

2009 WNAR/IMS Meeting

Portland State University, Oregon
June 14-17, 2009

WNAR Program Chair:

Gang Li, Ph.D.
University of California, Los Angeles
Department of Biostatistics
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IMS Program Chair:

Haiyan Huang, Ph.D.
University of California, Berkeley
Department of Statistics
hhuang@stat.berkeley.edu

Monday 15th:

WNAR Invited 1: Statistical Challenges in Design and Analysis of Clinical Trials

Chair:

Liansheng (Larry) Tang (George Mason University, ltang1@gmu.edu)

Organizer:

Kate Crespi (UCLA, ccrespi@ucla.edu)

Speakers:

Karen Messer (UCSD, kmesser@ucsd.edu)
“[Dose Establishment Designs for Phase I/II Oncology trials](#)”

John Boscardin (UCSF, John.Boscardin@ucsf.edu)
“[Hybrid Bayesian-Frequentist Designs for Medical Devices](#)”

Jane Fridlyand (Genentech, fridlyand.jane@gene.com)
“[Is Tumor Burden a Better Predictor of Drug Activity than Progression Free Survival?](#)”

J. Jack Lee (U. Texas M.D. Anderson Cancer Center, jjlee@mdanderson.org)
“[Biomarker Based Adaptive Designs for Targeted Agent Development - A Step Toward Personalized Medicine](#)”

WNAR Invited 2: Joint Modeling of Longitudinal and Survival Data or GLM Data

Chair:

Jianxin Pan (University of Manchester, UK, jianxin.pan@manchester.ac.uk)

Organizer:

Keming Yu (Brunel University, UK, keming.yu@brunel.ac.uk)

Speakers:

Geert Verbeke (University of Leuven, Belgium, geert.verbeke@med.kuleuven.be)

["Predicting renal graft failure using multivariate longitudinal profiles"](#)

Jeremy Taylor (University of Michigan, jmgt@umich.edu)

["Individual Prediction Using a Joint Longitudinal-Survival Model"](#)

Erning Li (Texas A&M University, eli@stat.tamu.edu)

["Joint models with regression analysis and variable selection in measurement error covariance of longitudinal covariate processes"](#)

Roseanne McNamee (University of Manchester, UK,

Roseanne.Mcnamee@manchester.ac.uk)

["Modelling of longitudinal blood pressure data and morbidity/mortality events in a trial of anti-hypertensives"](#)

IMS Invited 1: Applied Bayesian Modeling

Chair:

Jeffrey Morris (MD Anderson Cancer Center, jefmorris@mdanderson.org)

Organizer:

Feng Liang (University of Illinois at Urbana-Champaign, liangf@uiuc.edu)

Speakers:

Valen Johnson (MD Anderson Cancer Center, vejohanson@mdanderson.org)

["Bayesian Design of Single-Arm Phase II Clinical Trials with Continuous Monitoring"](#)

Chris Hans (Ohio State University, hans@stat.osu.edu)

["Covariance Decompositions for Improved Computation in Bayesian Scale-Usage Models"](#)

David Dahl (Texas A&M University, dahl@stat.tamu.edu)

["Modeling the Joint Distribution of Pairs of Dihedral Angles for Protein Structure Prediction"](#)

David van Dyk (University of California, Irvine, dvd@ics.uci.edu)

["Empirical Comparisons of Computer Models for Stellar Evolution"](#)

IMS Invited 2: New Frontiers in Functional Data Analysis

Chair:

Rhonda J. Rosychuk (University of Alberta, rhonda.rosychuk@ualberta.ca)

Organizer:

Jane-Ling Wang (University of California, Davis, wang@wald.ucdavis.edu)

Speakers:

Andrada Ivanescu (East Carolina University, IVANESCUA@ecu.edu)

["Adaptive inference for sparse signals in functional data"](#)

Jeffrey Morris (MD Anderson Cancer Center, jefmorris@mdanderson.org)

["Bayesian Hierarchical Functional Models for Detecting Shared Regions of Genomic Aberration in a Clinical Population"](#)

Debashis Paul (University of California, Davis, debashis@wald.ucdavis.edu)

["Modeling longitudinal data: FDA vs. ODE"](#)

Joint WNAR/IMS 1: Analysis of Event History Data: New Developments and Applications

Chair:

Rhonda J. Rosychuk (University of Alberta, rhonda.rosychuk@ualberta.ca)

Organizer:

X. Joan Hu (Simon Fraser University, joanh@stat.sfu.ca)

Speakers:

Mei-Ling Lee (University of Maryland, mltee@umd.edu)

["Threshold Regression and Analytical Time: With Applications in Epidemiology and Clinical Trials"](#)

Lihui Zhao (Simon Fraser University, Canada, lhzhao@stat.sfu.ca)

["Estimation with Nonhomogeneous Semi-Markov Processes"](#)

Peter Gilbert (University of Washington, pgilbert@scharp.org)

["Estimation of stratified mark-specific proportional hazards models with missing marks"](#)

Ning Li (University of Florida, nli@php.ufl.edu)

["Joint modeling of longitudinal ordinal data and competing risks survival"](#)

Tuesday 16th:

WNAR Invited 3: Multivariate Longitudinal Data Analysis

Chair:

Kate Crespi (UCLA, ccrespi@ucla.edu)

Organizer:

Robert Weiss, Dept. of Biostatistics (UCLA, robweiss@ucla.edu)

Speakers:

Michael J. Daniels (University of Florida, mdaniels@stat.ufl.edu)

