

Brian S. White, Ph.D.

CONTACT INFORMATION Computational Oncology *Phone:* (607) 351-8429
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SUMMARY Computational biologist with cross-disciplinary background in machine learning, bioinformatics, cancer biology, and statistical modeling. 11+ years of experience developing machine learning methods (e.g., variational Bayesian approximate inference and fuzzy spectral clustering); 7+ years of experience applying those methods to elucidate mechanisms of cancer (e.g., clonal evolution of colorectal cancer and dysregulated splicing in myelodysplastic syndromes) and therapeutic response (e.g., immune infiltration in tumors and biomarkers of BCL-2 inhibitor response in acute myeloid leukemia). Proven ability to work independently and to initiate and lead external multidisciplinary collaborations of experimentalists, clinicians, and computational biologists. Excellent written communication skills evidenced by first-author publications in high-impact journals and successful grant applications.

EDUCATION **Cornell University**, Ithaca, NY, USA
Ph.D., Electrical and Computer Engineering (Physics and Computer Science Minors), Mar 2008, GPA: 3.55

University of Virginia, Charlottesville, VA, USA
Master of Computer Science, May 2002, GPA: 3.81

Carnegie Mellon University, Pittsburgh, PA, USA
BS, Computer Science (Mathematics Minor), May 1998, GPA: 3.50

WORK EXPERIENCE **Computational Sciences**
The Jackson Laboratory, Farmington, CT, USA
Senior Computational Scientist, Oct 2020 – Present

Computational Oncology
Sage Bionetworks, Seattle, WA, USA
Senior Scientist, Oct 2016 – Oct 2020

- Co-organizing a DREAM Challenge (a community-wide competition) that is comparing deconvolution method predictions of tumor immune infiltration made from bulk RNA-seq against ground truth derived from single-cell platforms (e.g., CyTOF and single-cell RNA-seq).
- Predicted expression-based biomarkers of response in acute myeloid leukemia (AML) using penalized regression, random forest, and novel Bayesian multi-source approaches, which revealed an insensitivity of monocytic AMLs to venetoclax (“Beat AML” collaboration with Oregon Health & Science University and Institute of Molecular Medicine Finland).
- Mentoring a junior scientist in predicting expression-based biomarkers of response to tyrosine kinase inhibitors in chronic myeloid leukemia clinical trials

(collaboration with Prof. Jerry Radich and Novartis).

- Co-chairing an imaging analysis working group focused on high-dimensional microscopy (e.g., multiplexed/cyclic immunofluorescence, CODEX) within the NCI's Cancer Systems Biology Consortium (CSBC) and the Physical Sciences-Oncology Network (PS-ON).
- Dissected the Consensus Molecular Subtypes (CMS) of colorectal cancer (CRC) according to immune response.
- Defining a pathway- and network-based classification system for CRC that extends CMS to account for immuno-oncological features of disease.
- Integrated multi-modal data (i.e., molecular and clinical features) to predict disease progression in multiple myeloma using Cox proportional hazards model.
- Co-managing a team of six computational biologists and research associates that act as the data coordinating center for the CSBC / PS-ON.

Division of Oncology and McDonnell Genome Institute

Washington University School of Medicine, St Louis, MO, USA

Research Assistant Professor, Sept 2012 – Sept 2016

- Developed SciClone, a widely-used and highly-cited variational Bayesian mixture modeling approach for defining subclonal tumor architecture from whole-exome/whole-genome sequencing (WES/WGS) data, and used it to elucidate tumor heterogeneity in AML and to track progression to metastasis in CRC.
- Designed capture-based sequencing platforms for detecting B-cell receptor rearrangements (including IGH translocations), as well as single nucleotide variants and copy number alterations, in multiple myeloma (MM) and follicular lymphoma (FL). Used these platforms to discover frequent, progression-associated *IGLL5* mutations in MM and recurrent mutations affecting B-cell receptor signaling in FL.
- Inferred alterations in spliceosome/splicing site acceptor affinity induced by leukemia-associated mutations in the splicing factor U2AF1 by analyzing RNA-seq data with generalized linear models (collaboration with Prof. Matt Walter).
- Identified splicing disrupted in *H2AFY* by U2AF1 mutation, which may contribute to abnormal hematopoiesis in mice, and genes simultaneously dysregulated by U2AF1 mutation and spliceosome-targeted drugs, with a cumulative effect that may lead to a cell's sensitivity to pharmacological modulation (collaboration with Prof. Matt Walter).
- Designed a prototype NanoString-based clinical assay to evaluate the efficacy of splice-modulating drugs (collaboration with Prof. Matt Walter).

