

CURRICULUM VITAE

Stephen R. Piccolo

stephen_piccolo@byu.edu · [webpage](#) · (801) 422-7116

Personal Information

Current Position

Associate Professor, Department of Biology, Brigham Young University, Provo, UT, (Sept. 2020–present)

Assistant Professor, Department of Biology, Brigham Young University, Provo, UT, (Sept. 2014–Aug. 2020)

Member, Simmons Center for Cancer Research, Brigham Young University, Provo, UT, (2015–present)

Previous Employment

- OCT. 2011–AUG. 2014 *Postdoctoral Research Associate*
Division of Computational Biomedicine
Boston University School of Medicine
Advised by Dr. W. Evan Johnson
- FEB. 2011–AUG. 2014 *Postdoctoral Research Associate*
Department of Pharmacology and Toxicology
University of Utah
Advised by Dr. Andrea H. Bild
- SEPT. 2010–SEPT. 2011 *Research Associate*
Statistics Department, Brigham Young University
Advised by Dr. W. Evan Johnson
- SEPT. 2010–FEB. 2011 *Research Associate*
Department of Pharmacology and Toxicology, University of Utah
Advised by Dr. Andrea H. Bild
- MAY 2001–AUG. 2006 *Software developer / analyst*
Intel Corporation, Chandler, AZ
- APR. 2000–AUG. 2000 *Intern software developer / analyst*
Intel Corporation, Chandler, AZ

Education

University of Utah - Salt Lake City, UT

Ph.D. in Biomedical Informatics, FEBRUARY 2011

Advisor: Dr. Lewis J. Frey

Dissertation: “*Informatics framework for evaluating multivariate prognosis models: Application to human glioblastoma multiforme*”

Brigham Young University - Provo, UT

B.S. in Management Information Systems (minor in English), APRIL 2001, Cum laude

Ricks College (now Brigham Young University–Idaho) - Rexburg, ID

A.A.S. in Natural Sciences, APRIL 1998

Research and Scholarly Activities

Peer-reviewed Publications (*Corresponding Author, †Undergraduate student, ‡Graduate student)

Bodily WR[‡], Shirts BH, Walsh T, Gulsuner S, King MC, Parker A[†], Roosan M, and **Piccolo SR**. Effects of germline and somatic events in candidate BRCA-like genes on breast-tumor signatures. *PLoS One*, 30 Sep 2020. [\[link\]](#)

Miller DB[‡] and **Piccolo SR**. Compound heterozygous variants in pediatric cancers: A systematic review. *Frontiers in Genetics*, 19 May 2020. [\[link\]](#)

Piccolo SR, Lee TJ[†], Suh E[†], and Hill K[†]. ShinyLearner: A containerized benchmarking tool for machine-learning classification of tabular data. *Gigascience*, Volume 9, Issue 4, April 2020. [\[link\]](#).

Townsend MH, Tellez Freitas CM, Larsen D[†], **Piccolo SR**, Weber KS, Robison RA, and O’Neill KA. Hypoxanthine Guanine Phosphoribosyltransferase expression is negatively correlated with immune activity through its regulation of purine synthesis. *Immunobiology*, 2020. [\[link\]](#).

Mora-Lagos B, Cartas-Espinel I, Riquelme I, Parker AC[†], **Piccolo SR**, Viscarra T, Reyes ME, Zanella L, Buchegger K, Ili C, Brebi P. Functional and transcriptomic characterization of cisplatin-resistant AGS and MKN-28 gastric cancer cell lines. *PLoS One*, 2020, 15(1): e0228331 [\[link\]](#).

Sumsion GR[†], Bradshaw III MS[†], Beales JT[†], Ford E[†], Caryotakis GRG[†], Garrett DJ[†], LeBaron ED[†], Nwosu IO[‡], **Piccolo SR**. Diverse approaches to predicting drug-induced liver injury using gene-expression profiles. *Biology Direct*, 2020, 15:1 [\[link\]](#).

Viscarra T, Buchegger K, Jofre I, Riquelme I, Zanella L, Abanto M, Parker AC[†], **Piccolo SR**, Roa JC, Ili C, and Brebi P. Functional and transcriptomic characterization of carboplatin-resistant A2780 ovarian cancer cell line. *Biological Research*, 2019, 52:13 [\[link\]](#).

Townsend MH, Ence ZE[†], Felsted AM[†], Parker AC[†], **Piccolo SR**, Robison RA, and O’Neill KL. Potential new biomarkers for endometrial cancer. *Cancer Cell International*, 2019, 19:19 [\[link\]](#).

Townsend MH, Felsted AM[†], Ence ZE[†], **Piccolo SR**, Robison RA, and O’Neill KL. Falling from grace: HPRT is not suitable as an endogenous control for cancer-related studies. *Molecular and Cellular Oncology*, Volume 6, 2019 - Issue 2. [[link](#)].

Sumsion GR[†], Bradshaw MS[†], Hill KT[†], Pinto LDG[†], **Piccolo SR**^{*}. Remote sensing tree classification with a multilayer perceptron. *PeerJ*, 2019 Feb 28;7:e6101. eCollection 2019. doi: 10.7717/peerj.6101 [[link](#)].

