master of Arts in Biomedical Informatics January 2021
Columbia University

Bachelor of Science in Biochemistry June 2019
McGill University

RESEARCH EXPERIENCE

Bioinformatic Research 10/2021 – 06/2025
Dr. Ian Watson & Dr. Guillaume Bourque's labs
McGill University

Bioinformatic Research 01/2023 – 01/2024
Dr. Tasuku Honjo's lab
Kyoto University

Bioinformatic Research 01/2020 – 04/2021
Dr. Raúl Rabadán's Lab
Columbia University

Bioinformatic Research 06/2019 – 09/2019
Dr. Xiao Feng Dai's Lab
Jiangnan University, China

Bioinformatic Research 10/2017 – 12/2018
Dr. Uri David Akavia's Lab
Mcgill University

WORKING EXPERIENCE

Teaching assistant
New Oriental Education & Technology Group Inc. 07/2016 – 08/2016
Task & Achievement: My duties were teaching students about language exams such as IELTS and helping them to improve English. I received the 'Great Employee' award that year.

TED contributor (Volunteer) 06/2017 – Present
Tasks: Subtitle contributor for TED education videos.

PUBLICATIONS

EPIGENOMICS VOL. 11, NO. 16 | RESEARCH ARTICLE

Epigenetic profiles capturing breast cancer stemness for triple negative breast cancer control

Xiaofeng Dai‡, Rong Ma‡,Xijiang Zhao & Fengfeng Zhou
15 Nov 2019
https://doi.org/10.2217/epi-2019-0266

CONFERENCE PRESENTATIONS

15-minutes Presentation at CCII International Symposium
Title: Characterizing the epigenome of melanoma histological subtypes to reveal insights into immune therapy response
Names of the conference: CCII/CGM International Symposium
Location: Kyoto, Japan
Date: 2023/3/4

5-minutes Rapid-Fire Talk
Title: Characterizing the epigenome of melanoma subtypes to reveal insights into immune therapy response
Names of the conference: RRCancer Biennial Symposium in collaboration with the Quebec Node of the Terry Fox Research Institute and the Quebec Cancer Consortium
Location: Montreal, Canada
Date: 2022/9/23

Poster Presentation
Title: Characterizing the epigenome of melanoma subtypes to reveal insights into immune therapy response
Names of the conference: The Canadian Epigenetics, Environment and Health Research Consortium and International Human Epigenome Consortium Annual Meeting 2022
Location: Montreal, Canada
Date: 2022/10/4

HONORS AND AWARDS

01/Sept/2023	Donner Studentship Award (McGill Goodman Cancer Institute internal award)
10/Nov/2022	Cotutelle Graduate Mobility Award
28/Nov/2022	Grad Excellence Award in Human Genetics
Sept/2014	UKMT Silver Award

Projects Details

1. **The analysis of noncoding regulatory mutations in acute lymphoblastic leukemia (01/2020 – 04/2021)**

   In professor Raúl Rabadán's Lab at Columbia University, my current project is about analyzing the RNA-seq data of point mutation in non-coding regions from acute lymphoblastic leukemia (ALL) patients. The purpose of the project is to discover the potential noncoding regulatory mutations that could induce the development of ALL.

2. **Epigenetic profiles capturing breast cancer stemness for triple negative breast cancer control (06/2019 – 09/2019)**

   This project was completed during my summer holiday in 2019 in Dai Xiaofeng's lab at Jiangnan University. As we know, Triple-negative breast cancers (TNBCs) contain a higher percentage of breast cancer stem cells (BCSCs) than the other subtypes and lack effective yet safe-targeted therapies. We would like to unveil genes relevant to the therapeutic control of breast cancer stemness at the epigenetic level. More details can be found in the paper. I contributed equally to Professor Dai Xiaofeng as the first co-author.

3. **The cancer risks of glucosamine-containing nutritional supplements: a systematic review and meta-analysis (06/2018 – Present)**

   This is a literature review about predicting cancer risks of consuming nutritional supplements through collecting and analyzing data from relevant papers. I participate in the project as the second author and my duty is to read scientific papers and to check data accuracy. Here is the link of the protocol - http://www.crd.york.ac.uk/PROSPERO/display_record.php?ID=CRD42018100510

4. **Design Sato Aptamer (10/2017 – 10/2018)**

   Due to complex environments and many uncertainties in cells, it is difficult to visualize RNA in vivo. However, live-cell RNA imaging is critical to identify the subcellular localization of endogenous mRNA which can answer questions like morphogenesis or even detect the causes of diseases such as fragile X syndrome 7. By now, scientists have developed many techniques that allow people to visualize live-cell RNAs and one of them is based on quencher- and fluorophore-binding Aptamer (Sato Aptamer). However, designing a suitable RNA Aptamer that can bind to the target RNA accurately is time- and labor- consuming. Therefore, writing a reasonable and efficient program to design a suitable Aptamer can benefit many researchers who use this RNA imaging technique.

   I completed the whole project in Professor Uri David Akavia's Lab and constructed a website to present the results.

5. Analyzing readouts of Sanger sequence (01/2018 – 10/2018)

Sanger sequencing is a technique that can identify the sequences of provided unknown DNAs. It is usually used to check the deletion, insertion, or point mutation in specific DNA after CRISPR-Cas9 processing. However, it is difficult to analyze the results of Sanger sequence manually because of a mixture of products (wild type & mutations). In other words, writing a program to decompose the readouts into humanly readable probabilities can benefit researchers significantly. For example, if a researcher aims to see a point mutation in the CRISPR-Cas 9 treated cell and the program predicts that the probability of the desired point mutation is 99.5% from the readouts of the Sanger sequence, it can ensure that the treatment is successful and on- target. Although the website 'Tide and Tider' can achieve the aim generally, it shows some critical drawbacks and limitations.

Our goal is to design a program which can function similarly to the website but without the restrictions. I contributed to the part of the data analysis.

6. Using Protein Localization Studies to Improve Genome-scale Metabolic Models (10/2018 – 06/2019)

The project was designed to improve the human metabolic model (Recon 2.2) by introducing additional information on protein localization. In the original model (Recon 2.2), it does not consider the localization of proteins, and that could give the wrong prediction if the reactants are in different sub- cellular spaces. We combined the information of proteins' localization from various literature and Recon2.2 to provide a model with higher accuracy of prediction. This project was finished in Professor Uri David Akavia's Lab at McGill University. My contributions of the project were writing codes, doing data analysis, and reviewing the draft.

REFERENCES

Dr. Ian Watson, Associate Professor
Department of Biochemistry, McGill University

Dr. Guillaume Bourque, Professor & Head of Bioinformatics
Department of Human Genetics

Raul Rabadan
Columbia University