Curriculum Vitae

Ina Hoeschele

Mailing Address: Biocomplexity Institute, 1015 Life Sciences Drive
Virginia Polytechnic Institute and State University
Blacksburg, VA 24061-0477
phone: (540) 231-3135
fax: (540) 231-2606
email: inah@vbi.vt.edu
http://vbi.vt.edu/people/people-profile/Ina-Hoeschele
http://www.stat.vt.edu/people/faculty/Hoeschele-Ina.html

Education

German National Science Foundation Postdoctoral Fellow, Department of Animal Sciences, (mentor: D. Gianola), University of Illinois, Champaign-Urbana, *1987*.

German National Science Foundation Postdoctoral Fellow, Departments of Animal Science and Statistics, (mentors: M.F. Rothschild, A.E. Freeman, D.A. Harville), Iowa State University, Ames, *1986 - 1987*.

Ph.D., Quantitative Genetics and Biometry, Hohenheim University, Stuttgart, Germany, *1983-1986*.

Diploma (Dipl. Ing. Agr., B.S. & MS equivalent), Animal Genetics and Biometry, Hohenheim University, Stuttgart, Germany, *1978-1983*.

Employment

Assistant Professor of Genetics, Department of Dairy Science, Virginia Polytechnic Institute and State University, Blacksburg, VA, 1988 - *1993*.

Associate Professor of Genetics, Department of Dairy Science, Virginia Polytechnic Institute and State University, Blacksburg, VA, *1993 - 1998*.

Adjunct Professor of Statistics, Department of Statistics, Virginia Polytechnic Institute and State University, Blacksburg VA, *1997 - 2002*.

Professor of Genetics, Department of Dairy Science, Virginia Polytechnic Institute and State University, Blacksburg VA, *1998 - 2002*.

Professor, Department of Statistics, Virginia Polytechnic Institute and State University, Blacksburg VA, *2002 - present*.

Professor, Biocomplexity Institute, Virginia Polytechnic Institute and State University, Blacksburg VA, *2002 - present*.

Adjunct Professor, Wake Forest University School of Medicine, Winston-Salem, NC, *2006-present*.

Professional Honors and Awards

German Foreign Academic Exchange Organization (DAAD) Fellow, Station de Genetique Quantitative et Appliquee, Jouy-en-Josas, France, *1985*.

Young Scientist's Research Award of the European Association for Animal Production (EAAP), *1985*.

Summa Cum Laude Dissertation Award, Hohenheim University, Stuttgart, Germany, *1986*.

Postdoctoral Fellowship of the German National Science Foundation, *1986-87*.

Visiting Professor, Australian Meat Corporation Fund, Animal Genetics and Breeding Unit, University of New England, Armidale, NSW, Australia, *1993*.

Visiting Professor, Human Capital and Mobility Fund, Wageningen Agricultural University, The Netherlands, *1995*.

Visiting Professor, Department of Statistics, North Carolina State University (Host: Dr. Bruce S. Weir, NIH supported 6-month sabbatical), *1999*.

Professional Memberships

American Statistical Association

Genetics Society of America

Professional Consultantships

Department of Agriculture, Stuttgart, Germany, *1985 - 1992*

Genmark Inc., Salt Lake City, Utah, *1989 - 1993*

Medical College of Virginia, Richmond, *1993 to 1995*

MILQTL (The Netherlands - New Zealand collaboration on the identification of economic trait loci in dairy cattle), *1994 - 1995*

Foundation for Developmental and Medical Genetics, Helena, Montana, *1994 – 1995*

Infigen Inc., DeForrest, WI, *1995-2002*.

Pennington Biomedical Center and NuPotential Inc., Baton Rouge LA, *2003 – 2006*

The Monsanto Company, *2001 – 2007*.

Wake Forest University School of Medicine, Comprehensive Cancer Center, 2006-2011.

Software and Patents

(1) Fortran program INVERS. I. Hoeschele and P.M. VanRaden. *1990*. Computes the inverses of additive, dominance, and additive-by-additive genetic relationship matrices and inbreeding coefficients for large populations; was used for research purposes at multiple universities in the U.S., Germany, The Netherlands, and Austria, and by USDA and the Holstein Association.

(2) Fortran programs NONADD and NONAD2. I. Hoeschele. *1990*. Perform prediction and variance component estimation for nonadditive genetic models; was used for research purposes at multiple universities in the U.S., Germany, The Netherlands, and Austria, and by USDA and the Holstein Association.

(3) Fortran program GMATRX. I.J.M. DeBoer and I. Hoeschele. *1993*. Calculates covariance matrices for populations with additive and dominance genetic variation and inbreeding, computed with tabular method. Used at several universities.

(4) Fortran90 programs MQHREML and MQFREML. F.E. Grignola and I. Hoeschele. *1996*. Performs Residual Maximum Likelihood analysis of linkage between multiple linked markers and quantitative trait loci for half-sib and full-sib designs. Was used at several universities but has been replaced by (6) below.

(5) Set of SAS, R and Matlab programs for analysis of microarray gene expression data including standard eQTL mapping. Mostly in-house use. Hua Li, Yongcai Mao, Bing Liu, Lei Bao, Ina Hoeschele, *2004-2008*.

(6) C++ code for haplotype inference in large human pedigrees, for calculation of identity-by-descent matrices, and for joint linkage and linkage disequilibrium mapping. Used at multiple universities in multiple countries. Guimin Gao and Ina Hoeschele, *2004 to present*.

(7) C++ and R codes for expression QTL mapping and causal network inference in Systems Genetics experiments. Mostly in-house use at the present time. Alberto de la Fuente, Bing Liu, Ina Hoeschele. *2006-present*.

(8) SysGenSIM, a Matlab package for the simulation of artificial datasets in Genetical Systems Biology. http://sysgensim.sourceforge.net/. Andrea Pinna, Nicola Soranzo, Ina Hoeschele, Alberto de le Fuente. *2010-present.*

External Committee and Panel Memberships

NC-209 Multi-State Project “Genetic improvement of dairy cattle using molecular markers” (Chair 1997), *1993 - 2002.*

NC1010 Multi-State Project "Interpreting Cattle Genomic Data: Biology, Applications and Outreach", *2002 – 2003*.

NCR-204 Multi-State Project "The interface of molecular and quantitative genetics in plant and animal breeding", *2002-2003*.

NRSP-8 National Animal Genome Project, *1997-2000*.

MILQTL Research Project Scientific Review Panel, *1994 – 1995.*

NIH Genome Study Section grant proposal review panel, *2003*.

USDA Integrated Functional Genomics grant proposal review panel, *2004*.

NIH-NSF Math Bio program review panel, *2005*.

NIH NCBC Collaboratories review panel, 2006.

NIH GCAT study section review panel, 2009, and prior multiple years.

NIH Genomics Profiling and Genomic Technologies in Mental Disorders GO applications review panel, 2009

NIH The Genes, Environment and Health Initiative (GEI) review panel, 2009

NIH Challenge Grants in Health and Science Research review panel, 2009

NSF Advances in Biological Informatics program review panel, 2009

NIH Special Emphasis Proposal Review panels, 6/28-29, 2010; 11/11-12, 2010

NIH Special Emphasis Proposal Review panel in Computational Genetics and Genomics, March 29, 2011

NIH Special Emphasis Proposal Review Panels (Review Group 2012/05 ZDK1 GRB-J (M4))

Jeffress Trust Awards Program in Interdisciplinary Research, 2013 – 2017, Proposal Review Committee member

Evaluator of the candidates for a full Professorship at the University of Helsinki (Finland, November 2013)

Proposal reviewer for Medical Research Council, Great Britain, 2014, 2016.

Major Collaborations
(many minor collaborations are not listed)

Past:

(1)
Collaboration on genetic evaluation and parameter estimation for multiple categorical and continuous traits with the Animal Genetics and Breeding Unit, a joint venture of the University of New South Wales and the Australian Department of Agriculture in Australia, *1993-1995*.

