

George Wright

National Institutes of Health/NCI/DCDT/BRB
9609 Medical Center Dr Rm 5-W108 MSC 9735
Bethesda MD 20892
(240) 276-6027
wrightge@mail.nih.gov

Education

University of Maryland at College Park

M.A. (1998) Major: Statistics

Ph.D. (December 2000) Major: Statistics

Dissertation: "Efficient Semiparametric Estimation via Finite Dimensional Likelihoods"

Reed College

B.A. (1993) Major: Mathematics

Elected to **Phi Beta Kappa** Honor Society

Under graduate thesis "Approach to Randomness of the Bernoulli-Leplace Model of Diffusion"

Experience

National Cancer Institute Mathematical Statistician (May 2001-present)

Provides statistical support in the analysis of gene expression and chromosomal abnormalities, particularly as they relate to the molecular characterization of Lymphoma. Acts as Leader of the bioinformatics/biostatistics core for the Lymphoma Leukemia Molecular profiling project. Develops diagnostic tools for lymphoma classification.

National Cancer Institute Post Doctoral Fellow (Dec. 2000-May 2001)

Provided statistical support in the analysis of micro array data.

Food and Drug Administration Research assistant (June 1996-Dec. 1997)

Worked under an Oak Ridge Fellowship funded by the Institute of Women's Health. Analyzed data from Large sample clinical trials in order to investigate observed gender differences in mortality from Myocardial infarction. Findings resulted in the paper "Clinical trial (GUSTO-1 and INJECT) Evidence of Earlier Death for men than Women after Acute Myocardial Infarction"

University of Maryland at College Park Teaching Assistant (1993-1999)

Presented Lectures and led Discussions for undergraduate mathematics courses in topics ranging from introductory statistics to mathematical calculus.

Los Alamos National Laboratory Research Assistant (Summers 1992-1995)

Worked on a public-private partnership in the area of neural networked automotive control. Provided computer and mathematical support for the design and implementation of several neural networked architectures, to be used in controlling fuel injection, anti-lock brakes and four wheel steering. Wrote the technical report "Using Function Non-Linearity to Determine centers for Local Linear Models."

Awards

Web of Science Highly Cited Researcher (2019)

NCI Director's Award of Merit (2018)

NIH Director's Award (2010)

NCI Merit Award (2010)

Elected to Phi Beta Kappa Reed College (1993)

