

Zeynep I. Kalaylıođlu-Wheeler

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Education:

PhD in Statistics from North Carolina State University, Raleigh, NC (Jan 2002)

Advisors: Prof. Dr. Sastry Pantula and Assoc. Prof. Dr. Sujit K. Ghosh

Dissertation Title: Frequentist and Bayesian Unit Root Tests in Stochastic Volatility Models

Keywords: Unit-root test, Stochastic volatility models, Instrumental variable, Dickey-Fuller, Gibbs sampling, Markov chain Monte Carlo

MS in Statistics from North Carolina State University, Raleigh, NC (May 2000)

Minor in Computational Engineering and Sciences

BS in Statistics from Middle East Technical University, Ankara, Turkey (June 1995)

Concentration in Computer Architecture and Programming

Honor student on Chancellor's list

Professional Experience:

Instructor, Department of Statistics, METU, 2007-.

Biostatistics (3rd. year undergraduate)- Spring 2007

Nonparametric Statistics (4th. year undergraduate) - Spring 2007

Biostatistics (graduate) - Fall 2007

Categorical Data Analysis (4th. year undergraduate) - Fall 2007

Biostatistician and Biostatistical Programmer, Information Management Services/National Cancer Institute, 2002-2007

Development of statistical methods for health sciences, analyzing cancer data

Tutoring, North Carolina State University, 2000

Statistical Theory I-II

Linear Models and Variance Components

Graduate Teaching&Research Assistant, Department of Statistics, METU, 1995-1997.

Principles of Statistics I-II

Mathematical Statistics I-II

Sampling and Survey Methods

Regression Analysis

Awards:

Full Time Scholarship for Master and Doctorate from Turkish Higher Education Council and Middle East Technical University, 1997-2002

Publications:

Chatterjee, N., **Kalaylioglu, Z.**, Shih J., Gail M., (2007), "Letter to the editor," *Biometrics*, 63, 964-966.

Saatci, E., Kocak, Y., Akpınar, E., **Kalaylioglu-Wheeler, Z.** (2007), "Effect of chemotherapy on quality of life in patients with lymphoma," *Marmara Medical Journal*, Volume 20, Number 2

Sherman, M.E., Rimm, D.L., Yang, X., Chatterjee, N., Brinton, C., Lissowska, J., Peplonska, B., Szeszenia D., Mikolajczak, A.B., Zatonski, W., Cartun, R., Mandich, D., Rymkiewicz, G., Sikor, D.M., Lukaszek, S., Kordek, R., **Kalaylioglu, Z.**, Harigopal, M., Charrette, L., Falk, R.T., Richesson, D., Anderson, W.F., Hewitt, S.M., Clossas, M.G., (2007), "Variation in breast cancer hormone receptor and HER2 levels by etiologic factors: A population-based analysis," *International Journal of Cancer*, September 1; 121(5): 1079-85

Chatterjee, N., **Kalaylioglu, Z.**, Moslehi, R., Peters, U., Wacholder, S., (2006), "Powerful multi-locus tests for genetic association in the presence of gene-gene and gene-environment interactions," *American Journal of Human Genetics*, Vol. 79(6), 1002-1016

Garcia-Closas, M., Brinton, L. A., Chatterjee, N., Peplonska B., Szeszenia-Dabrowska, N., Bardin-Mikolajczak, A., Zatonski, W., Blair, A., Anderson, W. F., Rymkiewicz, G., Mazepa-Sikora, D., Kordek, R., Lukaszek, S., **Kalaylioglu, Z.**, Sherman, M. (2006), "Established risk factors for breast cancer by tumor characteristics in Poland," *British Journal of Cancer*, 95(1):123-129

Chatterjee, N., **Kalaylioglu, Z.**, Shih J., Gail M., (2006), "Case-control and case-only designs with genotype and family history data: Estimating relative-risk, familial aggregation and absolute risk," *Biometrics*, 62(1), 36-48.

Chatterjee, N., **Kalaylioglu, Z.**, Carroll, R. J. (2005), "Exploiting gene-environment independence in family-based case-control studies: Increased power for detecting as-

sociations, interactions, and joint effects,” *Genetic Epidemiology*, 28, 138-156

Hisada, M., Chatterjee, N., **Kalaylioglu, Z.**, Battjes, R. J., Goedert, J. J. (2005), “Hepatitis C virus load and survival among injection drug users in the United States,” *Hepatology*, Vol. 42, No. 6, 1446-1452

Kalaylioglu, Z., Pantula, S. G. and Ghosh, S. K. (2003), “Frequentist unit root tests in stochastic volatility models,” *Joint Statistical Meetings Proceedings, Business and Economics Statistics Section*[CD-ROM], Alexandria, VA: American Statistical Association.

Kalaylioglu, Z. and Ghosh, S. K. (2002), “Bayesian unit-root tests in stochastic volatility models,” *Joint Statistical Meetings Proceedings, Business and Economics Statistics Section*[CD-ROM], Alexandria, VA: American Statistical Association.

Kalaylioglu, Z., Pantula, S. G. and Ghosh, S. K. (2002), “Frequentist and Bayesian unit root tests in stochastic volatility models,” *unpublished Ph.D. thesis*

Other Professional Activities:

Seminars and Conferences

December 26, 2007. Collaboration of health scientists and biostatisticians for a successful biomedical research: Two examples from NIH.
Department of Biological Sciences, METU, Ankara.

