Guolian Kang, Ph.D.

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1. Current Position at St Jude

Associate Member, Department of Biostatistics 09/2017 - Present
St. Jude Children's Research Hospital
Memphis, TN 38105

2. Education and Training (list all degrees awarded and training programs completed)

B.S. in Mathematics, Qufu Normal University, Qufu, Shandong Province, China 07/2000
M.S. in Applied Mathematics, Qufu Normal University, Qufu, Shandong Province, China 07/2003
Ph.D. in Systems Modeling and Control with specialization in Biostatistics, Institute of Systems Science, Chinese Academy of Sciences, China 07/2006

3. Key Accomplishments Summary

For over twelve years I have been working on developing and applying mathematical and statistical methods to detect genetic and non-genetic factors that affect complex diseases and clinical outcomes of interest, and on constructing/modeling genetic networks and then relating these networks to clinical traits of interest. Along the way, I have accumulated in-depth interdisciplinary knowledge of biostatistics, statistical genetics/genomics, broad expertise in system modeling of complex traits, and clinical trials design.

On the methodological side, I have developed a generalized sequential testing procedure for a homogeneous population and a two-stage procedure capitalizing on admixture for an admixed population for genome wide association studies. I have also examined the power of two-phase case-control designs for the assessment of multiplicative gene-environment (G-E) interactions or for assessing genetic or environmental effects in the presence of G-E interactions. Currently, I am investigating the efficiency and power of an extreme phenotype sequencing design for the identification of rare variants in next generation sequencing studies. I have published a number of methodological papers in prestigious journals such as *Biostatistics*, *Statistics in Medicine*, *Genetics*, *Bioinformatics*, and *Statistical Applications in Genetics and Molecular Biology*. I have developed four user-friendly R packages: SV, SV_{2bc}, TRIM, and STEPS. To the end, two of my methodological works have been featured in many international medias such as *Nature Reviews Genetics* (UK) and *International Adaptogens* (Venezuela), one has been included in the book of *Transgénicos* (Cuba), and another two works have been highlighted in St. Jude Scientific Report and St. Jude PROMISE magazine, respectively.

On the applied side, I have been very successful and productive in conducting collaborative scientific researches covering all three components: pre-clinical, clinical and translational, regarding designing, monitoring and reporting clinical trials, paper publication, and securing national grant supports. Details are below:

For translational research: I have been/am co-investigator on several NIH-funded grants and a statistical geneticist on a recently funded study of "Genomic analysis of familial leukemia". I designed one largest population-based St. Jude genomics studies of 1000 Sickle Cell Disease Genomics Projects (1000SGP), and two largest family-based St. Jude genomics studies of non-malignant hematologic diseases (INSIGHT) and cancers (FAMILY). I have been successfully collaborating with researchers from very diverse backgrounds by applying methodologies I developed and publicly available statistical genetic and bioinformatics software and R program and providing crucial guidance to analyze the large-scale genomic data. I have been involved in the study of many phenotypes including schizophrenia, chronic kidney disease, acute lymphoblastic leukemias, adrenocortical tumor, and sickle cell diseases, which lead to peer-reviewed publications in top

journals such as *Nature Genetics*, *Journal of Clinical Oncology*, *Clinical Cancer Research,* and *Journal of the National Cancer Institute*.

For pre-clinical and clinical research: as the sole faculty member in our department who collaborates with investigators in Departments of Hematology and Bone Marrow Transplantation and Cellular Therapy, I provide statistical supports, including statistical designs for new protocols, monitoring the active treatment St. Jude studies, data analyses and interpretation, and writing of relevant manuscripts and of statistical sections of grant applications. I am the biostatistician for several federally funded grants aiming at developing gene therapy for patients with sickle cell disease (SCD) and the lysosomal storage disease galactosialidosis. I am the principal investigator (PI) of the Data Coordinating Center for finding the optimal dose of the Hydroxyurea in treating SCD patients, which is multi-center randomized clinical trial. I have also designed and been conducting two international multiple-site clinical trials for the Children's Oncology Group. The related findings lead to peer-reviewed publications in top journals such as *Nature Cell Biology*, *Journal of Clinical Oncology*, and *Journal of Experimental Medicine*.

In summary, my demonstrated interdisciplinary research experiences in statistical genomics, biostatistics and clinical trials, as well as successful collaboration experiences have prepared me to successfully conduct the projects.

4. Professional Career

Research Assistant 09/2003-02/2006
Chinese Academy of Sciences, China
Beijing, China

Visiting Scholar 03/2006-06/2007
Department of Statistics and Probability
Michigan State University
East Lansing, MI

Postdoctoral Fellow 07/2007-12/2009
Department of Biostatistics
The University of Alabama at Birmingham
East Lansing, MI

Postdoctoral Researcher 12/2009-12/2011
Department of Biostatistics and Epidemiology
University of Pennsylvania
Philadelphia, PA

Assistant Member 12/2011-09/2017
Department of Biostatistics
St. Jude Children's Research Hospital
Memphis, TN 38105

5. Professional Memberships

American Statistical Association	2008-present
American Society of Human Genetics	2008-present
Children's Oncology Group	2012-present
International Chinese Statistical Association	2014-present

6. Editorial Board Appointments

Editorial team: Journal of Public Health and Epidemiology 2009-

Editorial team: Journal of Medical Genetics and Genomics 2010-

Review editorial board: Frontiers in Statistical Genetics and Methodology 2011-

Editorial Board (Computational Biology Domain), The Scientific World Journal 2013-2017

Guest Associate Chief Editor: special issue about “Design and analysis of genome-wide association and next generation sequencing studies in cancer pharmacogenomics” on Frontiers in Genetics 05/2014

7. Grant Review / Study Activities

NIH-ZRG1-PSE-U(90)-S 06/2015

MRC DPFS, UK 11/2017

8. Honors and Awards

Research Assistant Fellowship, Chinese Academy of Science (China) 07/2003-02/2006

Spring 2008 Career Enhancement Award, The University of Alabama at Birmingham (USA) 2008

Travel fellowship from International Genetic epidemiology Society (USA) 2008

The Science Unbound Foundation Best Paper Award in Statistical Genetics Research (USA) 2009

Genetic Analysis workshop 17 travel award (USA) 2010

The Science Unbound Foundation Best Paper Award in General Statistics Research (USA) 2012

Travel awards from the 3rd Workshop on Biostatistics and Bioinformatics held at Georgia State University (USA) 2014

2014 National Institute of General Medical Sciences (NIGMS) Bursary Award 2014

Travel fellowship from the 4th NIGMS-funded Short Course on Statistical Genetics & Genomics, UAB (USA) 2014

9. Institutional and Committee Assignments

Biostatistics Protocol Review Committee 12/2011-

Lead Biostatistician for Department of Bone Marrow Transplantation and Cellular Therapy 12/2011-

Lead Biostatistician for Department of Hematology 12/2011-

Biostatistics Biostatistician Promotion Committee 06/2015-05/2018

Biostatistics Social Committee 07/2017-

10. Professional Administrative Services

The 24th Chinese Control Conference, Guangzhou, China (Co-chair) 07/2005
The 2009 Joint statistical meetings, Washington DC (Chair) 08/2009