(2)
Collaboration on the estimation of nonadditive genetic effects and on linkage mapping with the Institute of Animal Genetics (ZODIAC) at Wageningen University, The Netherlands, *1990-1995*.

(3)
Collaboration with Dr. Georg Thaller at the Technical University of Munich (Germany) on the fine-mapping of complex trait genes in livestock, *1993-2002*.

(4)
Collaboration on a comprehensive genome scan in dairy cattle and on implementation of marker-assisted selection with ABS Global / Infigen Inc., *1995-1999*.

(5)
Collaboration on a comprehensive genome scan in humans for plasma HDL cholesterol level and risk of coronary heart disease with the Department of Internal Medicine, University of Oulu, Finland, *1998-2000.*

(6)
Collaboration on a series of gene expression experiments to advance our understanding of the molecular basis of successful reprogramming for developmental competency of nuclear transfer cloned bovine and porcine embryos with Infigen Inc. (Drs. M. Bishop, K. Eilertsen), De Forrest, Wisconsin, *2000-2003*.

(7)
Collaboration on gene expression experiments aimed at advancing our understanding of the molecular basis of successful reprogramming for developmental competency of nuclear transfer cloned bovine and porcine embryos with Pennington Biomedical Research Center (Dr. K. Eilertsen), Louisiana, *2004-2006*.

(8)
Collaboration with the Monsanto Company on fine-mapping and gene network analysis, *2001-2005*.

(9)
Collaborations with the Cancer Biology Department of Wake Forest University Medical School, Winston-Salem, NC, on a mouse model for lung cancer, *2005-2007.*

(10)
Collaboration with researchers at Virginia Tech and at the Ohio State University on the genetic basis of quantitative resistance in soybean to P. Sojae infection. *2002-2008*.

(11)
Collaboration with Dr. Fei Zou and colleagues in the Department of Biostatistics at the

University of North Carolina (Chapel Hill) on nonparametric Bayesian variable selection, *2006 to 2009*.

(12)
Collaboration with John Robertson (VT Vet Med) and others on the comparative genomics of brain cancer in dogs and humans. *2010.*

(13)
Collaboration with Dr. Guimin Gao and colleagues in the Department of Biostatistics (Section in Statistical Genetics) at Virginia Commonwealth the University on haplotype inference and joint linkage and linkage disequilibrium mapping in large, complex human pedigrees. *2005-2011.*

(14)
Collaboration with Dr. Alberto de la Fuente and colleagues at CRS4 Bioinformatica (Italy) on causal network inference and simulation in systems genetics, *2006-2012*.

Current:

(15)
Collaborations with investigators at the VA-MD College of Veterinary Medicine (Drs. John Robertson, John Rossmeisl, Kurt Zimmerman) on the genomics of brain cancer in dogs and of atypical hyperadrenocorticism in Scottish Terriers. *2010-present*.

(16)
Collaborations with investigators at Wake Forest School of Medicine (Drs. Yongmei Liu, Jingzhong Ding, Timothy Howard and David Herrington) on the genomics and epigenomics of cardiovascular and other common diseases, *2008-present.*.

Other Major Services to the Profession

Associate Editor, Genetics-Selection-Evolution, *1996-2010*.

Associate Editor, Biometrics, *2000-2008*.

Associate Editor, Genetics, *2010-2016*.

Associate Editor, Frontiers in Systems Biology, *2010-present*.

Associate Editor, BMC Genetics, *2012-present*.

Grant proposal reviewer for National Science Foundation, National Institutes of Health, US Department of Agriculture, The United States – Israel Binational Agricultural Research and Development Fund, Vienna Science and Technology Fund (Austria), Human Frontier Science Program (France), Medical Research Council (UK).

Reviewer for many scientific journals including: Genetics, Heredity, Genetics-Selection-Evolution, Biometrics, Journal of Theoretical Biology, Journal of the American Statistical

Association, Journal of Agricultural and Environmental Statistics, Genetical Research, Theoretical and Applied Genetics, Computational Statistics and Data Analysis, Journal of Dairy Science, Journal of Animal Science, BMC Genomics, BMC Bioinformatics, BMC Genetics, PLoS Genetics, Bioinformatics, IEEE Journal of Biomedical and Health Informatics.

External Ph.D. thesis reviewer (two students from Australia, two from the Netherlands, two from Finland).

Research Grants (*1988-present*)

Completed:

American Jersey Cattle Club, (*1988*), "Association between genetic defects and performance for traits of economic importance in dairy cattle", $1,000, I. Hoeschele.

Eastern A.I. Cooperative, (*1988*), "Methods accounting for heterogeneous variances for dairy cattle sire and cow evaluation", $5,000, I. Hoeschele and R.E. Pearson.

Eastern A.I. Cooperative, (*1988*), "The use of quantitative trait loci in dairy cattle sire and cow evaluation", $5,000, I. Hoeschele, R.L. Fernando (University of Illinois), and D. Gianola (University of Illinois).

Eastern A.I. Cooperative, (*1989*), "Influence of nonadditive genetic effects on milk production", $10,000, I. Hoeschele.

Eastern A.I. Cooperative, (*1990*), "Influence of nonadditive genetic effects on milk production (continuation)", $5,000, I. Hoeschele.

National Association of Animal Breeders, (*1990*), "Additive and nonadditive genetic variation in measures of female fertility", $10,000, I. Hoeschele.

Holstein Association USA, (*1990*), "Detection of genetic markers and their use in selection of dairy cattle", $27,500, I. Hoeschele.

United States Department of Agriculture National Research Initiative Competitive Grants Program, (*1992*), "Method to include genetic marker data in genetic evaluation of livestock", $36,047, I. Hoeschele.

Holstein Association USA, (*1993*), "Development of an integrated genetic evaluation system utilizing phenotypic and genetic marker data", $37,106, I. Hoeschele.

Eastern A.I. Cooperative, (*1993*), "Optimizing selection for economic gain in dairy cattle", $32,000, B.G. Cassell and I. Hoeschele.

Australian Department of Industry, Training, and Regional Development, (*1994*), "Implementation of multiple trait genetic evaluation for categorical and continuous traits using Gibbs Sampling", $4,800, I. Hoeschele and B Tier.

United States Department of Agriculture National Research Initiative Competitive Grants Program, (*1994*), "Method to include genetic marker data in genetic evaluation of livestock", continuation, $59,626 (2 years), I. Hoeschele.

National Science Foundation, DBI-9696265, (*1994*), "Covariance component analyses of continuous and discontinuous traits and statistical mapping of quantitative trait loci using Markov Chain Monte Carlo methods", $342,434 (3 years), I. Hoeschele.

National Science Foundation Supercomputing Grant, (*1994*), "Covariance component analyses of continuous and discontinuous traits and statistical mapping of quantitative trait loci using Markov Chain Monte Carlo methods", 600 SU, I. Hoeschele.

National Science Foundation Supercomputing Grant, (*1995*), "Covariance component analyses of continuous and discontinuous traits and statistical mapping of quantitative trait loci using Markov Chain Monte Carlo methods", 2000 SU, I. Hoeschele.

ABS Global Inc, (*1995*), "Analysis of granddaughter design to map economic trait loci", $18,000, I. Hoeschele.

Holstein Association USA, (*1995*), "Development of an integrated genetic evaluation system utilizing phenotypic and genetic marker data", continuation, $10,000, I. Hoeschele.

MONTS (Montana’s NSF EpScor Program), (*1996*), "Statistical gene mapping and genetic parameter estimation using Markov chain Monte Carlo methods", $30,000, I. Hoeschele. (Returned).

United States Department of Agriculture National Research Initiative Competitive Grants Program, 96-35205-3662, (*1996*), "Method to include genetic marker data in genetic evaluation of livestock", continuation, $184,772 (3 years), I. Hoeschele.

National Science Foundation Supercomputing Grant, (*1996*), "Covariance component analyses of continuous and discontinuous traits and statistical mapping of quantitative trait loci using Markov Chain Monte Carlo methods", 3000 SU, I. Hoeschele.