Dept. of Molecular Biology and Genetics, Cornell University, Ithaca, NY USA

Research Associate, Apr 2011 – Sept 2012

Advisor: David Shalloway

- Mathematically modeled and experimentally validated RNA/protein binding in SELEX (Systematic Evolution of Ligands by Exponential Enrichment) experiments, leading to an optimized experimental protocol that is actively used by our molecular biology collaborators.

- Developed a bioinformatic pipeline to integrate next-generation sequencing into SELEX experiments, resulting in improved sensitivity compared to traditional, Sanger sequencing-based techniques.

Dept. of Molecular Biology and Genetics, Cornell University, Ithaca, NY USA

Postdoc, Mar 2008 – Apr 2011

Advisor: David Shalloway

- Developed a fuzzy (i.e., probabilistic), spectral (i.e., eigenvector-based) clustering algorithm modeled on statistical coarse-graining of “diffusive” transitions between similar data items, with improved efficiency and applicability over previous methods.
- Mathematically modeled migration of stem cells in collaboration with mouse geneticists, revealing an unexpected organization of the surrounding tissue.
- Quantified stem cell replication dynamics by analyzing fluorescence-activated cell sorting (FACS) data using Bayesian Gaussian mixture modeling, resulting in the discovery that the cell cycle regulator p21 represses stem cell proliferation.

Center for Advanced Scientific Computing, Lawrence Livermore National Laboratory, Livermore, CA, USA

Summer Student Guest, May 2004 – Aug 2005; Jun 2005

School of Computing, University of Utah, Salt Lake City, UT, USA

Visiting Graduate Research Assistant, Sept 2001 – Sept 2002

Computing Sciences Research Center, Bell Laboratories, Murray Hill, NJ, USA

(Summer) Member of Technical Staff, May 2000 – Aug 2000

Transarc Corporation, Pittsburgh, PA, USA

Summer Intern 1997 – 1998

SKILLS

Machine learning: supervised learning (e.g., SVMs, neural networks, LASSO/ridge/elastic net penalized regression, logistic regression), unsupervised learning (e.g., fuzzy spectral clustering, *k*-means, hierarchical clustering, expectation maximization), ensemble methods (e.g., random forest), dimensionality reduction (e.g., PCA, MDS)

Statistical modeling: generalized linear models, variational Bayesian inference, probabilistic graphical models, Monte Carlo techniques, survival analysis (e.g., Cox proportional hazards, Kaplan-Meier)

Pathway analysis: module detection (e.g., WGCNA, SPIA), gene-set enrichment (e.g., GSEA, GSVA, GSeq, DAVID, hypergeometric)

Genomic analysis: (pseudo-)alignment (e.g., bwa, tophat, STAR, cufflinks, kallisto), variant calling of whole-genome and exome/capture sequencing data (single nucleotide variants, insertions/deletions, structural variants, and copy number alterations; e.g., VarScan 2, pindel, lumpy), differential gene/splicing expression of RNA-seq and microarray expression data (e.g., cuffdiff, edgeR, DESeq, DEXSeq, rMATS, limma)

Single-cell RNA-seq analysis: scater (novice), scran (novice)
Databases and repositories: KEGG, Reactome, Biocarta, GO, CCLE, TCGA, ImmPort/ImmuneSpace
Natural language processing: feature representation (bag of words, tf-idf, word2vec, n-grams), topic modeling (LSA, LDA)
Programming languages: R/Bioconductor, python (novice), C/C++, perl, latex
Data visualization: R/ggplot2, python/Matplotlib (novice)
Scientific programming: NumPy (novice), pandas (novice), scikit-learn (novice)
Computing environments/software development: git/github, Docker, AWS
Experimental techniques: basic molecular biology (e.g., qPCR, protein quantitation)

MENTORING

Juan Vizcarra (Jun 2020 – Present)

