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Date of Birth: January 19, 1952

Academic Positions

- Research Assistant, Department of Animal Science, University of Illinois, 1978–1984.
- Research and Teaching Associate, Department of Animal Sciences, University of Illinois, 1984–1985.
- Assistant Professor of Biometry and Computer Applications, Department of Animal Sciences, University of Illinois, 1985–1991.
- Sabbatical Leave, Department of Biometry and Genetics, Louisiana State University, Medical Center, 1991–1992.
- Associate Professor of Biometry and Computer Applications, Department of Animal Sciences, University of Illinois, 1991–1996.
- Professor of Quantitative Genetics, Department of Animal Science, Iowa State University, 1996–

Education

- Diploma in Agriculture (First Class Honors) Aquinas College, Colombo, Sri Lanka. 1972–1975 (graduated first in class).
- B.S. (Summa Cum Laude) Agricultural Science with emphasis in animal science, California State University, Fresno. 1976–1978 (graduated first in class).
- M.S. Animal Science, University of Illinois at Urbana-Champaign. 1978–1981.

- Participated in the 3rd International Summer School in Agriculture “Modern Techniques in Animal Breeding”, Dublin, Ireland. June 26 – July 9, 1983.
- Ph.D. Animal Science, University of Illinois at Urbana-Champaign. 1981–1984.

Publications

* Indicates the research was directed by Rohan L. Fernando while first author was a graduate student, postdoctoral associate or visiting scientist.

Chapters in Books

1. Fernando, R. L. and D. Gianola. 1990. Optimal designs for sire evaluation schemes. In “Advances in Statistical Methods for Genetic Improvement of Livestock”. Springer-Verlag, New York.
2. Fernando, R. L. and D. Gianola. 1990. Statistical inferences in populations undergoing selection or non-random mating. In “Advances in Statistical Methods for Genetic Improvement of Livestock”. Springer-Verlag, New York.
3. Gianola, D., S. Im, R. L. Fernando and J. L. Foulley. 1990. Mixed model methodology and the Box-Cox theory of transformations: a Bayesian approach. In “Advances in Statistical Methods for Genetic Improvement of Livestock”. Springer-Verlag, New York.
4. Weller, J. and R. L. Fernando. 1991. Strategies for the improvement of animal production using marker assisted selection. In “Gene Mapping: Strategies, Techniques and Applications”. Marcel Dekker, New York.
5. *Fernández, S. A., R. L. Fernando and A. L. Carriquiry. 2000. “Analysis in complex pedigrees. Bayesian Case Studies”, pages 307-326. Springer-Verlag.
6. *Fernández, S. A., R. L. Fernando, A. L. Carriquiry. 2001. An algorithm to sample unobservable genotypes in complex pedigrees. In “Bayesian Methods with Applications to Science, Policy and Official Statistics (Selected papers from ISBA 2000)”, Monographs in Official Statistics, Eurostat, 125-134.
7. Fernando, R.L. and L.R. Totir. 2003. Incorporating Molecular Information in Breeding Programs: Methodology. In “Poultry Breeding and Biotechnology”. CABI Publishing, Cambridge.
8. Fernando, R. L. Kinship and Inbreeding. 2003. In “Encyclopedia of the Human Genome”. Nature Publishing Group, New York.

9. Stricker, C. and R. L. Fernando. 2003. Segregation analysis software. In "Encyclopedia of the Human Genome". Nature Publishing Group, New York.
10. *Totir, R. and R. L. Fernando. 2005. Selectia asistată de markeri. In "Programe De Ameliorare Genetică Zootehnie". Editura Ceres, Bucharest.
11. Abraham, K. J. and R. L. Fernando. 2012. Applications of Graphical Clustering Algorithms in Genome Wide Association Mapping, New Frontiers in Graph Theory, Dr. Yagang Zhang (Ed.), ISBN: 978-953-51-0115-4, InTech.
12. Fernando R.L. and D.J. Garrick. 2013. Bayesian methods applied to GWAS. In "Genome-Wide Association Studies and Genomic Prediction". Gondro, C., J.H.J. van der Werf and B. Hayes (2013). Springer Series: Methods in Molecular Biology, Berlin.
13. Garrick, D.J. and R.L. Fernando. 2013. Implementing a QTL detection study (GWAS) using genomic prediction methodology. In "Genome-Wide Association Studies and Genomic Prediction". Gondro, C., J.H.J. van der Werf and B. Hayes (2013). Springer Series: Methods in Molecular Biology, Berlin.

Articles in Journals

1. Fernando, R. L., R. D. Billingsley and D. Gianola. 1983. Effects of method of scaling in heritability estimates and sire evaluations for frame size at weaning in Angus cattle. *J. Anim. Sci.* 56:1047–1056.
2. Rattanarongchart, S., M. Grossman, R. L. Fernando, and R. D. Shanks. 1983. A Monte-Carlo comparison of estimators of average daily gain in body weight. *J. Anim. Sci.* 57:885–891.
3. Fernando, R. L., D. Gianola, and M. Grossman. 1984. Identifying all connected subsets in a two-way classification without interaction. *J. Dairy Sci.* 66:1399–1402.
4. Fernando, R. L., Susan A. Knights and D. Gianola. 1984. On a method of estimating the genetic correlation between characters measured in different experimental units. *Theor. Appl. Genet.* 67:175–178.
5. Fernando, R. L. and D. Gianola. 1984. Rules for assortative mating in relation to selection for linear merit functions. *Theor. Appl. Genet.* 68:227–237.
6. Staples, C. R., R. L. Fernando, G. C. Fahey, Jr, L. L. Berger and E. H. Jaster. 1984. Effect of intake of a mixed diet by dairy steers on digestion events. *J. Dairy Sci.* 67:995–1006.

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8. Caro, R. F., M. Grossman and R. L. Fernando. 1985. Effects of data imbalance on estimation of heritability. *Theor. Appl. Genet.* 69:523–530.
9. Fernando, R. L. and D. Gianola. 1986. Effect of assortative mating on genetic change due to selection. *Theor. Appl. Genet.* 72:395–404.
10. Fernando, R. L. and D. Gianola. 1986. Optimum properties of the conditional mean as a selection criterion. *Theor. Appl. Genet.* 72:822–825.
11. Gianola, D. and R. L. Fernando. 1986. Bayesian methods in animal breeding theory. *J. Anim. Sci.* 63:217–244.
12. Gianola, D. and R. L. Fernando. 1986. Random effects models for binary responses. *Biometrics* 42:217–218.
13. Gipson, T. A., M. Grossman and R. L. Fernando. 1986. Relationships between predicted difference for milk production traits and buck designation in dairy goats. *J. Dairy Sci.* 69:591–594.
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19. Brown, D. A., P. C. Harrison, R. L. Fernando and T. W. Odom. 1988. Reversal of depressed miduterine arterial flow during hyperthermia induced respiratory alkalosis. *Proc. Soc. Exp. Biol. and Med.* 189:152–157.