Atherosclerosis	2007 -
Behavior Genetics	2008 -
BMC Genomics	2008 -
Computational Statistics and Data Analysis	2009 -
Journal of Medical Genetics and Genomics	2009 -
Journal of Public Health and Epidemiology	2009 -
NeuroQuantology	2009 -
Statistical Applications in Genetics and Molecular Biology	2010 -
Human Heredity	2011 -
Journal of Applied Statistics	2012 -
Journal of Statistical Computation and Simulation	2012 -
Journal of Theoretical Biology	2012 -
Briefings in Bioinformatics	2012 -
PLOS One	2013 -
The Scientific World Journal	2013 -
Bioinformatics	2014 -
BMC Genetics	2014 -
Current Genomics	2015 -
BMC Cancer	2016 -
Cancer	2017 -
BMC Bioinformatics	2018 -
Genomics	2018 -
G3	2018 -

11. Formal Education/Teaching Activities

Lecturer for Short Courses or Workshops

Statistical Genetics Workshop, Taiyuan, China, Lecturer 06/2016

Statistical Programming Language R, Memphis, USA, Lecturer 11/2017

Academic Supervision

Postdoc
Wenjian Bi 08/2015-

Current Biostatistics Team Members

Anusha Sunkara, Senior Biostatistician 12/2011-

Jeffrey Gossett, Senior Biostatistician 03/2018-

Past Biostatistics Team Member

Matthew Paul Smeltzer 12/2011-05/2015
Current position, Assistant Professor, School of Public Health, The University of Memphis

Qinlei Huang 10/2014-12/2015
Current position, Biostatistician, Everest Clinical Research, Exceptional Quality CRO, New Jersey

Joseph Moen 06/2015-09/2016
Current position, Statistical Data Analyst, Division of Biostatistics, Washington University in St. Louis

Chen Li, Statistical Analyst 01/2017-03/2018

12. Grant Awards

A. Active Grants:

1 R34HL127162-01A1 Guolian Kang (PI) 04/01/2016 - 10/31/2019
Hydroxyurea Management in Kids: Intensive versus Stable Dosage Strategies (HUGKISS) (Data Coordinating Center)
Will be responsible for all computing and statistical components of the trial; design and develop the computing infrastructure that will provide a secure, paperless data management and reporting system for the trial.
Role: PI
Percent of Effort: 10%

HL1236999-01 Charles G Mullighan (PI) 11/08/2016 - 11/07/2017
Genomic analysis of familial leukemia
Will be responsible for statistical genetics
Role: Statistical Geneticist
Percent of Effort: 5%

1U01HL133996-01 Jane Hankins (PI) 08/08/2016 - 06/30/2020
Text Messaging to Improve Hydroxyurea Utilization
Will be responsible for all the statistical components of the three phases study.
Role: Biostatistician
Percent of Effort: 10%

COG-Univ of Florida sub Arzu Onar-Thomas (PI) 07/01/2013 – 02/28/2019
The Brain Tumor Team in the Department of Biostatistics at SJCRH will work with the COG statisticians to provide statistical support for COG CNS clinical trials and studies. They participate in the weekly COG statistical calls and will participate in the semi-annual COG meetings.
Role: Biostatistician
Percent of Effort: 25%

P30 CA021765-36 Biostat Kumar Srivastava (PI) 03/01/2013 – 02/28/2019
To provide investigators access to uniformly high quality, innovative statistical science; a centralized randomization system; access to statistical software, technical support for a web-based distributed data management system; and advice on data management issues.
Role: Biostatistician
Percent of Effort: 20%

Doric Duke Charitable Foundation Mitch Weiss (PI) 09/01/2017 – 08/31/2020
Genome Editing of Bone Marrow and Plerixafor-mobilized CD34+ Cells to Raise Fetal Hemoglobin Levels in Sickle Cell Disease. This project studies the safety and efficacy of plerixafor to mobilize hematopoietic stem cells in sickle cell disease patients and compares the on- and off-target effects of genome editing in plerixafor mobilized vs. bone marrow HSCs from sickle cell patients.
Role: Biostatistician
Percent of Effort: 5%

K23: ASH Honors Jeremie Estepp (PI) 07/01/2017 – 06/30/2018
Major goals are: 1) to better identify patients with both asthma and sickle cell disease, 2) once identified, treat this population appropriately to decrease the risk of associated pulmonary complications, and 3) identify easier ways to objectively define asthma in children with sickle cell disease.
Role: Biostatistician
Percent of Effort: 2%

F31 award Trent Hall (PI) 07/01/2018 – 06/30/2020
Characterizing a novel developmental checkpoint during hematopoietic stem cell ontogeny
Role: Biostatistician
Percent of Effort: 2%

ASH Physician Scientist Award: Anjelica Saulsberry (PI) 07/01/2018 – 06/30/2019
Exploring Predictors of Successful Transition from Pediatric to Adult Care for Patients with SCD.
Role: Biostatistician
Percent of Effort: 2%

B. Pending Grants:

Assessing the Impact of Long-Term Hydroxyurea on Fertility in Young Adult Males with Sickle Cell Disease (PI: Jeremie Estepp)
Will be responsible for all statistical components: design, conduct analyze, and report the study.
Role: Biostatistician 09/01/2018 - 06/30/2020
Percent of Effort: 5%

2P01 HL053749-21A1 Proj. 1 Mitch Weiss (PI) 07/01/2018 – 06/30/2019
Gene Therapy for SCA
To develop gene therapy for sickle cell anemia.
Role: Biostatistician
Percent of Effort: 5%

2P01 HL053749-21A1 Proj. 2 Brian Sorrentino (PI) 07/01/2018 – 06/30/2019
Gene Therapy for Wiskott-Aldrich Syndrome (WAS)
To develop gene therapy for Wiskott-Aldrich Syndrome (WAS).
Role: Biostatistician
Percent of Effort: 5%

2P01 HL053749-21A1 Proj. 3 Brian Sorrentino (PI) 07/01/2018 – 06/30/2019
Lentiviral Gene Therapy for SCID-X1
To develop gene therapy for SCID-X1.
Role: Biostatistician
Percent of Effort: 5%

1R01 DK116835-01 Shannon Mckinney-Freeman (PI) 04/01/2018 – 03/31/2019
Improving HSC transplantation by defining novel regulators of engraftment (R01)
Will be responsible for all statistical components: design, conduct analyze, and report the study.
Role: Biostatistician
Percent of Effort: 5%

F31 Kaitly Woodard (PI)
Functional Validation of Genomic Variants Affecting Fetal Hemoglobin.
Role: Biostatistician
Percent of Effort: 2%

C. Completed Grants:

R01 HL098239-02 Baylor Sub James M. Boyett (PI) 12/19/2011 – 03/30/2014
Sparing Conversion to Abnormal TCD Elevation (Data Coordinating Center)
Will be responsible for all computing and statistical components of the trial; design and develop the computing infrastructure that will provide a secure, paperless data management and reporting system for the trial.
Role: Biostatistician
Percent of Effort: 10%

