
| | | |
|---------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------|
| CONTACT INFORMATION | A218f Animal Science Building Department of Animal Science University of Nebraska-Lincoln Lincoln, NE 68583-0908 USA | <i>E-mail:</i> morota@unl.edu <i>Phone:</i> (402)-472-6031 <i>WWW:</i> morotalab.org |
| RESEARCH INTERESTS | I am a quantitative geneticist interested in incorporating statistics, machine learning, and bioinformatics to the study of animal genetics in the omics era. The core line of my research is connecting the quantitative genetics and animal breeding theories to currently available molecular information. I am particularly interested in statistical methods for prediction of complex traits using whole-genome molecular markers. | |
| EDUCATION | University of Wisconsin-Madison , Madison, Wisconsin USA Ph.D., Animal Sciences, May 2014 <ul style="list-style-type: none">• Dissertation: “Whole-genome Prediction of Complex Traits Using Kernel Methods.”• Advisor: Prof. Dr. Daniel Gianola• Committee: Drs. Corinne D. Engelman, Guilherme J. M. Rosa, Grace Wahba and Kent A. Weigel University of Wisconsin-Madison , Madison, Wisconsin USA M.S., Dairy Science, December 2011 <ul style="list-style-type: none">• Thesis: “Application of Bayesian and Sparse Network Models for Assessing Linkage Disequilibrium in Animals and Plants.”• Advisor: Prof. Dr. Daniel Gianola• Committee: Drs. Guilherme J. M. Rosa and Kent A. Weigel Obihiro University of Agriculture and Veterinary Medicine , Obihiro, Hokkaido Japan B.S., Agricultural Science, March 2008 <ul style="list-style-type: none">• Thesis: “Genetic Analysis of Threshold Traits.”• Advisor: Prof. Dr. Mitsuyoshi Suzuki | |
| PROFESSIONAL POSITIONS | Department of Animal Science University of Nebraska-Lincoln , Lincoln, Nebraska USA Assistant Professor (70% Research & 30% Teaching) | 08/2014 - Present |
| WORK EXPERIENCE | Department of Animal Sciences University of Wisconsin-Madison , Madison, Wisconsin USA Graduate Research Assistant Animal Genetics Research & Development Group Zoetis, Inc. , Kalamazoo, Michigan USA Quantitative Geneticist (student internship) | 06/2011 - 05/2014 06/2013 - 11/2013 |

PROFESSIONAL
SOCIETY
MEMBERSHIPS

- The International Society for Animal Genetics. 2015 - Present
- The American Society of Animal Science. 2014 - Present
- The Japanese Society of Animal Breeding and Genetics. 2013 - Present
- The International Biometric Society (ENAR). 2012 - Present

EDITORIAL
ACTIVITIES

Ad hoc Reviewer for: Animal Production Science (1), Computers and Electronics in Agriculture (1), DNA Research (1), G3 (Bethesda) (1), Genetics (1), PLOS ONE (1), Poultry Science (1), Scientia Agricola (1)

Number of reviewed papers: 2012 (1), 2013 (1), 2014 (6)

MANUSCRIPTS IN
REVIEW

12. Valente BD, **Morota G**, Peñagaricano F, Gianola D, Weigel KA, and Rosa GJM. The causal meaning of genomic predictors and how it affects construction and comparison of genome-enabled selection models. *BioRxiv* doi: [10.1101/001511](https://doi.org/10.1101/001511) , *arXiv*: <http://arxiv.org/abs/1401.1165>

PEER REVIEWED
JOURNAL PAPERS

Citations

- [Google Scholar](#)
- [Web of Science](#)
- [ResearcherID](#)
- [PubMed](#)
- [Europe PubMed Central](#)

2015

11. **Morota G**, Peñagaricano F, Petersen JL, Ciobanu DC, Tsuyuzaki K, and Nikaido I. An application of MeSH enrichment analysis in livestock. *Animal Genetics*. In press.
10. Abdollahi-Arpanahi R, **Morota G**, Valente BD, Kranis A, Rosa GJM, and Gianola D. (2015) Assessment of bagging GBLUP for whole genome prediction of broiler chicken traits. *Journal of Animal Breeding and Genetics*. Early View.
9. Tsuyuzaki K, **Morota G**, Ishii M, Nakazato T, Miyazaki S, and Nikaido I. (2015) MeSH ORA framework: R/Bioconductor packages to support MeSH over-representation analysis. *BMC Bioinformatics*. **16**:45 .