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47. Bunge, R, D. L. Thomas, T. G. Nash and R. L. Fernando. 1993. Performance of hair breeds and prolific wool breeds of sheep in southern Illinois: Effect of breed of service sire on lamb production of Suffolk and Targhee ewes. *J. Anim. Sci.* 71:321-325.
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114. *Habier D, RL Fernando, DJ Garrick. 2012. The three types of quantitative-genetic information in genomic prediction. Abstracts of the Plant & Animal Genome XXI conference, San Diego, abstract W359.
115. Wolc A, J Arango, P Settar, JE Fulton, NP OSullivan, R Preisinger, D Habier, R Fernando, DJ Garrick and JCM Dekkers. 2012. Genome wide association study for egg production and egg quality in layer chickens. World Poultry Conference held 5-9 August 2012 at Bahia convention center, Brazil.
116. Saatchi M, RL Fernando and DJ Garrick. 2012. QTL mapping and prediction of direct genomic breeding value using 1 Mb SNP windows and Bayesian inference. Abstract, 16th QTL-MAS workshop held in Alghero, Italy.
117. Wang C, D Habier, L Peiris, A Wolc, A Kranis, KA Watson, S Avendano, DJ Garrick, RL Fernando, SJ Lamont, and JCM Dekkers. 2012. Identification of genomic regions affecting body weight and hen house production using genomic prediction methods in broiler chickens. Abstract 60, <http://adsa.asas.org/midwest/2012/MW2012Abstracts.pdf>
118. Wolc A, J Arango, P Settar, JE Fulton, NP OSullivan, R Preisinger, D Habier, R Fernando, DJ Garrick and JCM Dekkers. 2012. Analysis of egg production using a random regression model with genomic relationships in layer chickens. *J Anim Sci Vol 90 Suppl. 3/J Dairy Sci Vol 95 Suppl 2* : 726. <http://www.jtmtg.org/2012/abstracts/686.pdf>
119. Peters, SO, K Kizilkaya, DJ Garrick, RL Fernando, EJ Pollak, M DeDonato, E Chaffee, T Hussain, and IG Imumorin. 2012. Model comparison for genetic parameter estimation of birth and weaning weight traits in beef cattle. *J Anim Sci Vol 90 Suppl. 3/J Dairy Sci Vol 95 Suppl 2*: M35. <http://www.jtmtg.org/2012/abstracts/15.pdf>
120. Wolc, A, J Arango, P. Settar, JE Fulton, NP OSullivan, R Preisinger, D Habier, R Fernando, DJ Garrick, and JCM Dekkers. 2012. Genome wide association study for egg defects in layer chickens. Abstracts of the Plant & Animal Genome XX conference, San Diego, W592. <http://pag.confex.com/pag/xx/webprogram/Paper2564.html>
121. Peters, SO, K Kizilkaya, M Thomas, RL Fernando, J Reecy, A Yakubu, M De Donato, I Imumorin. 2012. Whole Genome Linkage Disequilibrium Pattern in US Brangus Heifers. Abstracts of the Plant & Animal Genome

- XX conference, San Diego, P0558.
<http://pag.confex.com/pag/xx/webprogram/Paper3583.html>
122. Saatchi, M, DJ Garrick, RL Fernando, N Boddicker. 2012. Comparison of Different Bayesian Methods for QTL Mapping in Hereford Beef Cattle Using 1 Mb Windows. Abstracts of the Plant & Animal Genome XX conference, San Diego, P0552.
<http://pag.confex.com/pag/xx/webprogram/Paper3217.html>
 123. *Edriss, V, RL Fernando, G Su, Mogens, S Lund, B Gulbrandtsen. 2012. Haplotypes based on local genealogies for genomic prediction. 4th International Conference on Quantitative Genetics. Edinburgh.
 124. Stricker, C. and RL Fernando. 2013. Genauigkeit genomischer Zuchtwerte: Cosegregation or Linkage Disequilibrium? Swiss Association for Animal Production.
 125. Wolc, A., J. Arango, P. Settar, J.E. Fulton, N.P. OSullivan, R. Preisinger, D. Habier, R.L. Fernando, D.J. Garrick, S.J. Lamont, and J.C. Dekkers. 2013. Genomic selection in layer chickens outperforms pedigree-based selection. Proceedings ASAS/ADSA 45th Midwestern sectional scientific sessions and business meeting, abstract O071.
 126. *Sun, X., R.L. Fernando, D.J. Garrick, and J.C.M. Dekkers. 2013. Accurate prediction of genomic breeding values across families combining linkage disequilibrium and co-segregation. Proceedings ASAS/ADSA 45th Midwestern sectional scientific sessions and business meeting, abstract O181.
 127. Fernando, R.L., D. Garrick, J.C.M. Dekkers. 2013. Bayesian regression method for genomic analyses with incomplete genotype data. Abstracts of EAAP, 64th Annual meeting held in Nantes, France, page 225.
 128. Su, H., J. Lee, M. Saatchi, R.L. Fernando, D.J. Garrick. 2014. Population structure of ten US beef cattle breeds revealed by principal components analysis on genomic data. Abstracts of the Plant & Animal Genome XXII conference, San Diego, abstract P531. <https://pag.confex.com/pag/xxii/webprogram/Paper11207.html>
 129. Wolc, A., J. Arango, P. Settar, J.E. Fulton, R.L. Fernando, D.J. Garrick, J. Dekkers, N.P. Sullivan. 2014. Genome wide association study for heat stress mortality in a white egg layer line. Abstracts of the Plant & Animal Genome XXII conference, San Diego, abstract P641. <https://pag.confex.com/pag/xxii/webprogram/Paper11328.html>
 130. Baes, C.F., M.A. Dolezal, E. Fritz-Waters, J. Koltjes, B. Bapst, C. Flury, H. Signa-Hasler, C. Stricker, R.L. Fernando, J.M. Reecy, D. J. Garrick, R. Fries, B. Gredler. 2014. Comparison of variant calling pipelines for whole-genome sequencing data in dairy cattle. Abstracts of the Plant & Animal Genome XXII conference, San Diego, abstract P1053. <https://pag.confex.com/pag/xxii/webprogram/Paper11328.html>

131. Fernando, R.L., H. Cheng, X. Sun. Implications of using identity-by-descent versus identity-by-state matrices in genetic analyses. Abstracts of the Plant & Animal Genome XXII conference, San Diego, abstract W766. <https://pag.confex.com/pag/xxii/webprogram/Paper10910.html>
132. Garrick, D.J., J.C.M. Dekkers, R.L. Fernando. 2014. Genomic analysis combining genotyped and non-genotyped individuals. Abstracts of the Plant & Animal Genome XXII conference, San Diego, abstract W766. <https://pag.confex.com/pag/xxii/webprogram/Paper10906.html>
133. *Cheng, H., R.L. Fernando, D.J. Garrick. 2014. A Gibbs sampler for BayesB. Proceedings ASAS/ADSA 46th Midwestern sectional scientific sessions and business meeting.
134. Su, H., J. Koltcs, M. Saatchi, J. Lee, R. Fernando, D.J. Garrick. 2014. Haplotype diversity analysis in ten US cattle breeds. Proceedings ASAS/ADSA 46th Midwestern sectional scientific sessions and business meeting.