August, 2007. A two-stage logistic regression application: predictors of breast cancer risk
by tumor size, grade, and nodal status
Graduate Summer School on New Advances in Statistics
Department of Statistics, METU, Ankara.

February 23, 2006. Exploiting gene-environment independence in family-based case-control studies
Department of Statistics, METU, Ankara.

August, 2003. Frequentist unit root tests in stochastic volatility models
American Statistical Association Meetings, San Francisco, CA.

August, 2002. Bayesian unit root tests in stochastic volatility models

American Statistical Association Meetings, New York City, NY.

2001. Bayesian unit root tests in stochastic volatility models
NBER/NSF Time Series Workshop, Raleigh, NC.

Contribution to Papers

Berndt, S. I., Huang, W. Y., Chatterjee, N., Yeager, M., Welch, R., Chanock, S. J., Weissfeld, J. L., Schoen, R. E., Hayes, R. B. "Transforming growth factor beta 1 (TGFB1) gene polymorphisms and risk of advanced colorectal adenoma," *Carcinogenesis*, Vol 28, No. 9, 1965-1970 (2007).

Garcia-Closas M., Malats N., Real F. X., Yeager M., Welch R., Silverma, D., Kogevinas M., Dosemeci M., Figueroa J., Chatterjee N., Tardon A., Serra C., Carrato A., Garcia-Closas R., Murta-Nascimento C., Rothman N., Chanock S., (2007), "Large-Scale Evaluation of Candidate Genes Identifies Associations between VEGF Polymorphisms and Bladder Cancer Risk", *Plos Genetics* 3(2):e29

Garcia-Closas M., Malats N., Real F. X., Welch R., Kogevinas M., Chatterjee N., Pfeiffer R., Silverman D., Dosemeci M., Tardon A., Serra C., Carrato A., Garcia-Closas R., Castano-Vinyals G., Chanock S., Yeager M., and Rothman N. (2006), "Genetic Variation in the Nucleotide Excision Repair Pathway and Bladder Cancer Risk," *Cancer Epidemiology Biomarkers and Prevention*, Vol. 15, 536-542

Chatterjee, N. and Carroll, R. J. (2005), "Semiparametric maximum likelihood estimation exploiting gene-environment independence in case-control studies," *Biometrika*, 92, 399-418

Spinka, C., Carroll, R. J., Chatterjee, N. (2005), "Analysis of case-control studies of genetic and environmental factors with missing genetic information and haplotype-phase ambiguity," *Genetic Epidemiology*, 29, 108-127

Garcia-Closas M., Malats N., Silverman D., Dosemeci M., Kogevinas M., Hein D. W., Tardon A., Serra C., Carrato A., Garcia-Closas R., Lloreta J., Castano-Vinyals G., Yeager M., Welch R., Chanock S., Chatterjee N., Wacholder S., Samanic C., Tora M., Fernandez F., Real F. X., Rothman N. (2005), "NAT2 slow acetylation, GSTM1 null genotype, and risk of bladder cancer: results from the Spanish Bladder Cancer

Study and meta-analyses,” *Lancet*, 366(9486):649-659

Projects

A stratified matched case-control study for estimating the risk of developing carcinoma among women diagnosed with endometrial hyperplasia,

Global p-value based on likelihood ratio test to identify the genes related with Non-Hodgkins Lymphoma,

Two stage polytomous logistic regression analysis for evaluating the association between gene polymorphisms of interest and renal cell tumor characteristics,

Computer Functions Written

R

INFORMATION.LOGISTIC: Information matrix of logistic regression likelihood function,

MULTTEST.PERM: Permutation based methods to compute p-values for simultaneous hypothesis testing,

SCORE.LOGISTIC: Score function of logistic regression likelihood function,

MATLAB

CCCLR : Conditional maximum likelihood estimation for matched case- control studies,

CLR : Conditional logistic regression analysis for 1:k matching,

HLOGREGMISSING: Estimation of the haplotype frequencies and logistic regression coefficients for diplotype based genetical studies,

MULTINOUTCOME: Generation of multinomial random variables,

SELECTWOR : Random number selection without replacement,

WR : Correlation matrix for weighted data,

WMEANVAR : Mean and variance of weighted data,

WPHM : Proportional hazards model estimation for weighted data,

SCORE.LOGISTIC: Score function of logistic regression likelihood function,

INFORMATION.LOGISTIC: Information matrix of logistic regression likelihood function,

EH.ANALYSIS: A two stage modeling approach for the logistic regression analysis of the data where disease subtypes are defined using multiple characteristics.

GAUSS

CCKKJOINT: Maximum likelihood estimates of relative risks, survival function estimates of carriers and noncarriers of the mutated genes based on a kin-cohort design using joint likelihood function,

CCKKCOMPOSITE: Maximum likelihood estimates of relative risks, survival function estimates of carriers and noncarriers of the mutated genes based on a kin-cohort design using composite(marginal) likelihood function.

Programming Skills:

Matlab, Gauss, SAS, S-plus, R, BUGS, WinBugs, Maple, LaTeX, Pascal, Fortran, C, Cobol

Language Skills:

Turkish(native), English(reading,writing,speaking), German(reading)

Other Professional Skills:

Ten finger typing

Professional Memberships:

The International Biometric Society

Nonprofessional Memberships:

United States Tennis Association

Montgomery County Tennis Association

Bridge to Türkiye Fund

TEMA

Supporting:
İLKYAR
UNICEF