ASPIRES (*1997*) “Computational methods for statistical analysis of genetic data”, $26,700, I. Hoeschele.

ASPIRES (*1997*) “Establishment of an Institute for Genomics”, $64,795, M. Potts (PI), S. Boyle (Co-PI), R. Helm (Co-PI), I. Hoeschele (Co-PI).

National Science Foundation, DBI-9723022, (*1998-2002*), "Model choice and improvement for Bayesian analysis of Generalized Linear Mixed Models and Bayesian multiple polygene mapping in pedigreed, outcross populations", $250,768 (3 years), I. Hoeschele.

Holstein Association USA, (*1997-2002*), "Development of an integrated genetic evaluation system utilizing phenotypic and genetic marker data", $11,000, I. Hoeschele.

United States Department of Agriculture National Research Initiative Competitive Grants Program, 99-35205-8568**,** (*1999-2002*), "Method to include genetic marker data in genetic evaluation of livestock", continuation, $200,000, I. Hoeschele.

Infigen Inc. (*2000-2003*), “Design and analysis of a microarray gene expression experiment for predicting developmental competency of nuclear transfer bovine and porcine embryos", $121,387. I. Hoeschele.

The Monsanto Company (*2002-2005*), Statistical methods and software development for fine-mapping of QTLs in swine populations, $139,063, I. Hoeschele.

Comprehensive Cancer Center of Wake Forest University Pilot Grant Program (2004), "Microarray analysis of the effects of the mutant human Ki-*ras* gene on pulmonary gene expression in a bitransgenic murine model of lung tumorigenesis", $10,000, M. Miller, I. Hoeschele and S. Martino-Catt.

National Institutes of Health, R01 GM66103-01, (*2002-2006*), "Polygenic linkage and linkage disequilibrium mapping", $320,708, I. Hoeschele

National Science Foundation DBI-0211863, (*2002-2008*), "Dissecting soybean resistance to Phytophthora by QTL analysis of host and pathogen expression profiles", $6,764,465, B.M. Tyler (PI), M.A. Saghai Maroof, I. Hoeschele (Co-PI), A. Dorrance, S. St. Martin.

RHL092572A, National Institutes of Health (*2008-2010*), "Angiotensis Receptor Blockade and Adipose Tissue Inflammation in Obesity". $435,344. K. Davy, I. Hoeschele (Co-PI).

Wake Forest University (NIH) (2007-2009), "Research Collaboration and TSI Program", $17,903, I. Hoeschele (PI).

P30 CA12197, Comprehensive Cancer Center Of Wake Forest University, (2006-2011), "Biostatistics Consulting", $255,612, I. Hoeschele (PI).

1R01GM073766-01A2, National Institutes of Health (*2007-2013*), "Haplotyping and QTL mapping in pedigrees with missing data". $177,582 (Hoeschele portion). G. Gao (PI), I Hoeschele (Co-I).

1R01HG005254-01, National Institutes of Health (2010-2014), "Highly Multivariate Quantitative Trait Loci Mapping In Systems Genetics". $773,732, I Hoeschele (PI).

1R01HL101250-01, National Institutes of Health (*2009-2016*), "Epigenome-wide association study of DNA methylation and artherosclerosis", $559,641 (Hoeschele: PI of subcontract to VT, Y. Liu (WFU): PI).

5R01AG032098, National Institutes of Health (2011-2016), "Genetic determinants of visceral adiposity: A genome-wide association study. $449,060 (Hoeschele sub-contract for the period 02/01/11-1/31/16; Y. Liu, PI).

AKC Canine Health Foundation (2011-2016) Longitudinal Study Investigating the Progression and Pathogenesis of Atypical Hyperadrenocorticism in Scottish Terriers. $25,200, Kurt Zimmerman (PI), Hoeschele Co-I.

Active:

National Institutes of Health (*2012-2017*), "Genomic and proteomic features of premature atherosclerosis". $1,965,933 (Wattam AR: PI of subcontract to VT, Hoeschele I at 14%, Herrington D (WFU): PI).

National Institutes of Health (*2014-2018*), “Epigenetic roles in cholesterol metabolism and CVD risk”. $731,631 (Hoeschele: PI of subcontract to VT, Y. Liu (WFU): PI).

National Institutes of Health (*2015-2020*), “Obesity-Related Epigenetic Changes and Type-2 Diabetes”. $384,407 (Hoeschele: PI of subcontract to VT, J. Ding (WFU): PI).

National Institutes of Health (*2016-2021*), “Epigenetics of Weight Loss and Glycemic Improvement”. $301,006 (Hoeschele: PI of subcontract to VT, J. Ding (WFU): PI).

National Institutes of Health (*2018-2020*), “A Longitudinal Epigenetic Study of Atherosclerosis”. $764,765 (Hoeschele: PI of subcontract to VT, Y. Liu (WFU): PI).

Major Invited Talks and Lectureships

1. Annual Meeting of the German Committee for Statistical Genetics, *March 1985*, Rauisch-Holzhausen, Germany. "Comparison of genetic evaluation procedures for categorical data."

2. Annual Meeting of the German Committee for Statistical Genetics, *March 1986*, Rauisch-Holzhausen, Germany. "Estimation of variance and covariance components with categorical data."

3. 37th Annual National Poultry Breeder's Roundtable, *May 1988*, St. Louis, MO. "Statistical analysis of field data with major genes segregating."

4. 14th International Biometric Conference, *July 1988*, Namur, Belgium. "Genetic analysis of animal breeding data combining major gene and polygenic inheritance."

5. Joint Annual Meeting of the American Dairy Science Association and the American Society of Animal Science, *July 1989*, Lexington, KY. "The role of animal breeding in an age of molecular and zygotic manipulation. Potential gains from major gene insertion in dairy cattle."

6. Internordic course for graduate students and postdoctoral fellows, *May 1990*, Uppsala, Sweden. "Statistical methods for detection and utilization of major genes."

7. NC-209/NC-210 National Animal Genome Technical Committee Meeting, *November 1993*, Salt Lake City, UT. "Statistical methods for the mapping of quantitative trait loci in livestock populations."

8. International course "Markov Chain Monte Carlo in Genetic Analyses", *May 1994*, Wageningen, The Netherlands. "Bayesian QTL mapping via MCMC algorithms."

9. International course "Markov Chain Monte Carlo in Genetic Analyses", *May 1994*, Wageningen, The Netherlands. "Bayesian analysis of a Generalized Linear Mixed Model for categorical traits".

10. International workshop "Markov Chain Monte Carlo algorithms: Theory and Applications in Animal Genetics", *June 12-13, 1995*, Salzburg, Austria.

11. Workshop "Markov Chain Monte Carlo algorithms: Theory and Applications in Animal Genetics", *July 5-6*, Wageningen University, The Netherlands.

12. International Conference on Mapping Quantitative Trait Loci in Animals, Plants and Humans, *June 1996*, Gotland, Sweden. "Statistical methods for the mapping of Quantitative Trait Loci"

13. Annual Meeting of the American Statistical Association, Chicago, USA, *August 1996*, Continuing Education Course "Markov Chain Monte Carlo Methods for likelihood and Bayesian inference".

14. Annual Meeting of the American Statistical Association, Chicago, USA, *August 1996*, “Statistical mapping of polygenic loci in livestock".

15. Allerton II: Genetic analysis of economically important traits in livestock, Monticello, IL, *November 1996*, “Bayesian and Residual Maximum Likelihood statistical gene mapping”.

16. Sixth Gordon Conference on Quantitative Genetics and Biotechnology, Ventura, CA, USA, *February 1997*. "QTL: Beyond experimental populations, methods"

17. Module 8, Summer Institute for Statistical Genetics at North Carolina State University, *June 1997*, “Pedigree analysis and Bayesian gene mapping”.

18. Module 7, Summer Institute for Statistical Genetics at North Carolina State University, *June 1998*, “Pedigree analysis and Bayesian gene mapping”.

19. Module 12, Summer Institute for Statistical Genetics at North Carolina State University, *June 1999*, “Pedigree analysis and Bayesian gene mapping”.