Golightly NP[†], Bell A[†], Bischoff AI[†], Hollingsworth PD[†], **Piccolo SR**^{*}. Curated compendium of human transcriptional biomarker data. *Scientific Data*, volume 5, Article number: 180066 (2018), [[link](#)].

Singh B, Trincado JL, Tatlow PJ[†], **Piccolo SR**, and Eyraas E. Genome sequencing and RNA-motif analysis reveal novel damaging non-coding mutations in human tumors. *Molecular Cancer Research*, March 28, 2018, [[link](#)].

Weagel EG, Burrup W[†], Kovtun R[†], Velazquez EJ, Felsted AM[†], Townsend MH, Ence ZE[†], Suh E[†], **Piccolo SR**, Weber KS, Robison RA, and O’Neill KL. Membrane expression of thymidine kinase 1 and potential clinical relevance in lung, breast, and colorectal malignancies. *Cancer Cell International*, 2018, 18:135, [[link](#)].

Dayton JB[†] and **Piccolo SR**^{*}. Classifying cancer genome aberrations by their mutually exclusive effects on transcription. *BMC Medical Genomics*, 2017, 10(Suppl 4):66, <https://doi.org/10.1186/s12920-017-0303-0>. [[link](#)].

Bolouri H, Farrar JE, Triche TJ, Ries RE, Lim EL, Alonzo TA, Ma Y, Moore R, Mungall AJ, Marra MA, Zhang J, Ma X, Liu Y, Liu Y, Auviel JMG, Davidsen TM, Gesuwan P, Hermida LC, Salhia B, Capone S, Ramsingh G, Zwaan CM, Noort S, **Piccolo SR**, Kolb EA, Gamis AS, Smith MA, Gerhard DS, and Meshinchi S. The molecular landscape of pediatric acute myeloid leukemia reveals recurrent structural alterations and age-specific mutational interactions. *Nature Medicine*, 2017 Dec 11. doi: 10.1038/nm.4439. [[link](#)].

Brady SW, McQuerry JA, Qiao Y, **Piccolo SR**, Shrestha G, Jenkins D, Layer RM, Pedersen BS, Miller R, Esch A, Selitsky S, Parker J, Anderson L, Dalley BK, Factor RE, Reddy CB, Boltax J, Li DY, Moos PJ, Gray JW, Heiser LM, Buys SS, Cohen AL, Johnson WE, Quinlan AR, Marth G, Werner TL, and Bild AH. Combating subclonal evolution of resistant cancer phenotypes. *Nature Communications*, 2017 Nov 1;8(1):1231. doi: 10.1038/s41467-017-01174-3. [[link](#)].

Townsend MH, Felsted AM[†], Ence ZE[†], **Piccolo SR**, Robison RA, and O’Neill KL. Elevated expression of hypoxanthine guanine phosphoribosyltransferase within malignant tissue. *Cancer and Clinical Oncology*; 2017; 6(2). DOI: <https://doi.org/10.5539/cco.v6n2p19> [[link](#)].

Townsend MH, Felsted AM[†], **Piccolo SR**, Robison RA, and O’Neill KL. Metastatic colon adenocarcinoma has a significantly elevated expression of IL-10 compared to primary colon adenocarcinoma tumors. *Cancer Biology & Therapy*; 2017 Aug 16:0. doi: 10.1080/15384047.2017.1360453 [[link](#)].

Seyednasrollah F, Koestler DC, Wang T, **Piccolo SR**, Vega R, Greiner R, Fuchs C, Gofer E, Kumar L, Wolfinger RD, Winner KK, Bare C, Neto EC, Yu T, Shen L, Abdallah K, Norman T, Stolovitzky G, PCC-DREAM Community, Soule H, Sweeney CJ, Ryan CJ, Scher HI, Sartor O,

Elo LL, Zhou FL, Guinney J, Costello JC. A DREAM Challenge to build prediction models for short-term discontinuation of docetaxel in metastatic castration-resistant prostate cancer. *JCO Clinical Cancer Informatics*; published online August 4, 2017. DOI: 10.1200/CCI.17.00018 [\[link\]](#).

Rahman M, MacNeil SM, Jenkins DF, Shrestha G, Wyatt SR, McQuerry JA, **Piccolo SR**, Heiser LM, Gray JW, Johnson WE and Bild AH. Activity of distinct growth factor receptor network components in breast tumors uncovers two biologically relevant subtypes. *Genome Medicine*, 2017; 9:40. doi:10.1186/s13073-017-0429-x [\[link\]](#).

Cohen AL, Neumayer L, Boucher K, Factor RE, Shrestha G, Wade M, Lamb JG, Arbogast K, **Piccolo SR**, Riegert J, Schabel M, Bild AH, Werner TL. Window-of-opportunity study of valproic acid in breast cancer testing a gene expression biomarker. *JCO Precision Oncology*, published online April 7, 2017. doi:10.1200/PO.16.00011 [\[link\]](#).

Naylor BC, Porter MT, Wilson E, Herring A, Lofthouse S, Hannemann A, **Piccolo SR**, Rockwood AL, Price JC. DeuteRater: a tool for quantifying peptide isotope precision and kinetic proteomics. *Bioinformatics*, 2017; 33 (10): 1514-1520. [\[link\]](#).

