# Douglas C. Wu
*Bioinformatics Scientist*

- +1-310-658-1540
- /wckdouglas
- @wckdouglas
- wckdouglas.github.io
- wckdouglas
- wckdouglas@gmail.com

## ⊙ Professional summary

Highly-motivated fast learner with > 7 years of bioinformatics consultation and research experiences in next-generation sequencing analysis. Collaborative and innovative with strong communication and interpersonal abilities. Staying up-to-date with industrial trends in sequencing and programming technologies. Comfortable with working in a fast-paced environment.

## ⚙ Skills

**Bioinformatics** Multiplex PCR primer design, WGS-seq, Targeted DNA-seq, RNA-seq, 16S-seq, methyl-seq, experimental design, familiar with public -omics databases and their APIs, such as UCSC and Ensembl

**Coding** Python, R, Bash, MySQL, C/C++, Matlab, LaTeX

**Computing** Familiar with Amazon web service and High performance computing, web development

**Deep learning framework** PyTorch, Keras/Tensorflow

**Experimental** Cell-free DNA and RNA, RNA-seq, DNA-seq, Methyl-seq, Molecular diagostics, Liquid biopsies, Live cell imaging

**Language** English, Chinese, Cantonese

## 🎓 Education

**Univeristy of Texas at Austin**                                         2013 – 2019
*Ph.D specialized in Bioinformatics*                                       *Austin, TX*

**University of Illinois at Urbana Champaign**                            2009 – 2013
*BS in Biochemistry*                                                       *Champaign, IL*

## ◔ Experience

**QIAGEN**                                                         July 2019 – Present
*Bioinformatics Scientist*                                                 *Frederick, MD*

> Founding member of the bioinformatics group in QIAGEN Genomics Services
> Bioinformatics consultation for different sizes of external projects with revenue ranging from $0.1 to 5 million USD
> Expert in data visualization and progress reporting presentations for academic, pharmaceutical and biotech researcher customers
> Increased revenue by enabling analyses of larger projects by developing internal data pipelines to streamline and scale up NGS data processing
> Expanded business scope by designing and integrating R&D NGS products into customer projects
> Provided bioinformatics training and worked directly with internal sales team and field scientists to improve business development processes
> Collaborated with software engineers and IT teams to setup local servers for data analysis and deliveries
> Worked with global product managers to adjust cost calculations to provide more competitive service rates
> Built internal web tools using RESTful API to automate data delivery for wetlab scientist

**University of Texas at Austin**                                   Sep. 2013 – May. 2019
*Graduate Research Assistant*                                              *Austin, TX*

> Developed streamlined whole transcriptome RNA-seq, small RNA-seq and single-stranded DNA-seq with a novel reverse transcriptase
> Characterized human plasma genetic materials using cell-free DNA and RNA-seq
> Devised statistical and quantitative metrics for benchmarking methods in collecting and analyzing terabytes of genomic data