Project: *Active Learning in Analysis of Highly-Multiplexed Images*

Thomas Corey (Aug 2019 – Feb 2020)

Project: *CSBC/PSON Knowledge Portal: Semi-automating Curation and Enhancing Semantic Connectivity*

Dr. Matthew Wall (Jun 2019 – Oct 2020)

Project: *Predicting TKI response and discontinuation in CML*

Andrew Lamb (Jan 2018 – Oct 2020)

Project: *A tumor deconvolution DREAM Challenge*

Dr. Milen Nikolov (Jul 2018 – Jan 2019)

Project: *Genotype-phenotype characterization of a cancer cell-line panel*

Dr. Irena Lanc (Oct 2014 – Sept 2016)

Project: *A Second Generation, Multiple Myeloma-Specific, Targeted Sequencing Platform for Detecting Translocations, Copy Number Alterations, and Single Nucleotide Variants*

AWARDS

NIH K12 Calabresi Career Development Award (Clinical Oncology), 2014 – 2016

International Myeloma Foundation Brian D. Novis Junior Research Grant, 2014

SPORE in Leukemia Career Development Award, 2013 – 2014

Dept. of Energy Krell High-Performance Computer Science Fellowship, 2003 – 2007

University of Virginia Dean's Scholarship, 1998 – 1999

Electronic Data Systems Textbook Scholarship (Carnegie Mellon University), 1994

OPEN-SOURCE SOFTWARE

bmm: variational Bayesian mixture modeling

- Performs **variational Bayesian inference** with mixtures of Gaussian, beta, or binomial distributions.
- Available on <http://github.com/genome/bmm> (R package)

sciclone: statistical inference of tumor clones from next-generation sequencing

- Detects evolution of tumor clones using **variational Bayesian** approaches

- Available on <http://github.com/genome/sciclone> (R package)

PATENTS

White BS, Lanc I, Fulton R, Auclair D, Tomasson MH, Automated exposition of known and novel multiple myeloma genomic variants using a single sequencing platform. United States Patent Application 20180126354. May, 2018.

PUBLICATIONS IN SUBMISSION

White BS*, Khan SA*, Ammad-ud-din M, Potdar S, Mason MJ, Tognon CE, Druker BJ, Heckman CA, Kallioniemi O, Kurtz SE, Porkka K, Tyner JW, Aittokallio T, Wennerberg K, Guinney J, Comparative analysis of independent *ex vivo* functional drug screens identifies predictive biomarkers of BCL-2 inhibitor response in AML. **(*: co-first authors)**

Kim S, Srivatsan N, Chavez M, Duncavage E, Vij K, Shirai CL, **White BS**, Jayasinghe R, Ahmed T, Shao J, Nunley R, Ding L, Pehrson JR, Walter MJ, *H2afy* (macroH2A1) Haploinsufficiency Induces Hematologic Malignancies and its Alternative Splicing Regulates B-Lymphopoiesis.

REFEREED PUBLICATIONS

Links to publications available at:

<http://www.ncbi.nlm.nih.gov/sites/myncbi/1PWfbcnlnSaQM/bibliography/40735948/public/?sort=date&direction=descending>

Dang HX, Krasnick BA, **White BS**, Grossman JG, Strand MS, Zhang J, Cabanski CR, Miller CA, Fulton RS, Goedegebuure SP, Fronick CC, Griffith M, Larson DE, Goetz BD, Walker JR, Hawkins WG, Strasberg SM, Linehan DC, Lim KH, Lockhart AC, Mardis ER, Wilson RK, Ley TJ, Maher CA, Fields RC, The clonal evolution of metastatic colorectal cancer, *Sci Adv* 2020; 6(24):eaay9691. doi: 10.1126/sciadv.aay9691. eCollection 2020 Jun. PubMed PMID: 32577507; PubMed Central PMCID: PMC7286679.