Theses

1. Fernando R. L. 1981. Scaling ordered categorical variables in relation to sire evaluation for frame score at weaning in Angus cattle. M.S. Thesis. University of Illinois. 116 pp.
2. Fernando, R. L. 1984. Assortative mating and selection. Ph.D. Thesis. University of Illinois. 138 pp.

Theses Supervised

1. Ang, Iris Hui-Chi. 1990. Comparison of alternative mixed linear model analyses of unbalanced data. M.S. Thesis. 163 pp.
2. Cantet, R. C. 1990. Estimation and prediction problems in mixed linear models for maternal genetic effects. Ph.D. Thesis. 183 pp. (supervised jointly with Dan Gianola)
3. Soto-Murillo, H. W. 1991. Methods for checking the goodness of fit of alternative nonlinear mixed models with an application in fertility traits of beef cows. Ph.D. Thesis. 149 pp. (supervised jointly with Dan Gianola)
4. Lo, L. L. 1993. Genetic evaluation and selection in multibreed populations. Ph.D. Thesis. 168 pp.
5. Wang, T. 1998. Genetic evaluation and parameter estimation using marker and trait information. Ph.D. Thesis. 102 pp.
6. McPherson, S. K. 1999. Estimation of genetic covariances between antibody response and bacterial burden. M.S. Thesis. 47 pp.

7. Santos, N. 2001. Estimation of adjustment factors for 3X milking. Ph.D. Thesis. 186 pp. (supervised jointly with A. E. Freeman)
8. Benson, T. J. 2001. Use of the expected log likelihood to evaluate designs for mapping quantitative trait loci. M. S. Thesis. 96 pp.
9. Fernández, S. A. 2001. An algorithm to sample genotypes in complex pedigrees. Ph.D. Thesis 132 pp. (supervised jointly with Alicia Carriquiry)
10. Totir, L. R. 2002. Genetic evaluation with finite locus models. Ph.D. Thesis. 124 pp.
11. Fonseca, da R. 2003. Use of information on identified genes to reduce the selection bias on genetic evaluation. Ph.D. Thesis. 56 pp. (supervised jointly with Ricardo Euclides).
12. Pita, F. V. da C. 2003. Construction of the gametic covariance matrix for quantitative trait loci analyses in outbred populations. Ph.D. Thesis. 61 pp. (supervised jointly with Paulo Savio Lopes)
13. Grapes, L. 2004. Molecular, bioinformatic and statistical approaches to identify genes underlying complex traits in livestock. Ph.D. Thesis. 118 pp. (supervised jointly with Max Rothschild)
14. He, Wei. 2011. A combined linkage disequilibrium and cosegregation method for fine mapping of QTL and approaches to study the long-term accuracy of genomic selection. Ph.D. Thesis. 183 pp.
15. Zeng, Jian. 2011. Genomic selection of purebred animals for crossbred performance under dominance. M.S. Thesis. 65 pp.
16. Toosi, Ali. 2012. Genome-wide prediction of breeding values and mapping of quantitative trait loci in stratified and admixed populations. Ph.D. Thesis. 208 pp.

Postdoctoral Research Supervision

1. Bruce Southey. 1996-1998. Research topic: “QTL mapping by pedigree analysis”.
2. Soledad A. Fernandez. 2001 (8 months). Research topic: QTL mapping using the IBD approach”, (jointly with Jack Dekkers).
3. Liviu R. Totir. 2002-2005. Research topic: “Use of sampling techniques for refined QTL analysis in complex pedigrees” (jointly with Jack Dekkers)..
4. Mehmet Firat. 2003-2004. Research topic: “QTL detection using linkage and linkage disequilibrium”, (jointly with Jack Dekkers).
5. Helene Gilbert. 2003-2004. Research topic: “Use of linkage-disequilibrium and cosegregation information for marker assisted selection”.

6. Joseph Abraham, 2004-2005 Research topic: “Use of MCMC methods for marker assisted selection”.
7. Tian Kechuan. 2005-2006. Research topic: “Use of marker data for computing gametic relationship matrices”.
8. David Habier. 2006-2008. Research topic: “Improved methods for marker assisted and genomic selection”.
9. Kadir Kizilkaya. 2008-2013. Research topic: “Utilization of natural genomic variation”, (jointly with Dorian Garrick).
10. Mahdi Saatchi. 2012-2014. Research topic: “Factors affecting prediction accuracy of complex human traits and diseases”.
11. Wan-Ling Hsu. 2014-.Research topic. “Accounting for breed differences in whole-genome analyses that combine information from genotyped and non-genotyped animals”.

Courses Taught

Semester-year	Course	Hours	Enrollment
Fall-1985	Advanced Quantitative Genetics	4	6 students about 10 others
Spring-1986	Statistical Methods	4	27 students
Spring-1987	Statistical Methods	4	38 students
	Animal Breeding Seminar	1	16 students
	Research Studies in Animal Science	1	1 student
Spring-1988	Statistical Methods	4	26 students
	Research Studies in Animal Science	1	1 student
Spring-1989	Statistical Methods	4	27 students
Spring-1990	Statistical Methods	4	17 students
	Research Studies in Animal Science	1	1 student
Summer-1990	Research Studies in Animal Science	1	1 student
Spring-1991	Statistical Methods	4	14 students
Fall-1992	Animal Breeding Seminar	1	6 students
Spring-1993	Statistical Methods	4	30 students
	Quantitative Genetics	4	3 students 4 others
Spring-1994	Statistical Methods	4	30 students
	Quantitative Genetics	4	5 students
	Animal Breeding Seminar	1	10 students
Fall-1994	Statistical Methods to Map QTL	4	7 students about 5 others
Spring-1995	Statistical Methods	4	22 students
	Quantitative Genetics	4	5 students
Spring-1996	Quantitative Genetics	4	7 students
Summer-1996	Statistical Methods to Map QTL	3	20 students and others
Fall-1996	Statistical Methods to Map QTL	2	30 students and others
Spring-1997	Population Genetics	3	14 students
Summer-1997	Linear Models in Animal Breeding	4	37 students and others
Fall-1997	Applied Animal Breeding	2	14 students
Spring-1998	Statistical Methods to Map QTL	2	10 students
Fall-1998	Population Genetics	4	14 students
Spring-1999	Statistical Methods to Map QTL	2	15 students 3 faculty
Fall-1999	Population Genetics	4	16 students
Spring-2000	Statistical Methods to Map QTL	2	10 students
Spring-2000	Bioinformatics	2	10 students
Fall-2000	Population Genetics	4	8 students
Fall-2001	Computing Methods for Animal Breeders	2	8 students
Fall-2001	Population Genetics	4	14 students