20. Module 12, Summer Institute for Statistical Genetics at North Carolina State University, *June 2000*, “Pedigree analysis, Bayesian linkage mapping, and disequilibrium fine-mapping”.

21. Highly Structured Stochastic Systems Workshop on "Bayesian and MCMC Methods in Gene Mapping", Lammi (Finland), *March 24 - 27, 1999*, “Mapping complex trait genes in a dairy cattle pedigree for milk production and health and in a human pedigree for cholesterol, using Bayesian and other methods”.

22. 50th Anniversary Conference of the Department of Statistics at Virginia Tech, *August 1999*, “Bayesian mapping of quantitative trait genes in complex pedigrees”.

23. 50th Anniversary Conference of the Department of Statistics at Virginia Tech, *August 1999*, “Statistical Genomics: Current and Future”, NSF panel discussant.

24. Short-course (Mathematical Approaches to the Analysis of Complex Phenotypes) at

The Jackson Laboratory, *October 2000*, “QTL mapping in complex pedigrees via Bayesian methods and genotype samplers”.

25. Plant and Animal Genome IX (International Conference on the Status of Plant and Animal Genome Research), *January 2001*, “QTL mapping in complex pedigrees”.

26. Module 12 (QTL II), Summer Institute for Statistical Genetics at North Carolina State University, *June 2001*, “Pedigree analysis, Bayesian linkage mapping, and disequilibrium fine-mapping”.

27. Short-course (Mathematical Approaches to the Analysis of Complex Phenotypes) at The Jackson Laboratory, *October 2001*, “Identification of genes and pathways affecting quantitative traits in complex pedigrees using genetic marker and microarray gene transcription data”.

28. Short-course (Mathematical Approaches to the Analysis of Complex Phenotypes) at The Jackson Laboratory, *September 2002*, “Identification of genes and pathways affecting quantitative traits in complex pedigrees using genetic marker and microarray gene transcription data”.

29. Workshop on Analysis of Gene Expression Data: Principles and Applications, Mathematical Biosciences Institute at The Ohio State University, *October 2004*, “Genetical genomics analysis to infer gene regulatory networks”.

30. Symposium: Systems Biology: Integrative, Comparative, and Multi-Scale Modeling. Iowa State University, June 11-14, 2009.

Invited Seminars (*1987 - present*)

1. Iowa State University, Department of Animal Science (*January 1987*), "Estimation of covariance components in generalized mixed linear models for discrete traits."

2. Iowa State University, Department of Statistics (*February 1987*), "Applications of mixture distribution models in animal breeding."

3. University of Illinois, Department of Animal Science (*August 1987*), "Identification of major genes using statistical approaches." (Biotechnology and animal improvement: A discussion on needs and opportunities.)

4. VPI & SU, Department of Statistics (*December 1988*), "Statistical methods in genetic evaluation of livestock."

5. Medical College of Virginia, Department of Human Genetics, Richmond (*February 1989*), "Methods for genetic evaluation of livestock."

6. Cornell University, Department of Animal Science (*September 1989*), "Potential gains from major gene insertion in dairy cattle."

7. Cornell University, Department of Animal Science (*September 1989*), "Rapid methods to

compute inverses of dominance and additive-by-additive relationship matrices."

8. Hohenheim University (Germany), Department of Animal Breeding and Animal Genetics (*December 1989*), "Genetic models including nonadditive and single gene effects."

9. Virginia Polytechnic Institute and State University, Department of Dairy Science (*May 1990*), "Genetic models with nonadditive, single gene, and marker effects."

10. Utah State University, Genmark, Inc. and Department of Human Genetics (*March 1990*), "Estimation of nonadditive genetic variance and its use in breeding programs."

11. Utah State University, Genmark, Inc. and Department of Human Genetics (*March 1990*), "Potential gains from use of genetic markers in dairy cattle genetic evaluation."

12. Swedish Agricultural University, Uppsala, Department of Animal Science (*May 1990*), "Estimation of nonadditive genetic variance and its use in breeding programs."

13. Medical College of Virginia, Department of Human Genetics, Richmond (*March 1991*), "Bayesian analysis of linkage between genetic markers and quantitative trait loci."

14. Hohenheim University (Germany), Department of Animal Breeding and Animal Genetics (*May 1991*), "An update on the Weaver locus."

15. Hohenheim University (Germany), Department of Animal Breeding and Animal Genetics (*May 1991*), "Bayesian method for linkage analysis of animal breeding data."

16. Wageningen Agricultural University (The Netherlands), Department of Animal Breeding (*May 1991*), "Bayesian method for linkage analysis of animal breeding data."

17. Wageningen Agricultural University (The Netherlands), Department of Animal Breeding (*May 1991*), "Estimation of nonadditive genetic effects from animal breeding data."

18. Wageningen Agricultural University (The Netherlands), Department of Animal Breeding (*May 1991*), "The effect of the Weaver locus on milk production.

19. Virginia Polytechnic Institute and State University, Department of Dairy Science (*May 1992*) "Method to incorporate genetic marker data in animal model genetic evaluations."

20. Medical College of Virginia, Department of Human Genetics (*December 1992*), "Estimating five component models for family resemblance."

21. Genmark Inc., Salt Lake City, UT (*January 1993*), "Results from single marker Bayesian linkage analysis."

22. University of New England (Australia), Department of Animal Science and Animal Genetics and Breeding Unit (*April 1993*), "Markov Chain Monte Carlo Methods for implementing multiple trait genetic evaluation procedures for continuous and categorical traits."

23. University of Queensland (Australia), Molecular Animal Genetics Center (*May 1993*), "Bayesian linkage analysis for the mapping of quantitative trait loci."

24. University of Queensland (Australia), Molecular Animal Genetics Center (*May 1993*), "Utilization of genetic marker data in dairy cattle breeding."

25. Montana State University, Department of Mathematics (*February 1994*), "Generalized linear mixed models."

26. Montana State University, Plant Genetics and Molecular Biology group (*November 1994*), "Experimental designs and statistical analyses for the mapping of quantitative trait loci".

27. Virginia Polytechnic Institute and State University, Department of Statistics (*February 1995*), "Applications of Markov Chain Monte Carlo algorithms in animal and human genetics".

28. Michigan State University, Campus Theory Seminar (*April 1996*), "Bayesian polygene mapping via Markov chain Monte Carlo algorithms"

29. Michigan State University, Department of Animal Science (*April 1996*), "Categorical data analysis via Markov chain Monte Carlo algorithms"

30. Duke University, Institute of Statistics and Decision Sciences (*September 1996*), ”Statistical gene mapping and generalized linear mixed models”

31. University of Wisconsin (Madison), Department of Animal Science, (*November 1996*), “Residual Maximum Likelihood and Bayesian statistical gene mapping”

32. North Carolina State University, Department of Statistics, (*December 1996*), “Residual Maximum Likelihood and Bayesian statistical gene mapping”

33. Beadle Center for Biotechnoloy, Lincoln, Nebraska, (*April 1997*), ”Statistical mapping of quantitative trait loci in outcross populations”

34. Infigen Inc. and ABS Global Inc. (July 1997), “A first complete genome scan for milk production and health traits in the ABS granddaughter design”.

35. Virginia Polytechnic Institute and State University, Interdepartmental Genetics Program (*November 1997*), “Gene mapping in large complex pedigrees with application to a genome scan in a large dairy cattle pedigree”.

36. University of Illinois at Champaign-Urbana, Departments of Animal Sciences and Statistics (*November 1997*), "Gene mapping in large complex animal and human pedigrees".

37. Virginia Polytechnic Institute and State University, Department of Statistics (*April 1998*), "Gene mapping in large complex animal and human pedigrees".

38. Infigen Inc. and ABS Global Inc. (*May 1998*), “Update on the ABS granddaughter

design, fine-mapping of QTLs, and marker-assisted selection in dairy cattle”.

39. Jokioinen Agricultural Research Center, Finland, (*March 1999*), “Finite polygenic models, and linkage and linkage disequilibrium mapping of complex trait genes”.