Pre-Morota lab publications

2014

8. **Morota G** and Gianola D. (2014) Kernel-based whole-genome prediction of complex traits: a review. *Frontiers in Genetics*. **5**:363 .
7. **Morota G**, Boddhireddy P, Vukasinovic N, Gianola D and DeNise S. (2014) Kernel-based variance components estimation and whole-genome prediction of pre-corrected phenotypes and progeny tests for dairy cow health traits. *Frontiers in Genetics*. **5**:56 .

6. **Morota G**, Abdollahi-Arpanahi R, Kranis A and Gianola D. (2014) Genome-enabled prediction of broiler traits in chickens using genomic annotation. *BMC Genomics*. **15**:109
 5. Abdollahi-Arpanahi R, Pakdel A, Nejati-Javaremi A, Moradi-Shahrbabak M, **Morota G**, Valente BD, Kranis A, Rosa GJM, and Gianola D. (2014) Dissection of additive genetic variability for quantitative traits in chickens using SNP markers. *Journal of Animal Breeding and Genetics*. **131**:183-193.
 4. Abdollahi-Arpanahi R, Nejati-Javaremi A, Pakdel A, Moradi-Shahrbabak M, **Morota G**, Valente BD, Kranis A, Rosa GJM, and Gianola D. (2014) Effect of allele frequencies, effect sizes and number of markers on prediction of quantitative traits in chickens. *Journal of Animal Breeding and Genetics*. **131**:123-133
- 2013
3. **Morota G**, Koyama M, Rosa GJM, Weigel KA, and Gianola D. (2013) Predicting complex traits using a diffusion kernel on genetic markers with an application to dairy cattle and wheat data. *Genetics Selection Evolution*. **45**:17.
 2. **Morota G** and Gianola D. (2013) Evaluation of linkage disequilibrium in wheat with an L1 regularized sparse Markov network. *Theoretical and Applied Genetics*. **126**:1991-2002.
- 2012
1. **Morota G**, Valente BD, Rosa GJM, Weigel KA, and Gianola D. (2012) An assessment of linkage disequilibrium in Holstein cattle using a Bayesian network. *Journal of Animal Breeding and Genetics*. **129**:474-487. ★ **Highlighted in the Genomic Selection Virtual Issue.**

PAPERS IN PROCEEDINGS

- 2014
3. Gianola D, **Morota G**, and Crossa J. (2014) Genome-enabled Prediction of Complex Traits with Kernel Methods: What Have We Learned? Proceedings, 10th World Congress of Genetics Applied to Livestock Production. August 17-22, Vancouver, BC, Canada. [PDF](#)
 2. Valente BD, **Morota G**, Rosa GJM and Gianola D and Weigel KA (2014) Causal meaning of genomic predictors: Implication on genome-enabled selection modeling. Proceedings, 10th World Congress of Genetics Applied to Livestock Production. August 17-22, Vancouver, BC, Canada. [PDF](#)
- 2011
1. Bueno Filho JS*, **Morota G***, Tran Q, Maenner MJ, Vera-Cala LM, Engelman CD, and Meyers KJ. (2011) Analysis of human mini-exome sequencing data from Genetic & Analysis Workshop 17 using a Bayesian hierarchical mixture model. *BMC Proceedings*, **5**(Suppl 9):S93. *equal contribution

INVITED PRESENTATIONS

- 2015
4. **Morota G**. Quantitative genetics in the functional genomics era. Animal Breeding & Genetics Seminar. Iowa State University. March 3.

- 2014 3. **Morota G.** Quantitative genetics in the functional genomics era. Special Seminar. PIC, Inc., Hendersonville TN. November 12.
- 2013 2. **Morota G.** Whole-genome prediction of complex traits using kernel methods. Department of Animal Science, University of Nebraska-Lincoln. December 19.
- 2011 1. **Morota G.** OBIHIRO GCOE Animal Global Health Seminar. Obihiro University of Agriculture and Veterinary Medicine. January 7.