Tatlow PJ[†] and **Piccolo SR**. A cloud-based workflow to quantify transcript-expression levels in public cancer compendia. *Scientific Reports*, 2016; 6:39259. doi:10.1038/srep39259 [\[link\]](#); highlighted in Science Translational Medicine [\[link\]](#).

Archer TC, Fertig EJ, Gosline SJC, Hafner M, Hughes SK, Joughin BA, Meyer AS, **Piccolo SR**, Shajahan-Haq A (authors listed alphabetically). Systems approaches to cancer biology. *Cancer Research*, 2016 Dec 1;76(23):6774-6777. Epub 2016 Nov 18.

Piccolo SR* and Frampton MB[†]. Tools and techniques for computational reproducibility. *Gigascience*, 2016; 5:30. doi: 10.1186/s13742-016-0135-4. [\[link\]](#)

Wang ZL, Li B, **Piccolo SR**, Zhang XQ, Li JH, Zhou H, Yang JH, Qu LH. Integrative analysis reveals clinical phenotypes and oncogenic potentials of long non-coding RNAs across 15 cancer types. *Oncotarget*, 2016 Jun 7;7(23):35044-55. doi:10.18632/oncotarget.9037. [\[link\]](#)

Allen GI, Amoroso N, Anghel C, Balagurusamy V, Bare CJ, Beaton D, Bellotti R, Bennett DA, Boehme K, Boutros PC, Caberlotto L, Caloian C, Campbell F, Neto EC, Chang Y, Chen B, Chen C, Chien T, Clark T, Das S, Davatzikos C, Deng J, Dillenberger D, Dobson RJB, Dong Q, Doshi J, Duma D, Errico R, Erus G, Everett E, Fardo DW, Friend SH, Frohlich H, Gan J, St George-Hyslop P, Ghosh SS, Glaab E, Green RC, Guan Y, Hong M, Huang C, Hwang J, Ibrahim J, Inglese P, Jiang Q, Katsumata Y, Kauwe JSK, Klein A, Kong D, Krause R, Lalonde E, Lauria M, Lee E, Lin X, Liu Z, Livingstone J, Logsdon BA, Lovestone S, Lyappan A, Ma M, Malhotra A, Mangravite LM, Maxwell TJ, Merrill E, Nagorski J, Namasivayam A, Narayan M, Naz M, Newhouse SJ, Norman TC, Nurtdinov RN, Oyang Y, Pawitan Y, Peng S, Peters MA, **Piccolo SR**, Praveen P, Priami C, Sabelnykova VY, Senger P, Shen X, Simmons A, Sotiras A, Stolovitzky G, Tangaro S, Tateo A, Tung Y, Tustison NJ, Varol E, Vradenburg G, Weiner MW, Xiao G, Xie L, Xie Y, Xu J, Yang H, Zhan X, Zhou Y, Zhu F, Zhu H, Zhu S, Alzheimer's Disease Neuroimaging Initiative. Crowdsourced estimation of cognitive decline and resilience in Alzheimer's disease, *Alzheimer's & Dementia*, 2016 Jun; 12(6): 645-653. [\[link\]](#)

Piccolo SR, Hoffman LM, Conner T, Shrestha G, Cohen AL, Marks JR, Neumayer LA, Agarwal CA, Beckerle MC, Andrulis IL, Spira AE, Moos PJ, Buys SS, Johnson WE, Bild AH. Integrative

analyses reveal signaling pathways underlying familial breast cancer susceptibility. *Molecular Systems Biology*, 2016 Mar; 12(3): 860. [\[link\]](#)

Piccolo SR, Andrulis IL, Cohen AL, Conner T, Moos PJ, Spira AE, Buys SS, Johnson WE, Bild AH. “Gene-expression patterns in peripheral blood classify familial breast cancer susceptibility”. *BMC Medical Genomics*, 2015, 8:72 doi:10.1186/s12920-015-0145-6. [\[link\]](#)

Rahman M, Jackson LK, Johnson WE, Li DY, Bild AH, **Piccolo SR***. “Alternative preprocessing of RNA-Sequencing data in The Cancer Genome Atlas leads to improved analysis results”. *Bioinformatics*, 2015, 31(22): 3666-3672. [\[link\]](#)

MacNeil SM, Johnson WE, Li DY, **Piccolo SR***, Bild AH. “Inferring pathway dysregulation in cancers from multiple types of omic data”. *Genome Medicine*, 2015 Jun 26;7(1):61. [\[link\]](#)

Mortenson JB, Heppler LN, Banks CJ, Weerasekara VK, Whited MD, **Piccolo SR**, Johnson WE, Thompson JW, Andersen JL. “Histone deacetylase 6 (HDAC6) promotes the pro-survival activity of 14-3-3 via deacetylation of lysines within the 14-3-3 binding pocket”. *Journal of Biological Chemistry*, 2015 May 15;290(20):12487-96. [\[link\]](#)

Shen Y, Rahman M, **Piccolo SR**, Gusenleitner D, El-Chaar NN, Cheng L, Monti S, Bild AH, Johnson WE. “ASSIGN: Context-specific Genomic Profiling of Multiple Heterogeneous Biological Pathways.” *Bioinformatics*, 2015 31 (11): 1745-1753. [\[link\]](#)

Lee S, **Piccolo SR**, Allen-Brady K. “Robust meta-analysis shows that glioma transcriptional subtyping complements traditional approaches.” *Cellular Oncology*, 2014 Oct; 37(5):317-29. [\[link\]](#)