40. Virginia Polytechnic Institute and State University, Molecular Cell Biology and Biotechnology Seminar (*November 1999*), "Linkage and Linkage disequilibrium gene mapping in large complex animal and human pedigrees".

41. Bioinformatics Conference, Virginia Polytechnic Institute and State University, (October 1999), "Gene mapping in large complex animal and human pedigrees".

42. Computational Biology seminar series (organized by Dr. John Tyson, Biology), Virginia Tech, *Spring 2000*, 3 seminars on complex trait gene mapping.

43. The Monsanto Company, *June 2000*, “Statistical design and analysis methods for gene mapping and gene transcription experiments”.

44. Infigen Inc., *November 2000*, “Statistical design and analysis methods for gene mapping and gene transcription experiments”.

45. Virginia Tech Workshop on Bioinformatics and Computational Biology, *March 2001*, Panel discussant on “Bioinformatics curriculum”.

46. Second RECOMB Satellite Workshop on Computational Methods for SNPs and Haplotypes, Pittsburgh, PA, *2003* “A Note on a Conditional Enumeration Haplotyping Method in Pedigrees”. G. Gao and I. Hoeschele.

47. Wake Forest University School of Medicine, Winston-Salem, NC, 2006 “An introduction to systems genetics to better understand cancer and other complex diseases”. I Hoeschele.

48. Section on Statistical Genetics seminar series, Department of Biostatistics, University of Alabama at Birmingham, 2007, “Causal inference in Systems Genetics via Structural Equation Modeling”. I. Hoeschele.

49. Wake Forest University School of Medicine, Winston-Salem, NC, 2009 “A systems approach to investigate the genetic basis of complex diseases”. I. Hoeschele.

50. Annual meeting of the BTCOE (Brain Tumor Center Of Excellence) at Wake Forest University, Winston-Salem, NC. Canine Brain Genome Atlas – preliminary results from the first gene expression study of canine brain tumors. July 2010. I. Hoeschele.

51. Annual meeting of the BTCOE (Brain Tumor Center Of Excellence) at Wake Forest University, Winston-Salem, NC. Comparative canine and human glioma genomics.. September 2012. I. Hoeschele.

Numerous seminars at Virginia Tech (VBI, Statistics, VT-Bioinformatics, GBCB) not listed.

Graduate and Undergraduate Course Development

Undergraduate:
ALS 3104 (Virginia Polytechnic Institute and State University)
"**Animal Genetics**". An undergraduate course covering population genetics, selection index, and crossbreeding theory and practice. 3 C).

Graduate:
ALS 6114 (Virginia Polytechnic Institute and State University)
"Mixed Model Applications in Genetics". An advanced graduate level course covering selection index theory, Best and Best Linear Prediction, Best Linear Unbiased Prediction, Linear Mixed Model Equations, Linear Mixed Model theory issues (estimability, connectedness, hypothesis testing, incorrect data models, linearly equivalent models), selection theory, computing strategies, Generalized Mixed Linear Models, random regression and multivariate models, Linear Mixed Model Equations for balanced data with application to microarray gene expression experiments. 3C.

STAT 5554 (Virginia Polytechnic Institute and State University)
"**(Co)variance Components Estimation**". An advanced graduate level course dealing with various methods (ANOVA, Henderson's methods, MINQUE/MIVQUE/Dispersion Mean Model, ML, REML, Bayesian) and computing strategies (e.g., derivative-free, derivative-intense optimization, Markov chain Monte Carlo) for (co)variance component estimation under linear and generalized linear mixed models from unbalanced data. 3C.

STAT 5564 (Virginia Polytechnic Institute and State University)
"Statistical Genetics". An advanced graduate course on statistical methods for linkage mapping of quantitative/complex trait genes in populations ranging from inbred lines to complex pedigrees, statistical methods for fine-mapping including linkage disequilibrium mapping, and statistical design and analyses of systems genetics experiments. 3C.

STAT 5984 (Virginia Polytechnic Institute and State University)
"Design and Analysis of Microarray expression Experiments". An introduction to design and analysis of microarray experiments and systems biology/genetics. 1C.

STAT 5984 (Virginia Polytechnic Institute and State University)
"High-Dimensional Data Analysis in Bioinformatics". Significance analysis of microarray expression data, high-dimensional QTL mapping, regulatory network inference. Bayesian methods, penalized regression. 1C.

STAT 5605 (Virginia Polytechnic Institute and State University)
Biometry I. 3C.

Short-courses:

"Markov chain Monte Carlo methods for likelihood and Bayesian inference". Annual Meeting of the American Statistical Association, *1996*, Continuing Education Course.

"QTL: mapping II: Part A: QTL mapping in segregating, pedigreed populations via Least-Squares and Residual Maximum Likelihood. Part B: Genotype sampling and Bayesian QTL mapping in large, complex pedigrees”. Summer Institute in Statistical Genetics at North Carolina State University (multiple years).

“Identification of genes and pathways affecting quantitative traits in complex pedigrees using genetic marker and microarray gene transcription data” Short-course Mathematical Approaches to the Analysis of Complex Phenotypes, Jackson Laboratory, Bar Harbor, Maine (multiple years).

Academic Committee Assignments

<u>Virginia Polytechnic Institute and State University (member):</u>

Departmental Honors Committee (*Spring 1988 - Spring 1990*)

Departmental Graduate Seminar Committee (*Spring 1988 - Fall 1988, Fall 1992 - Spring 1995*)

Departmental Hospitality Committee - (*Spring 1988 - Spring 1992*)

Departmental Library Committee (*Fall 1992 - Spring 1995*)

Interdisciplinary Animal and Poultry - Dairy Genetics Committee (*Spring 1988 - Spring 1995*)

College Committee on Graduate Studies and Affairs (*Fall 1992 - Spring 1995*)

College Committee on Information Technology Planning (*Spring 1993 - Spring 1995*)

<u>Montana State University (member):</u>

University Search Committee for Executive Director of Information Technology Services (*Fall 1995 - Spring 1996*)

Search Committee for Head of Plant, Soil and Environmental Sciences (*Spring 1996*)

<u>Virginia Polytechnic Institute and State University (member):</u>

University Honors Committee (*Fall 1996 - 2000*)

Departmental Graduate Seminar Committee (*Fall 1996 - 1999*)

Departmental Retreat Committee (*Fall 1996 - 1998*)

Departmental Library Committee (*Fall 1996 - 2002*)

Interdisciplinary Animal and Poultry - Dairy Genetics Committee (*Spring 1996 - 2002*)

University Research Computing Task Force (*2001-2002*)

University Genetics, Bioinformatics and Computational Biology Graduate Curriculum Committee (*2000-2003*).

Several faculty search committees in Statistics and in Animal and Poultry Sciences (*1996-2004*)

GBCB (Genetics, Bioinformatics and Computational Biology (interdisciplinary) Ph.D. program) steering committee (*2003-present*)

GBCB (Genetics, Bioinformatics and Computational Biology (interdisciplinary) Ph.D. program) admissions committee (*2003-present*)

Statistics Personnel and Faculty Search Committee (*2006-2008*)

Virginia Bioinformatics Institute Faculty Search Committee (*2007-2009*)

College of Science Promotion and Tenure Committee (2009-2012)

Administrative Experience

Administrative Chair, University-wide Genetics Ph.D. program, Virginia Tech, *1997 - 2002*.

