Douglas C. Wu

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PROFESSIONAL SUMMARY

Highly-motivated fast learner with > 5 years of quantitative and computational research experiences in next-generation sequencing method developments. 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.

EDUCATION

UNIVERSITY OF TEXAS AT AUSTIN
PhD, specialized in Bioinformatics
2013 - 2019 | Austin, TX
Advisor: Alan M. Lambowitz
University Graduate Continuing Fellowships (2017-2018)

UNIVERSITY OF ILLINOIS AT URBANA CHAMPAIGN
BS in Biochemistry
May 2013 | Champaign, IL
Biochemistry High Distinction Award
Dean List (Fall 2010, Spring 2011)

LINKS

Github:// **wckdouglas**
LinkedIn:// **wckdouglas**
Twitter:// **@wckdouglas**
Google Scholar:// **Douglas C. Wu**

SKILLS

PROGRAMMING
Ordered by proficiency
• Python • R • Bash
• Matlab • Octave • LaTeX
• C/C++ • MySQL
• Experienced with Scikit-learn and SciPy ecosystem
• Deep learning framework: Pytorch, Keras/Tensorflow
• Familiar with -omics databases and their APIs
• High-performance computing

EXPERIMENTAL
• Cell-free DNA-seq/RNA-seq/bisulfite-seq
• Molecular diagnostics
• Liquid biopsies
• Live cell imaging

OPEN SOURCE PROJECTS

MAINTAINER
• **wckdouglas/sequencing_tools** (python package)
• **wckdouglas/deep_cfNA** (python package)

CONTRIBUTOR
• **pysam-developers/pysam** (python package)
• **jdidion/atropos** (python package)
• **cran/colorspace** (R shiny package)

RESEARCH EXPERIENCE

METHOD DEVELOPMENTS IN HIGH-THROUGHPUT SEQUENCING | Graduate Research Assistant
Dec 2013 – present | University of Texas at Austin, Austin, TX

- Developed streamlined RNA-seq and ssDNA-seq methods using thermostable group II intron reverse transcriptase
- Developed and deployed large scale simulation and data analytic tools (python and R) to identify biases in genomic data collections
- Built software to extract information from genomic data for training and predicting biologically-relevant signatures in existing genomic datasets
- Devised statistical and quantitative metrics for benchmarking methods in collecting and analyzing terabytes of genomic data
- Developed data pipeline for reproducible data analysis
- Worked with Center for Quantitative Biology to build and manage remote scalable storage server

MECHANOBIOLOGY | Research Assistant/Rotation student
Feb 2011 – Feb 2014 | University of Illinois at Urbana Champaign, Champaign, IL & University of Texas at Austin, Austin, TX

- Designed and deployed computer simulations to quantify magnetic-induced force that directs embryoid bodies into mesodermal lineages
- Identified force-induced biochemical changes in embryonic stem cells and tumorigenic cells with live-cell imaging
- Identified biophysical regulations during the formation of organized germ layers from a single mouse embryonic stem cell

RECENT PUBLICATIONS

- Xu H*, Yao J*, Wu DC* and Lambowitz AM (2018). Improved TGIRT-seq methods for comprehensive transcriptome profiling with decreased adapter dimer formation and bias correction. Scientific Reports. 9:7953 (*contributed equally).
- Wu DC, Yao J, Ho KS, Lambowitz AM and Wilke CO (2018). Limitations of alignment-free tools in total RNA-seq quantification. BMC Genomics. 19:510.
- Wu DC and Lambowitz AM (2017). Facile single-stranded DNA sequencing of human plasma DNA via thermostable group II intron reverse transcriptase template switching. Scientific Reports. 7:8421.