["Analysis of multivariate longitudinal ordinal data using marginalized models"](#)

Robert Weiss (UCLA, robweiss@ucla.edu)

["The Common Predictor Effects \(COPE\) Model for Multivariate Longitudinal Data"](#)

Dongchu Sun (University of Missouri-Columbia, dsun@stat.missouri.edu)

["Objective Bayesian Analysis for Multivariate Longitudinal Data"](#)

WNAR Invited 4: Regression Tree and its Applications

Chair/Organizer:

Ying Lu, Ph.D. (UCSF, ying.lu@radiology.ucsf.edu)

Speakers:

Heping Zhang, Ph.D. (Yale University, heping.zhang@yale.edu)

["Tree – and Forest-based Genomic Analysis"](#)

Ilya Lipkovich, Ph.D. (Eli Lilly, lipkovichia@lilly.com)

["STEP: A new tree-based procedure for identifying subgroups of subjects with treatment effect"](#)

Caixia Li, Ph.D. (UCSF, caixia.li@radiology.ucsf.edu)

["Using Bootstrap Aggregating or Random Forests to Select Optimal Diagnostic Tests"](#)

IMS Invited 3: Statistical Issues in Protein Folding

Chair:

Jane Fridlyand (Genentech, fridlyand.jane@gene.com)

Organizer:

Mark Segal (University of California, San Francisco, mark@biostat.ucsf.edu)

Speakers:

Ingo Ruczinski (Johns Hopkins University, ingo@jhu.edu)

["Some statistical issues in protein folding kinetics"](#)

Scott Schmidler (Duke University, schmidler@stat.duke.edu)

["Statistical estimation for protein folding simulations"](#)

Phil Bradley (Fred Hutchinson Cancer Research Center (FHCRC),
pbradley@fhcrc.org)

["From folding to binding: using three-dimensional structures to predict protein interactions "](#)

Mark Segal (University of California, San Francisco, mark@biostat.ucsf.edu)

["A novel topology for representing protein folds"](#)

IMS Invited 4: Statistical Methods for Diagnostic Medical Imaging Data

Chair:

Debashis Paul (University of California, Davis, debashis@wald.ucdavis.edu)

Organizers:

Xiao-Hua Andrew Zhou (University of Washington, azhou@u.washington.edu)

Liansheng Larry Tang (George Mason University, ltang1@gmu.edu)

Speakers:

Kumar Bharat Rajan (Rush University and Medical Center, Kumar_Rajan@rush.edu)

["A Regression Method for the Area Under the Curve for Diagnostic Studies with Ordinal Scale Outcomes "](#)

Liansheng Larry Tang (George Mason University, ltang1@gmu.edu)

["A Random-Sum Wilcoxon Statistic with Applications to LROC Data "](#)

Dev Chakraborty (University of Pittsburgh, dpc10@pitt.edu)

["Clinical relevance of the ROC and FROC paradigms "](#)

Andriy Bandos (University of Pittsburgh, anb61@pitt.edu)

["Clustered ROC and FROC analyses"](#)

Joint WNAR/IMS 2: Next-Generation High-Throughput Sequencing

Chair/Organizer:

Sandrine Dudoit, Division of Biostatistics, UC Berkeley
(Sandrine@stat.berkeley.edu)

Speakers:

James Bullard, Division of Biostatistics, UC Berkeley (bullard@stat.berkeley.edu)
“[EDA and Inference in mRNA-Seq](#)”

Hector Corrada Bravo, Department of Biostatistics, Johns Hopkins University
(hcorrada@jhsp.hopkins.edu)
“[Model-Based Quality Assessment and Base-Calling for Second-Generation Sequencing Data](#)”

Raphael Gottardo, Institut de recherches cliniques de Montreal (ICRM)
(raphael.gottardo@ircm.qc.ca)
“[PICS: Probabilistic inference for ChIP-sequencing data](#)”

Paul Spellman, Life Sciences Division, Lawrence Berkeley National Laboratory
(ptspellman@lbl.gov)
“Deep sequencing for investigation of the cancer genome”

Wednesday 17th:

WNAR Invited 5: Variable Selection and High Dimensional Data Analysis

Chair:

Ning Li (University of Florida, nli@phhp.ufl.edu)

Organizer:

Gareth James (University of Southern California, gareth@marshall.usc.edu)

Speakers:

Rob Tibshirani (Stanford University, tibs@stat.stanford.edu)
“[A penalized matrix decomposition, with applications to sparse canonical correlation analysis and principal components](#)”

Xinwei Deng (Georgia Institute of Technology, xdeng@gatech.edu)
“[Sparse Discriminant Analysis for Multi-categorical Classification](#)”

Jinchi Lv (University of Southern California, jinchilv@marshall.usc.edu)
“[A Unified Approach to Model Selection and Sparse Recovery Using Regularized Least Squares](#)”

IMS Invited 5: Population Genetics

Chair:

Paul Joyce (University of Idaho, joyce@uidaho.edu)

Organizer:

Rasmus Nielsen (University of California, Berkeley, rasmus@binf.ku.dk)

Speakers:

Paul Joyce (University of Idaho, joyce@uidaho.edu)

["Maximum likelihood estimates under k-Allele models with selection can be numerically unstable"](#)

Su Yeon Kim (University of California, Berkeley, suyeonkim@berkeley.edu)

["Design of association studies with pooled next-generation sequencing data"](#)

Yun S. Song (University of California, Berkeley, yss@stat.berkeley.edu)

["Approximate conditional sampling distributions for the coalescent with recombination"](#)