GBCB (Genetics, Bioinformatics and Computational Biology (interdisciplinary) Ph.D. program) Admissions and Steering committees (*2003-present*)

Graduate Students supervised

1. Anita L. DeStefano (M.S. Dairy Science 1991, now Professor of Biostatistics, Associate Professor of Neurology, and Associate Director of the BUMC Genome Science Institute, Boston University Medical Center).
2. Ant R. Vollema (visiting Ph.D. student 1993, now Project Leader, Rijksdienst voor Ondernemend Nederland, The Netherlands)
1. Imke J.M. DeBoer (visiting Ph.D. student 1993, now Professor of Animal Production Systems Wageningen, The Netherlands)
2. Eduardo O. Romano (M.S., *1993*, now Senior Research Scientist, Pacific Institute for Research and Evaluation)
3. Fernando E. Grignola (Ph.D., *1996*, now Senior Biostatistician at The Monsanto Company)
4. Katherine M. Gage (M.S. Dairy Science, 1997, unknown)
5. Peter Sorensen (visiting Ph.D. student 1998, now senior research scientist, Center for Quantitative Genetics and Genomics, Aarhus University, Denmark)
6. Tina Van der Horst (visiting student, 2000)
7. David Henderson (Ph.D. Genetics, Bioinformatics and Computational Biology, 2001, now Senior Scientist at LabCorp Clinical Trials).
8. Xiao Yang (Ph.D. Statistics, 2003, co-chair with professor Keying Ye, now Senior Statistical Scientist at The Monsanto Company)
9. Nan Bing (Ph.D. Genetics, Bioinformatics and Computational Biology, 2004, now Director of Human Genetics, Pfizer).

10. Chiranjeeet Chetia (M.S. Statistics, 2005, now Manager, Risk Detection at PayPal)
11. Bing Liu (Ph.D. Statistics, 2006, now Statistical Project Manager at the Monsanto Company)
12. Xu Yang (M.S. Biological Sciences, 2009; co-chair with Professor Iuliana Lazar, now PhD student, Biological Sciences, VT)
13. Hui Li (Ph.D., Genetics, Bioinformatics and Computational Biology Program, 2009-2015)
14. Charles Weeks (Genetics, Bioinformatics and Computational Biology Ph.D. Program, 2009-2010)
15. Ting Guan (Statistics, 2013-2014)
16. Angela Dement (Genetics, Bioinformatics and Computational Biology Ph.D. Program, co-chair, 2013-2015)

Postdoctoral and Senior Research Associates supervised

1. Dr. Lizhen Wang (1993, now Genetic Evaluation Specialist, PIC USA)
2. Dr. Daniel Weigel (1994, now Associate Director at Pfizer)
3. Dr. Georg Thaller (1995, now Professor, Christian-Albrechts-University of Kiel, Germany).
4. Dr. Pekka Uimari (1996, now Professor, University of Helsinki, Finland)
5. Dr. Christian Fuerst (1996, now Senior Research Scientist, ZuchtData EDV-Dienstleistungen GmbH, Vienna, Austria)
6. Dr. Birgit Waltl (1996, now Professor, University of Natural Resources and Life Science, Vienna, Austria, 1996).
7. Dr. Qin Zhang (1996 – 1998, now Professor of Genetics, Beijing Agricultural University)
8. Dr. Yi-Ju Li (1997, now Professor, Department of Biostatistics and Bioinformatics and Center for Human Genetics, Duke University)
9. Dr. Mogens Lund (visiting scientist 1998, Head of Center for Quantitative Genetics and Genomics, Aarhus University, Denmark)
10. Dr. Fengxing Du (1998 – 1999, now Senior Statistical Geneticist, The Monsanto Company)
11. Dr. Gertraude Freyer (visiting scientist 1999, now senior research scientist, Leibniz Institute for Farm Animal Biology, Dummersdorf, Germany)
12. Dr. Peter von Rohr (1999-2000, now Nebion AG, Switzerland)
13. Dr. Shun-Hwa Li (2000 – 2002; unknown)
14. Dr. Peter Sorensen (2001-2002, now senior research scientist, Center for Quantitative Genetics and Genomics, Aarhus University, Denmark)
15. Dr. Hirokazu Matsuda (2003; unknown)
16. Dr. Guimin Gao (2002-2005, now Associate Professor, Department of Biostatistics, Virginia Commonwealth University)
17. Dr. Hua Li (2003-2005, unknown)
18. Dr. Kathrin-Friederike Stock (2005-2006, Assistant Professor (Dr. Vet. Med. Habil.), Hannover Veterinary University, Germany)
19. Dr. Alberto de la Fuente (2004-2006, Ph.D. Bioinformatics, now Leader of Unit on Biomathematics and Bioinformatics, Section on Genetics and Biometry, Leibniz Institute for Farm Animal Biology (FBN), Dummersdorf, Germany)
20. Dr. Yongcai Mao (2005-2006, Ph.D. Biostatistics), now Senior Research Scientist, Forest Research Institute NJ).
21. Dr. Lei Bao (2007-2008, now Principal Statistician, Moores Cancer Center at UC

San Diego)

22. Dr. Yan Ling (2010-2012, unknown)
23. Dr. Netsanet Iman (2013-2014), now data scientist at Boeing.

Research Publications (total of 99 research publications and 5 book chapters)

1. Hoeschele, I. and E. Niebel. 1983. Population analysis of beef performance characteristics by visual appraisal in young Fleckvieh heifers. Zuchtungskde. 55:321-329.

2. Karras, K., I. Hoeschele, and G. Averdunk. 1985. A first evaluation of stayability in the German Fleckvieh. Der Tierzuchter 37:116-118.

3. Hoeschele, I., J.L. Foulley, J.J. Colleau, and D. Gianola. 1986. Genetic evaluation for multiple binary responses. Genet. Sel. Evol. 18:299-319.

4. Hoeschele, I., D. Gianola, and J.L. Foulley. 1987. Estimation of variance components with quasi-continuous data using Bayesian methods. J. Anim. Breed. Genet. 104:334-349.

5. Foulley, J.L., S. Im, D. Gianola, and I. Hoeschele. 1987. Empirical Bayes estimation of parameters for n polygenic binary traits. Genet. Sel. Evol. 19: 197-224.

6. Hoeschele, I. 1988. "Comparison of Maximum A-Posteriori Estimation" and "Quasi Best Linear Unbiased Prediction" with quasi-continuous data. J. Anim. Breed. Genet. 105:337-361.

7. Hoeschele, I., M.F. Rothschild, and D. Gianola. 1988. Recursive estimation of breeding values with categorical data. J. Dairy Sci. 71:452-466.

8. Hoeschele, I. 1988. Genetic evaluation with data presenting evidence of mixed major gene and polygenic inheritance. Theor. Appl. Genet. 76:81-92.

9. Hoeschele, I. 1988. Statistical techniques for detection of major genes in animal breeding data. Theor. Appl. Genet. 76:311-319.

10. Misztal, I., D. Gianola, and I. Hoeschele. 1989. Note on threshold models with heterogeneous residual variance due to missing information. Genet. Sel. Evol. 20:511.

11. Komender, P. and I. Hoeschele. 1989. Use of mixed model methodology to improve estimation of crossbreeding parameters. Livst. Prod. Sci. 21:101-113.

12. Hoeschele, I. and D. Gianola. 1989. Bayesian versus Maximum Quasi-Likelihood methods for sire evaluation with categorical data. J. Dairy Sci. 72:1569-1577.

13. Hoeschele, I. 1989. A note on local maxima in maximum likelihood, restricted maximum likelihood and Bayesian estimation of variance components. J. Statist.

Comput. Simul. 33:149-160.

14. Hoeschele, I. and T.R. Meinert. 1990. Association of genetic defects with yield and type traits: a major production gene is linked to Weaver. J. Dairy Sci. 73:2503-2515.

15. Hoeschele, I. 1990. Potential gains from major gene insertion in dairy cattle. J. Dairy Sci. 73:2601-2618.

16. Hoeschele, I. and P.M. VanRaden. 1991. Rapid method to compute inverses of dominance relationship matrices for noninbred populations including sire x dam subclass effects. J. Dairy Sci. 74:557-569.

17. VanRaden, P.M. and I. Hoeschele. 1991. Rapid method to compute inverses of additive-by-additive relationship matrices including sire-dam combination effects. J. Dairy Sci. 74:570-579.

18. Hoeschele, I. 1991. Additive and nonadditive genetic variance in female fertility of Holsteins. J. Dairy Sci. 74:1743-1752.