5P01 HL053749-18 Proj. 1 Arthur W. Nienhuis (PI) 06/01/2013 – 07/31/2016
Lentiviral Gene Therapy for SCD and Immunodeficiency Disorders
To develop gene therapy for sickle cell disease.
Role: Biostatistician
Percent of Effort: 5%

5P01 HL053749-18 Proj. 2 Arthur W. Nienhuis (PI) 06/01/2013 – 07/31/2016
Lentiviral Gene Therapy for SCD and Immunodeficiency Disorders
To develop gene therapy for sickle cell disease.
Role: Biostatistician
Percent of Effort: 5%

5P01 HL053749-20 Proj. 3 Brian Sorrentino (PI) 08/01/2014 – 07/31/2016
Gene Therapy for Sickle Cell Disease and Pediatric Immunodeficiency Disorders
To develop gene therapy for sickle cell disease and pediatric Immunodeficiency disorders.
Role: Biostatistician

Percent of Effort: 5%

5R01HL092209 Daniel J. Rader (PI) 12/16/2009 – 12/15/2011
Genetics of Lipoprotein Metabolism and CVD in CKD
The goal of this project is to identify important risk factors including genetic and environmental for the development of CVD in CKD
Role: Co-investigator

5R01HL091663 Daniel L. Dries (PI) 12/16/2009 – 10/31/2011
Genetic Determinants of Hypertensive Heart Disease in CRIC
The goal of this project is to identify Genetic Variation in the CORIN gene, NPS, MMP/TIMP Candidate Gene Systems for Prevalent Heart Disease in CRI.
Role: Co-investigator

R01GM073766-01A2 Guimin Gao (PI) 07/01/2007 – 12/15/2009
Haplotyping and QTL Mapping in Pedigrees with Missing Data
Role: Co-investigator

13. Clinical Trials Involvement

1. GENIOS - GENES INFLUENCING IRON OVERLOAD STATE, St. Jude, Biostatistician, 2011. (active)

2. BRAIN2 - The Brigance Assessment of Individual Neurodevelopment in Young Children with Sickle Cell Disease-2, St. Jude, Biostatistician, 2011. (active)

3. HIFLEX - A REDUCED INTENSITY CONDITIONING REGIMEN WITH CD3-DEPLETED HEMATOPOIETIC STEM CELLS TO IMPROVE SURVIVAL FOR PATIENTS WITH HEMATOLOGIC MALIGNANCIES UNDERGOING HAPLOIDENTICAL STEM CELL TRANSPLANTATION), St. Jude, Biostatistician, 2011. (active)

4. REFLEX - HAPLOIDENTICAL HEMATOPOIETIC STEM CELL TRANSPLANTATION USING A NOVEL CLOFARABINE CONTAINING CONDITIONING REGIMEN FOR PATIENTS WITH REFRACTORY HEMATOLOGIC MALIGNANCIES, St. Jude, Biostatistician, 2011. (active)

5. HAP3R - T-CELL REPLETE HAPLOIDENTICAL DONOR HEMATOPOIETIC STEM CELL PLUS NK CELL TRANSPLANTATION IN PATIENTS WITH HEMATOLOGIC MALIGNANCIES RELAPSED OR REFRACTORY DESPITE PREVIOUS ALLOGENEIC TRANSPLANT), St. Jude, Biostatistician, 2011. (active)

6. MUDSIB - METHOTREXATE OR PENTOSTATINFOR GRAFT-VERSUS-HOST DISEASE PROPHYLAXIS IN RISK-ADAPTED ALLOGENEIC BONE MARROW TRANSPLANTATION FOR HEMATOLOGIC MALIGNANCIES), St. Jude, Biostatistician, 2011. (closed)

7. MOZBMT - A PHASE I PEDIATRIC STUDY OF A PLERIXAFOR CONTAINING REGIMEN IN SECOND ALLOGENEIC STEM CELL TRANSPLANTION), St. Jude, Biostatistician, 2011. (closed)

8. BEAL1 - CLINICAL PRACTICE PLAN: ALLOGENEIC STEM CELL TRANSPLANTATION FOR PATIENTS WITH HEMATOLOGIC MALIGNANCIES AND CLOSELY MATCHED DONORS, St. Jude, Biostatistician, 2011. (active)

9. BMTRV - PROSPECTIVE SURVEILLANCE FOR RESPIRATORY VIRUS INFECTIONS IN CHILDREN UNDERGOING HEMATOPOIETIC STEM CELL TRANSPLANTATION, St. Jude, Biostatistician, 2011. (closed)

10. NKCD19 - PILOT STUDY OF GENETICALLY MODIFIED HAPLOIDENTICAL NATURAL KILLER CELL INFUSIONS FOR B-LINEAGE ACUTE LYMPHOBLASTIC LEUKEMIA, St. Jude, Biostatistician, 2011. (Concept approved)

11. INFT2 - HLA-NONIDENTICAL STEM CELL AND NATURAL KILLER CELL TRANSPLANTATION FOR CHILDREN LESS THAN 2 YEARS OF AGE WITH HEMATOLOGIC MALIGNANCIES, St. Jude, Biostatistician, 2011. (closed)

12. NKHEM – PILOT STUDY OF HAPLOIDENTICAL NATURAL KILLER CELL INFUSIONS FOR POOR PROGNOSIS NON-AML HEMATOLOGIC MALIGNANCIES, St. Jude, Biostatistician, 2011. (closed)

13. SCDMR4 - STATE of the ART FUNCTIONAL IMAGING in SICKLE CELL DISEASE, St. Jude, Biostatistician, 2011. (active)

14. HUSTLE - LONG TERM EFFECTS OF HYDROXYUREA THERAPY IN CHILDREN WITH SICKLE CELL DISEASE, St. Jude, Biostatistician, 2012. (active)

15. NKID - NATURAL KILLER CELLS IN THE PEDIATRIC POPULATION, St. Jude, Biostatistician, 2012. (active)

16. ELYSIS - LONG TERM EFFECTS OF ERYTHROCYTE LYSIS, St. Jude, Biostatistician, 2012. (active)

17. AGT4HB – AN OPEN LABEL DOSE-ESCALATION STUDY OF A SELF COMPLEMENTARY ADENO-ASSOCIATED VIRAL VECTOR (scAAV2/8-LP1-hFIXco) FOR GENE TRANSFER IN SUBJECTS WITH HEMOPHILIA B, St. Jude, Biostatistician, 2012. (active)

18. RADIANT - A PHASE I STUDY OF CD45RA+ DEPLETED HAPLOIDENTICAL STEM CELL TRANSPLANTATION IN CHILDREN WITH RELAPSED OR REFRACTORY SOLID TUMORS OR LYMPHOMAS, St. Jude, Biostatistician, 2012. (active)

19. ACNS0334 - A Phase III Randomized Trial for the Treatment of Newly Diagnosed Supratentorial PNET and High Risk Medulloblastoma in Children < 36 months Old with Intensive Induction Chemotherapy with Methotrexate Followed by Consolidation with Stem Cell Rescue vs. the Same Therapy Without Methotrexate, COG, Biostatistician, 2012. (active)

