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## **Publications**

**K. Choi**, N. Raghupathy, G.A. Churchill, 2019. “A Bayesian mixture model for the analysis of allelic expression in single cells.” **Nature Communications**, 10(5188)  
doi:10.1038/s41467-019-13099-0.

C. Baker, M. Walker, S. Arat, G. Ananda, P. Petkova, N. Powers, H. Tian, C. Spruce, B. Ji, D. Rausch, **K. Choi**, P. Petkov, G. Carter, K. Paigen, 2019. Tissue-Specific Trans Regulation of the Mouse Epigenome. **Genetics**, 211(3), pp. 831-845.

N. Raghupathy, **K. Choi**, M.J. Vincent, G.L. Beane, K.S. Sheppard, S.C. Munger, R. Korstanje, F. Pardo-Manuel de Villena, and G.A. Churchill, 2018. Hierarchical Analysis of Multi-mapping RNA-seq Reads Improves the Accuracy of Allele-specific Expression. **Bioinformatics**, 34(13), pp. 2177–2184 (**Joint First Author**)

J.M. Chick, S.C. Munger, ... , **K. Choi**, ... , G.A. Churchill, and S.P. Gygi, 2016. Defining the consequences of genetic variation on a proteome-wide scale. **Nature**, 534(7608), pp.500-505.

H. Zheng, ... , **K. Choi**, ... , F. Rivadeneira, and J.B. Richards, 2015. Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. **Nature**, 526(7571), pp.112-117.

C.L. Baker, S. Kajita, M. Walker, ... , **K. Choi**, ... , K. Paigen, 2015. PRDM9 drives evolutionary erosion of hotspots in *Mus musculus* through haplotype-specific initiation of meiotic recombination. **PLoS Genetics**, 11(1), e1004916.

M. Walker, T. Billings, C.L. Baker, ... , **K. Choi**, ... , M.A. Handel, and K. Paigen, 2015. Affinity-seq detects genome-wide PRDM9 binding sites and reveals the impact of prior chromatin modifications on mammalian recombination hotspot usage. **Epigenetics & Chromatin**, 8(1), p.31.

J.P. Kemp, C. Medina-Gomez, ... , **K. Choi**, ... , F. Rivadeneira, and D.M. Evans, 2014. Phenotypic dissection of bone mineral density reveals skeletal site specificity and facilitates the identification of novel loci in the genetic regulation of bone mass attainment. **PLoS Genetics**, 10(6), p.e1004423.

S.C. Munger, N. Raghupathy, **K. Choi**, ... , E.J. Chesler, and G.A. Churchill, 2014. RNA-seq alignment to individualized genomes improves transcript abundance estimates in multiparent populations. **Genetics**, 198(1), pp.59-73.

S.M. Gomez, **K. Choi**, Y. Wu, 2014. Prediction of Protein-Protein Interaction Networks. **Current Protocols in Bioinformatics**, pp. 8.2.1-8.2.14.

**K. Choi**, S.M. Gomez, 2009. Comparison of phylogenetic trees through alignment of embedded evolutionary distances. **BMC bioinformatics**, 10(1), 423.

### **Manuscripts in review**

D.A. Skelly, A. Czechanski, C. Byers, S. Aydin, C. Spruce, C. Olivier, **K. Choi**, D.M. Gatti, N. Raghupathy, A. Stanton, M. Vincent, S. Dion, I. Greenstein, M. Pankratz, D.K. Porter, W. Martin, W. Qin, A.H. Harrill, T. Choi, G.A. Churchill, S.C. Munger, C.L. Baker, L.G. Reinholdt. "Genetic variation influences pluripotent ground state stability in mouse embryonic stem cells through a hierarchy of molecular phenotypes." bioRxiv. doi: <https://doi.org/10.1101/552059>. 2019

D.M. Gatti, P. Simecek, L. Somes, C.T. Jeffery, M.J. Vincent, **K. Choi**, X. Chen, G.A. Churchill, K.L. Svenson. "The Effects of Sex and Diet on Physiology and Liver Gene Expression in Diversity Outbred Mice." bioRxiv. doi: <https://doi.org/10.1101/098657>. 2017

### **Manuscripts in preparation**

**K. Choi**, Y. Chen, D.A. Skelly, G.A. Churchill. "Bayesian model selection approach for detecting zero-inflated genes in droplet-based single-cell RNA sequencing data."

**K. Choi**, H. He, D.M. Gatti, N. Raghupathy, V.M. Philip, S.C. Munger, E.J. Chesler, G.A. Churchill. "Genotype-free genome reconstruction of multi-parental population models by RNA sequencing data"

**K. Choi**, M.J. Vincent, G.A. Churchill "g2gtools: A toolset for creation of custom diploid genomes and transcriptomes for allele-aware analysis of next-generation sequencing data."

**K. Choi**, M.J. Vincent, G.A. Churchill. "alnTools: A toolset for pre-processing bulk and single-cell read alignments for efficient inventory and downstream computations."

**K. Choi**, M.A. Hibbs, K.L. Shultz, D. Godfrey, G.A. Churchill, C. Ackert-Bicknell. "Osteoblast development is driven by trans-acting regulations."

