

Cheng Lyu

(314) 520-8878 | cheng.lyu2@emory.edu
Atlanta, GA

EDUCATION

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| Emory University; Atlanta, GA | Aug 2018-Present |
| <ul style="list-style-type: none">• Doctor of Philosophy in <i>Biostatistics</i>, Department of Biostatistics and Bioinformatics | |
| Washington University in St. Louis; St. Louis, MO | Jun 2016-Dec 2017 |
| <ul style="list-style-type: none">• Master of Science in <i>Biostatistics</i>, Division of Biostatistics | |
| Nanjing University; Nanjing, China | Sep 2012-Jun 2016 |
| <ul style="list-style-type: none">• Bachelor of Science in <i>Computational and Applied Mathematics</i>, minor in <i>Statistics</i>, Department of Math• Undergraduate thesis: <i>Simulation of Epidemic Spread based on Branching Process</i> | |

PROFESSIONAL EXPERIENCE

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| Bioinformatics Research Core, Center of Regenerative Medicine,
Department of Developmental Biology, Washington University in St. Louis | St. Louis, MO |
| Bioinformaticist | Jan 2018-Jul 2018 |

RESEARCH EXPERIENCE

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| Division of Biology & Biomedical Sciences, Washington University in St. Louis | St. Louis, MO |
| Research Assistant | Sep 2016-Jan 2018 |

Principal Investigator: Bo Zhang, Ph.D., Ting Wang, Ph.D.

- Designed and constructed a quality control and analysis pipeline of ATAC-seq and RNA-seq data for TaRGET II consortium funded by NIEHS, taking charge of R scripts, python scripts and Dockerfile.
- Evaluated the epigenetic modification which affects STAT1 binding to genomic DNA; performed differential analysis to RNA-seq and ChIP-seq data between cancer cells and normal cells; discovered the dependent relationship between genomic DNA methylation and STAT1-responses immune genes in PBMC.
- Assessed the impact of osteoarthritis on the cartilage by comparing gene transcripts and biological processes in the cartilage, and the batch effects of patients' age, sex and BMI.
- Investigated the role of transposable elements in early embryo development of mouse, and compared the difference among intestine, liver, lung and stomach, as well as the difference among forebrain, midbrain and hindbrain.

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| Division of Public Health Sciences, Washington University in St. Louis | St. Louis, MO |
| Research Assistant | Nov 2016-Jul 2018 |

Supervisor: Esther Lu (Jingxia Liu), Ph.D.

- Proposed statistical discordancy test based on right-truncated gamma distribution of length of hospital stay data; performed Monte Carlo simulation study and power analysis under slippage alternative hypothesis; applied our method to length of stay of the adult patients with influenza infection.
- Proposed sample size calculation method for stepped wedge designs using a generalized estimating equation; reconstructed the treatment effect estimator in GEE model.

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| Division of Biology & Biomedical Sciences, Washington University in St. Louis | St. Louis, MO |
| Statistical Analyst | May 2017-Jan 2018 |

Principal Investigator: Tim R. Peterson, Ph.D.

- Identified the gene *ATRAID* as required for the effects of nitrogen-containing bisphosphonates on bone; investigated the effects of genes on phenotypes and their contributions to disease susceptibility, including myeloma, breast cancer and osteoporosis, in the presence of N-BPs.
- Compared gene ontologies between genes identified respectively by in-vitro and in-vivo experiments; discovered genes identified in screening with N-BPs that are also variant in people with altered drug responses to N-BPs; clustered orphan genes by genetic interactions with other well-known genes.

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SUBMITTED PUBLICATIONS

- Lauren E. Surface, Jiwoong Park, Sandeep Kumar, Damon T. Burrow, **Cheng Lyu**, ..., Erin K. O'Shea*, Timothy R. Peterson*. *ATRAID*, a genetic factor that regulates the clinical action of nitrogen-containing bisphosphonates on bone. (Submitted to *Nature Communication*. Available on [bioRxiv](#).)
- Jingxia Liu, **Cheng Lyu**, José E. Hagan, Steven J. Lawrence. Outlier detection of length of hospital stay. (Submitted to *Journal of the Royal Statistical Society: Series C Applied Statistics*.)
- Jingxia Liu, **Cheng Lyu**, Aimee S. James, and Graham A. Colditz. Sample size calculation using generalized estimating equation models in stepped wedge designs. (In preparation.)

AWARDS

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| • People's Scholarship; Nanjing University, China | 2013-2015 |
| • WU Scholarship and Grants; Washington University in St. Louis | 2016-2017 |

SKILLS AND COURSES

- Coding Languages: R (3 years), Shell Script (3 years), Python (3 years), SAS (2 years), C++ (2 years), MATLAB (2 years), SQL (1 years).
- Highlighted courses: Mathematical Analysis, Numerical Analysis, Higher Algebra, Abstract Algebra, Probabilities, Discrete Mathematics, Introduction to Database, Computer Programming, Statistical computation, Bioinformatics, Biostatistics, Advanced Linear Statistical Models, Data Mining, Machine Learning, Biostatistical Ethics, Survival Analysis, Clinical Study Design.