Meng Luo (骆孟)

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Position: Bioinformatics Engineer

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Summary

I am mostly interested in better understanding the genetic architecture of complex traits by using advanced statistical models and methods based on the quantitative genetic theory, molecular information and bioinformatics technology. I have developed new statistical approaches to use genome-wide SNPs marker data to dissect the genetic architecture of complex traits, e.g. GWAS and predicting unobserved future phenotypes based on genome-wide SNPs information. The developed statistical approaches can be used to analyze any of the health-related traits in humans and many other traits of interest in many species. Currently, I focus on using the new advanced statistical methods combined with bioinformatics technology pinpointing biological mechanisms. e.g. researched 880 rice samples that implemented GWAS for yield-related traits (eQTL(gene regulation) and mGWAS (metabolism)) and genome selection which in multiple environments and four years. And also included mRNA sequencing, lncRNA, circular RNA, and small RNA sequencing, etc. RNA-Seq also provides an affordable approach for gene expression quantification and differential gene expression analysis among groups of samples. It is widely used in disease research and personalized healthcare research which combined high-throughput multi-omics approaches. I have highly motivated computational analyses and tools for mining large scale omics and genetic data for trait lead discovery which is highly desired.

Research Interests: Statistical Genetics; Quantitative Genetics; Bioinformatics; Population Genetics; Genomics

Education

Degree: Master of Biostatistics/Bioinformatics at Yangzhou University

Date of award: June 2018

Title: Iterative screen regression----a new approach of dissecting genetic effects for complex traits

Supervisor: Prof. Shiliang Gu

Degree: Bachelor of Agriculture at Yangzhou University

Date of award: June 2015

Title: Genome-Wide Association Analysis between SNP Markers and Zinc Content in Wheat Grains

Supervisor: Prof. Tao Li and Prof. Shiliang Gu

Work Experiences

Position:

January 2019 - present

Bioinformatics Engineer (Biotech leader manager at Bioinformatics analysis department since Sep, 2019) at Plant and Animal (human) Omics department in Majorbio.

Position Accountabilities:

Compared with microarray analysis, mRNA sequencing (RNA-Seq for Eukaryotes and Prokaryotes) provides a more precise and complete snapshot of the transcriptome and enables the identification of novel transcripts, alternative splicing, and gene fusion events. In addition to mRNA sequencing, it also offers lncRNA, circular RNA, and small RNA sequencing. RNA-Seq also provides an alternative and affordable approach for gene expression quantification and differential gene expression analysis among groups of samples. It is widely used in disease research, drug response research, and personalized healthcare research.

- To ensure the successful completion of the NGS sequencing project. Also including the former responsible.
- Led a team (six members) and assist them to complete the analysis of projects.
- Analyze large scale omics datasets, interpret and communicate analysis results to stakeholders
- Contribute to the design of strategies on validating the function of candidate genes
- Provide consultations on experimental design, analytical methods, computational tools, and data interpretation

Developed Pipeline:

➢ Long non-coding RNA: LncRNA-Pipeline

- ➤ Circular RNA: circRNA-Pipeline
- ➤ Joined the Other developed project: comparative genomics and transcriptomics

Position:

July, 2018 - December, 2018

Bioinformatics Engineer (level 6 in total level 9) at Plant and Animal research department in Majorbio

Position Accountabilities:

With advancements in next-generation sequencing technology, whole-genome resequencing (WGS) has become the most rapid and effective method to unravel, at the genomic level, the underlying mechanisms of species origin, development, growth, and evolution.

- Responsible for the establishment and improvement of NGS sequencing data biological information analysis process.
- Cooperated with a researcher at colleges and research institutes for big projects.

Projects: including 880 rice samples that implemented GWAS (eQTL and mGWAS) and genome prediction in multiples environment and four years project (I finished all analysis that cooperated with prof.Junyi Gong at Zhejiang University), etc.

Developed Pipeline:

- ➤ Genetic mapping: Polymap
- ➤ Bulked Segregant Analysis: MBSA
- ➤ GWAS: MMGWAS-Pipeline
- ➤ DataViz: Circos-Pipeline, LocusZoom-Pipeline, and Others.
- ➤ Others: CRISPR-Pipeline, Env-pipeline, etc.

Teaching Experience:

July 2018 - present

- ➤ Teaching Bioinformatics (Linux, Perl and RNA-seq pipeline) and DataViz Course

Research experience (biostatistics, statistical genetics, and bioinformatics)

Project: Iterative screen regression ---- a new approach of dissecting genetic effects for complex traits

January 2017 - May 2018

- ✓ Iterative Screen Regression Models For Genetic Mapping Studies Of Epistasis Of Quantitative Traits

- ✓ Genetic Prediction Of Complex Traits With Iterative Screen Regression Models

- ✓ An Efficient Iterative Screen Regression Model For Genome-Wide Association Study In Structured Populations

My Supervisor conceived the study. He and I developed the software tool, first coded by M language, which R and python under developing. I designed the experiment and performed all simulations and data analyses. And wrote the manuscript (Unpublished). Then I talked at Yangzhou University and Marjorbio.

Project: Solving Traveling Salesman Problem with a new algorithm

May 2016 - January 2017

- ✓ Solve Traveling Salesman Problem Using EMF-CE Algorithm

My Supervisor conceived the study. He (mostly) and I developed the software tool, only coded by M language. I designed the experiment and performed all simulations and data analyses, and finished to write the manuscript (Unpublished).