20. ACNS1422 - A Phase 2 Study of Reduced Therapy for Newly Diagnosed Average-Risk WNT-Driven Medulloblastoma Patients, COG, Biostatistician, 2012. (active)

21. SCATE - Sparing Conversion to Abnormal TCD Elevation (SCATE) - a Phase III clinical trial to compare standard care (observation) with alternative therapy (hydroxyurea) for reducing the risk of converting to an abnormal TCD velocity in children with sickle cell anemia and conditional pre-treatment TCD velocities, International Trial, Biostatistician, 2012. (closed)

22. HAPNK1 - HAPLOIDENTICAL DONOR HEMATOPOIETIC PROGENITOR CELL AND NATURAL KILLER CELL TRANSPLANTATION WITH A TLI BASED CONDITIONING REGIMEN IN PATIENTS WITH HEMATOLOGIC MALIGNANCIES), St. Jude, Biostatistician, 2012. (active)

23. NCBP01 - A MULTICENTER SAFETY STUDY OF UNLICENSED, INVESTIGATIONAL CRYOPRESERVED CORD BLOOD UNITS (CBUs) MANUFACTURED BY THE NATIONAL CORD BLOOD PROGRAM (NCBP) AND PROVIDED FOR UNRELATED HEMATOPOIETIC STEM CELL TRANSPLANTATION OF PEDIATRIC AND ADULT PATIENTS, Multiple-Center, Biostatistician, 2012. (active)

24. LVXSCID-ND - A PILOT FEASIBILITY STUDY OF GENE TRANSFER FOR X-LINKED SEVERE COMBINED IMMUNODEFICIENCY IN NEWLY DIAGNOSED INFANTS USING A SELF-INACTIVATING LENTIVIRAL VECTOR TO TRANSDUCE AUTOLOGOUS CD34+ HEMATOPOIETIC CELLS, Multiple-Center, Biostatistician, 2012. (active)

25. TRIALS - Transfusional Iron Overload Among Leukemia Survivors, St. Jude, Biostatistician, 2013. (active)

26. SJRET6 - Protocol for the Study and Treatment of Participants with Intraocular Retinoblastoma. Biostatistician, 2013. (active)

27. SCCRIP – SICKLE CELL CLINICAL RESEARCH AND INTERVENTION PROGRAM, Multiple-Center, Biostatistician, 2013. (active)

28. HAPCORD - COMBINED T CELL DEPLETED HAPLOIDENTICAL PERIPHERAL BLOOD STEM CELL AND UNRELATED UMBILICAL CORD BLOOD TRANSPLANTATION IN PATIENTS WITH HEMATOLOGIC MALIGNANCIES USING A TOTAL LYMPHOID IRRADIATION BASED PREPARATIVE REGIMEN, St. Jude, Biostatistician, 2013. (active)

29. REFLEX - CD45RA-DEPLETED HAPLOIDENTICAL HEMATOPOIETIC PROGENITOR CELL AND NATURAL KILLER CELL TRANSPLANTATION FOR HEMATOLOGIC MALIGNANCIES RELAPSED OR REFRACTORY DESPITE PRIOR TRANSPLANTATION, St. Jude, Biostatistician, 2013. (active)

30. PMVOC - PAIN MANAGEMENT OF VASO-OCCLUSIVE CRISIS IN CHILDREN AND YOUNG ADULTS WITH SICKLE CELL DISEASE, St. Jude, Biostatistician, 2013. (active)

31. ASCIST - A PHASE I STUDY OF IMMUNOTHERAPY INCLUDING HAPLOIDENTICAL NK CELL INFUSION FOLLOWING CD133+ POSITIVELY-SELECTED AUTOLOGOUS HEMATOPOIETIC STEM CELLS IN CHILDREN WITH HIGH RISK SOLID TUMORS OR LYMPHOMAS, St. Jude, Biostatistician, 2013. (active)

32. KIRT - ANALYSIS OF KIR+CD56+ T-CELLS AND FcRg-CD56+CD3- NK CELLS IN PEDIATRIC ALLOGENEIC HEMATOPOIETIC STEM CELL TRANSPLANT PATIENTS AND DONORS, St. Jude, Biostatistician, 2013. (active)

33. PPCAGT - AN OPEN LABEL DOSE-ESCALATION STUDY OF A SELF COMPLEMENTARY ADENO-ASSOCIATED VIRAL VECTOR (scAAV2/8-LP1-hPPCA) FOR GENE TRANSFER IN SUBJECTS WITH GALACTOSIALIDOSIS, St. Jude, Biostatistician, 2014. (active)

34. TWIPES - A RANDOMIZED CONTROLLED TRIAL OF THE SAFETY AND EFFICACY OF THERAWORX™ BATH WIPES IN THE REDUCTION OF SKIN COLONIZATION WITH VANCOMYCIN-RESISTANT ENTEROCOCCI COMPARED TO STANDARD BATH WIPES IN CHILDREN UNDERGOING HEMATOPOIETIC STEM CELL TRANSPLANTATION, St. Jude, Biostatistician, 2014. (active)

35. G4K - GENOMES FOR KIDS, St. Jude, Biostatistician, 2014. (active)

36. REFNK1 – CD45RA-DEPLETED HAPLOIDENTICAL HEMATOPOIETIC PROGENITOR CELL AND NATURAL KILLER CELL TRANSPLANTATION FOR HEMATOLOGIC MALIGNANCIES RELAPSED OR REFRACTORY DESPITE PRIOR TRANSPLANTATION, St. Jude, Biostatistician, 2015. (active)

37. INSIGHT - INVESTIGATION OF THE GENETICS OF HEMATOLOGIC DISEASES, St. Jude, Biostatistician, 2015. (active)

38. SJFAMILY - FAMILIAL INVESTIGATIONS OF CHILDHOOD CANCER PREDISPOSITION, St. Jude, Biostatistician, 2016. (active)

39. HUGKISS - A PILOT STUDY OF HYDROXYUREA MANAGEMENT IN KIDS: INTENSIVE VERSUS STABLE DOSAGE STRATEGIES, Multiple-Center, Co-PI, 2016. (active)

40. REF2HCT – PROVISION OF TCRγδ T CELLS AND MEMORY T CELLS PLUS SELECTED USE OF BLINATUMOMAB IN NAÏVE T CELL DEPLETED HAPLOIDENTICAL DONOR HEMATOPOIETIC CELL TRANSPLANTATION FOR PATIENTS WITH HEMATOLOGIC MALIGNANCY RELAPSED OR REFRACTORY DESPITE PRIOR TRANSPLANTATION, St. Jude, Biostatistician, 2016. (active)

41. OSTPDL1 - A Phase II Trial of Avelumab, a Fully Human Antibody that Targets Cells Expressing PD-L1 in Patients with Recurrent or Progressive Osteosarcoma, St. Jude, Biostatistician, 2016. (active)

42. SCID2016 - HAPLOCOMPATAIBLE TRANSPLANT USING TCRα/β DEPLETION FOLLOWED BY CD45RA-DEPLETED DONOR LYMPHOCYTE INFUSIONS FOR SEVERE COMBINED IMMUNODEFICIENCY, St. Jude, Biostatistician, 2017. (active)