Publications

1. Dersh, D., et al., Genome-wide Screens Identify Lineage- and Tumor-Specific Genes Modulating MHC-I- and MHC-II-Restricted Immunosurveillance of Human Lymphomas. *Immunity*, 2021. 54(1): p. 116-131.
2. Ramis-Zaldivar, J.E., et al., MAPK and JAK-STAT pathways dysregulation in plasmablastic lymphoma. *Haematologica*, 2021. 106(10): p. 2682-2693.
3. Shaffer, A.L., et al., Overcoming Acquired Epigenetic Resistance to BTK Inhibitors. *Blood Cancer Discovery*, 2021. 2(6): p. 630-647.
4. Wilson, W.H., et al., Phase 1b/2 study of ibrutinib and lenalidomide with dose-adjusted EPOCH-R in patients with relapsed/refractory diffuse large B-cell lymphoma*. *Leukemia & Lymphoma*, 2021. 62(9): p. 2094-2106.
5. Wright, G.W., et al., A Probabilistic Classification Tool for Genetic Subtypes of Diffuse Large B Cell Lymphoma with Therapeutic Implications. *Cancer Cell*, 2020. 37(4): p. 551-568.
6. Roschewski, M., et al., Inhibition of Bruton tyrosine kinase in patients with severe COVID-19. *Science Immunology*, 2020. 5(48).
7. Fish, K., et al., Rewiring of B cell receptor signaling by Epstein-Barr virus LMP2A. *Proceedings of the National Academy of Sciences of the United States of America*, 2020. 117(42): p. 26318-26327.
8. Danforth, D.N., et al., Characteristics of Breast Ducts in Normal-Risk and High-risk Women and Their Relationship to Ductal Cytologic Atypia. *Cancer Prevention Research*, 2020. 13(12): p. 1027-1036.
9. Choi, J., et al., Regulation of B cell receptor-dependent NF-kappa B signaling by the tumor suppressor KLHL14. *Proceedings of the National Academy of Sciences of the United States of America*, 2020. 117(11): p. 6092-6102.
10. Young, R.M., et al., Taming the Heterogeneity of Aggressive Lymphomas for Precision Therapy, in *Annual Review of Cancer Biology*, Vol 3. 2019. p. 429-455.
11. Grande, B.M., et al., Genome-wide discovery of somatic coding and non-coding mutations in pediatric endemic and sporadic Burkitt lymphoma. *Blood*, 2019.
12. Wright, G.W., W.H. Wilson, and L.M. Staudt, Genetics of Diffuse Large B-Cell Lymphoma. *N Engl J Med*, 2018. 379(5): p. 493-494.
13. Schmitz, R., et al., Genetics and Pathogenesis of Diffuse Large B-Cell Lymphoma. *N Engl J Med*, 2018. 378(15): p. 1396-1407.
14. Phelan, J.D., et al., A multiprotein supercomplex controlling oncogenic signalling in lymphoma. *Nature*, 2018. 560(7718): p. 387-391.
15. Nakagawa, M., et al., Targeting the HTLV-I-Regulated BATF3/IRF4 Transcriptional Network in Adult T Cell Leukemia/Lymphoma. *Cancer Cell*, 2018. 34(2): p. 286-297 e10.
16. Mottok, A., et al., Molecular classification of primary mediastinal large B-cell lymphoma using routinely available tissue specimens. *Blood*, 2018. 132(22): p. 2401-2405.
17. Clot, G., et al., A gene signature that distinguishes conventional and leukemic nonnodal mantle cell lymphoma helps predict outcome. *Blood*, 2018. 132(4): p. 413-422.
18. Scott, D.W., et al., New Molecular Assay for the Proliferation Signature in Mantle Cell Lymphoma Applicable to Formalin-Fixed Paraffin-Embedded Biopsies. *Journal of Clinical Oncology*, 2017. 35(15): p. 1668-1677.
19. Jais, J.P., et al., Reliable subtype classification of diffuse large B-cell lymphoma samples from GELA LNH2003 trials using the Lymph2Cx gene expression assay. *Haematologica*, 2017. 102(10): p. E404-E406.