Courses Taught (continued)

Semester-year	Course	Hours	Enrollment
Spring-2002	Statistical Methods to Map QTL	2	7 students
	Advance Quantitative Genetics	2	3 students
Fall-2002	Population Genetics	4	13 students
Fall-2003	Computing Methods for Animal Breeders	4	5 students
Spring-2004	Statistical Methods to Map QTL	2	5 students
Summer-2004	QTL Mapping in Complex Pedigrees	2	25 students
Summer-2005	C++ Programming	2	17 students
Fall-2007	Computing Methods for Animal Breeders	2	5 students
Spring-2006	Statistical Methods to Map QTL	2	8 total 2 for credit
Fall-2007	Computing Methods for Animal Breeders	4	2 students
Spring-2008	Statistical Methods to Map QTL	2	6 students 8 total
Summer-2009	Genomic Selection in Livestock		70 participants
February-2010	Armidale, Australia		40 participants
Summer-2010			63 participants
Fall-2009	Computing Methods for Animal Breeders	4	2 students
Summer-2011	Genomic Selection Davos, Switzerland		41 participants
	Wageningen, Netherlands		50 participants
Summer-2012	Phoenix, Arizona		xx participants
Fall-2011	Computing Methods for Animal Breeders	4	2 student
Spring-2013	Statistical Methods to Map QTL	2	3 students 6 total
Fall-2013	Computing Methods for Animal Breeders	4	3 student
Summer-2013	Genomic Selection Quebec City, Canada		35 participats
	Samsun, Turkey		30 participants
	Davos, Switzerland		20 participants
Fall-2013	Piacenza, Italy		60 participants

Description of Courses

Statistical Methods I have had primary responsibility for teaching this course for 9 semesters to a total of 231 students. This is a 1-unit course with three one-hour lecture periods and two one-hour lab periods per week. I present the lectures and supervise one or two teaching assistants for the laboratory. This course in applied statistics is aimed at giving students an introduction to the analysis of unbalanced data, using computers. It is taken primarily by graduate students in the College of Agriculture, and it is cross listed with the Departments of Agricultural Engineering and Forestry.

Based on the evaluations of students taking this course, in the Spring of 1991, I was included in the list of teachers ranked excellent by their students.

Introductory Quantitative Genetics I have taught this course for 4 semesters to a total of 18 students. This is a 1-unit course with four one-hour lecture periods per week. This course is aimed at giving students a solid introduction to the fundamentals of Quantitative Genetics. It is taken primarily by graduate students in plant and animal breeding, and it is cross listed with Biology.

Based on the evaluations of students taking this course, in the Spring of 1994, I was included in the list of teachers ranked excellent by their students.

Advanced Quantitative Genetics In 1985, co-taught this course, with Dr. Gianola and with guest lectures by several other faculty to a group of about 20 including 8 to 10 faculty members and visiting scholars. I presented and discussed nine out of 37 key papers. Notes were provided for each paper with detailed derivations of formulae.

Statistical Methods to Map QTL I taught this course in 1994 to a group of 7 students and several faculty and research associates. This is a 1-unit course with four one-hour lecture periods per week. The material covered included the theory of maximum likelihood estimation, hypothesis testing in relation to linkage analysis, methods for linkage analysis between markers, between markers and QTL in crosses of inbred lines, and between markers and QTL in outbred populations. In the summer of 1996, this course was taught at the University of Wisconsin (Madison) to a group of about 20. In the fall of 1996 part of this material was taught to a group of about 30, including some faculty members, at Iowa State University. This course is offered every other year at ISU. In 1999, I taught some of this material in Argentina and Brazil. In Spring 2002, I introduced the use of Bayesian methods. In 2008, the focus of the course was changed to the analysis to whole-genome data. New material introduced included: 1) theory on the generation of linkage disequilibrium due to genetic drift in finite populations; 2) Bayesian variable selection methods; and 3) whole-genome selection.

Computing Techniques in Animal Breeding I helped Dr. Groeneveld develop and teach this course for the first time in 1989. I taught about 10 percent of the course. The code that was prototyped during the development of this course led to the package PEST.

Animal Breeding and Genetics Seminar I was responsible for organizing this seminar class for three semesters.

Research Studies in Animal Science I have directed students in independent research projects in Monte-Carlo simulation studies, estimation of genetic parameters, theory of covariance between relatives, and mitochondrial inheritance.

Population Genetics I taught this course for the first time in the Spring of 1997 at Iowa State University. This course is aimed at giving students a solid introduction to the fundamentals of Population and Quantitative Genetics. It is taken primarily by graduate students in Animal Breeding, Plant Breeding and Interdepartmental Genetics. In Fall 1998, this course was expanded to cover some more material relevant to plant breeding and was taught as a four hour course jointly by Jim Holland and me.

Linear Models in Animal Breeding I was invited to teach this as Nordic-Ph.D. course in the Summer of 1997 to 37 students and young research scientists. The topics included the theory underlying estimation of fixed effects and hypothesis testing, prediction of random effects, and estimation of variance components using maximum likelihood techniques.

Applied Animal Breeding I was responsible for teaching this course through distance learning methods (ICN and video tapes) to 14 students in the Fall of 1998. Half of this two hour course dealt with theory and concepts underlying animal breeding. I gave the lectures on theory and concepts. The second half of the course covered the application of these concepts to genetic improvement in the swine, beef, dairy, poultry, and sheep industries. The lectures on industry applications were given by five others.

Bioinformatics This was an informal workshop, organized by ETH, Zurich, Switzerland, to introduce the problems and concepts in the field of Bioinformatics and Computational Biology to Animal Breeders. I taught it once in May, 2000 at St. Moritz, Switzerland, and there were 10 Animal Breeders from Switzerland, Germany, and France. The topics covered included the analysis of biological sequence data, linkage analysis, and molecular phylogeny construction.