## Open Source Software Packages Developed

**g2gtools**: A toolset for creation of custom diploid genomes and transcriptomes for allele-aware analysis of next-generation sequencing data. <http://churchill-lab.github.io/g2gtools/#overview> (version 0.2.3)

**alntools**: A toolset for pre-processing bulk and single-cell read alignments for efficient inventory and downstream computations. <https://churchill-lab.github.io/alntools/> (version 0.1.1)

**kallisto-align**: A toolset for encoding kallisto pseudo-alignments as an alignment incidence matrix. <https://churchill-lab.github.io/kallisto-align/> (version 0.1.0)

**EMASE**: Expectation-Maximization algorithm for Allele-Specific Expression. <https://github.com/churchill-lab/emase> (version 0.10.11)

**EMASE-Zero**: C++ implementation of EMASE algorithm. <https://churchill-lab.github.io/emase-zero/> (version 0.3.0)

**GBRS**: Genotype-free genome reconstruction of multi-parental population models by RNA sequencing data. <http://churchill-lab.github.io/gbrs/> (version 0.1.5)

**scBASE**: Zero-and-one inflated model for estimating allelic proportion from scRNA-seq data. <https://churchill-lab.github.io/scBASE/> (version 0.1.1)

**scRATE**: Bayesian model selection approach for detecting zero-inflated genes in droplet-based single-cell RNA sequencing data. <https://github.com/churchill-lab/scRATE> (version 0.1.0)

## Platform Presentations

**K. Choi**, Y. Chen, D.A. Skelly, G.A. Churchill. "Model selection-based scRNA-seq quantitation algorithm that controls overfitting and unwarranted imputation of technical zeros." The annual meeting of the American Society of Human Genetics, Houston, TX. October 15-19, 2019.

**K. Choi**, D.A. Skelly, G.A. Churchill. "A new analytic pipeline that leverages multi-mapping reads for the quantitation of gene expression from droplet single-cell RNA sequencing data". Algorithms and Models for Single-Cell Genomics Annual Workshop, Irvine, CA. June 6-7, 2019.

**K. Choi**, D. Gatti, N. Raghupathy, P. Simacek. “Advanced Mouse Genetics: Diversity Outcross”. International Behavioural and Neural Genetics Society Annual meeting, Bar Harbor, ME, May 12-17, 2016.

**K. Choi**, D.M. Gatti, N. Raghupathy, S.C. Munger, G.A. Churchill. “Genotype-free genome reconstruction by RNA-seq”. Complex Trait Community 14th annual meeting, Portland, OR, June 8-11, 2015.

**K. Choi**, N. Raghupathy, S.C. Munger, G.A. Churchill. “PopulASE: Simultaneous Estimation of strain-, isoform-, and allele-specific expression. The 28th International Mammalian Genome Conference, Bar Harbor, ME, October 26-29, 2014.

**K. Choi**, K. Shultz, ..., C. Ackert-Bicknell. “Identifying Significant Molecular Events in Osteoblast Development by RNA-seq Time Course Analysis”. The 40th Annual Maine Biological and Medical Sciences Symposium, April 12-13, 2013.

**K. Choi** and S.M. Gomez SM, “A New Tool for Phylogeny Comparison Based on Multidimensional Scaling and Procrustes Analysis.” Theoretical & Systems Biology Seminar, UNC-CH.

## **Fellowship**

[2013-2015] TJL Fellowship, The Jackson Laboratory

[2005-2006] Bioinformatics and Computational Biology Fellowship, UNC-CH

## **Teaching**

N. Raghupathy, **K. Choi**. “RNA-seq: From study design to differential expression”. The Short Course on Systems Genetics, The Jackson Laboratory. Sep. 27-Oct. 3, 2015.

N. Raghupathy, **K. Choi**, P. Simacek. “Lab 2: RNA sequencing analysis”: From study design to differential expression”. The Short Course on Systems Genetics, The Jackson Laboratory. Sep. 27-Oct. 3, 2015.

N. Raghupathy, **K. Choi**, D.M. Gatti. “WORKSHOP: Gene Expression Analysis and QTL Mapping 1 and 2”. The Short Course on the Genetics of Addiction, The Jackson Laboratory. Aug. 24-29, 2015.

**K. Choi**, D. Hinerfeld, N. Raghupathy. "RNA-seq library preparation and data analysis". Workshop on Modern Approaches to High Throughput Sequencing, The Jackson Laboratory. Oct. 14-18, 2014.

**K. Choi**, "Genotyping by RNA sequencing data". The Short Course on Systems Genetics, The Jackson Laboratory. Sep. 27-Oct. 4, 2014.

S.C. Munger, N. Raghupathy, **K. Choi**. "Lab 5: RNA-seq". The Short Course on Systems Genetics, The Jackson Laboratory. Sep. 27-Oct. 4, 2014.

S.C. Munger, N. Raghupathy, **K. Choi**. "RNA-seq: From study design to differential expression". The Short Course on Systems Genetics, The Jackson Laboratory. Sep. 8-14, 2013.

**K. Choi**. "Introduction to Programming (Java)." Department of Computer Science, UNC-CH. I was in charge of teaching the intro programming course (COMP110-001) for a full **Summer 2009 semester**. The course is designed to lead students to use/make computer programs for solving research problems in their own academic field. Fundamental programming concepts (including object-oriented programming paradigm) and algorithm design skills have been covered.

## Education and Professional Experience

[2015-present] Research Scientist, **The Jackson Laboratory**, Bar Harbor, ME.

[2011-2015] Postdoctoral Associate, **The Jackson Laboratory**, Bar Harbor, ME.

[2005-2011] **Ph.D.**, Computer Science, **UNC, Chapel Hill**, NC.

[2003-2005] **M.S.**, Computer Science (Minor in Statistics), **NC State University**, Raleigh, NC.

[2001-2003] Non-degree undergraduate program (Computer Science), **University of Illinois, Urbana-Champaign**, IL.

[1994-2000] Assistant Manager, Choong-Ang Research Center, **Hanwha Corp.**, Inchon, South Korea.

[1994] Undergraduate Research Assistant, **Korea Institute of Science & Technology (KIST)**: Functional Polymer Lab, Seoul, Korea.

[1990-1994] B.S., Chemical Engineering, **Seoul National University**, Korea

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