20. Czuczman, M.S., et al., A Phase 2/3 Multicenter, Randomized, Open-Label Study to Compare the Efficacy and Safety of Lenalidomide Versus Investigator's Choice in Patients with Relapsed or Refractory Diffuse Large B-Cell Lymphoma. *Clinical Cancer Research*, 2017. 23(15): p. 4127-4137.
21. Yang, Y.B., et al., Targeting Non-proteolytic Protein Ubiquitination for the Treatment of Diffuse Large B Cell Lymphoma. *Cancer Cell*, 2016. 29(4): p. 494-507.
22. Rui, L.X., et al., Epigenetic gene regulation by Janus kinase 1 in diffuse large B-cell lymphoma. *Proceedings of the National Academy of Sciences of the United States of America*, 2016. 113(46): p. E7260-E7267.
23. Hodson, D.J., et al., Regulation of normal B-cell differentiation and malignant B-cell survival by OCT2. *Proceedings of the National Academy of Sciences of the United States of America*, 2016. 113(14): p. E2039-E2046.
24. Ceribelli, M., et al., A Druggable TCF4-and BRD4-Dependent Transcriptional Network Sustains Malignancy in Blastic Plasmacytoid Dendritic Cell Neoplasm. *Cancer Cell*, 2016. 30(5): p. 764-778.
25. Yuan, J., et al., Identification of Primary Mediastinal Large B-cell Lymphoma at Nonmediastinal Sites by Gene Expression Profiling. *American Journal of Surgical Pathology*, 2015. 39(10): p. 1322-1330.
26. Wilson, W.H., et al., Targeting B cell receptor signaling with ibrutinib in diffuse large B cell lymphoma. *Nature Medicine*, 2015. 21(8): p. 922-926.
27. Scott, D.W., et al., Prognostic Significance of Diffuse Large B-Cell Lymphoma Cell of Origin Determined by Digital Gene Expression in Formalin-Fixed Paraffin-Embedded Tissue Biopsies. *Journal of Clinical Oncology*, 2015. 33(26): p. 2848-2856.
28. Iqbal, J., et al., Global microRNA expression profiling uncovers molecular markers for classification and prognosis in aggressive B-cell lymphoma. *Blood*, 2015. 125(7): p. 1137-1145.
29. Yang, Y.B., et al., Essential Role of the Linear Ubiquitin Chain Assembly Complex in Lymphoma Revealed by Rare Germline Polymorphisms. *Cancer Discovery*, 2014. 4(4): p. 480-493.
30. Wright, G.W., L.E. Dodd, and E.L. Korn, Inherent difficulties in nonparametric estimation of the cumulative distribution function using observations measured with error: Application to high-dimensional microarray data. *Statistics and Its Interface*, 2014. 7(1): p. 69-73.
31. Scott, D.W., et al., Determining cell-of-origin subtypes of diffuse large B-cell lymphoma using gene expression in formalin-fixed paraffin-embedded tissue. *Blood*, 2014. 123(8): p. 1214-1217.
32. Schmitz, R., et al., Oncogenic Mechanisms in Burkitt Lymphoma. *Cold Spring Harbor Perspectives in Medicine*, 2014. 4(2).
33. Iqbal, J., et al., Gene expression signatures delineate biological and prognostic subgroups in peripheral T-cell lymphoma. *Blood*, 2014. 123(19): p. 2915-2923.
34. Ceribelli, M., et al., Blockade of oncogenic I kappa B kinase activity in diffuse large B-cell lymphoma by bromodomain and extraterminal domain protein inhibitors. *Proceedings of the National Academy of Sciences of the United States of America*, 2014. 111(31): p. 11365-11370.
35. Bouska, A., et al., Genome-wide copy-number analyses reveal genomic abnormalities involved in transformation of follicular lymphoma. *Blood*, 2014. 123(11): p. 1681-1690.
36. Xue, S.A., et al., Human MHC Class I-restricted high avidity CD4(+) T cells generated by co-transfer of TCR and CD8 mediate efficient tumor rejection in vivo. *Oncoimmunology*, 2013. 2(1).
37. Dunleavy, K., et al., Dose-Adjusted EPOCH-Rituximab Therapy in Primary Mediastinal B-Cell Lymphoma. *New England Journal of Medicine*, 2013. 368(15): p. 1408-1416.
38. Bodor, C., et al., EZH2 mutations are frequent and represent an early event in follicular lymphoma. *Blood*, 2013. 122(18): p. 3165-3168.
39. Barlow, J.H., et al., Identification of Early Replicating Fragile Sites that Contribute to Genome Instability. *Cell*, 2013. 152(3): p. 620-632.