Advanced Computational Methods in Animal Breeding This course is offered in two modules. In module 1, students learn how to use C++ to solve Henderson's mixed model equations by iterative techniques for very large pedigrees. In Module 2 estimation of parameters is considered. This module was taught for the first time in 2004 and estimation of variance components in mixed linear models by maximum likelihood was considered. Simple models were used to introduce concepts. Subsequently, the models were extended to accommodate multiple traits, correlated random effects, and marker data. In Summer of 2005, module 1 was taught as a two-week short course. In the Fall, I taught the second module where students learned to simulate genomic data and how to modify the mixed model programs to estimate parameters by Bayesian methods. In the Fall of 2009, the course was offered as an online course to students at Iowa State.

Advanced Quantitative Genetics Advanced linear and non-linear methods for analyses of quantitative traits. In Spring 2002, I taught this course for the first time with Jack Dekkers. My lectures were on the analysis of data from populations undergoing selection and non-random mating and on the theory underlying Markov Chain Monte Carlo methods.

QTL Mapping in Complex Pedigrees This course was offered as a summer workshop in 2004. Theory and algorithms were presented for QTL mapping in outbred populations using linear model and mixture model methods. Computer programs for implementing these methods were discussed and made available to the students.

Use of High-density SNP Genotyping for Genetic Improvement of Livestock This course focuses on theory and applications related to the use of whole-genome SNP data for genetic improvement of livestock. It has been taught jointly, and my contributions have been on the theory of Bayesian methods and their implementations. Taught Summer 2009 with Jack Dekkers (JD) and Dorian Garrick (DG), February 2010 in Armidale, Australia with DG, Summer 2010 with JD and DG, 2013 with JD and DG in Quebec City, with DG in Samsun, Turkey and Davos Switzerland, and by myself in Piacenza, Italy.

Research Support

1. Comparison of alternative analyses of unbalanced data with mixed models. Hatch funds, \$30,000, 1985–1988. R. L. Fernando (PI).
2. Heterospermic insemination as a tool for sire evaluation for sex limited traits and techniques for improvement of AI in swine. Hatch Funds, \$30,000 1985–1988. L. H. Thompson (PI), D.G. McLaren (Co-PI), and R. L. Fernando (Co-PI).

3. Development of methods for genetic analysis of discrete traits of economic importance in U.S. and Israeli dairy cattle, BARD, \$200,000, 1985–1989. D. Gianola (PI), R. L. Fernando (Co-PI), C. R. Henderson (Co-PI), R. Bar-Anon (Co-PI), and J. Weller (Co-PI).
4. Detection of major genes of growth using genetic markers (USDA, \$125,000, 1987–1990. H. A. Lewin (PI), P. D. George (Co-PI), R. L. Fernando (Co-PI).
5. Student work stations on a local Macintosh laserwriter network. (Univ. of Illinois, \$4,706, 1987. D. McLaren (PI) and R. L. Fernando (Co-PI).
6. The use of quantitative trait loci in dairy sire and cow evaluation (Eastern A. I. Cooperative, \$3000, 1988. Ina Hoeschele (PI), R. L. Fernando (Co-PI), and D. Gianola (Co-PI).
7. Marker assisted selection for genetic improvement of livestock. Hatch funds, \$70,000, 1989–1996. R. L. Fernando (PI).
8. Towards a 20 cM map of the Bovine genome. USDA, \$310,743, 1991–1994. H. A. Lewin (PI) and R. L. Fernando (Co-PI).
9. Segregation and linkage analysis to study the mode of inheritance of quantitative trait loci. Schweizerischer Nationalfonds, Switzerland, \$ 102,825, 1993–1994. C. Stricker (PI), N. Küenzi (Co-PI), and R. L. Fernando (Co-PI).
10. Estimation of Genetic Parameters. Hatch funds, 1993-1998 \$ 50,000. M. Grossman (PI) and R. L. Fernando (Co-PI).
11. Fine Mapping of Chicken Chromosome I with respect to loci affecting quantitative traits of economic importance. USA-Israel/BSF, \$135,000, 1994–97. M. Soller (PI), R. L. Fernando (Co-PI), and H. H. Cheng (Co-PI).
12. Methods to map QTL by pedigree analysis. USDA, \$108,244, 1994-1997. R. L. Fernando (PI) and Ignacy Misztal (Co-PI).
13. Segregation and linkage analysis for quantitative trait loci. Schweizerischer Nationalfonds, Switzerland, \$122,879 1995–1997. Christian Stricker (PI), N. Küenzi (Co-PI), and R. L. Fernando (Co-PI).
14. Mapping QTL for age at puberty, ovulation, rate of embryo survival using the Illinois Meishan/Yorkshire reference family. Pig Improvement Company, \$103,172, 1995–97. M. Ellis (PI) and R. L. Fernando (Co-PI).
15. A model to assess infertility and embryo mortality in dairy cattle and poultry. USDA/CSREES, \$24,000, 1995-97. M. Grossman (PI) and R. L. Fernando (Co-PI).

16. A molecular genomic scan analysis to identify genes influencing muscle quality in the pig. National Pork Producers Council, \$255,000, 1997-2000. M. F. Rothschild (PI), T. Baas (Co-PI), L. Christian (Co-PI), and R. L. Fernando (Co-PI).
17. USDA National Needs Graduate Fellowship Program in Animal Biotechnology. USDA, \$108,000, ISU \$30,000, 1998-2003. R. L. Fernando (PI) S. Lamont (Co-PI), and M. F. Rothschild(Co-PI).
18. Optimizing marker assisted selection for genetic improvement of livestock. USDA/NRI, \$130,000, 1998-2001. J. C. M. Dekkers (PI), M. F. Rothschild (Co-PI), and R. L. Fernando (Co-PI).
19. Marker assisted BLUP. Monsanto, \$41,860, 1999-2001. R. L. Fernando (PI).
20. Mapping and use of QTL for marker-assisted improvement of meat quality in pigs. USDA/IFAFS, \$587,722, 2000-2003. J. C. M. Dekkers (PI), M. F. Rothschild (Co-PI), and R. L. Fernando (Co-PI).
21. Pedigree-based QTL detection to identify valuable crop genes and understand long-term selection response. Plant Sciences Institute, \$25,000, 2001-2002. Jean-Luc Jannink (PI), R. L. Fernando (Co-PI), and Machael Lee (Co-PI).
22. Novel Sampling Techniques For Refined QTL Analysis In Complex Pedigrees. USDA/NRI, \$200,000, 2001-2006. R. L. Fernando (PI) and J.C.M. Dekkers (Co-PI).
23. Gene simulation software for teaching animal breeding and genetics. USDA/HECGP, \$99,392, 2001-2004. P.L. Spike (PI), R. L. Fernando (Co-PI), and J.C.M. Dekkers (Co-PI).
24. QTL detection using linkage and linkage disequilibrium in swine breeding populations. SYGEN and Monsanto, \$99,108, 2002-2006. J.C.M. Dekkers (PI) and R. L. Fernando (Co-PI).
25. Marker-Assisted Selection Using Population-Wide Linkage Disequilibrium. HY-Line Int., Monsanto Co., and SYGEN Int., \$108,846, 2003-2007. J.C.M. Dekkers (PI) and R. L. Fernando (Co-PI).
26. Use of Parallel Computing to Sample Genotypes. Iowa State University, 10% share of high performance computing cluster, 2004-2005. R. L. Fernando (PI).
27. National Beef Evaluation Consortium. USDA/CSREES, \$80,000, 2004-2005. J. Reecey (PI) and R. L. Fernando (Co-PI).
28. Statistical methods for fine mapping of QTL. ISU/CIAG, \$30,051, 2005-2007. R. L. Fernando (PI) and J.C.M. Dekkers (Co-PI).

