ANTONIO PÁEZ

Professor

🎓 EDUCATION

Beijing University of Chemical Technology
2010

B.S. in Information and Computing Sciences 📍 Beijing, China

Thesis: Dyadic wavelet and its application in edge detection

University of Chinese Academy of Sciences
2014

M.S. in Bioinformatics 📍 Beijing, China

Thesis: A multi-omics study for intra-individual divergence of the distributions between mRNA isoforms in mammals
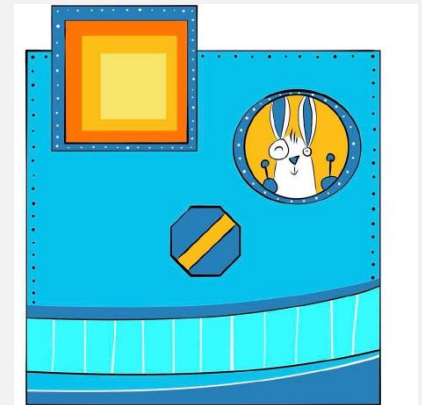
💻 RESEARCH EXPERIENCE

Graduate Research Assistant
2011
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2014

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.

Bioinformatican
2015
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2016

My Health Gene Technology Co., Ltd. 📍 Beijing, China

· Investigated how cancer cells spread to other parts of the body at the single cell level.

Visiting Scientist
2016
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2018

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 mutiple patients' blood genome.

💼 PROFESSIONAL EXPERIENCE

Data Scientist, intern
2014

SupStat Inc. 📍 Beijing, China

· Taught R language to beginners.
· Wrote Shiny app demos.
· Converted statistical tutorials from SPSS to R language.

CONTACT INFO

✉ paezha@mcmaster.ca

 github.com/paezha

📞 +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

2015
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2016

● **Bioinformatician**
My Health Gene Technology Co., Ltd. 📍 Beijing, China
- Analyzed whole-exome sequencing data.
- Wrote analysis pipelines of ChIP-seq, single cell DNA-seq and single cell RNA-seq.
- Studied tumor metastasis and wrote research reports.
- 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
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2017

● **Computational Biology and Bioinformatics.**
Teaching assistant of GBS CB2-201 courses at UAB 📍 AL, USA

📄 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.