40. Zhang, X., et al., Myc represses miR-15a/miR-16-1 expression through recruitment of HDAC3 in mantle cell and other non-Hodgkin B-cell lymphomas. *Oncogene*, 2012. 31(24): p. 3002-3008.
41. Yang, Y.B., et al., Exploiting Synthetic Lethality for the Therapy of ABC Diffuse Large B Cell Lymphoma. *Cancer Cell*, 2012. 21(6): p. 723-737.
42. Schmitz, R., et al., Burkitt lymphoma pathogenesis and therapeutic targets from structural and functional genomics. *Nature*, 2012. 490(7418): p. 116-120.
43. Rao, E., et al., The miRNA-17 similar to 92 cluster mediates chemoresistance and enhances tumor growth in mantle cell lymphoma via PI3K/AKT pathway activation. *Leukemia*, 2012. 26(5): p. 1064-1072.
44. Johnson, N.A., et al., Concurrent Expression of MYC and BCL2 in Diffuse Large B-Cell Lymphoma Treated With Rituximab Plus Cyclophosphamide, Doxorubicin, Vincristine, and Prednisone. *Journal of Clinical Oncology*, 2012. 30(28): p. 3452-3459.
45. Rimsza, L.M., et al., Accurate Classification of Diffuse Large B-Cell Lymphoma into Germinal Center and Activated B-Cell Subtypes Using a Nuclease Protection Assay on Formalin-Fixed, Paraffin-Embedded Tissues. *Clinical Cancer Research*, 2011. 17(11): p. 3727-3732.
46. Ngo, V.N., et al., Oncogenically active MYD88 mutations in human lymphoma. *Nature*, 2011. 470(7332): p. 115-U133.
47. Cardesa-Salzman, T.M., et al., High microvessel density determines a poor outcome in patients with diffuse large B-cell lymphoma treated with rituximab plus chemotherapy. *Haematologica-the Hematology Journal*, 2011. 96(7): p. 996-1001.
48. Williams, P.M., et al., A Novel Method of Amplification of FFPET-Derived RNA Enables Accurate Disease Classification with Microarrays. *Journal of Molecular Diagnostics*, 2010. 12(5): p. 680-686.
49. Wang, Y., et al., Critical role for transcriptional repressor Snail2 in transformation by oncogenic RAS in colorectal carcinoma cells. *Oncogene*, 2010. 29(33): p. 4658-4670.
50. Rui, L.X., et al., Cooperative Epigenetic Modulation by Cancer Amplicon Genes. *Cancer Cell*, 2010. 18(6): p. 590-605.
51. Hartmann, E.M., et al., Pathway discovery in mantle cell lymphoma by integrated analysis of high-resolution gene expression and copy number profiling. *Blood*, 2010. 116(6): p. 953-961.
52. Davis, R.E., et al., Chronic active B-cell-receptor signalling in diffuse large B-cell lymphoma. *Nature*, 2010. 463(7277): p. 88-U97.
53. O'Riain, C., et al., Array-based DNA methylation profiling in follicular lymphoma. *Leukemia*, 2009. 23(10): p. 1858-1866.
54. Leich, E., et al., Follicular lymphomas with and without translocation t(14;18) differ in gene expression profiles and genetic alterations. *Blood*, 2009. 114(4): p. 826-834.
55. Dunleavy, K., et al., Differential efficacy of bortezomib plus chemotherapy within molecular subtypes of diffuse large B-cell lymphoma. *Blood*, 2009. 113(24): p. 6069-6076.
56. Shaffer, A.L., et al., IRF4 addiction in multiple myeloma. *Nature*, 2008. 454(7201): p. 226-231.
57. Salaverria, I., et al., Chromosomal alterations detected by comparative genomic hybridization in subgroups of gene expression-defined Burkitt's lymphoma. *Haematologica-the Hematology Journal*, 2008. 93(9): p. 1327-1334.
58. O'Shea, D., et al., The presence of TP53 mutation at diagnosis of follicular lymphoma identifies a high-risk group of patients with shortened time to disease progression and poorer overall survival. *Blood*, 2008. 112(8): p. 3126-3129.
59. Lenz, G., et al., Molecular subtypes of diffuse large B-cell lymphoma arise by distinct genetic pathways. *Proceedings of the National Academy of Sciences of the United States of America*, 2008. 105(36): p. 13520-13525.
60. Lenz, G., et al., Stromal Gene Signatures in Large-B-Cell Lymphomas. *New England Journal of Medicine*, 2008. 359(22): p. 2313-2323.