29. Use of molecular data for breeding. Newsham Genetics, \$16,000. 2006. R. L. Fernando (PI).
30. Identification of DNA markers for important production traits in layer lines. Midwest Poultry Research Program (\$57,000) and Hy-Line Int. (\$15,000), 2006-2007. S.J. Lamont (PI), J.C.M. Dekkers (Co-PI), and R.L. Fernando (Co-PI).
31. Aviagen genomics initiative. Aviagen Int. \$230,747, 2005-2007. S.J. Lamont (PI), J.C.M. Dekkers (Co-PI), and R.L. Fernando (Co-PI).
32. Training in the development and application of quantitative methods and tools for animal genomics. USDA/National Needs Fellowship. \$243,000. 2007-2010. J.C.M. Dekkers (PI), D. Nettleton (Co-PI), R.L. Fernando (Co-PI), and M.F. Rothschild (Co-PI).
33. Use of genomics to select purebreds for crossbred performance in the field. USDA/NRI \$386,963. 2007-2010. Fernando, R. L. (PI) and J.C.M. Dekkers (Co-PI).
34. Identification of Molecular Markers to Improve Fertility in Beef Cattle. USDA/NRI \$449,721. 2008-2011. Thomas, M. (PI), Reecy, J. (Co-PI), Fernando, R. L. (Co-PI).
35. Genetic regulation and genomic selection of energy balance traits in dairy cattle. USDA/NRI \$446,972. 2008-2011. Spurlock, D.M. (PI), Dekkers, J.C.M. (Co-PI), Fernando, R. L. (Co-PI), Coffey, M. (Co-PI).
36. Utilization of natural genomic variation. Pfizer. \$1,444,868. Reecy, J.M. (PI), Beitz, D.C. (Co-PI), Garrick, D. (Co-PI) Fernando, R.L. (Co-PI).
37. Bioinformatics to implement genomic selection (BIGS). USDA/NRI \$899,936. 2009-2012. Garrick, D.J. (PI) Dekkers, J.C.M., Fernando, R.L. and others.
38. PRRS CAP Host genetics: Characterization of host factors that contribute to PRRS disease resistance and susceptibility. PRRS CAP2 Objective 3 Host Genetics. \$279,938 (ISU budget). JK Lunney (PI), J Dekkers, R Fernando, JM Reecy, M Rothschild, C Tuggle, and others.
39. Use of high-density SNP genotyping for genetic improvement of livestock. USDA/AFRI. \$449,939. 2010-2012. Dekkers, J. C. M. (PI), Fernando, R. L. (Co-PI), Garrick, D. (Co-PI), Lamont, S (Co-PI).
40. Investigation of novel whole genome analysis techniques for marker based genetic evaluation of complex pedigrees. Pioneer Hi-Bred. \$80,000. 2010-2011. Fernando, R. L. (PI)
41. Enhanced Bioinformatics to Implement Genomic Selection (e-BIGS). USDA-NIFA-AFRI. \$488,501. 2012-2016. Garrick, DJ (PI) Dekkers JCM (Co-PI), Fernando RL (Co-PI), Reecy JM (Co-PI), Rothschild MF (Co-PI).

42. Factors affecting prediction accuracy of complex human traits and diseases. NIH (R01GM099992-01A1) \$421,939 (ISU) 2012-2016. De los Campos, G. (PI), Allison, D. (Co-PI), Fernando, R.L. (Co-PI).
43. Combining between and within breed variability for genome-wide association mapping of QTL. The Scientific and Technological Research Council of Turkey (TUBITAK). \$24,000, 2012-2013. Kizilkaya, K. (PI), R.L. Fernando (Co-PI).
44. Single-Step Bayesian method for genomic prediction that combines information from genotyped and non-genotyped animals. USDA-NIFA-AFRI. \$350,000. 2015-2017. Fernando, RL (PI), Garrick, D. (Co-PI), Wolc, A. (Co-PI), Dekkers, JCM (Co-PI).

Honors and Awards

1. Ralph and Mabel Hunter Fellowship, College of Agriculture, University of Illinois. 1978–1979.
2. Jessie E. Hackett Fellowship, College of Agriculture, University of Illinois. 1981–1982.
3. Full Scholarship to participate in the 3rd International Summer School in Agriculture “Modern Techniques in Animal Breeding”, Dublin, Ireland. 1983.
4. Norton Prize in Statistics (for outstanding student contributions to Theoretical or Applied Statistics), Graduate College Statistics Program, University of Illinois. 1985.
5. University of Illinois Teachers Ranked Excellent by Their Students: Statistical Methods–1991, Quantitative Genetics–1994.
6. Over 50 invited lectures in U.S. and 14 foreign countries. 1984–present.
7. Associate editor for Genetics, Selection and Evolution. 1992–1994.
8. Advisory Board, Genetics, Selection and Evolution. 1998–2000.
9. Scientific Program Chair for session on Estimation of Genetic Parameters, 6th World Congr. Genetics Appl. Livest. Prod. Armidale, Australia. 1998.
10. Henderson Lecturer, 1998. Department of Animal Science, Cornell University, Ithaca, New York.
11. Review Panel, USDA Scientific Quality Control. 2002.
12. ASAS travelling fellow to European Association of Animal Production, 2004.

13. Rotary LeClerc Lecture, University of Maryland. 2009.
14. Associate Editor, *Frontiers in Livestock Genomics*, 2011–
15. Rockefeller Prentice Memorial Award in Animal Breeding and Genetics. American Society of Animal Science. 2012.
16. ASAS travelling fellow to European Association of Animal Production, 2013.