43. SJCAR19 - SJCAR19: A PHASE I/II STUDY EVALUATING SJCAR19 (CD19-SPECIFIC CAR ENGINEERED AUTOLOGOUS T-CELLS) IN PEDIATRIC AND YOUNG ADULT PATIENTS ≤ 21 YEARS OF AGE WITH RELAPSED OR REFRACTORY CD19+ ACUTE LYMPHOBLASTIC LEUKEMIA, St. Jude, Biostatistician, 2017. (active)

44. PMVOC-VR- PAIN MANAGEMENT OF VASO-OCCLUSIVE CRISIS IN CHILDREN AND YOUNG ADULTS WITH SICKLE CELL DISEASE - EFFECT OF VIRTUAL REALITY TECHNOLOGY, St. Jude, Biostatistician, 2017. (active)

45. RE-HASH - RE-AIMING AT HYDROXYUREA ADHERENCE FOR SICKLE CELL WITH MHEALTH, St. Jude, Biostatistician, 2017. (active)

46. PACT - PRECLINICAL ASSESSMENT OF CELL THERAPIES, St. Jude, Biostatistician, 2017. (active)

47. HOPE – Hydroxyurea therapy: Optimizing Access in Pediatric Populations Everywhere, St. Jude, Biostatistician, 2018. (In review)

48. LGTWAS - LENTIVIRAL GENE THERAPY FOR TREATMENT OF INDIVIDUALS WITH X-LINKED WISKOTT-ALDRICH SYNDROME, Multiple-Center, Biostatistician, 2018 (in development)

49. HAP2HCT - TCRαβ-DEPLETED PROGENITOR CELL GRAFT WITH ADDITIONAL MEMORY T-CELL DLI, PLUS SELECTED USE OF BLINATUMOMAB, IN NAÏVE T-CELL DEPLETED HAPLOIDENTICAL DONOR HEMATOPOIEITC CELL TRANSPLANTATION FOR HEMATOLOGIC MALIGNANCIES St. Jude, Biostatistician, 2018 (in BPRC review)

50. CD45RAD - A Phase II Study of the Efficacy and Kinetics of Lymphoid Reconstitution After Donor Lymphocyte Infusion (DLI) with CD45RA-Depleted Apheresed Product in Children Post-Allogeneic Hematopoietic Stem Cell Transplantation, St. Jude, Biostatistician, 2018 (in development)

14. Publication Record (*Co-first author, #Corresponding author, and Trainee)

I have co-authored **73** papers: 67 peer-reviewed scientific publications, including 26 publications (I am either the first-author or senior author on 23 out of 26) on statistical and mathematical methodology and 41 biomedical publications on topics including clinical trial results, preclinical research, and translational genomics; and another 6 conference papers. The full list of my publications can be found https://www.ncbi.nlm.nih.gov/myncbi/browse/collection/46494942/?sort=date&direction=ascending.

A. Peer Reviewed Publications

i. Original Statistical Methodology Research Articles:

1. Kang G. Some generalizations and applications on some integral inequalities. Journal of Engineering Mathematics 21(5):715-721, 2004. (In Chinese)

2. Kang G. Oscillation theorems of solutions of nonlinear difference equations of second order. Journal Of Binzhou Teachers College 18(4):6-10, 2004.

3. Kang G, Zhang H. Oscillation criteria of solutions of nonlinear difference equations of second order. Annals of Differential Equations 20(1):41-48, 2004.

4. Kang G. Oscillation criteria for second-order nonlinear difference equation with "summation small" coefficient. Bull Korean Math Society 42(2):245-256, 2005.

5. Kang G. Oscillation criteria for second-order half-linear neutral difference equations. Journal of Mathematical Research and Exposition 26(2):247-252, 2006.

6. Kang G, Meng F. Oscillation criteria for second-order quasi-linear neutral difference equations. Journal of Engineering Mathematics 23(1):923-926, 2006.

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21. Partanen M, Schreiber J, Porter J, Krull K, **Kang G**, Hodges J, King A, Hankins J, Jacola L. Associations between hydroxyurea and neurocognitive functioning in adolescents with sickle cell disease (SCD). (In preparation) 2018.

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23. Incidence, severity, and duration of sinusoidal obstruction syndrome in high risk neuroblastoma: contributions, management, and outcomes in modern multi-institutional cohort. ASTRO 2018 meeting.

24. Whipple N, Naik, RJ, **Kang G**, Moen J, Govindaswamy SD, Fowler JA, Dowdy J, Joshi VM, Hankins J. Altered Ventricular Global Longitudinal Strain in Children with Sickle Cell Disease. British Journal of Haematology (In review), 2018.

25. Oyebimpe Adesina, James Gurney, **Guolian Kang**, Martha Villavincienco, Jason Hodges, Wassim Chemaitilly, Sue Kaste, Babette Zemel, Jane S. Hankins. LOW BONE MINERAL DENSITY PERSISTS IN ADOLESCENTS WITH SICKLE CELL DISEASE, DESPITE HEIGHT ADJUSTMENT: RESULTS FROM THE SICKLE CELL CLINICAL RESEARCH AND INTERVENTION PROGRAM (SCCRIP). (To be submitted) 2018.

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v. Reviews and Conference Proceedings:

1. **Kang G**, Li S, Zhang J. Evolution analysis of life systems via entropy theory. Proc. of the 24th Chinese Control Conference 1567-1572, 2005.

2. **Kang G**, Childers DK, Liu N, Zhang K, Gao G. Genome-wide association studies of Rheumatoid Arthritis data via multiple hypothesis testing methods for correlated tests. BMC Proceedings 3(S38):1-5, 2009.

3. Childers DK, **Kang G**, Liu N, Gao G, Zhang K. Application of imputation methods for the analysis data from genome-wide association studies. BMC Proceedings 3(S24):1-5, 2009.

4. Martin LJ, Gao G, **Kang G**, Fang Y, Woo JG. Improving the signal-to-noise ratio in genomewide association studies. Genetic Epidemiology 33:S29-S32, 2009.

5. **Kang G**, Jiang B, Gao G. A generalized sequential Bonferroni procedure incorporating information of Hardy-Weinberg disequilibrium among cases for genome-wide association studies. In JSM Proceedings, Section on Statistics in Epidemiology. Washington, DC: American Statistical Association. 4434-4448, 2009.

6. Bi W, **Kang G**, Stanley Pounds. Statistical selection of biological models for genome-wide association analyses. IEEE International Conference on Bioinformatics and Biomedicine (BIBM), 150-157, 2017. *** BIBM 2017 student travel award**

vi. Abstracts

1. Gao G, **Kang G**. A generalized sequential Ŝidk procedure for multiple hypothesis testing. Genet Epidemiol 32:690, 2008.

2. **Kang G**. An efficient multilocus Monte Carlo approach for gene-centric genome-wide association studies. Genet Epidemiol 32:698, 2008.

3. Gao G, **Kang G**. A generalized sequential Bonferroni procedure for genome-wide association studies incorporating information on Hardy-Weinberg disequilibrium among cases. Genet Epidemiol 33:790, 2009.

