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Education

[2011-2015] Postdoctoral Associate, The Jackson Laboratory
[2005-2011] Ph.D., Computer Science, UNC at Chapel Hill
[2003-2005] M.S., Computer Science (Minor in Statistics), NC State University
[2001-2003] Non-degree undergraduate program in Computer Science, University of Illinois at Urbana-Champaign
[1990-1994] B.S., Chemical Engineering, Seoul National University, Korea

Publications

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**. (**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.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 098657. 2017

Manuscripts in preparation

K. Choi, N. Raghupathy, S.C. Munger, G.A. Churchill. "Combining information across cells improves estimation of allele-specific and total gene expression for single-cell RNA Sequencing data."

K. Choi, N. Raghupathy, S.C. Munger, G.A. Churchill. "GBRS: Genotype-free genome reconstruction using RNA-Seq data derived from multiparental population models"

K. Choi, M.J. Vincent, G.A. Churchill "g2gtools: A versatile tools for creation and comparison of custom diploid genomes."

K. Choi, M.J. Vincent, G.A. Churchill. "alntools: A versatile tools for pre-processing read alignment files for efficient downstream computation and storage."

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 or Supervised

g2gtools: A set of tools for creation of custom genomes and genome-to-genome coordinate conversion. <http://churchill-lab.github.io/g2gtools/#overview> (version 0.2)

alnTools: A set of tools for pre-processing read alignment files (bam, maf, psix) for efficient downstream computation and storage. <https://churchill-lab.github.io/alnTools/> (version 0.1.0)

kallisto-align: A tool for exporting kallisto pseudo-alignments as a compressed three-dimensional incident 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. <https://churchill-lab.github.io/emase-zero/> (version 0.1.0)

GBRS: Genotype-free genome reconstruction using RNA-Seq data derived from multiparental population models. <http://churchill-lab.github.io/gbrs/> (version 0.1.5)

scBASE: Implementation of hierarchical mixture model for allele-specific expression from single-cell RNA-Seq data (Soon to be released)

Platform Presentations

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. “PopuIASE: 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.

Posters

D.A. Skelly, N. Raghupathy, **K. Choi**, A. Srivastava, G.A. Churchill. "Examining age, tissue, and genetic effects on RNA splicing with allele-specific resolution in a diverse mouse population". The 67th Annual Meeting of the American Society of Human Genetics, Orlando, FL, October 17-21, 2017.

K. Choi, A. Srivastava, R. Korstanje, G.A. Churchill. "Accurate quantification of allele-specific methylation from genetically diverse population". The 67th Annual Meeting of the American Society of Human Genetics, Orlando, FL, October 17-21, 2017.

R. Maynard, M. Doolittle, M. Beltejar, **K. Choi**, C. Ackert-Bicknell. "Establishing the functional role of Cped1 in the osteoblast". 2017 Annual Meeting of the American Society for Bone and Mineral Research, Denver, Co, September 8-11, 2017.

K. Choi, N. Raghupathy, S.C. Munger, G.A. Churchill. "Allele-specific expression from single-cell RNA-Seq data". The 66th Annual Meeting of the American Society of Human Genetics, Vancouver, BC, Canada, October 18-22, 2016.

S.C. Munger, J. Chick, P. Simacek, **K. Choi**, ..., S. Gygi, G.A. Churchill. "Conserved and tissue-specific effects of natural genetic variation on transcript and protein abundance". The 66th Annual Meeting of the American Society of Human Genetics, Vancouver, BC, Canada, October 18-22, 2016.

R.D. Maynard, F. Rivadeneira, C. Medina-Gomez, **K. Choi**, C. L Ackert-Bicknell. "Functional validation of a key bone mineral density locus determined by genome-wide association studies". 2016 Annual Meeting of the American Society for Bone and Mineral Research, Atlanta, GA, September 16-19, 2016.