Invited Lectures

1. Discussant in symposium, “New Statistical Methods in Animal Breeding and Genetics”, at the American Society of Animal Science Annual Meeting. 1984.
2. Optimum designs for sire evaluation schemes. At the “International Symposium on Advances in Statistical Methods for Genetic Improvement of Livestock”, Armidale, Australia. 1987.
3. Statistical inferences in populations undergoing selection or non-random mating. At the “International Symposium on Advances in Statistical Methods for Genetic Improvement of Livestock”, Armidale, Australia. 1987.
4. Prioritizing Animal Breeding Research for the 90’s: Statistics. At the Annual Meeting of the American Society of Animal Science, Midwestern section. 1989.
5. Integrated Strategies and methodologies for the genetic improvement of animals. At the “Symposium on the Role of Animal Breeding in an Age of Molecular and Zygotic Manipulation”, at the Annual Meeting of the American Society of Animal Science. 1989.
6. Marker assisted selection. At conference on “Mapping Domestic Animal Genomes: Needs and Opportunities”. Allerton Park, IL. 1990.
7. Statistical problems in marker assisted selection for QTL. At workshop on “Genetic Parameter Estimation”, 4th Wld. Cong. Genet. App. Liv. Prod., Edinburgh, Scotland. 1990.
8. Best linear unbiased prediction. At the Department of Biometry and Genetics, Louisiana State University, Medical Center. 1991.
9. An alternative formulation of the mixed model of inheritance for segregation and linkage analysis. At E.T.H. Zürich, Switzerland. 1992.
10. Best linear unbiased prediction theory for marker assisted selection. At E.T.H. Zürich, Switzerland. 1992.

11. Statistical problems in marker assisted selection for QTL. At I.N.R.A. Jouy-en-Josas, France. 1992.
12. An alternative formulation of the mixed model of inheritance for segregation and linkage analysis. At I.N.R.A. Jouy-en-Josas, France. 1992.
13. Comparison of alternative approaches for analysis of data with mixed model inheritance. At I.N.R.A. Jouy-en-Josas, France. 1992.
14. Best linear unbiased prediction theory for marker assisted selection. At I.N.R.A. Jouy-en-Josas, France. 1992.
15. Best linear unbiased prediction theory for marker assisted selection. At I.N.R.A. Toulouse, France. 1992.
16. Genetic means and covariances between relatives in crossbred populations under dominance. At the University of Wisconsin, Madison, Wisconsin. 1993.
17. Design of QTL experiments in cattle. At workshop on "The Design of Experimental Populations to Detect and Map Livestock QTL", 5th Wld. Cong. Genet. App. Liv. Prod. Guelph, Canada. 1994.
18. Likelihood analysis of extended pedigrees under mixed inheritance. At Annual Meeting of the International Biometric Society, German Region. Hohenheim University, Stuttgart. Germany. 1995.
19. Theory for genetic evaluation in crossbred populations. At E.T.H. Zürich, Switzerland. 1995.
20. Theory for genetic evaluation in crossbred populations. At Hohenheim University, Stuttgart. Germany. 1995.
21. Statistical methods for marker-QTL studies. At Hebrew University of Jerusalem, Rehovot, Israel. 1995.
22. Theory for genetic evaluation in crossbred populations under dominance inheritance. At University of Guelph, Guelph, Canada. 1995.
23. Genetic evaluation in crossbred populations. At National Breeders Roundtable. 1996.
24. Multiple tests in linkage analysis. At Allerton II: Genetic Analysis of Economically Important Traits in Livestock. 1996.
25. Detection and utilization of single genes without DNA assays. At the "Dairy Cattle Improvement Symposium in Honor of Prof. Charles Smith on Breeding Objectives and Strategies", at the Annual Meeting of the American Dairy Science Association. 1997.

26. Controlling error rates in mapping QTL. At Agricultural University of Norway, Å s, Norway. 1997.
27. Controlling error rates in mapping QTL. At Danish Institute of Animal Science, Tjele, Denmark. 1997.
28. Controlling error rates in mapping QTL. At E.T.H. Zürich, Switzerland. 1997.
29. Genetic evaluation and selection using genotypic, phenotypic and pedigree information, 6th Wld. Cong. Genet. App. Liv. Prod. Armidale, Australia. 1998.
30. Controlling error rates in mapping QTL. At Department of Epidemiology and Biostatistics, Case Western Reserve University, Cleveland, Ohio, 1998.
31. Identification of QTL and ETL. Ensminger International Workshop. Central Agricultural University, Wuhan, China. 1998.
32. Genomics and Computational Biology. Ensminger International Workshop. Central Agricultural University, Wuhan, China. 1998.
33. Genomics and Computational Biology. Ensminger International Workshop. China Agricultural University, Beijing, China. 1998.
34. Genetic Evaluation in Crossbred Populations. Department of Animal Science, Cornell University, Ithaca, New York. 1998.
35. A two-stage test for mapping QTL. University of Wisconsin. Madison, Wisconsin. 1999.
36. An alternative approach to control false discoveries in detecting QTL. Biotechnology Seminar, University of Nebraska, Lincoln, Nebraska. 1999.
37. Analysis of data from crossbred populations. International Symposium on Animal Breeding and Genetics. Federal University of Vicosa, Brazil. 1999.
38. Theory for analysis of data from multibreed populations. Genetic Prediction Workshop of the Beef Improvement Federation. 1999.
39. Controlling the relative frequency of false positives in a multiple test situation. Baker Center for Bioinformatics and Biological Statistics, Iowa State University, Ames, Iowa. 2000.
40. An Algorithm to Obtain an Irreducible Markov Chain to Sample Marker Genotypes. Statistical Methods of Pedigree Analysis Workshop, IX International Plant and Animal Genome Conference. San Diego, California. 2001.

41. An alternative approach to control false positives in QTL scans. Session I: Advances in genetic analysis and evaluation. 512th EAAP Conference, Budapest, Hungary. 2001.
42. Controlling the proportion of false positives in genome scans for QTL. NCR-199 Committee Meeting, Cornell University, Ithaca, NY. 2001.
43. Advances in genetic and statistical models to predict breeding values. 7th World Congress Genet. Appl. Livest. Prod. France. 2002.
44. Statistical Issues In Marker Assisted Selection. 8th Genetic Prediction Workshop of the Beef Improvement Federation. 2003.
45. Use of Linkage Disequilibrium for Fine Mapping Quantitative Trait Loci. Department of Statistics, Iowa State University, Ames, Iowa. 2003.
46. Incorporating molecular markers into genetic evaluation. EAAP Conference, Bled, Slovenia. 2004.
47. Controlling the proportion of false positives in multiple dependent tests. Department of Epidemiology and Biostatistics, Case Western Reserve University School of Medicine, Cleveland, Ohio. 2004.
48. Incorporating Molecular Markers into Genetic Evaluation. Pioneer Hi-Bred International, Johnston, Iowa. 2005.
49. Combining Disequilibrium and Cosegregation Information to Map Quantitative Trait Genes. Department of Epidemiology and Biostatistics, Case Western Reserve University School of Medicine, Cleveland, Ohio. 2005.
50. Theory for genetic evaluation given genotypes at a trait locus. Roslin Institute, Edinburgh, Scotland, UK. 2005.
51. Marker assisted BLUP. Genesis Faraday Symposium on High throughput genotyping, numerical genomics and quantitative genetics in farm animals. Edinburgh, Scotland, UK. 2006.
52. Algorithms to compute allele state and origin probabilities for QTL mapping. 8th World Congress Genet. Appl. Livest. Prod. Brazil. 2006.
53. Genomic selection. Symposium on "Statistics in animal breeding and quantitative genetics: the next 60 years". Sonderborg, Denmark. 2007.
54. Unraveling a paradox in marker assisted selection. Statistical Genomics Workshop, International Plant and Animal Genome Conference XVI. San Diego, California. 2008.
55. Alternative approaches for whole-genome analyses. Joint Biometric Conference of the German Region. Munich, Germany. 2008.