4. **Kang G**, Jiang B. Analysis of two gene-centric approaches for genomewide association studies. Genet Epidemiol 33:795-796, 2009.

5. **Kang G**, Gao G. A Bonferroni procedure using weights accounting for Hardy-Weinberg disequilibrium information in genome-wide association studies. The 2009 meeting of the American Society of Human Genetics S82:475, 2009.

6. Jiang B, Zhang X, Zuo Y, **Kang G**. A truncated tail strength method for testing an overall hypothesis in a dataset. The 2010 meeting of the American Society of Human Genetics 874, 2010.

7. **Kang G**, Gao G, Shete S, Redden DT, Chang B-L, Rebbeck TR, Barnholtz-Sloan JS, Patterson N, Pajewski NM, Allison DB. Capitalizing on admixture in genome-wide association studies: A two-stage testing procedure and application to height in African-Americans. The 2010 meeting of the American Society of Human Genetics 819, 2010.

8. **Kang G**, Lin D, Li M, Chen J. A powerful and efficient two-stage design for next generation sequencing data analysis using extreme phenotype sequencing. The 2011 meeting of the American Society of Human Genetics 2011.

9. Wilson CL, Liu W, Neale G, Srivastava D, Gurney JG, **Kang G**, Mehta P, Ojha R, Hudson MM, Robison LL, Ness KK. Potential gene variants associated with obesity following cranial radiation treatment for childhood cancer in a genome-wide association study. The 2013 meeting of the American Association for Cancer Research 2013.

10. Perko R, Thomas P, **Kang G**, Dallas MH. Elevated Gamma Delta T Cell Recovery Following Hematopoietic Stem Cell Transplantation Associated with Improved Long Term Overall Survival in Pediatric Patients with Acute Leukemia, Biology of Blood and Marrow Transplantation, 19: S207-S208, 2013.

11. **Kang G**. Power and sample size of two-stage extreme phenotype sequencing design for next generation sequencing studies. BMC Bioinformatics. 14:A16, 2013.

12. Bi W, **Kang G**[#], Cui Y, Li Y, Hartford CM, Leung W, Zhang JF. A new set-valued system identification approach to identifying rare genetic variants for ordered categorical phenotype. BMC Bioinformatics. 15:P29, 2014.

13. **Kang G**, Liu W, Cheng C, Wilson C, Neale G, Yang J, Ness KK, Robison LL, Hudson MM, Srivastava K. Evaluation of two-step iterative resampling procedure for internal validation of genome-wide association studies. BMC Bioinformatics. 15:P34, 2014.

14. Estepp JH, Smelter MP, **Kang G**, Aygun B, Ware RE, Nottage K. Higher fetal hemoglobin following escalation of hydroxyurea to maximum tolerated dose provides clinical benefit to children with sickle cell anemia. Blood. 124 (21), 85-85, 2014.

15. Yates AM, Joshi VJ, Nottage KA, Smeltzer MP, **Kang G**, Govindaswamy D, Dowdy J, Cotton A, Ware RE, Hankins JS. Elevated tricuspid regurgitation jet velocity in patients with sickling and non-sickling hemolytic anemias: prevalence and correlates. Blood. 124(21): 4906-4906, 2014.

16. Bi W[*], **Kang G**[*#], Zhao Y, Cui Y, Yan S, Li Y, Cheng C, Pounds SB, Borowitz MJ, Relling MV, Yang JJ, Pui CH, Hunger SP, Hartford C, Leung W, Zhang JF[#]. SVSI: fast and powerful set-valued system identification approach to identifying rare variants in sequencing studies for ordered categorical traits. The 2014 meeting of the American Society of Human Genetics 819, 2014.

17. Whipple N, Joshi V, Naik R, Smeltzer M, **Kang G**, Govindaswamy SD, Dowdy J, Ware RE, Yates A, Hankins J. Altered Ventricular Global Longitudinal Strain in Children with Sickle Cell Disease. The ASPHO 2015 Annual Meeting. *Pediatric Blood & Cance*r.

18. Wang WC, Freeman MB, Carroll YM, Hamilton L, Smeltzer MP, **Kang G**, Hankins J, Aygun B. High Failure Rate with Brigance Developmental Screening in 3 Year-Old Children with Sickle Cell Disease. Blood. 124 (21), 4926-4926, 2014.

19. Srinivasan S, Srinivasan S, Sunthankar S, Sunkara A, Kang G, Stokes D, Leung W. Pre-hematoloietic stem cell transplantation lung function and pulmonary complications in children. Biology of Blood and Marrow Transplantation. 21(2): S106, 2015.

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21. Estepp JH, Qinlei Huang, Wang W, **Kang G**. Prognostic factors for hospitalization of children with sickle cell anemia treated with hydroxyrea at maximum tolerated dose. Blood 126:2177, 2015.

22. Yasui Y, Rampersaud E, **Kang G**, Hankins J, Estepp J, Wang Z, Yanai H, Robison L, Zhang J, Wu Gang, Tokunaga K, Weiss M. A statistical exploration of how multiple enhancers affect traits jointly. The 13th International Congress of Human Genetics, 2016.

23. Rampersaud E, **Kang G**, Yasui Y, Wang S, JiangY, Palmer L, Feng R, Estepp J, Zhang J, Hankins J, Wu Gang, Weiss M. Whole genome sequence analysis of genetic determinants of fetal hemoglobin in children with sickle cell disease. The 13th International Congress of Human Genetics, 2016.

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26. Mastellaro Z, **Kang G**, Miranda E, Abrahao R, Fihueiredo B, Ana Luiza, Pounds S, Rodriguez-Galindo C, Unicamp, Ribeiro R. (2016) Contribution of the TP53 R337H mutation to cancer burden in families with a proband with adrenocortical tumor. J Clin Oncol 34, 2016 (suppl; abstr 1538). 2016 American Society of Clinical Oncology Annual Meeting

27. Abrams C, Moen J, **Kang G**, Wang W, Hankins J, Estepp JH. Hydroxyurea at maximal tolerated dose (MTD) prior to completion of the β-globin switch has additive but not sustained benefits in fetal hemoglobin production. Blood 128(:22): 125-125, 2016. [*](**Oral presentation**)

28. Whipple N, Joshi V, Naik R, **Kang G**, Moen J, Govindaswamy SD, Dowdy J, Ware RE, Yates A, Hankins J. The association of age, disease modifying therapy, and ventricular global longitudinal strain in children with hemolytic anemias. Pediatric Blood & Cancer 63: S57-S58, 2016.

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30. Mack JM, Wiczling P, Moen J, Kang G, Liem RI, Panepinto JA, Kearns G, Neville KA, Estepp JH. Pharmacokinetics in Children with Sickle Cell Anemia Following Single Dose Versus Chronic Treatment with Hydroxyurea. Blood 128(:22): 1314-1314, 2016.

31. Puri L, Flanagan J, **Kang G**, Bi W, McCarville B, Sajja A, Ralf L, Villavicenzio M, Hillenbrand C, Hankins J. Genetic modifiers of iron overload in sickle cell disease. ASPHO, 2017.