El Chaar NN, **Piccolo SR**, Boucher KM, Cohen AL, Chang JT, Moos PJ, Bild AH. “Genomic classification of the RAS network identifies a personalized treatment strategy for lung cancer.” *Molecular Oncology* 2014, pii: S1574-7891(14)00110-0.[\[link\]](#)

Bild AH, Chang JT, Johnson WE, **Piccolo SR**. “A field guide to genomics research.” *PLOS Biology* 2014, 1:12, e1001744. [\[link\]](#)

Piccolo SR, Withers MR, Francis OE, Bild AH, Johnson WE. “Multi-platform single-sample estimates of transcriptional activation.” *Proceedings of the National Academy of Sciences of the United States of America* 2013, 110:44, 17778-17783. [\[link\]](#) Highlighted in [Nature Methods](#).

Cohen AL, **Piccolo SR**, Cheng L, Soldi R, Han B, Johnson WE, Bild AH. “Genomic pathway analysis reveals that EZH2 and HDAC4 represent mutually exclusive epigenetic pathways across human cancers.” *BMC Medical Genomics* 2013, 6:35. [\[link\]](#)

Piccolo SR, Frey LJ. “Clinical and molecular models of glioblastoma multiforme survival.” *International Journal of Data Mining and Bioinformatics* 2013, 7:3, 245-265. [\[link\]](#)

Piccolo SR, Sun Y, Campbell JD, Lenburg ME, Bild AH, Johnson WE. “A single-sample microarray normalization method to facilitate personalized-medicine workflows.” *Genomics* 2012, 100:6, 337-344. [\[link\]](#)

Kim SH, Lee SH, **Piccolo SR**, Allen-Brady K, Park EJ, Chun JN, Kim TW, Cho NH, Kim IG, So I, Jeon JH. “Menthol induces cell-cycle arrest in PC-3 cells by down-regulating G2/M genes, including polo-like kinase 1.” *Biochemical and Biophysical Research Communications* 2012, Jun 8; 422(3), 436-41. [\[link\]](#)

Piccolo SR, Frey LJ. “ML-Flex: A flexible framework for performing classification analyses in parallel.” *Journal of Machine Learning Research* 2012, 13, 555-559. [[link](#)]

Frey LJ, **Piccolo SR**, Edgerton ME. “Multiplicity: an organizing principle for cancers and somatic mutations.” *BMC Medical Genomics* 2011, 4:52. [[link](#)]

Crockett DK, **Piccolo SR**, Ridge PG, Margraf RL, Lyon E, Williams MS, Mitchell JA. “Predicting phenotypic severity of uncertain gene variants in the RET proto-oncogene.” *PLoS ONE* 2011, 6:3, e18380. [[link](#)]

Peer-reviewed Publications as Consortium Author

Mason MJ, et al., along with the **Multiple Myeloma DREAM Consortium**. Multiple Myeloma DREAM Challenge reveals epigenetic regulator PHF19 as marker of aggressive disease. *Leukemia*, 2016. [[link](#)]

Guinney J, et al., along with the **Prostate Cancer Challenge DREAM Community**. Prediction of overall survival for patients with metastatic castration-resistant prostate cancer: development of a prognostic model through a crowdsourced challenge with open clinical trial data. *Lancet Oncology*, Online first: 15 Nov 2016. [[link](#)]

Oral Conference Presentations (*Presenter, †Undergraduate student, ‡Graduate student)

Miller DB^{*‡} and **Piccolo SR**. “Containerized pipeline for the identification of compound heterozygous variants in trios”. *Rocky Mountain Bioinformatics Conference*, December 2019, Snowmass, CO.

Dayton JB^{*‡} and **Piccolo SR**. “Using adversarial deep neural networks to remove nonlinear batch effects from expression data”. *Rocky Mountain Bioinformatics Conference*, December 2018, Snowmass, CO.

Sumsion GR^{*†}, Bradshaw III MS[†], Beales JT[†], Ford E, Caryotakis GRG[†], Garrett DJ[†], LeBaron ED[†], Nwosu IO[‡], and **Piccolo SR**. “An ensemble approach to predicting drug-induced liver injury based on RNA expression levels”. *Intelligent Systems for Molecular Biology*, July 2018, Chicago, IL.

Dayton JB^{*‡} and **Piccolo SR**. “Classifying cancer genome aberrations by their mutually exclusive effects on transcription.” *The 16th International Conference on Bioinformatics*, September 2017, Shenzhen, China. [[link](#)]

Bodily WR^{*‡} and **Piccolo SR**. “Integrative analysis to evaluate similarity between ‘BRCAness’ tumors and BRCA tumors.” *Great Lakes Bioinformatics Conference*, May 2017, Chicago, IL. [[link](#)]

Piccolo SR^{*}. “Experiences teaching bioinformatics skills to novices and to advanced undergraduates.” *Great Lakes Bioinformatics Conference*, May 2017, Chicago, IL. [[link](#)]

Piccolo SR^{*}. “Preprocessing, alignment, and quantification of thousands of RNA-Sequencing samples in the cloud for a minimal cost.” *American Association for Cancer Research Annual Meeting*, April 2017, Washington DC. [[link](#)]