56. Genomic selection of purebreds for crossbred performance. National Breeders Roundtable. 2008.
57. Genomic selection of purebreds for crossbred performance. I.N.R.A. Jouyen-Josas, France. 2008.
58. Genomic selection of purebreds for crossbred performance. I.N.R.A. Toulouse, France. 2008.
59. DNA technology: estimation of genetic merit from large DNA marker panels. American Society of Animal Science, Annual Meeting. 2008.
60. Controlling Error Rates in QTL Mapping and Marker Assisted Selection. Rotary LeClerg Lecture, University of Maryland. 2009.
61. Genomic Selection in Admixed and Crossbred Populations. Rotary LeClerg Lecture, University of Maryland. 2009.
62. A mixture model for genomic selection. Symposium on Statistical Genetics of Livestock for the Post-Genomic Era. University of Wisconsin, Madison, Wisconsin. 2009.
63. Combining information from genotyped and ungenotyped individuals. Aviagen Advisory Group Meeting. Edinburgh, Scotland, UK. 2009.
64. Accuracy of genomic prediction. Aviagen Advisory Group Meeting. Chicago, Illinois. 2010.
65. Controlling false positives in genome-wide association studies: a Bayesian approach. Department of Biometry, University of Alabama at Birmingham. 2011.
66. Bayesian regression method for genomic analyses with incomplete genotype data. EAAP Conference, Nantes, France. 2013.
67. Bayesian regression as an alternative implementation of genomic-enhanced genetic evaluation. Beef Improvement Federation 10th Genetic Prediction Workshop held in Kansas City. 2013.
68. Implications of using identity-by-descent versus identity-by-state matrices in genetic analyses. Plant and Animal Genome XXII conference, San Diego. 2014.
69. Application of whole-genome prediction methods for genome-wide association studies: a Bayesian approach. 10th World Congress on Genetics Applied to Livestock Production. Vancouver, Canada.

Invited Courses

1. Statistical Methods to Map QTL. Summer 1996. University of Wisconsin, Madison Wisconsin.
2. Inter-Nordic Course: Linear Models in Animal Breeding. Summer 1997. Biri, Norway.
3. FOMECA Visiting Professor: Statistical Methods to Map QTL. 1999. University of Buenos Aires, Argentina.
4. Statistical Methods to Map QTL. 1999. Federal University of Vicosa, Brazil.
5. Bioinformatics workshop organized by ETH, Zurich, Switzerland. 2000, St. Moritz, Switzerland.
6. QTL Mapping in Complex Pedigrees. Iowa State University. 2004, Ames, Iowa, USA.
7. C++ Programming for Animal Breeding. Iowa State University. 2005, Ames, Iowa, USA. (taught jointly with Steve Kachman)
8. Use of High-density SNP Genotyping for Genetic Improvement of Livestock. Iowa State University. 2009, Ames, Iowa, USA. (taught jointly with Jack Dekkers and Dorian Garrick)
9. Armidale Animal Breeding Summer Course: Bayesian Methods in Genome Association Studies. University of New England. 2010. Armidale, Australia (taught jointly with Dorian Garrick)
10. Summer Workshop: Genomic Selection of Livestock. Iowa State University. Ames, Iowa, USA. 2010. (taught jointly with Jack Dekkers and Dorian Garrick)
11. Genomic Selection in Livestock. 2011. agn Genetics Davos, Switzerland. (taught jointly with Dorian Garrick)
12. Genomic Selection in Livestock. 2011. Animal Breeding and Genomics Centre, Wageningen, The Netherlands. (taught jointly with Dorian Garrick)
13. Workshop on Genomic Selection in Livestock. 2012. Funded by USDA-NIFA Higher Education Challenge Program. Phoenix, Arizona. (taught jointly with Jack Dekkers and Dorian Garrick)
14. Workshop on Genomic Selection in Livestock. 2013. Funded by USDA-NIFA Higher Education Challenge Program. Quebec City, Canada. (taught jointly with Jack Dekkers and Dorian Garrick)

15. Workshop on Genomic Selection in Livestock. 2013. Samsun, Turkey. (taught jointly with Dorian Garrick)
16. Workshop on Genomic Selection in Livestock. 2013. Davos, Switzerland. (taught jointly with Dorian Garrick)
17. Theory and Methods for Genomic Prediction. 2013. Gen2Farm Winter School. Piacenza, Italy.

Service

1. Member of the QTL group of the National Consortium for Beef Cattle Evaluation. 2001-
2. Interdepartmental Genetics, Supervisory Committee. 1999-2003.
3. Interdepartmental Genetics, Admissions Committee. 2001.
4. USDA Scientific Quality Control Review Panel. 2002.
5. BCB Admissions Committee 2002,2003,2004,2007, 2008

Areas of Research

- Theory and methods for use of genetic markers in breeding. This includes the development of theory and methods for:
 1. detection of QTL by linkage analysis
 2. linkage disequilibrium methods for fine mapping
 3. estimation of marker-QTL parameters
 4. comparison alternative designs
 5. marker assisted selection
 6. evaluation of the advantage of marker assisted selection
 7. Markov chain Monte Carlo methods
 8. statistical and computational issues related to analysis of whole-genome data
 9. semi-parametric methods for genome assisted selection
 10. use of parallel computing to reduce computing time in whole-genome analyses
- Theory and methods for genetic evaluation of crossbred animals. This includes the development of theory and methods for:
 1. covariance between relatives
 2. estimation of genetic parameters
 3. genetic evaluation and selection

4. finite locus models using Markov chain Monte-Carlo
 5. comparison of breeding schemes
 6. use of whole-genome data for QTL mapping and prediction of breeding values using crossbreds and mixed breed populations
- Other areas of research include
 1. methodology related to the estimation of genetic parameters and the prediction of genetic merit in populations undergoing selection and non-random mating.
 2. Bayesian methodology for analysis of unbalanced mixed model data
 3. Optimization of breeding programs.
 4. Use of computer simulation to study dynamics of genetic systems.