19. DeStefano, A.L. and I. Hoeschele. 1992. Utilization of dominance variance through mate allocation strategies. J. Dairy Sci. 75:1680-1690.

20. VanRaden, P.M., T.J. Lawlor, T.H. Short, and I. Hoeschele. 1992. Use of reproductive technology to investigate gene interactions. J. Dairy Sci. 75:2892-2901.

21. Hoeschele, I. and P.M. VanRaden. 1993. Bayesian analysis of linkage between genetic markers and quantitative trait loci. I. Prior knowledge. Theor. Appl. Genet. 85:953-960.

22. Hoeschele, I. and P.M. VanRaden. 1993. Bayesian analysis of linkage between genetic markers and quantitative trait loci. II. Combining prior knowledge with experimental evidence. Theor. Appl. Genet. 85:946-952.

23. Hoeschele, I. 1993. Elimination of quantitative trait loci equations in an animal model incorporating genetic marker data. J. Dairy Sci. 76:1693-1713.

24. Smothers, C.D., R.E. Pearson, I. Hoeschele, and D.A. Funk. 1993. Herd level for final score and its relationship to genetic and environmental parameters of conformation traits in U.S. Holsteins. J. Dairy Sci. 76:1671-1677.

25. Hoeschele, I. and A.R. Vollema. 1993. Estimation of variance components with dominance and inbreeding in dairy cattle. J. Anim. Breed. Genet. 10:93-104.

26. DeBoer, I.J.M. and I. Hoeschele. 1993. Genetic evaluation methods for populations with dominance and inbreeding. Theor. Appl. Genet. 86:245-258.

27. Hoeschele, I. and E.O. Romano. 1993. On the use of marker information from granddaughter designs. J. Anim. Breed. Genet. 110:429-449.

28. Weigel, D.J., R.E. Pearson, and I. Hoeschele. 1994. Impact of different strategies and levels of preferential treatment on different methods of bull dam selection. J. Dairy

Sci. 77:3163-3173.

29. Grignola, F.E., I. Hoeschele, and K. Meyer. 1994. Empirical Best Linear Unbiased Prediction to map QTL. 5th World Congr. Genet. Appl. Livest. Prod., Guelph, Canada, Vol 21:245.

30. Hoeschele, I. 1994. Bayesian QTL mapping via the Gibbs sampler. 5th World Congr. Genet. Appl. Livest. Prod., Guelph, Canada, Vol 21:241.

31. Georges, M., D. Nielsen, M. Mackinnon, A. Mishra, R. Okimoto, A.T. Pasquino, L.S. Sargeant, A. Sorensen, M.R. Steele, X. Zhao, J.E. Womack, and I. Hoeschele*. 1994. Exploiting progeny-testing to identify polygenes controlling milk production in cattle. 5th World Congr. Genet. Appl. Livest. Prod., Guelph, Canada, Vol 21:81.

32. Hoeschele, I., B. Tier, and H.-U. Graser. 1995. Multiple trait genetic evaluation for one polychotomous and several continuous traits with missing data and different models. J. Anim. Sci. 73:1609-1627.

33. Weigel, D.J., B.G. Cassell, I. Hoeschele, and R.E. Pearson. 1994. Multiple trait prediction of transmitting abilities for herd life and estimation of economic weights using relative net income adjusted for opportunity cost. J. Dairy Sci. 78:639-649.

34. Georges, M., D. Nielsen, M. Mackinnon, A. Mishra, R. Okimoto, A.T. Pasquino, L.S. Sargeant, A. Sorensen, M.R. Steele, X. Zhao, J.E. Womack and I. Hoeschele. 1995. Mapping genes controlling milk production: toward marker-assisted selection in livestock. Genetics 139:907-920.

35. Hoeschele, I. and B. Tier. 1995. Marginal Maximum Likelihood estimation of variance components of threshold characters via Gibbs sampling. Genet. Sel. Evol. 27:519-540.

36. Thaller, G. and I. Hoeschele. 1996a. A Monte Carlo method for Bayesian analysis of linkage between single markers and quantitative trait loci: I. Methodology. Theor Appl Genet 93:1161-1166.

37. Thaller, G. and I. Hoeschele. 1996b. A Monte Carlo method for Bayesian analysis of linkage between single markers and quantitative trait loci: II. A simulation study. Theor Appl Genet 93:1167-1174.

38. Thaller, G., L. Dempfle and I. Hoeschele. 1996. Investigation of the inheritance of birth defects in swine by complex segregation analysis. J. Anim. Breed. Genet. 113:77-92.

39. Uimari, P., G. Thaller and I. Hoeschele. 1996. A Monte Carlo method for Bayesian analysis of linkage between multiple linked markers and quantitative trait loci. Genetics 143:1831-1842.

40. Grignola F.E., I. Hoeschele and B. Tier. 1996. Mapping Quantitative Trait Loci in outcross populations via Residual Maximum Likelihood. I. Methodology. Genet. Sel. Evol. 28:479-490.

41. Grignola F.E., I. Hoeschele, Q. Zhang and G. Thaller. 1996. Mapping Quantitative Trait Loci in outcross populations via Residual Maximum Likelihood. II. A simulation study. Genet. Sel. Evol. 28:491-504.

42. Thaller, G., L.. Dempfle and I. Hoeschele. 1996. Maximum Likelihood analysis of binary traits under different modes of inheritance. Genetics 143:1819-1829.

43. Uimari, P., Q. Zhang, F.E. Grignola, I. Hoeschele and G. Thaller. 1996. Analysis of QTL workshop I granddaughter design data using Least-Squares, Residual Maximum Likelihood, and Bayesian methods. Journal of Quantitative Trait Loci 7: No. 2.

44. Hoeschele, I., P. Uimari, F.E. Grignola, Q. Zhang and K.M. Gage. 1996. Statistical mapping of polygene loci in livestock. Proceedings of the Biometrics Section, p.21-25.

45. Grignola, F.E., Q. Zhang and I. Hoeschele. 1997. Mapping linked quantitative trait loci via Residual Maximum Likelihood. Genet. Sel. Evol. 29:529-544.

46. Hoeschele I. 1997. Bayesian and Residual Maximum Likelihood statistical gene mapping. Animal Biotechnology 8:47-54.

47. Uimari, P. and I Hoeschele. 1997. Mapping linked quantitative trait loci using Bayesian analysis and Markov chain Monte Carlo algorithms. Genetics 146:735-743.

48. Hoeschele, I., P. Uimari, F.E. Grignola, Q. Zhang and K.M. Gage. 1997.Advances in statistical methods to map quantitative trait loci in outbred populations. Genetics 147: 1445-1456.

49. Zhang, Q., D. Boichard, M. C. Bishop, I. Hoeschele, C. Ernst *et al*.. 1998. Mapping quantitative trait loci for milk production and health of dairy cattle in a large outbred pedigree. Genetics 149:1959-1973.

50. Fuerst-Waltl, B., J. Soelkner, A. Essl and I. Hoeschele. 1997. Estimation of non-linear genetic relationships between yield and type traits in Holstein cattle. 6th World Congr. Genet. Appl. Livest. Prod., January 11-16, 1988, Armidale, NSW, Australia, Vol 23:415-418.

51. Zhang, Q., and I. Hoeschele. 1997. Multiple QTL mapping via Residual Maximum Likelihood in outbred populations. 6th World Congr. Genet. Appl. Livest. Prod., January 11-16, 1988, Armidale, NSW, Australia, Vol 26: 265-268.

52. Fuerst, C., I. Hoeschele, J. Sölkner and A. Essl. 1997. The potential use of specific combining ability as selection criterion. 6th World Congr. Genet. Appl. Livest. Prod., January 11-16, 1988, Armidale, NSW, Australia, Vol. 26:109-111.

53. Hoeschele, I., F.E. Grignola, Y.-J. Li, G. Thaller, P. Uimari and Q. Zhang. 1996. MQREML, MQAREML, MPLGIB, and NQTLGIB: Software for QTL mapping in outcross or complex pedigrees. 6th World Congr. Genet. Appl. Livest. Prod., January 11-16, 1988, Armidale, NSW, Australia, Vol 27:441-442.