Piccolo SR*, Lee TJ[†], and Taylor SA[†]. “ShinyLearner: Enabling biologists to perform robust machine-learning classification.” *Rocky Mountain Bioinformatics Conference*, December 2016, Snowmass, CO. [[link](#)]

Piccolo SR*, Lee TJ[†], and Taylor SA[†]. “ShinyLearner: Enabling biologists to perform robust machine-learning classification.” *Rocky Mountain Bioinformatics Conference*, December 2016, Snowmass, CO. [[link](#)]

Tatlow PJ^{*,†} and **Piccolo SR**. “How to quantify expression for thousands of RNA-Sequencing samples in a day for a minimal cost.” *Biological Data Science*, October 2016, Cold Spring Harbor, NY. [[link](#)]

Golightly NP^{*,†}, Guyer AI[†], and **Piccolo SR**. “Evaluating how well we can predict biomedical outcomes with gene-expression profiles.” *Publishing Better Science through Better Data*, October 2016, London, England. [[link](#)]

Piccolo SR*. “Performance Above Random Expectation: A more intuitive and versatile metric for evaluating probabilistic classifiers.” *UseR! Conference*, June 2016, Palo Alto, CA. [[link](#)]

Piccolo SR* and Guyer AI[†]. “Compendium of gene-expression data sets to facilitate machine-learning benchmarks.” *International Society for Biocuration, annual meeting*, April 2016, Geneva, Switzerland. [[link](#)]

Piccolo SR*. “A Prototype Software Pipeline to Identify Mutated Genes that Have a Similar Effect on Tumor Transcription”. *AMIA Summit on Translational Bioinformatics*, March 2015, San Francisco, CA. [[link](#)]

Piccolo SR*. “Building portable analytical environments to improve sustainability of computational-analysis pipelines in the sciences.” *2nd Workshop on Sustainable Software for Science: Practice and Experiences*, November 2014, New Orleans, LA. [[link](#)]

MacNeil SM, Johnson WE, **Piccolo SR***, Bild AH. “Gene Set Omic Analysis: A gene-set analysis approach that can be applied to many omic types.” *Biological Data Science*, November 2014, Cold Spring Harbor Laboratories, NY.

Crockett DK, **Piccolo SR**, Narus SP, Mitchell JA, Facelli JC. “Machine-learning classification of RET mutation severity.” *AMIA Summit on Translational Bioinformatics*, 2010, San Francisco, CA.

Piccolo SR*, Abo RP, Allen-Brady K, Camp NJ, Knight S, Anderson JL, Horne BD. “Evaluation of genetic risk scores for lipid levels using genome-wide markers in the Framingham Heart Study.” *BMC Proceedings* 2009, 3(Suppl 7):S46 (15 December 2009). [[link](#)]

Piccolo SR*, Frey LJ. “Somatic mutation signatures of cancer.” *AMIA Annual Symposium Proceedings* 2008, 202–206. [[link](#)]

Invited Talks

“Using somatic-mutation signatures to identify BRCA-like genes.” *Cancer Control and Population Sciences Clinical Research Conference seminary series*, City of Hope Medical Center, Duarte, CA (held virtually due to pandemic), August 2020.

“Using somatic-mutation signatures to identify BRCA-like genes.” *Seminar Series of the Research Center and the Graduate Program in Oncology*, Rio de Janeiro, Brazil, April 2019.

“Containerization of shallow and deep classification algorithms and benchmarks on gene-expression data.” *NCI Containers and Workflows Interest Group Seminar (webinar)*, April 2019.

“Comprehensive benchmark of supervised-learning algorithms for predicting cancer states.” *BioC 2017: Where Software and Biology Connect*, July 2017, Boston, MA. [\[link\]](#)

“Reproducible curation and analysis of public gene-expression data.” *Medical College of Wisconsin*, March 2017, Milwaukee, WI.

“Using Machine Learning to Identify Aberrant Pathway Activity.” *BD2K-LINCS Webinar*, September 2015. [\[link\]](#)

Keynote speaker. “Making pathway-level inferences from omic data.” *Biotechnology and Bioinformatics Symposium*, December 2014, Provo, UT.

Conference Posters (*Presenter, †Undergraduate student, ‡Graduate student)

Miller DB^{*‡} and **Piccolo SR**. “The landscape of compound heterozygous variation across pediatric disease”. *American Society of Human Genetics Annual Meeting*, October 2020, San Diego, CA (held virtually due to pandemic).

Townsend MH^{*}, Ewell ZD[†], Tellez CM[†], Larsen DJ[†], Lawrence EL[‡], Bennion KA[†], †, **Piccolo SR**, Weber KS, Robison RA, O’Neill KL. “HPRT Overexpression May Contribute to the Immunosuppressive Tumor Microenvironment.” *American Association for Cancer Research Annual meeting*, 2019, Atlanta, GA.

Townsend MH^{*}, Bennion KA[†], Ence ZE[†], Bitter EEK[†], Felsted AM[†], Lattin JE[†], Reese MD[†], **Piccolo SR**, O’Neill KL. “Differential expression of HPRT in prostate cancer leads to investigation of its ADCC effects.” *American Association for Cancer Research Annual meeting*, 2019, Atlanta, GA.