Mason MJ*, Schinke C*, Eng CLP*, Towfic F*, Gruber F*, Dervan A*, **White BS**, Pratapa A, Guan Y, Chen H, Cui Y, Li B, Yu T, Neto EC, Mavrommatis K, Ortiz M, Lyzogubov V, Bisht K, Dai H, Schmitz F, Flynt E, Rozelle D, Danziger SA, Ratushny A, Multiple Myeloma DREAM Consortium, Dalton WS, Goldschmidt H, Avet-Loiseau H, Samur M, Hayete B, Sonneveld P, Shain KH, Munshi N, Auclair D, Hose D, Morgan G, Trotter M, Bassett D*, Goke J*, Walker BA*, Thakurta A*, Guinney J*, Multiple Myeloma DREAM Challenge Reveals Epigenetic Regulator *PHF19* As Marker of Aggressive Disease, *Leukemia*, In Press.

White BS*, Lanc I*, O'Neal J, Gupta H, Fulton RS, Schmidt H, Fronick C, Belter EA Jr, Fiala M, King J, Ahmann GJ, DeRome M, Mardis ER, Vij R, DiPersio JF, Levy J, Auclair D, Tomasson MH, A multiple myeloma-specific capture sequencing platform discovers novel translocations and frequent, risk-associated pointed mutations in IGLL5, *Blood Cancer J* 2018; 8(3):35. **(*: co-first authors)**

Lal N*, **White BS***, Goussous G, Pickles O, Mason MJ, Beggs AD, Tanriere P, Willcox BE, Guinney J, Middleton GW, KRAS Mutation and Consensus Molecular

Subtypes 2 and 3 Are Independently Associated with Reduced Immune Infiltration and Reactivity in Colorectal Cancer, *Clin Cancer Res* 2018; 24(1):224-233. (*: **co-first authors**)

Dang HX, **White BS**, Foltz SM, Miller CA, Luo J, Fields RC, Maher CA, ClonEvol: clonal ordering and visualization in cancer sequencing, *Annals of Oncology* 2017; 28(12):3076-3082

Krysiak K, Gomez F, **White BS***, Matlock M, Miller CA, Trani L, Fronick CC, Fulton RS, Kreisel F, Cashen AF, Carson KR, Berrien-Elliott MM, Bartlett NL, Griffith M, Griffith OL, Fehniger TA, Recurrent somatic mutations affecting B-cell receptor signaling pathway genes in follicular lymphoma, *Blood* 2017; 129(4):473-483.

Shirai CL*, **White BS***, Tripathi M*, Tapia R, Ley JN, Ndonwi N, Kim S, Shao J, Carver A, Saez B, Fulton RS, Fronick C, O'Laughlin M, Lagisetti C, Webb TR, Graubert TA, Walter MJ, Mutant U2AF1-expressing cells are sensitive to pharmacological modulation of the spliceosome, *Nat Commun* 2017; 8:14060. (*: **co-first authors**)

Sada A, Jacob F, Leung E, Wang S, **White BS**, Shalloway D, Tumber T, Defining the cellular lineage hierarchy in the interfollicular epidermis of adult skin, *Nat Cell Biol* 2016; 18(6):619-31.

Eissenberg LG, Rettig MP, Ritchey JK, Prior JL, Schwarz SW, Frye J, **White BS**, Fulton RS, Ghobadi A, Cooper ML, Couriel DR, Seegulam ME, Piwnica-Worms D, Dehdashti F, Cornetta K, DiPersio JF, [(18)F]FHBG PET/CT imaging of CD34-TK75 transduced donor T cells in relapsed allogeneic stem cell transplant patients: safety and feasibility, *Mol Ther* 2015 Jun;23(6):1110-22.

Shirai CL, Ley JN, **White BS**, Kim S, Tibbitts J, Shao J, Ndonwi M, Wadugu B, Duncavage EJ, Okeyo-Owuor T, Liu T, Griffith M, McGrath S, Magrini V, Fulton RS, Fronick C, O'Laughlin M, Graubert TA, Walter MJ, Mutant U2AF1 expression alters hematopoiesis and pre-mRNA splicing in vivo, *Cancer Cell* 2015 May 11;27(5):631-43.

Okeyo-Owuor T, **White BS**, Chatrikhi R, Mohan DR, Kim S, Griffith M, Ding L, Ketkar-Kulkarni S, Hundal J, Laird KM, Kielkopf CL, Ley TJ, Walter MJ, Graubert TA., U2AF1 mutations alter sequence specificity of pre-mRNA binding and splicing, *Leukemia* 2015 Apr; 29(4):909-917.