54. Fuerst-Waltl, B., J. Soelkner, A. Essl, I. Hoeschele and C. Fuerst (1998) Non-linearity in the genetic relationship between milk yield and type traits in Holstein cattle. Livst. Prod. Sci 57:41-47.

55. Du F.-X., I. Hoeschele and K.M. Gage-Lahti (1999) Estimation of additive and dominance variances components in finite polygenic models and complex pedigrees. Genetical Research 74:179-187.

56. Du, F., and I. Hoeschele (2000) Estimation of additive, dominance, and epistatic variance components using finite-locus models implemented with a single-site Gibbs and a descent graph sampler. Genetical Research 76:187-198.

57. Thaller G., and I. Hoeschele (2000) Fine-mapping of quantitative trait loci in half-sib families using current recombinations. Genetical Research 76:87-104.

58. Du, F. and I. Hoeschele (2000) A note on genotype and allele elimination in complex pedigrees with incomplete genotype data. Genetics 156:2051-2062.

59. Von Rohr, P. and I. Hoeschele (2002) Robust Bayesian QTL mapping using skewed Student- t distributions. Genetics, Selection, Evolution 34:1-21.

60. Freyer G., C. Kühn, R. Weikard, Q. Zhang, M. Mayer and I. Hoeschele (2002) Multiple QTL on chromosome six in dairy cattle affecting yield and content traits. J. Anim. Breed. Genet. 119:69-82.

61. Kakko S, Kelloniemi J, P von Rohr, I Hoeschele, M Tamminen, ME. Brousseau, YA Kesäniemi, and MJ Savolainen (2002) ATP-binding cassette transporter A1 locus was not a major locus for HDL-C regulation in a population with high risk of coronary heart disease. Arteriosclerosis 166:285-290.

62. Du. F.-X., P. Sorensen, G. Thaller and I. Hoeschele (2002) Joint linkage disequilibrium and linkage mapping of quantitative trait loci. Proc. 7th World Congr. Genet. Appl. Livest. Prod. 32:661-668.

63. Stricker C., M. Schelling, F.-X. Du, I. Hoeschele, S. A. Fernández and R. L. Fernando (2002) A comparison of efficient genotype samplers for complex pedigrees and multiple linked loci. Proc. 7th World Congr. Genet. Appl. Livest. Prod. 32:637-644.

64. Freyer G., P. Sorensen, C. Kuhn, R. Weikard and I. Hoeschele (2003) Search for pleiotropic QTL on chromosome BTA6 affecting milk production traits. J. Dairy Sci. 86: 999-1008.

65. Gao, G., Hoeschele, I., Sorensen, P., and F.-X. Du (2004) Conditional probability methods for haplotyping in pedigrees. Genetics 167:2055-2065.

66. De la Fuente, A., N. Bing, I. Hoeschele and P. Mendes (2004) Discovery of meaningful associations in genomic data using partial correlation coefficients. *Bioinformatics* 20, 3565-3574

67. Pfister-Genskow, M., Myers, C., Childs, L., Lacson, J.C., Betthauser, J., Gouleke, P.J.,

Forsberg, E., P., Zheng, Y., Leno, G., Schultz, R., Liu, B., Chetia, C., Yang, X., Hoeschele, I., and Eilertsen, K.J. (2005) Identification of differentially expressed genes in individual bovine preimplantation embryos produced by nuclear transfer: Improper reprogramming of genes required for trophoblast development. Biology of Reproduction 72:546-555.

68. Hoeschele, I., and Li, H. (2005) A note on joint versus gene-specific mixed model analysis of microarray gene expression data. Biostatistics 6:183-186.

69. Bing, N., Hoeschele, I., Ye, K., and Eilertsen, K.J. (2005) Finite mixture model analysis of microarray expression data on samples of uncertain biological type with application to reproductive efficiency. Veterinary Immunology and Immunopathology 105:187-196.

70. Bing, N., and Hoeschele, I., (2005) Genetical genomics analysis of a yeast segregant population for transcription network inference. Genetics 170:533-542.

71. Gao, G., and Hoeschele, I. (2005) Approximating identity-by-descent matrices using multiple haplotype configurations on pedigrees. Genetics 171:365-376.

72. Betthauser, J.M., Pfister-Genskow, M., Xu, H., Gouleke, P.J., Lacson, J.C., Koopang, R.W., Liu, B., Hoeschele, I., Eilertsen, K.J., and Leno, G.H. (2006) Nucleoplasmin facilitates reprogramming and in vivo development of bovine nuclear transfer embryos. Molecular Reproduction and Development 73:977-986.

73. Stock, K.F., Distl, O., and Hoeschele, I. (2007) Influence of priors in Bayesian estimation of genetic parameters for multivariate threshold models using Gibbs sampling. Genetics-Selection-Evolution 39:123-137.

74. Stock, K.F., Hoeschele, I. and Distl, O. (2007) Bayesian estimation of genetic parameters for multivariate threshold and continuous phenotypes and molecular genetic data in simulated horse populations using Gibbs sampling. BMC Genetics 8:19.

75. Stock, K.F., I. Hoeschele and O. Distl (2007) Estimation of Genetic parameters and prediction of breeding values for multivariate threshold and continuous data in a simulated horse population using Gibbs sampling and residual maximum likelihood. J. Anim. Breed. Genet. 124:308-319.

76. Gao, G. and I. Hoeschele (2007) A note on a haplotyping method in pedigrees. Genetics, Selection, Evolution 40: 25-36.

77. Liu, B., de la Fuente, A., and Hoeschele, I. (2008) Gene network inference via structural equation modeling in genetical genomics experiments. Genetics 178: 1763-1776.

78. Tyler, B.M., R.J.Y. Jiang, L. Zhou, S. Tripathy, D. Dou, T. Torto-Alalibo, H. Li, Y. Mao, B. Liu, M. Vega-Sanchez, S.X. Mideros, R. Hanlon, B.M. Smith, K. Krampis, K. Ye, S. St. Martin, A.E. Dorrance, I. Hoeschele and M.A. Saghai Maroof (2007) Functional genomics and bioinformatics of the Phytophthora-soybean interaction. Stadler Genetics Symposium book.

79. Bao, L and I. Hoeschele (2008) Comment: Quality assessment of short oligonucleotide microarray data. Technometrics 50: 268-271.

80. Gao, G., D.B. Allison and I. Hoeschele (2008) A review of haplotyping methods in pedigrees. Human Heredity 67:248-266.

81. Huang, H., H. Zhu, F. Cheng, I. Hoeschele and F. Zou (2010) Gaussian process based Bayesian semiparametric quantitative trait loci interval mapping. Biometrics 66:222-232. Selected by the Co-Editors for Showcase session.

82. Zhou, L., S. X. Mideros, L. Bao, R. Hanlon, F. Arredondo, S. Tripathy, K. Kampis, A. Jerauld, C. Evans, S.K. St. Martin, S. Maroof, I. Hoeschele, A.E. Dorrance and B.M. Tyler (2009) Infection and genotype remodel the entire soybean transcriptome. BMC Genomics 10:49.

83. Armenta, J., I.M. Lazar and I. Hoeschele (2009) A quantitative proteomic study of the MCF-7 breast cancer cell line using iTRAQ/PQD linear ion trap MS technology. Journal of the American Society for Mass Spectrometry 20:1287-1302.

84. Kangas-Kontio, T., S. Kakko, S., M. Tamminen, P. Von Rohr, I. Hoeschele, T. Juvonen, J. Kere, and M.J. Savolainen (2010) Genome scan for loci regulating HDL-cholesterol levels in Finnish extended pedigrees with early coronary heart disease. European Journal of Human Genetics 18(5):604-13.

85. Zou, F., H. Huang and I. Hoeschele (2010) Nonparametric Bayesian multiple quantitative trait loci mapping with epistasis and gene-environment interaction. Genetics 186:385-394.

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