32. Mesleh A, **Kang G**, Su Y, Lama E, Reiss U. Outcomes after off-label use of recombinant factor VIIa for severe bleeding in pediatric hematology/oncology patients. ASPHO, 2017.

33. Sharma A, **Kang G**, Cunningham L, Madden R, Qudeimat A, Triplett BM. Allogeneic Hematopoietic Cell Transplantation for Acute Megakaryoblastic Leukemia: A Single Center Experience. Biology of Blood and Marrow Transplantation, 23(3): S299-S300, 2017.

34. Srinivasan A, Mitchell W, Sunkara A, Sunthankar S, **Kang G**, Stokes DC, Srinivasan S. Recovery of Pulmonary Function after Allogeneic Hematopoietic Cell Transplantation in Children Predicts Improved Survival. Biology of Blood and Marrow Transplantation, 23(3): S242-S243, 2017.

35. Lucas Jr. JT, Braunstein S, Sunkara A, Kang G, Krasin M, Federico S, Santana V, Furman W, Goldsby R, Dvorak C, Tolbert V, Matthay K, Cunningham L. External beam radiotherapy is not associated with the incidence, severity or duration of veno-occlusive disease. PEDIATRIC BLOOD & CANCER 64, S233-S233, 2017.

36. Wang W, Schreiber J, **Kang G**, Li C, Hankins J, Estepp J, Helton K. Effects of Hydroxyurea (HU) on Neurocognitive Performance in Children with Sickle Cell Disease: A Prospective Trial. 2017 ASH Conference. *(**Oral Presentation**)

37. Alberts NM, Hankins J, **Kang G**, Li C, Hodges J, Villavicencio M, Klosky J. A Developmental Examination of Pain among Youth with Sickle Cell Disease. Blood 130:4722, 2017.

38. Saulsberry A, Hodges J, Williams J, Anderson S, Cole A, **Kang G**, Li C, Cronin R, Porter J, Hankins J. Caregiver Perceptions of Adolescent Self-Management Skills Predicts Higher Disease Knowledge Among Adolescents with SCD. Blood 130 (Suppl 1), 3350-3350, 2017.

39. Hall T, Walker M, Ganuza M, Holmfeldt P, Bordas M, **Kang G**, Bi W, Palmer LE, Finkelstein D, McKinney-Freeman S. Nfix promotes survival of immature hematopoietic cells via regulation of c-Mpl. Blood, 130:2423-2423, 2017.

40. Wells JRL, Sunkara A, Kang G, Hale J, Carlton H, Alloush L, Madden RM, Qudeimat A, Mamcarz E, Leung W, Janssen W, Triplett B, Srinivasan A. Infused total nucleated cell dose is a better predictor of transplant outcomes than CD34+ cell number for peripheral blood allogeneic hematopoietic cell transplantation in children. 2018 SIOP Conference.

41. Harreld J, Kaufman R, William M, Thompson J, Sunkara A, **Kang G**, Srinivasan A. Utility of pre-transplant screening sinus CT in children. 2018 ACR.

42. Claassen D, Chen L, **Kang G**, Reiss U. Characterization, Treatment and Toxicities in a Pediatric Diamond Blackfan Anemia Cohort. 2018 ASPHO Conference, 2018.

43. Partanen, M., Schreiber, J., Porter, J., Krull, K., **Kang, G.**, Hodges, J., King, A., Hankins, J., & Jacola, L. Associations between hydroxyurea and neurocognitive functioning in adolescents with sickle cell disease (SCD). Paper presented at the American Academy of Clinical Neuropsychology Annual Conference, San Diego, CA, 2018.

44. INCIDENCE, SEVERITY, AND DURATION OF SINUSOIDAL OBSTRUCTION SYNDROME IN HIGH RISK NEUROBLASTOMA: CONTRIBUTORS, MANAGEMENT, AND OUTCOMES IN A MODERN MULTI-INSTITUTIONAL COHORT. ASTRO 2018 meeting.

15. Presentations

A. Oral Presentations

1. Evolution analysis of life systems via entropy theory, The 24th Chinese Control Conference, Guangzhou, China, 07/15/2005.

2. Two-stage designs for genome-wide association studies, Department of Epidemiology, Michigan State University, 03/27/2007.

3. Mixed analysis for genomewide association studies, Department of Biostatistics, University of Alabama at Birmingham, 05/08/2007.

4. A generalized sequential Bonferroni procedure for genome-wide association studies incorporating information of Hardy-Weinberg disequilibrium among cases, “Section on Statistics in Epidemiology”, 2009 Joint Statistical Meetings, Washington, DC, 08/05/2009.

5. A generalized sequential Bonferroni procedure for genome-wide association studies, Department of Biostatistics and Epidemiology, University of Pennsylvania, 09/16/2009.

6. Two-stage design: SNP discovery of mini-exome data by using extreme phenotype sequencing, Genetic Analysis Workshop 17, Boston, 10/13/2010.

7. Efficient designs of gene-environment interaction studies: implications of Hardy-Weinberg equilibrium and gene-environment independence, Institute of Systems Science, Chinese Academy of Sciences, Beijing, China, 03/10/2011.

8. Efficient designs of gene-environment interaction studies: implications of Hardy-Weinberg equilibrium and gene-environment independence, Department of Biostatistics, Tulane University, New Orleans, LA, 05/06/2011.

9. Two-stage design for identifying and testing common and rare genetic variants in next generation sequencing studies using extreme phenotype sequencing, Department of Molecular Pharmacology and Therapeutics, Loyola University Stritch School of Medicine, Chicago, IL, 08/18/2011.

10. Extreme phenotype sequencing for next generation sequencing studies: efficiency and power, Center for Public Health Genomics and Division of Biostatistics, University of Virginia, Charlottesville, VA, 08/29/2011.

11. Efficient designs of gene-environment interaction studies: implications of Hardy-Weinberg equilibrium and gene-environment independence, Department of Biostatistics, St. Jude Children’s Research Hospital, Memphis, TN, 09/19/2011.

12. Efficient designs of gene-environment interaction studies: implications of Hardy-Weinberg equilibrium and gene-environment independence, Division of Biostatistics and Epidemiology, Cincinnati Children’s Hospital Medical Center, University of Cincinnati, 10/06/2011.

13. Two-stage design for identifying and testing common and rare genetic variants in next generation sequencing studies using extreme phenotype sequencing. “Section on Statistics in Epidemiology”, 2012 Joint Statistical Meetings, San Diego, CA, 07/30/2012.

14. Power and sample size of two-stage extreme phenotype sequencing design for next generation sequencing studies. 2013 Bioinformatics Summit, Buchanan, TN, 03/23/2013.

15. A powerful and robust system identification approach to testing genotype-phenotype associations. The 2013 pSTAR analysis workshop. Nashville, TN, 12/11/2013.

16. A fast and powerful set-valued system identification approach to identifying rare genetic variants in sequencing studies for ordered categorical traits. The 2014 Bioinformatics Summit. Cadiz, KY. 04/12/2014.