Project: Curve and Surface Fitting with Contraction-Expansion Algorithm

March 2015 - May 2016

- ✓ Optimization by A New Improved Contraction Expansion Algorithm And Its Application

My Supervisor conceived the study. He developed the software tool, only coded by M language. I designed the experiment and optimize the selection model (see my blog for details), and also performed all simulations and data analyses (Unpublished). Talk At Yangzhou University.

Project: Bachelor project at Yangzhou University

Sep 2014 - July 2015

- ✓ <u>Effective marker alleles associated with type 2 resistance of wheat to Fusarium head blight infection in fields.</u>
- ✓ Genome-Wide Association Analysis between SNP Markers and Zinc Content in Wheat Grains (Unpublished).

My Supervisor prof.Tao Li conceived the study. Then I both performed all data analyses and finished to write the manuscript.

Teaching Courses and Workshops

Attending Workshops:

- ✓ Onsite: "<u>GWAS Workshop (2016 Wuhan, China)</u>"instructed by <u>Dr.Zhiwu Zhang</u>
- ✓ Onsite: "<u>GS Workshop (2017 Harbin, China)</u>"instructed by <u>Dr.Zhiwu Zhang</u>
- ✓ Onsite: "<u>Bioinformatics Workshop (2016 Yangzhou University, China)</u>"instructed by <u>Dr.Yunchen Gong</u>
- ✓ Onsite: "<u>Principles of Statistical Genomics Workshop (2018 Yangzhou University, China)</u>" Main instructed by <u>Prof.Shizhong Xu</u>

Senior lecturer:

- ✓ <u>Teaching Bioinformatics and R for DataViz courses (Rstats)</u>
- ✓ <u>Talk</u> (presentation)

Technical skills

Programming languages: Skilled in a variety of statistical and bioinformatical programs that included SAS（my first statistics language）, <u>MATLAB</u>, <u>R</u>, <u>Perl</u>, <u>Python</u> and also, shell, awk, and sed. All of the code of the project both pushed to my <u>Github</u>.

Built Website: Web designed which my personal website developed by JavaScript, Node.js, HTML5, CSS, jQuery, Jekyll and Grunt + Gulp.

DataViz ：M and R for DataViz, also using the Gephi and Cytoscape for networking DataViz. Others included Adobe Illustrator CC 2019 and Adobe Photoshop CC 2019 for logo design and optimize the image and MS 2019.

Language：English (IELTS: 6, and now preparing for another IELTS testing); Bouyei language（native language, minority）; Mandarin (score 80 in total 100 at collage); Guizhou dialect.

Operating systems：CentOS 7, Linux Mint and Win10 (Subsystem for Linux).

Hobbies

Movies, biking, table tennis, traveling and photography (Leica D-Lux 7).

Publications

*Co-first Author Publications; #contributed equally to this work

Unpublished:

1, **Meng Luo,** Shiliang Gu. An Efficient Iterative Screen Regression Method for Genome-Wide Association Studies in Structured Populations. 2018.

2, **Meng Luo,** Shiliang Gu. Iterative Screen Regression Models for Genetic Mapping Studies of Epistasis of Quantitative Traits. 2018.

3, **Meng Luo,** Shiliang Gu. Genetic Prediction of Complex Traits with Iterative Screen Regression Models. 2018.

4, **Meng Luo,** Shiliang Gu. Solve traveling salesman problems using the EMF-CE algorithm. Transactions on Evolutionary Computation. (under review).

5**, #LUO Meng,** #ZHANG Ming-Yan, PENG Yong-Xin, GUO Wen-Shan, ZHU Xin-Gai, LI Chun-Yan, BAI Gui-Hua, LI Tao and FENG Chao-Nian. Genome-Wide Association Analysis between SNP Markers and Zinc Content in Wheat

Grains. Acta Agronomica Sinica, (in Chinese and under review). Core Journals!

Published:

1, #Tao Li, #**Meng Luo**, Dadong Zhang, Di Wu, Lei Li, Guihua Bai. Effective marker alleles associated with type 2 resistance of wheat to Fusarium head blight infection in fields. Breeding Science, 2016, 66(3):350-357.

2, *Li Tao, ***Luo Meng**, Qian Dan, Dong JingJing, Gu ShiLiang. Evaluation of Phenotypic Variation of EMS-induced Mutants of Chinese Wheat Landraces Huangfangzhu and Haiyanzhong Resistant to Fusarium Head Blight. Journal of Plant Genetic Resources,2016, doi:10.13430/j.cnki.jpgr.2016.06.018. (In chinese). Core Journals!

3, *Qian Dan, ***Luo Meng**, Dong Jingjing, Li Changcheng, Li Lei, Li Tao. Evaluation of Agronomic Traits and Resistance to Fusarium Head Blight of Ning 7840 and Its Mutants. Journal of Triticeae Crops, 2016, doi:10.7606/j.issn.1009-1041.2016.02.16. (In chinese). Core Journals!

4, #Gong Xuan, **#Luo Meng**, Xiao Tianjing, Cao Jing, Li Lei, Li Tao. Variations in agronomic traits and resistance to Fusarium head blight in wheat mutants. Journal of Yangzhou University (Agricultural and Life Science Edition), 2017, doi: 10.16872/j.cnki.1671-4652.2017.04.011. (In chinese). Core Journals!

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