Miller CA*, **White BS***, Dees ND, Griffith M, Welch JS, Griffith OL, Vij R, Tomasson MH, Graubert TA, Walter MJ, Ellis MJ, Schierding W, DiPersio JF, Ley TJ, Mardis ER, Wilson RK, Ding L, SciClone: inferring clonal architecture and tracking the spatial and temporal patterns of tumor evolution, *PLoS Comput Biol* 2014 Aug 7;10(8):e1003665. (*: **co-first authors**)

Hughes AE, Magrini V, Demeter R, Miller CA, Fulton R, Fulton LL, Eades WC, Elliott K, Heath S, Westervelt P, Ding L, Conrad DF, **White BS**, Shao J, Link DC, DiPersio JF, Mardis ER, Wilson RK, Ley TJ, Walter MJ, Graubert TA, Clonal architecture of secondary acute myeloid leukemia defined by single-cell sequencing, *PLoS Genet* 2014 Jul 10;10(7):e1004462.

White BS, DiPersio JF, Genomic tools in acute myeloid leukemia: from the bench to the bedside, *Cancer* 2014 Apr 15;120(8):1134-44.

Meng HW, Pagano JM, **White BS**, Toyoda Y, Min IM, Craighead HG, Shalloway D, Lis JT, Xiao K, Jin MM, Discovering aptamers by cell-SELEX against human soluble growth factors ectopically expressed on yeast cell surface, *PLoS One* 2014 Mar 27;9(3):e93052.

Pagano JM, Kwak H, Waters CT, Sprouse RO, **White BS**, Ozer A, Szeto K, Shalloway D, Craighead HG, Lis JT, Defining NELF-E RNA binding in HIV-1 and promoter-proximal pause regions, *PLoS Genet* 2014 Jan;10(1):e1004090.

Szeto K, Latulippe DR, Ozer A, Pagano JM, **White BS**, Shalloway D, Lis JT, Craighead HG, RAPID-SELEX for RNA aptamers, *PLoS One* 2013 Dec 20;8(12):e82667.

Walter MJ, Shen D, Shao J, Ding L, **White BS**, Kandath C, Miller CA, Niu B, McLellan MD, Dees ND, Fulton R, Elliot K, Heath S, Grillot M, Westervelt P, Link DC, DiPersio JF, Mardis E, Ley TJ, Wilson RK, Graubert TA, Clonal diversity of recurrently mutated genes in myelodysplastic syndromes, *Leukemia* 2013 Jun;27(6):1275-82.

Ozer A*, **White BS***, Lis JT, Shalloway D, Density-dependent cooperative non-specific binding in solid-phase SELEX affinity selection, *Nucleic Acids Res* 2013 Aug 1;41(14):7167-75. (*: co-first authors)

Latulippe DR, Szeto K, Ozer A, Duarte FM, Kelly CV, Pagano JM, **White BS**, Shalloway D, Lis JT, Craighead HG, Multiplexed microcolumn-based process for efficient selection of RNA aptamers, *Anal Chem* 2013 Mar 19;85(6):3417-24.

Lee J, Hoi CS, Lilja KC, **White BS**, Lee SE, Shalloway D, Tumber T, Runx1 and p21 synergistically limit the extent of hair follicle stem cell quiescence in vivo, *Proc Natl Acad Sci U S A* 2013 Mar 19;110(12):4634-9.

Huang J, Yao L, Xu R, Wu H, Wang M, **White BS**, Shalloway D, Zheng X, Activation of Src and transformation by an RPTPalpha splice mutant found in human tumours, *EMBO J* 2011 Jul 1;30(15):3200-11.

Zhang YV, **White BS**, Shalloway DI, Tumber T, Stem cell dynamics in mouse hair follicles: a story from cell division counting and single cell lineage tracing, *Cell Cycle* 2010 Apr 15;9(8):1504-10.

White BS, Shalloway D, Efficient uncertainty minimization for fuzzy spectral clustering, *Phys Rev E Stat Nonlin Soft Matter Phys* 2009 Nov;80(5 Pt 2):056705.

White BS, McKee SA, Quinlan D, A projection-based optimization framework for abstractions with application to the unstructured mesh domain, *In: Proceedings of the 2008 International Conference on Supercomputing* (2008).