Townsend MH^{*}, Bitter EEK[†], Larsen DJ[†], Tellez CM[†], **Piccolo SR**, Weber KS, Robison RA, O’Neill KL. “HPRT impact on immune regulation influences the tumor microenvironment.” *Midwinter Conference of Immunologists*, 2019, Monterey, CA.

Townsend MH^{*}, Bennion KA[†], Ence ZE[†], Suh E[†], Felsted AM[†], Lattin JE[†], **Piccolo SR**, Robison RA, O’Neill KL. “Stepping into the ring of cancer immunotherapy: HPRT as a therapeutic target.” *Midwinter Conference of Immunologists*, 2019, Monterey, CA.

Mella N^{*†}, Heaton T[†], and **Piccolo SR**. “Predicting progression-free interval for cancer patients based on heterogeneous combinations of high-throughput molecular data.” *Rocky Mountain Bioinformatics Conference*, December 2019, Snowmass, CO.

Anderson EC^{*†} and **Piccolo SR**. “A web application for annotating tabular data with terms from biomedical ontologies.” *Rocky Mountain Bioinformatics Conference*, December 2019, Snowmass, CO.

Wengler J^{*†} and **Piccolo SR**. “Optimizing storage and querying of massive biological datasets of a tabular nature.” *Rocky Mountain Bioinformatics Conference*, December 2019, Snowmass, CO.

Suh E^{*†} and **Piccolo SR**. “geneHarmony: An Interactive Web Application that Automates the Manual Process of Bacteriophage Genome Annotation.” *Rocky Mountain Bioinformatics Conference*, December 2019, Snowmass, CO.

Parker AC^{*†} and **Piccolo SR**. “Good Nomen: An interactive web application for cleaning clinical data using standardized terminologies.” *Rocky Mountain Bioinformatics Conference*, December 2018, Snowmass, CO.

Hill K^{*†} and **Piccolo SR**. “Predicting cancer outcomes based on gene-expression profiles more accurately with deep neural networks.” *Rocky Mountain Bioinformatics Conference*, December 2018, Snowmass, CO.

Fry B^{*†} and **Piccolo SR**. “ShapeShifter: Making it easy to transform genomic and transcriptomic data from one file format to another.” *Rocky Mountain Bioinformatics Conference*, December 2018, Snowmass, CO.

Piccolo SR^{*}, Bell A[†], Golightly NP[†]. How well can we predict cancer states using transcriptional profiles? *Precision Medicine in Cancer*, Keystone Symposia, May 2018, Stockholm, Sweden.

Townsend MH^{*†}, Brindley TD[†], Uhl RA[†], Felsted AM[†], **Piccolo SR**, Robison RA, and O’Neill KL. Expression of IL-10 and TGF-B in Primary and Metastatic Colorectal Adenocarcinoma Tumors. *American Association for Cancer Research*, Annual Meeting, April 2018, Chicago IL.

Townsend MH^{*†}, Cox TP[†], Felsted AM[†], Lattin JE[†], Ence Z[†], Robison RA, **Piccolo SR**, and O’Neill KL. Determining the Molecular Mechanism of HPRT Surface Expression in Prostate Cancer. *American Association for Cancer Research*, Annual Meeting, April 2018, Chicago IL.

Townsend MH^{*†}, Ewell ZD[†], Ence Z[†], Burrup W[†], Velazquez EJ, Robison RA, **Piccolo SR**, and O’Neill KL. Evaluation of Potential Protein Biomarkers for Burkitt’s Lymphoma. *American Association for Cancer Research*, Annual Meeting, April 2018, Chicago IL.

Townsend MH^{*†}, Felsted AM[†], Cox TP[†], Ence ZE[†], **Piccolo SR**, Robison RA, and O’Neill KL. HPRT surface localization on prostate cancer cells as a biomarker for immunotherapy. *American Association for Cancer Research*, Annual Meeting, April 2018, Chicago IL.

Townsend MH^{*†}, Cox TP[†], Felsted AM[†], **Piccolo SR**, Robison RA, and O’Neill KL. IL-10 as an indicator of metastatic potential in colorectal carcinoma. *American Association for Cancer Research*, Annual Meeting, April 2018, Chicago IL.

Townsend MH^{*†}, Felsted AM[†], Ence ZE[†], **Piccolo SR**, Robison RA, and O’Neill KL. Unique HPRT1 upregulation in malignant tissue: Potential use as a diagnostic biomarker. *American Association for Cancer Research*, Annual Meeting, April 2018, Chicago IL.

Townsend MH^{*†}, Felsted AM[†], Ence ZE[†], **Piccolo SR**, Robison RA, and O’Neill KL. Unusual HPRT1 upregulation in malignant tissue and potential use as a diagnostic biomarker. *American Association for Cancer Research*, Undergraduate Student Caucus and Poster competition, April 2018, Chicago, IL.

Townsend MH^{*†}, Brindley T[†], Felsted AM[†], Ence ZE[†], **Piccolo SR**, Robison RA, and O’Neill KL. Evaluation of TGF-B and IL-10 as potential prognostic biomarkers in primary and metastatic colorectal adenocarcinoma. *American Association of Microbiologist Tri-Branch Meeting*, April 2018, Durango, CO.

Bell AA^{*†} and **Piccolo SR**. “GEOcurate: Enabling biologists to easily curate annotations from GEO datasets.” *Rocky Mountain Bioinformatics Conference*, December 2017, Snowmass, CO.