N. Raghupathy, **K. Choi**, S.C. Munger, G.A. Churchill. "Splice-EMASE: Quantifying allele-specific alternative splicing in diploid genomes". The 65th Annual Meeting of the American Society of Human Genetics, Baltimore, MD, October 6-10, 2015.

K. Choi, N. Raghupathy, S.C. Munger, ..., G.A. Churchill. "Accurate quantification of allele-specific expression from single-cell RNA-Seq data". The 65th Annual Meeting of the American Society of Human Genetics, Baltimore, MD, October 6-10, 2015.

S.C. Munger, N. Raghupathy, **K. Choi**, D.M. Gatti, P. Simacek, G.A. Churchill. "Allele-specific expression and eQTL in diploid genomes". The 64th Annual Meeting of the American Society of Human Genetics, San Diego, CA, October 18-22, 2014.

K. Choi, K. Shultz, D. Godfrey, M. Hibbs, C. Ackert-Bicknell, G.A. Churchill. "Osteoblast development is driven by trans-acting regulations". The 64th Annual Meeting of the American Society of Human Genetics, San Diego, CA, October 18-22, 2014.

H. Zheng, V. Forgetta, Y. Hsu, ..., **K. Choi**, ..., D. Kiel, B. Richards. "A large-scale whole genome sequence-based analysis discovered novel genetic variants influencing bone mineral density: Results from the GEFOS and UK10K Consortia". 2014 Annual Meeting of the American Society for Bone and Mineral Research, Houston, TX, September 12-15, 2014.

K. Choi, D. Godfrey, M. Hibbs, C. Ackert-Bicknell. "Comprehensive profiling of gene expression temporal dynamics during osteoblastogenesis in the context of differing genetic backgrounds". 2014 Annual Meeting of the American Society for Bone and Mineral Research, Houston, TX, September 12-15, 2014.

K. Choi, N. Raghupathy, S.C. Munger, D.M. Gatti, G.A. Churchill. "Estimation of isoform-specific and allele-specific expression from RNA-Seq data of genetically diverse population". The 63th Annual Meeting of the American Society of Human Genetics, Boston, MA, October 22-26, 2013.

S.C. Munger, N. Raghupathy, **K. Choi**, A.K. Simons, D.M. Gatti, D.A. Hinerfeld, ..., G.A. Churchill. "RNA-Seq alignment to individualized genomes". The 63th Annual Meeting of the American Society of Human Genetics, Boston, MA, October 22-26, 2013.

N. Raghupathy, **K. Choi**, S.C. Munger, G.A. Churchill. "Quantifying gene expression and allele-specific expression simultaneously using personal human genomes". The 63th Annual Meeting of the American Society of Human Genetics, Boston, MA, October 22-26, 2013.

L. Oei, S. Reppe, ..., **K. Choi**, ..., C. Ackert-Bicknell, the GEFOS consortium. "Functional characterization of GWAS loci associated with fracture risk". 2013 Annual Meeting of the American Society for Bone and Mineral Research, Baltimore, MD, October 4-7, 2014.

K. Choi, K. Shultz, ..., C. Ackert-Bicknell. "Identification of Slc9a9 as a candidate gene for a bone mineral density locus on mouse Chromosome 9". 2013 Annual Meeting of the American Society for Bone and Mineral Research, Baltimore, MD, October 4-7, 2014.

L. Oei, P. Nordstrom, ..., **K. Choi**, ..., F. Rivadeneira, the GEFOS consortium. "The genetic basis of cross-phenotype correlation with bone fracture risk: the GEFOS consortium". 2013 Annual Meeting of the American Society for Bone and Mineral Research, Baltimore, MD, October 4-7, 2014.

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-seq". 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. "Intro 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.

Professional Experience

[2017-present] Associate Computational Scientist, **The Jackson Laboratory**, Bar Harbor, ME.

[2015-2017] Associate Research Scientist, **The Jackson Laboratory**, Bar Harbor, ME.

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

[2005-2011] Research Assistant, Biomedical Engineering: Gomez Lab, **UNC, Chapel Hill**, NC.

[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.

References

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(More references are available upon request)