61. Lenz, G., et al., Oncogenic CARD11 mutations in human diffuse large B cell lymphoma. *Science*, 2008. 319(5870): p. 1676-1679.
62. Lam, L.T., et al., Cooperative signaling through the signal transducer and activator of transcription 3 and nuclear factor-kappa B pathways in subtypes of diffuse large B-cell lymphoma. *Blood*, 2008. 111(7): p. 3701-3713.
63. Lam, L.T., et al., Compensatory IKK alpha activation of classical NF-kappa B signaling during IKK beta inhibition identified by an RNA interference sensitization screen. *Proceedings of the National Academy of Sciences of the United States of America*, 2008. 105(52): p. 20798-20803.
64. Wiestner, A., et al., Point mutations and genomic deletions in CCND1 create stable truncated cyclin D1 mRNAs that are associated with increased proliferation rate and shorter survival. *Blood*, 2007. 109(11): p. 4599-4606.
65. Salaverria, I., et al., Specific secondary genetic alterations in mantle cell lymphoma provide prognostic information independent of the gene expression-based proliferation signature. *Journal of Clinical Oncology*, 2007. 25(10): p. 1216-1222.
66. Lusa, L., et al., Appropriateness of some resampling-based inference procedures for assessing performance of prognostic classifiers derived from microarray data. *Statistics in Medicine*, 2007. 26(5): p. 1102-1113.
67. Lenz, G., et al., Aberrant immunoglobulin class switch recombination and switch translocations in activated B cell-like diffuse large B cell lymphoma. *Journal of Experimental Medicine*, 2007. 204(3): p. 633-643.
68. Iqbal, J., et al., Distinctive patterns of BCL6 molecular alterations and their functional consequences in different subgroups of diffuse large B-cell lymphoma. *Leukemia*, 2007. 21(11): p. 2332-2343.
69. Davies, A.J., et al., Transformation of follicular lymphoma to diffuse large B-cell lymphoma proceeds by distinct oncogenic mechanisms. *British Journal of Haematology*, 2007. 136(2): p. 286-293.
70. Annunziata, C.M., et al., Frequent engagement of the classical and alternative NF-kappa B pathways by diverse genetic abnormalities in multiple myeloma. *Cancer Cell*, 2007. 12(2): p. 115-130.
71. Shaffer, A.L., et al., A library of gene expression signatures to illuminate normal and pathological lymphoid biology. *Immunological Reviews*, 2006. 210: p. 67-85.
72. Roberts, R.A., et al., Loss of major histocompatibility class II gene and protein expression in primary mediastinal large B-cell lymphoma is highly coordinated and related to poor patient survival. *Blood*, 2006. 108(1): p. 311-318.
73. Iqbal, J., et al., BCL2 expression is a prognostic marker for the activated B-cell-like type of diffuse large B-cell lymphoma. *Journal of Clinical Oncology*, 2006. 24(6): p. 961-968.
74. Dave, S.S., et al., Molecular diagnosis of Burkitt's lymphoma. *New England Journal of Medicine*, 2006. 354(23): p. 2431-2442.
75. Zou, H. and T. Hastie, Regularization and variable selection via the elastic net. *Journal of the Royal Statistical Society Series B-Statistical Methodology*, 2005. 67: p. 301-320.
76. Fu, K., et al., Cyclin D1-negative mantle cell lymphoma: a clinicopathologic study based on gene expression profiling. *Blood*, 2005. 106(13): p. 4315-4321.
77. Dunleavy, K., et al., B-cell recovery following rituximab-based therapy is associated with perturbations in stromal derived factor-1 and granulocyte homeostasis. *Blood*, 2005. 106(3): p. 795-802.
78. Bea, S., et al., Diffuse large B-cell lymphoma subgroups have distinct genetic profiles that influence tumor biology and improve gene-expression-based survival prediction. *Blood*, 2005. 106(9): p. 3183-3190.
79. Dave, S.S., et al., Prediction of survival in follicular lymphoma based on molecular features of tumor-infiltrating immune cells. *New England Journal of Medicine*, 2004. 351(21): p. 2159-2169.

