

Yun YAN

RNA Bioinformatics

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Interview In Person at U.S.: Available

"you shall know the truth and the truth shall set you free"

Research Experience

Computational Biology Center

2013.08–2014.06

Memorial Sloan-Kettering Cancer Center

New York City, U.S

- Research Associate in internationally collaborative project (in progress) for exploring co-transcriptional splicing in *Arabidopsis thaliana* at Prof. Gunnar Räscher's lab.
- Web architect building the Chinese Wiki with cutting-edge Bootstrap3 to make PALMapper, the RNA-seq aligner developed in the lab, more international and friendly access to Chinese users.

"Dragon Star" Program

2012.06–2012.07

Jilin University

Jilin, China

For further professional trainings I selected "Bioinformatics" subject in 2012, trained by Prof. Ting Wang, Washington University, U.S.. The program is fully supported by Chinese Academy of Sciences (CAS), which provides timely and comprehensive training to graduated students on selected research subjects.

Unit of Synthetic Biology (USB)

2011.02–2011.09

Sci.&Tech. Department, Beijing Genomics Institute (BGI)

Shenzhen, China

Chief tech executive, greatly contributed to new-born team construction, developed stable and rapid bench-work platform when collaborated with BIOFAB to work on C.dog (Central Dogma on *E.coli*) project. At the early stage, I also contributed to collaboration with John Hopkins University to work on Yeast 2.0 project.

Cancer Research Group

2010.10–2011.02

Sci.&Tech. Department, Beijing Genomics Institute (BGI)

Shenzhen, China

Bioinformatics Intern, and my bioinformatics career launched as a student of WHU-BGI two-sides Educational Collaboration. I focused on detecting InDel (insertion /deletion) and Structural Variances when participating in lung cancer researches.

Publication

Xiaorong Zhang, Xinxin Zuo, Bo Yang, Zongran Li, Yuanchao Xue, Yu Zhou, Jie Huang, Xiaolu Zhao, Jie Zhou, **Yun Yan**, Huiqiong Zhang, Peipei Guo, Hui Sun, Lin Guo, Yi Zhang, Xiang-Dong Fu*. *MicroRNA directly enhances mitochondrial translation during muscle differentiation*. Cell 158, 607–619 (2014).

Public Resources Under Maintain

- CLIP-seq Toolkit implemented in R/Perl – see CLIPseqToolkit
- Figure library dependently produced by R – see aRtist
- On-line toolkit for data mining in Chemoinformatics – see Minery
- RNA-seq aligner PALMapper Chinese Manual – see PALMapper_zh-cn
- My open-source book: "A Little Book about CLIP-seq" – see here

Master Thesis

Title: Genome-wide Identify Distance Effect of RNA Binding Protein PTB on RNA Splicing

Supervisors: Professor Xiang-dong Fu, UCSD

Description: "**Humid**" lab approaches, molecular biology experiments (wet) integrated with next-generation sequencing analysis (dry), were used in my thesis for hypothesis validation.

- Uncovered the distance effect that cassette or alternative exon would be less inhibited spliced-out with gradient increased distance to binding site of Polypyrimidine Tract Binding protein (PTB) using RNA-seq and Cross-Linking Immunoprecipitation sequencing (CLIP-seq) approaches.
- Independently developed R nested with Perl toolkit dedicated to CLIP-seq analysis pipeline and deployed at GitHub friendly to reproducible research.

"Humid" Skills

Benchwork –Typical Molecular Biology Experiments.....

Plasmids Sub-clone, PCR, Transformation, Human Cell Culturing, Transfection, RNA exaction.

Bioinformatics, Statistics, Machine Learning.....

Skillful at NGS (RNA-seq & CLIP-seq) analysis; Basic implement experience in HMM, SVM.

Programming Language & Experience Years/Months.....

Advanced: **R** (3y), **Perl** (3y) ; Mid: **Python** (~1y), **Bash** (1y); New: Octave, C++

Bioinformatics Tag Clouds

- Bowtie2, STAR, TopHat, BEDTOOLS, Bioconductor, BioPerl, Pysam
- Rstudio, Vim, SublimeText, Xcode, Bio-Linux6, GitHub
- ggplot2, knitr, Circos, UCSC Genome Browser, IGV
- T_EX, Markdown, HTML5, CSS3, Bootstrap3

Education

MScRes (with honor), Biochemistry and Molecular Biology

2011.09–2013.06

College of Life Sciences, Wuhan University

Wuhan, China

- Cumulative GPA: 3.47/4.00 (with full scholarship)

Graduate Student Summer School

2012.08–2012.09

Helsinki University

Helsinki, Finland

Visiting graduate student (only 10 selected out of the entire grade) attended Summer School at Institute of Biotechnology, Helsinki University, fully supported by Biocenter Finland, Helsinki University, Wuhan University tri-sides collaboration, welcomed by Prof. Erkki Raulo, Helsinki University.

B.S., Biology Base Class

2007.09–2011.06

College of Life Sciences, Wuhan University

Wuhan, China

- Last Year at campus GPA: 3.48/4.00 (with Wuhan University Scholarship); Cumulative GPA: 3.22/4.00
- Thesis: Preliminary Researches in Central Dogma of *E.coli*. (International collaboration of BGI and BIOFAB)

My MOOC

- StatLearning: Statistical Learning, by Trevor Hastie & Rob Tibshirani – Ongoing
- Machine Learning, by Andrew Ng , 2013.10 – Earned 98.2/100
- Computing for Data Analysis, by Roger Peng, 2013.04 – Earned 89/100