17. Set-valued system identification approach to identifying genetic variants in sequencing studies. Department of Biostatistics, The University of Texas, M.D. Anderson Cancer Center, Houston, TX. 03/27/2015.

18. Set-valued system identification approach to identify rare genetic variants in sequencing studies. Joint 24th ICSA Applied Statistics symposium and 13th Graybill Conference. Fort Collins, Colorado. 06/15/2015.

19. Set-valued system identification approach to identifying genetic variants in sequencing studies. Institute of Systems Science, Chinese Academy of Sciences, Beijing, China, 06/25/2015.

20. Set-valued system identification approach to identify rare genetic variants in next generation sequencing studies. Institute of Reliability Engineering, Beihang University, Beijing, China, 06/26/2015.

21. Set-valued system identification approach to identify rare genetic variants in sequencing studies. 2015 ICSA China Statistics Conference. Shanghai, China, 07/06/2015.

22. Binary and continuous trait rare variant association analyses in case-control sequencing studies. Institute of Systems Science, Chinese Academy of Sciences, Beijing, China 06/10/2016.

23. Set-valued system identification approach to identify rare genetic variants in sequencing studies. 2016 Statistical Genetic Workshop. Taiyuan, China, 06/22/2016.

24. Binary and continuous trait rare variant association analyses in case-control sequencing studies part2. Institute of Systems Science, Chinese Academy of Sciences, Beijing, China 06/23/2016.

25. Set-valued approach to identify rare genetic variants in case-control sequencing studies. 2016 ICSA China Statistics Conference. Qingdao, China, 06/25/2016.

26. Set-valued approach to identify rare genetic variants in case-control sequencing studies. School of Mathematics, Qufu Normal University. Qufu, China, 06/29/2016.

27. Set-valued approaches for rare variant association analyses in case-control sequencing studies. Department of Biostatistics, The University of Kansas Medical Center, Kansas City, MO, 10/31/2016.

28. A robust and powerful set-valued approach to identify rare genetic variants in case-control sequencing studies. Department of Mathematics, Jining University. Jining, China, 11/23/2016.

29. A novel set-valued approach to identify rare genetic variants in case-control sequencing studies. School of Statistics, Qufu Normal University. Qufu, China, 11/24/2016.

30. A robust and powerful set-valued approach to identify rare genetic variants in case-control sequencing studies. Department of Hematology and Hematopoietic Cell Transplantation, City of Hope, Duarte, California, 12/14/2016.

31. Set-valued approaches for rare variant association analyses in case-control sequencing studies. Michigan State University, East Lansing, Michigan, 02/09/2017.

32. Statistical considerations in designing clinical trials and conducting large genomic studies. Department of Pediatrics, Medical College of Wisconsin, Wisconsin, 02/17/2017.

33. Secondary traits - rare variants association analyses in case-control sequencing studies. The 2017 ICSA Applied Statistics Symposium, Chicago, IL, 06/26/2017.

34. STEPS: An Efficient Prospective Likelihood Approach to Genetic Association analyses of Secondary Traits in Extreme Phenotype Sequencing. ICSA 2018 Applied Statistics Symposium, New Jersey, USA 06/16/2018.

35. Post-GWAS Secondary Phenotype Analysis is Cost-Benefit Only with Valid Analytical Approach. Institute of Systems Science, Chinese Academy of Sciences, Beijing, China 06/27/2018.

36. An Efficient Prospective Likelihood Approach to Genetic Association analyses of Secondary Traits in Extreme Phenotype Sequencing. School of Statistics, Qufu Normal University. Qufu, China, 07/02/2018.

B. Poster Presentations

1. An entropy approach for gene-centric genomewide association study. Cambridge Healthtech Institute 7th annual Conference for New Applications for Microarray Data Analysis: Integrating Genetics with Omics. (Washington DC), 2007

2. A generalized sequential Ŝidák procedure for multiple hypothesis testing. The 17th Annual International Genetic Epidemiology Society Conference. (St. Louis, Missouri), 2008

3. An efficient multilocus Monte Carlo approach for gene-centric genome-wide association studies. The 17th Annual International Genetic Epidemiology Society Conference. (St. Louis, Missouri), 2008

4. A generalized sequential Bonferroni procedure for genome-wide association studies incorporating information on Hardy-Weinberg disequilibrium among cases. The 18th Annual International Genetic Epidemiology Society Meeting. (Kahuku Hawaii), 2009

5. Analysis of two gene-centric approaches for genomewide association studies. The 18th Annual International Genetic Epidemiology Society Meeting. (Kahuku, Hawaii), 2009

6. A Bonferroni procedure using weights accounting for Hardy-Weinberg disequilibrium information in genome-wide association studies. The 59th Annual Meeting of The American Society of Human Genetics. (Honolulu, Hawaii), 2009

7. A truncated tail strength method for testing an overall hypothesis in a dataset. The 60th Annual Meeting of The American Society of Human Genetics. (Washington, DC), 2010

8. Capitalizing on admixture in genome-wide association studies: A two-stage testing procedure and application to height in African-Americans. The 60th Annual Meeting of The American Society of Human Genetics. (Washington, DC), 2010

9. Two-stage design for identifying and testing common and rare genetic variants using extreme phenotype sequencing. The 61th Annual Meeting of The American Society of Human Genetics. (Montreal, Canada), 2011

10. Power and sample size of two-stage extreme phenotype sequencing design for next generation sequencing studies. 2013 Bioinformatics Summit. (Buchanan, TN), 2013

11. A powerful and robust system identification approach to testing genotype-phenotype associations. The 2013 Impact of Large-Scale Genomic Data on Statistical Quantitative Genetics Conference, Seattle, WA, 2013

16. Official Reports Done Related to Clinical Trials

Clinical Trials Government Report/CTG Report
U.S. Food and Drug Administration report/FDA Report
St. Jude Data Safety and Monitoring Board Report/DSMB Report
NHLBI Data Safety and Monitoring Board Report/ NHLBI DSMB Report
Children's Oncology Group Data Safety and Monitoring Board Report/COG DSMB Report

17. Computing and Software Experience

Languages: Matlab, SAS, R/Splus, C/C++
Operating Systems: Windows, Unix/Linux
Typesetting Systems: Latex, Microsoft Word, Excel, Power Point, Dreamweaver
Genetic Software: ADMIXPROGRAM, ANCESTRYMAP, EIGENSTRAT, fast-PHASE, FBAT/PBAT, HAP-SAMPLE, Haploview, MACH/minimach, MERLIN, MS, PLINK, SNAP, STRUCTURE, EPACT, SOLAR, LocusZoom, GCTA, CaTS, Quanto, SKAT, TDTASP
Bioinformatics Software: ARACNE, Bioconductor, Bioinformatics Toolbox in Matlab, Cytoscape, GenomeStudio, Genotyping Console, GSEA, KEGG, MDR, PennCNV, BWA (Burrows-Wheeler Aligner), SRA-toolkit, fastx-toolkit, picard, GATK, ANNOVAR, VCFtools, UCSC genome browser, VEP, LDlink, EMMAX, King

18. Software We Developed

SV: creator

SV2bc: creator

STEPS: creator

TRIM: creator