80. Wright, G.W. and R.M. Simon, A random variance model for detection of differential gene expression in small microarray experiments. *Bioinformatics*, 2003. 19(18): p. 2448-2455.
81. Wright, G., et al., A gene expression-based method to diagnose clinically distinct subgroups of diffuse large B cell lymphoma. *Proceedings of the National Academy of Sciences of the United States of America*, 2003. 100(17): p. 9991-9996.
82. Wiestner, A., et al., ZAP-70 expression identifies a chronic lymphocytic leukemia subtype with unmutated immunoglobulin genes, inferior clinical outcome, and distinct gene expression profile. *Blood*, 2003. 101(12): p. 4944-4951.
83. Rosenwald, A., et al., The proliferation gene expression signature is a quantitative integrator of oncogenic events that predicts survival in mantle cell lymphoma. *Cancer Cell*, 2003. 3(2): p. 185-197.
84. Rosenwald, A., et al., Molecular diagnosis of primary mediastinal B cell lymphoma identifies a clinically favorable subgroup of diffuse large B cell lymphoma related to Hodgkin lymphoma. *Journal of Experimental Medicine*, 2003. 198(6): p. 851-862.
85. Kovanen, P.E., et al., Analysis of gamma(c)-family cytokine target genes - Identification of dual-specificity phosphatase 5 (DUSP5) as a regulator of mitogen-activated protein kinase activity in interleukin-2 signaling. *Journal of Biological Chemistry*, 2003. 278(7): p. 5205-5213.
86. Glebov, O.K., et al., Distinguishing right from left colon by the pattern of gene expression. *Cancer Epidemiology Biomarkers & Prevention*, 2003. 12(8): p. 755-762.
87. Rosenwald, A., et al., The use of molecular profiling to predict survival after chemotherapy for diffuse large-B-cell lymphoma. *New England Journal of Medicine*, 2002. 346(25): p. 1937-1947.
88. Rieves, D., et al., Clinical trial (GUSTO-1 and INJECT) evidence of earlier death for men than women after acute myocardial infarction. *American Journal of Cardiology*, 2000. 85(2): p. 147-153.

Patents

1. CA2659194(A1) METHODS FOR IDENTIFYING, DIAGNOSING, AND PREDICTING SURVIVAL OF LYMPHOMAS (Canada)
2. CA2726811(A1) SURVIVAL PREDICTOR FOR DIFFUSE LARGE B CELL LYMPHOMA (Canada)
3. CA2897828(A1) METHODS FOR IDENTIFYING, DIAGNOSING, AND PREDICTING SURVIVAL OF LYMPHOMAS (Canada)
4. EP2294420(B1) SURVIVAL PREDICTOR FOR DIFFUSE LARGE B CELL LYMPHOMA (Europe)
5. EP2299377(A1) METHODS FOR IDENTIFYING, DIAGNOSING, AND PREDICTING SURVIVAL OF LYMPHOMAS (Europe)
6. US131475(B2) METHODS FOR IDENTIFYING, DIAGNOSING, AND PREDICTING SURVIVAL OF LYMPHOMAS (United States)
7. US20110152115(A1) METHODS FOR IDENTIFYING, DIAGNOSING, AND PREDICTING SURVIVAL OF LYMPHOMAS (United States)
8. US20110195064(A1) SURVIVAL PREDICTOR FOR DIFFUSE LARGE B CELL LYMPHOMA (United States)
9. US20120225793(A1) METHODS FOR IDENTIFYING, DIAGNOSING, AND PREDICTING SURVIVAL OF LYMPHOMAS (United States)
10. US20150132297(A1) SURVIVAL PREDICTOR FOR DIFFUSE LARGE B CELL LYMPHOMA (United States)
11. US20150167088(A1) METHODS FOR IDENTIFYING, DIAGNOSING, AND PREDICTING SURVIVAL OF LYMPHOMAS (United States)
12. WO2008013910(A2) METHODS FOR IDENTIFYING, DIAGNOSING, AND PREDICTING SURVIVAL OF LYMPHOMAS (Worldwide)
13. WO2009149359(A2) SURVIVAL PREDICTOR FOR DIFFUSE LARGE B CELL LYMPHOMA (Worldwide)
14. WO2015069790(A1) METHODS FOR IDENTIFYING, DIAGNOSING, AND PREDICTING SURVIVAL OF LYMPHOMAS (Worldwide)

Patent Applications

1. No. 62/325,213 EVALUATION OF MANTLE CELL LYMPHOMA AND METHODS RELATED THERETO (United States)