

# LIJIA YU

## Currently searching for a PhD student position

Please note that this is a *real* resume, and I'm really looking for a PhD student position at the moment. I made this resume because Yihui asked me if I'd like to test the **pagedown** package with my resume. If you are interested in my background and skills, please feel free to contact me.

## EDUCATION

- 2010 • **Beijing University of Chemical Technology**  
B.S. in Information and Computing Sciences 📍 Beijing, China
- Thesis: Dyadic wavelet and its application in edge detection
- 2014 • **University of Chinese Academy of Sciences**  
M.S. in Bioinformatics 📍 Beijing, China
- Thesis: A multi-omics study for intra-individual divergence of the distributions between mRNA isoforms in mammals

## RESEARCH EXPERIENCE

- 2011 | 2014 • **Graduate Research Assistant**  
Beijing Institute of Genomics, Chinese Academy of Sciences 📍 Beijing, China
- Performed computational biology research towards understanding regulation of alternative splicing in human and mouse transcriptome.
  - Found EGFR pathway related mutations, aimed to understand the impacts of cancer mutations on EGFR signaling pathway.
- 2015 | 2016 • **Bioinformatician**  
My Health Gene Technology Co., Ltd. 📍 Beijing, China
- Investigated how cancer cells spread to other parts of the body at the single cell level.
- 2016 | 2018 • **Visiting Scientist**  
University of Alabama at Birmingham 📍 AL, USA
- Investigated the role of mitochondria in development of cancer.
  - Investigated the evolution of genome architecture and its role in important evolutionary events.
  - Detected thrombotic thrombocytopenic purpura related mutations in multiple patients' blood genome.



## CONTACT INFO

✉ [lijia.yu@outlook.com](mailto:lijia.yu@outlook.com)

🌐 [github.com/yulijia](https://github.com/yulijia)

☎ +1 000-000-0000

For more information, please contact me via email.

## SKILLS

Experienced in statistical analysis, statistical learning models, and optimization methods.



Full experience with next generation sequencing data analysis.

Highly skilled in R, Bash, Perl, Python, LaTeX



*This resume was made with the R package **pagedown**.*

*Last updated on 2021-09-13.*


## PROFESSIONAL EXPERIENCE

- 2014 • **Data Scientist, intern**  
SupStat Inc.  Beijing, China
- Taught R language to beginners.
  - Wrote Shiny app demos.
  - Converted statistical tutorials from SPSS to R language.
- 2015 • **Bioinformatician**  
My Health Gene Technology Co., Ltd.  Beijing, China
- 2016
- Analyzed whole-exome sequencing data.
  - Studied tumor metastasis and wrote research reports.
  - Wrote analysis pipelines of ChIP-seq, single cell DNA-seq and single cell RNA-seq.
  - Also did case studies to identify the genetic defect causing rare disease.

## TEACHING EXPERIENCE

- 2014 • **Introduction to R Language for Beginners.**  
Instructor of R and Data Mining Training Courses at SupStat Inc.  Beijing, China
- 2016 • **Computational Biology and Bioinformatics.**  
Teaching assistant of GBS CB2-201 courses at UAB  AL, USA
- 2017

## SELECTED PUBLICATIONS AND POSTERS

- 2014 • **Genetic and epigenetic signals are found predictive to the distribution of intra-individual divergence of alternative splicing.**  
Poster for 2013 International Conference of Genomics  Qingdao, China
- Yu L, Chen B, Zhang Z.
- 2016 • **ESCRT-0 complex modulates Rbf mutant cell survival by regulating Rhomboid endosomal trafficking and EGFR signaling.**  
J Cell Sci. 2016 May 15;129(10):2075-84.  
Sheng Z, Yu L, Zhang T, Pei X, Li X, Zhang Z and Du W.