Dmitri Zaykin, Ph.D.

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Education:

Ph.D. 1999 Biomathematics North Carolina State University

M.S. 1988 Biology and Population Genetics Far Eastern State University, Vladivostok, Russia

Dmitri Zaykin joined the Biostatistics Branch at NIEHS in October 2004. His previous positions in statistical and population genetics were at the Institute of Marine Biology (Vladivostok, Russia), North Carolina State University (Statistical Genetics and Biomathematics, Statistics Department - where he received his PhD), and at GlaxoSmithKline Inc. His scientific interests are in the areas of statistical, population genetics and genetic epidemiology with applications to genetics of human diseases and pharmacogenetics. His research focus is on:

- Approaches for simultaneous association analysis of multiple polymorphisms with human traits such as disease predisposition and adverse reactions to drugs
- Multilocus association methods when the haplotype phase is unobserved
- Statistical methods for estimation of genetic susceptibility
- Population-genetic aspects of effective population size
- Studies of genetic associations in the presence of population heterogeneity
- Characterizing disequilibria within and between multiple genetic loci with applications to studies of population structure and forensics
- Properties and estimation of two-locus disequilibria
- Haplotype and linkage disequilibrium based marker selection methods for large-scale association studies and other issues of selecting polymorphisms that tag common haplotypic variation in human populations
- Meta-analysis methods in the presence of effect size heterogeneity, "file drawer effects" and

other sources of publication bias
- Multiple-testing problems in genome scans
- Relative distributions of true and false discoveries and false discovery rates

A Selection of Relevant Publications:

Zaykin DV, Zhivotovsky L 2004. Ranks of genuine associations in whole genome scans (submitted)

Zaykin DV, Ehm MG, Weir BS 2004. The composite haplotype method for association mapping of complex traits in outbred populations (submitted)

Zaykin DV, Young SS 2004 Large recursive partitioning analysis of complex disease pharmacogenetic studies: II. Statistical considerations (Pharmacogenomics, in press)

Nielsen DM, Ehm MG, Zaykin DV, Weir BS 2004 Effect of two- and three-locus linkage disequilibrium on the power to detect marker/phenotype associations. Genetics 168: 1029-1040.

Zaykin DV 2004. Bounds and normalization of the composite linkage disequilibrium coefficient. Genetic Epidemiology 27:252-257

Zaykin DV, Meng Z, Ghosh SK 2004. Interval estimation of genetic susceptibility for retrospective case-control studies. BMC Genetics. 2004 May 11;5(1):9.

Meng Z, Zaykin DV, Xu C-F, Wagner M, Ehm M. 2003. Selecting genetic markers for association analyses using LD and haplotypes Am J of Hum Genet 73: 115-130.

Zaykin DV, Westfall PH, Young SS, Karnoub MC, Wagner MJ, Ehm MG. 2002. Testing association of statistically inferred haplotypes with discrete and continuous traits in samples of unrelated individuals. Human Heredity 53: 79-91.

Zaykin DV, Zhivotovsky LA, Westfall PH, and Weir BS. 2002. Truncated product method for combining P-values. Genetic Epidemiology 22:170-185.

Xu C-F, Lewis K, Cantone CL, Khan P, Donnelly C, White N, Crocker N, Boyd PR, Zaykin DV, Purvis IJ. 2002. The effectiveness of computational methods in haplotype prediction. Hum Genet 110:148-156.

Westfall PH, Zaykin DV, and Young SS. 2001. Multiple tests for genetic effects in association studies. In "Biostatistics Methods", series "Methods in Molecular Biology, Biotechnology and Medicine", Stephen Looney, Ed., The Humana Press, Inc.

Nielsen DM, Zaykin DV. 2001. Association mapping: where we've been, where we're going. Expert Reviews in Molecular Diagnostics 1:89-97.

Meng Z, Zaykin DV, Karnoub MC, Sreekumar GP, St Jean PL, Ehm MG 2001. Identifying susceptibility genes using linkage and linkage disequilibrium analysis in large pedigrees. Genetic Epidemiology, 21S:453-458.

Almasy L, Terwilliger JD, Nielsen D, Dyer TD, Zaykin D, Blangero J. 2001. GAW12: Simulated genome scan, sequence, and family data for a common disease. Genetic Epidemiology, 21S:332-

338.

Thomas DC, Borecki IB, Thomson G, Weiss K, Terwilliger JD, Nielsen D, Zaykin D, Blangero J, Almasy L, Macluer J. 2001. Evolution of the GAW 12 simulated data problem. Genetic Epidemiology, 21S:325-331.

Zaykin DV, Young SS, and Westfall PH. 2000. Using false discovery rate approach in the genetic dissection of complex traits: a response to Weller et al. Genetics 154: 1917-1918.

Zaykin D and Pudovkin A. 2000. The variance effective population size for mitochondrial genes. Russian Journal of Genetics 36:965-967.

Nielsen D, Zaykin D. 1999. Novel tests for marker-disease association using the COGA data. Genetic Epidemiology S265-S270, 1999.

Pudovkin AI, Zaykin D, and Dolganov S. 1998. Interlocus genotypic associations in Sea of Japan settlements of the scallop Mizuhopecten (Patinopecten) yessoensis. Russian Journal of Genetics 34:299-305.

Pudovkin AI, Zaykin D, and Hedgecock D. 1996. On the potential for estimating the effective number of breeders from heterozygote-excess in progeny. Genetics 144:383-387.

Weir BS and Zaykin D. 1996. Tests for disequilibrium in Illinois databases. Illinois State Police and Chicago Police Department, technical report.

Pudovkin AI, Zaikin D, and Tatarenkov AH. 1996. A computer program for calculation of genetic distances and their bootstrap confidence intervals. Russian Journal of Genetics 32:1017-1020.

Zaykin D, Zhivotovsky LA, and Weir BS, 1995. Exact test for association between alleles at arbitrary number of loci. Genetica 96:169-178.

Surmach SG and Zaykin DV. 1994. The scaly-sided merganser Mergus squamatus (Gould) in the Iman basin, Far East Russia. Threatened Waterfowl Research Group. B. Hughes and J. Hunter, Ed., p.11-17.

Zaykin DV and Pudovkin AI 1993. Two programs to estimate significance of Chi-square values using pseudo-probability test. J. of Heredity 84:152.

Polyakova NE, Malinina TV, Galeev AV, Zaikin DV, Brykov VA, Altukhov YP. 1992. Variability in the mitochondrial DNA of the pink salmon Oncorhynhus gorbusha (Walbaum). Russian Journal of Genetics 28:122-129.

Zaykin DV and Pudovkin AI. 1991. Programme MULTTEST: calculation of indices of statistical significance for multiple tests. Russian Journal of Genetics 27:2034-2038.

Balakirev ES and Zaykin DV. 1990. Allozyme polymorphism of glutathione reductase in marine invertebrates. Isozyme Bulletin, 23:90.

Balakirev ES and Zaykin DV. 1990. Allozyme variability of formaldehyde dehydrogenase - a new gene marker in marine invertebrates. Isozyme Bulletin, 23:91.

Balakirev ES and Zaykin DV. 1988. Allozyme variability of formaldehyde dehydrogenase in marine

invertebrates. Russian Journal of Genetics 24:1504-1507.

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