White BS, McKee SA, de Supinski BR, Miller B, Quinlan D, Schulz M, Improving the computational intensity of unstructured mesh applications, *In: Proceedings of the 2005 International Conference on Supercomputing* (2005).

Schulz M, **White BS**, McKee SA, Lee H-H, Jeitner J, Owl: next generation system monitoring, *In: Proceedings of Computing Frontiers* (2005).

Quinlan D, Yi Q, Kumfert G, Epperly T, Dahlgren T, Schordan M, **White B**, Toward the automated generation of components from existing source code *In: Second Workshop on Productivity and Performance in High-End Computing (P-PHEC), held in conjunction with HPCA* (2005).

White B, Lepreau J, Stoller L, Ricci R, Guruprasad S, Newbold M, Hibler M, Barb C, Joglekar A, An integrated experimental environment for distributed systems and networks, *In: Fifth Symposium on Operating Systems Design and Implementation* (2002).

White B, Lepreau J, Guruprasad S, Lowering the barrier to wireless and mobile experimentation, *In: HotNets-I* (2002).

White BS, Walker M, Humphrey M, Grimshaw AS, LegionFS: a secure and scalable file system supporting cross-domain high-performance applications, *In: Proceedings of Supercomputing Conference* (2001).

Stoker G, **White BS**, Stackpole E, Highley TJ, Humphrey M, Toward realizable restricted delegation in computational grids, *In: European High Performance Computing and Networking* (2001).

White BS, Grimshaw AS, Nguyen-Tuong A, Grid-based file access: the Legion I/O model, *In: Proceedings of the Ninth IEEE International Symposium on High Performance Distributed Computing* (2000).

Zeigarnik AV, Valdés-Pérez RE, **White BS**, Proposed methodological improvement in the elucidation of chemical reaction mechanisms based on chemist-computer interaction, *Journal of Chemical Education* 2000;77:214.

TEACHING
EXPERIENCE

Division of Oncology, Washington University, St Louis, MO, USA
Genomics and the Era of Personalized Medicine (2015)
Guest Lecturer: Analysis of the Transcriptome

Dept. of Molecular Biology and Genetics, Cornell University, Ithaca, NY, USA
Mathematical Modeling and Computational Statistics of the Molecular Cell (2011)
Guest Lecturer

PRESENTATIONS

White BS*, Khan SA*, Ammad-ud-din M, Potdar S, Mason MJ, Tognon CE, Druker BJ, Heckman CA, Kallioniemi O, Kurtz SE, Porkka K, Tyner JW, Aittokallio T, Wennerberg K, Guinney J, Comparative analysis of independent *ex vivo* functional drug screens identifies predictive biomarkers of BCL-2 inhibitor response in AML. American Society of Hematology (ASH) Annual Meeting, San Diego, CA (2018; Poster; * **co-first author**).

White BS*, Khan SA*, Ammad-ud-din M, Potdar S, Mason MJ, Tognon CE, Druker BJ, Heckman CA, Kallioniemi O, Kurtz SE, Porkka K, Tyner JW, Aittokallio T, Wennerberg K, Guinney J, Comparative analysis of independent *ex vivo* functional drug screens identifies predictive biomarkers of BCL-2 inhibitor response in AML. Beat AML Research Symposium, Portland, OR (2018; Talk; * **co-first author**).

White BS, Khan SA, Ammad-ud-din M, Potdar S, Mason MJ, Tognon CE, Druker BJ, Heckman CA, Kallioniemi O, Kurtz SE, Porkka K, Tyner JW, Aittokallio T, Wennerberg K, Guinney J, Gene expression predicts *ex vivo* drug sensitivity in acute myeloid leukemia. American Association for Cancer Research (AACR) Annual Meeting, San Diego, CA (2018; Poster).

White BS, Shirai CL, Ley JN, Ndonwi M, Okeyo-Owuor T, Kim S, Graubert TA, Walter MJ. U2AF1 Splicing Factor Mutation Dysregulates Other Splicing Factors and Cancer-Associated Genes. Eukaryotic mRNA Processing, Cold Spring Harbor, NY (2015; Poster).