Jensen S^{*†}, Cranney C[†], and **Piccolo SR**. “Efficiently generating unique vector permutations in R.” *Rocky Mountain Bioinformatics Conference*, December 2017, Snowmass, CO.

Ence Z^{*†}, Tatlow PJ[†], Dayton JB[‡], and **Piccolo SR**. “Geney: A data ecosystem that enables biologists to efficiently subset, visualize, and analyze genomic data.” *Genome Informatics*, November 2017, Cold Spring Harbor Laboratories, NY.

Piccolo SR^{*} and Gill RA. “Using ecology to teach bioinformatics: Novel connections between disciplines.” *Ecological Society of America, annual meeting*, August 2017, Portland, OR.

Triche TJ^{*}, Farrar JE, Bolouri H, Ries RE, Lim EL, Alonzo TA, Ma Y, Moore R, Mungall AJ, Marra MA, Auvil JMG, Davidsen TM, Gesuwan P, Hermida LC, Kolb EA, Gamis A, Smith MA, **Piccolo SR**, Gerhard DS and Meshinchi S. “Divergent Epigenomes in Pediatric and Adult Acute Myeloid Leukemia Implicate Cell of Origin and Transcriptional Silencing of Immune Responses As Sources of Clinically Relevant Heterogeneity: A Report from the Children’s Oncology Group and NCI/COG Therapeutically Applicable Research to Generate Effective Treatments (TARGET) Initiative.” *American Society of Hematology, annual meeting*, December 2016, San Diego, CA.

Piccolo SR^{*}, Lee TJ[†], and Taylor SA[†]. “ShinyLearner: Enabling biologists to perform robust machine-learning classification.” *Biological Data Science*, October 2016, Cold Spring Harbor, NY.

Cohen AL^{*}, Neumayer L, Factor R, Boucher K, Wade M, Lamb G, Arbogast K, **Piccolo SR**, Shrestha G, Riegert J, Schabel M, Bild AH, Werner TL. “A phase 1 window of opportunity study of valproic acid (VPA) in breast cancer testing a 200 gene expression biomarker.” *American Society for Clinical Oncology Annual Meeting*, 2016, Chicago, IL.

Piccolo SR^{*}, Hoffman LM, Conner T, Shrestha G, Cohen AL, Marks JR, Neumayer LA, Agarwal CA, Beckerle MC, Andrulis IL, Spira AE, Moos PJ, Buys SS, Johnson WE, Bild AH. Disrupted cell adhesion is a candidate risk factor for familial breast cancer. *Systems Approaches to Cancer Biology*, April 2016, Marine Biological Laboratory, Woods Hole, MA.

Lee TJ^{*†} and **Piccolo SR**. “Predicting cancer patient survival by analyzing clinical and molecular data using a machine-learning approach”. *BIOT*, Provo, UT, November 2015.

Hawkes DR^{*†} and **Piccolo SR**. “Examining gene-expression patterns across rare colon cancer syndromes to identify early diagnosis and treatment options”. *BIOT*, Provo, UT, November 2015.

Guyer AI^{*†} and **Piccolo SR**. “How well can machine-learning algorithms predict biomedical outcomes based on gene-expression data?” *BIOT*, Provo, UT, November 2015.

Piccolo SR^{*} and Johnson WE. “Mixture models that estimate gene-expression activation on a single-sample basis for any expression platform”. *Genome Informatics*, Cold Spring Harbor Laboratory, NY, October 2015.

Eddington HS^{*†}, **Piccolo SR**. “Examining Overall Mutation Frequency In Breast Cancer Patients Who Carry Germline Variants in DNA Repair Genes”. *The Cancer Genome Atlas Annual Symposium*, Bethesda, MD, May 2015.

Johnson WE* and **Piccolo SR**. “SCAN.UPC: Single sample estimates of transcriptional activation.” *BioC 2014*, Boston, MA. July 2014.

Piccolo SR*, Cohen AL, Johnson WE, Moos PJ, and Bild AH. “Genomic predictors of sensitivity to 17-AAG treatment for individual breast cancer patients.” *Pacific Symposium on Biocomputing*, Big Island, HI. January 2013.

Piccolo SR, Johnson WE, Sun Y, Conner T, Cohen AL, Moos PJ, Goldgar D, Andrulis I, Buys SA and Bild AH. “Genomic variation in peripheral blood can predict hereditary breast-cancer development.” *Quantitative Issues in Genomic Medicine*, Harvard School of Public Health, Boston, MA. November 2011.

Piccolo SR*, Withers MR, Sun Y, Bild AH, Johnson WE. “Enabling cross-platform pathway analyses via universal probability codes.” *Keystone Symposia: Changing Landscape of the Cancer Genome*, Boston, MA. June 2011.

Crockett DK, **Piccolo SR**, Ridge PG, Escobar H, Reyes-Vargas E, Jensen PE, Delgado JC. “A novel representation of HLA allele specificity and prediction algorithm for HLA class I binding.” *BCB’ 10: ACM International Conference on Bioinformatics and Computational Biology*, Niagara Falls, NY. August 2010.