White BS, Shirai CL, Ley JN, Ndonwi M, Okeyo-Owuor T, Kim S, Graubert TA, Walter MJ. Meta-analysis increases power and reduces false discoveries in detecting alternative splicing. Integrative RNA Biology Special Interest Group, Dublin, Ireland (2015; Poster).

White BS, Shirai CL, Ley JN, Ndonwi M, Okeyo-Owuor T, Kim S, Graubert TA, Walter MJ. Meta-analysis increases power and reduces false discoveries in detecting alternative splicing. International Conference on Intelligent Systems for Molecular Biology/European Conference on Computational Biology (ISMB/ECCB), Dublin, Ireland (2015; Poster).

Dees, ND*, Miller CA*, **White, BS***, Schierding W, Vij R, Tomasson MH, Welch JS, Graubert TA, Walter MJ, Ley TJ, DiPersio J, Mardis ER, Wilson RK, Ding L. Tumor clonality detection using next generation sequencing data. American Association for Cancer Research (AACR) Annual Meeting, New Orleans, LA (2013; Poster; * **co-first author**).

Okeyo-Owuor T, **White BS**, Mohan DR, Chatrikhi R, Kim S, Griffith M, Ding L, Ketkar-Kulkarni S, Hundal J, Laird KM, Kielkopf CL, Ley TJ, Walter MJ, Graubert TA. U2AF1 Mutations Alter pre-mRNA Splicing in Hematological Disorders.

- Gordon Research Conference on Post-Transcriptional Gene Regulation, Newport, RI (2014; Poster).
- White BS**, Ozer A, Lis JT, Shalloway D. Optimizing SELEX with high-throughput sequencing. American Association for Cancer Research (AACR) Annual Meeting, Philadelphia, PA (2012; Poster)
- White B**, Shalloway D. Macrostate Data Clustering: A new analysis tool for biological data sets. Cold Spring Harbor Laboratory Meeting on Systems Biology: Global Regulation of Gene Expression, Cold Spring Harbor, NY (2010; Poster).
- White B**, Korenblum D, Shalloway D. Geometric Perspectives on Uncertainty Minimization for Fuzzy Spectral Clustering. New York Conference on Applied Mathematics, Rochester, NY (2009; Poster and talk).
- White B**, Zhang YV, Lee J, Tumber T, Shalloway D. Inferring Stem Cell Dynamics: Mathematical Modeling of Division-Induced H2B-GFP Expression Dilution in the Hair Follicle Bulge. Stem Cell Symposium, Ithaca, NY (2009; Poster).
- White B**, Zhang YV, Tumber T, Shalloway D. Mathematical Modeling of Stem Cell Dynamics in the Mouse Hair Follicle System. Symposium of the Tri-Institutional Program in Computational Biology and Medicine, Ithaca, NY (2009; Poster).
- White B**, Shalloway D. Macrostate Data Clustering: A new analysis tool for biological data sets. Symposium of the Tri-Institutional Program in Computational Biology and Medicine, Ithaca, NY (2008; Poster).
- White B**, McKee S, de Supinski B, Miller B, Quinlan, D, Schulz M. A Semantics-Based Approach to Optimizing Unstructured Mesh Abstractions. University of Rochester Systems Meeting, Rochester, NY (2006; Talk).
- White BS**, McKee SA, de Supinski BR, Miller B, Quinlan D, Schulz M. Improving the Computational Intensity of Unstructured Mesh Applications. International Conference on Supercomputing (2005; Talk).
- White B**, Lepreau J, Stoller L, Ricci R, Guruprasad S, Newbold M, Hibler M, Barb C, Joglekar A. An Integrated Experimental Environment for Distributed Systems and Networks. Symposium on Operating Systems Design and Implementation (2002; Talk).
- White BS**, Walker M, Humphrey M, Grimshaw AS. LegionFS: A Secure and Scalable File System Supporting Cross-Domain High-Performance Applications. Supercomputing Conference (2001; Talk).
- Stoker G, **White BS**, Stackpole E, Highley TJ, Humphrey M. Toward Realizable Restricted Delegation in Computational Grids. European High Performance Computing and Networking Conference (2001; Talk).
- White BS**, Grimshaw AS, Tuong AN. Grid-Based File Access: The Legion I/O Model. International Symposium on High Performance Distributed Computing (2000; Talk).