Ridge PG, **Piccolo SR**, Escobar H, Jensen PE, Delgado JC, Crockett DK. “Feature selection for characterizing HLA class I peptide motif anchors.” *BCB’ 10: ACM International Conference on Bioinformatics and Computational Biology*, Niagara Falls, NY. August 2010.

Piccolo SR*, Frey LJ. “Model of glioblastoma multiforme survival using clinical and somatic mutation data.” *AMIA Summit on Translational Bioinformatics*, San Francisco, CA. March 2009.

Piccolo SR*, Camp N, Frey LJ. “Polygenic model for predicting breast cancer risk via genome-wide polymorphisms.” *AMIA Annual Symposium*, Washington D.C. November 2008 (Nov 6:1094).

Piccolo SR*. “Combining the power of graphical user interfaces and command-based input: A medical literature search tool with no buttons.” *AMIA Spring Congress*, Orlando, FL. May 2007.

Patents

U.S. patent; “Streaming File Transfer Apparatus, Systems, and Methods”; US 7,797,405 B2; September 14, 2010.

Fellowships and Scholarships

Postdoctoral Research Training Fellowship, National Institutes of Health–National Cancer Institute (T32CA093247) via Multidisciplinary Cancer Research Training Program at Huntsman Cancer Institute, 2010–2012.

PhD Training Fellowship, National Library of Medicine (5T15LM007124), 2006-2010.

University Academic Scholarship, Brigham Young University, 2000–2001.

Awards and Honors

Disciplinary Breadth Award, Maize Genetics Conference, March 2020, Kailua-Kona, Hawai'i. Award sponsored by the National Science Foundation (did not travel due to pandemic).

Travel Award, Publishing Better Science through Better Data, October 2016, London, England. Funding provided via Wellcome Trust.

Top Performer, Prostate Cancer DREAM Challenge (Subchallenge 2), 2015. [[link](#)]

Finalist, Design Challenge, AMIA Translational Summit, San Francisco, CA, 2015. [[link](#)]

Travel Award, 2nd Workshop on Sustainable Software for Science: Practice and Experiences, New Orleans, LA, 2014. Funding provided via NSF award #1434218. [[link](#)]

Travel Award, Personalized Health Care Travel Grants Program, University of Utah, 2012.

John D. Morgan Fellowship Award, University of Utah, Department of Biomedical Informatics, 2010 (<http://medicine.utah.edu/bmi/scholarship>).

Bruce A. Houtchens, MD Award in Medical Informatics and Telemedicine, University of Utah, Department of Biomedical Informatics, 2010 (best student paper).

3rd place, Student Paper Competition (out of 80 submitted papers), American Medical Informatics Association Annual Symposium, 2008.

Travel Award, Genetic Analysis Workshop 16, 2008.

Grants

Developing and evaluating a process to distribute whole-genome variant calling across dispersed computing environments, Pilot Project for NIH 1U54CA209978-01A1, \$23,321 (direct costs), 2018.

Illumina Array SCAN, Alex's Lemonade Stand, \$10,000, 2017.

Mentoring Environment Grant, Brigham Young University, \$20,000, 2017-2018.

Teaching Environment Grant, Brigham Young University, 2017.

Life Sciences Startup Grants, Brigham Young University, \$60,000, 2014-2016.

AWS in Education research grant, \$10,000 research credits, Amazon Web Services LLC, 2011.

Teaching

Instructor

- 2019–PRESENT BIO 665, *Bioinformatics & Data Analysis 2*, Brigham Young University
- 2018–PRESENT BIO 365, *Computational Biology*, Brigham Young University
- 2017–PRESENT BIO 165, *Introduction to Bioinformatics*, Brigham Young University
- 2015–PRESENT BIO 100, *Principles of Biology*, Brigham Young University
- 2015–2018 BIO 465, *Bioinformatics*, Brigham Young University
- 2012–2014 *Applied Genomics*, PHTX 7777, University of Utah

Teaching Assistant

- SPRING 2009 *Bioinformatics*, BMI 6950, University of Utah
- SPRING 2008 *Statistics for Biomedical Informatics*, BMI 6105, University of Utah

Service

- 2019–PRESENT Curriculum Committee chair, Dept. of Biology, Brigham Young University
- 2017–PRESENT Co-chair, Association of Early Career Cancer Systems Biologists
- 2017–2018 Co-chair, Organizing Committee, Systems Approaches to Cancer Biology, Woods Hole, MA
- 2018 Bioinformatics Faculty Search Committee, Dept. of Biology, Brigham Young University
- 2017–PRESENT Graduate Committee member, Dept. of Biology, Brigham Young University
- 2017–2019 Adjunct Curriculum Committee member, Dept. of Biomedical Informatics, University of Utah
- 2017–PRESENT Bioinformatics Faculty Search Committee member, Dept. of Biology, Brigham Young University
- 2015 Biodiversity Faculty Search Committee member, Dept. of Biology, Brigham Young University
- 2014–2019 Curriculum Committee member, Dept. of Biology, Brigham Young University
- 2014–2016 Participant, Early Stage Investigators in Cancer Systems Biology steering committee National Cancer Institute
- 2010 Admissions Committee Member, Dept. of Biomedical Informatics, Univ. of Utah
- 2008–2010 Curriculum Committee member, Dept. of Biomedical Informatics, Univ. of Utah
- 2006–2010 Volunteer, Huntsman Cancer Hospital, Salt Lake City, Utah