CONTRIBUTED PRESENTATIONS

- 2015 3. **Morota G.**, Peñagaricano F, Petersen JL, Ciobanu DC, Tsuyuzaki K, and Nikaido I. An application of MeSH enrichment analysis in livestock. ADSA-ASAS Joint Annual Meeting. Rosen Shingle Creek, Orlando FL. July 12-16.
2. **Morota G.** Prediction of complex quantitative traits using functional annotations and bootstrap aggregating. Special Seminar. National Livestock Breeding Center, Shirakawa Japan. January 10.
- 2012 1. **Morota G.**, Rosa GJM, Weigel KA, and Gianola D. Application of Bayesian and Sparse Network Models for Assessing Linkage Disequilibrium in Animals and Plants. 26th International Biometric Conference. Kobe International Conference Center, Kobe Japan. August 26-31. <http://secretariat.ne.jp/ibc2012/30Aug.html#aug-30-14:00-Contributed36>. ★ **Second Oral Prize Winners.**

POSTERS

- 2015 • **Morota G.** Estimating genomic heritability in the presence of population stratification. NGS Field 4th Meeting. Tsukuba International Congress Center, Tsukuba Japan. July 1-3.
- 2013 • **Morota G.**, Tsuyuzaki K, and Nikaido I. MeSHR: R/Bioconductor package for finding statistically overrepresented MeSH terms in a set of genes. Annual Bioconductor Conference BioC 2013. July 18-19, Seattle, USA. <https://secure.bioconductor.org/BioC2013/posters.php#8>.
- **Morota G.** Predicting complex traits using a diffusion kernel on genetic markers with an application to dairy cattle and wheat data. Annual Bioconductor Conference BioC 2013. July 18-19, Seattle, USA. <https://secure.bioconductor.org/BioC2013/posters.php#7>.

INTRAMURAL SEMINARS

- 2014 • Animal Genetics Seminar. University of Nebraska-Lincoln. September 18.
- Ph.D. Thesis Defense. University of Wisconsin-Madison. May 12.
- Dairy Science Graduate Seminar. University of Wisconsin-Madison. February 14.
- 2013 • Special Seminar. Zoetis, Inc., Kalamazoo, Michigan USA. August 8.

- 2012 • Animal Breeding & Genomics Seminar. University of Wisconsin-Madison. April 10.
- 2011 • Master's Thesis Defense. University of Wisconsin-Madison. December 5.
- 2010 • Animal Breeding & Genomics Seminar. University of Wisconsin-Madison. November 30.
- Animal Breeding & Genomics Seminar. University of Wisconsin-Madison. March 23.
- 2008 • Animal Breeding & Genomics Seminar. University of Wisconsin-Madison. November 25.

TEACHING **University of Wisconsin-Madison**, Madison, Wisconsin USA

Teaching Assistant
 ANSCI/DYSCI 363: Principles of Animal Breeding **Spring, 2011**

Teaching Assistant
 ANSCI/DYSCI 361: Introduction to Animal and Veterinary Genetics **Spring, 2011**

RESEARCH SUPPORT

Internal Funding

- Layman Award - \$9,910.00 UNL
 PI: Gota Morota **June 1, 2015 - May 31, 2016**
 Proposal: Cracking the Blackbox of Whole-genome Prediction: Genome Partitioning of Predictive Ability
 Role: Principal Investigator

SERVICE ACTIVITIES

Departmental

- 2016 • Spring 2016 Animal Genetics Seminar organizer. Department of Animal Science, University of Nebraska-Lincoln
- 2015 • Fall 2015 Animal Genetics Seminar organizer. Department of Animal Science, University of Nebraska-Lincoln

OSS
CONTRIBUTIONS

- R packages
- [dkDNA](http://cran.r-project.org/web/packages/dkDNA/index.html): <http://cran.r-project.org/web/packages/dkDNA/index.html>
- Bioconductor packages
- [meshr](#)
 - [MeSH.db](#)
 - [MeSH.AOR.db](#)

- [MeSH.PCR.db](#)
- [org.MeSH.XXX.db](#) (120 packages)
 - org.MeSH.Aca.db
 - org.MeSH.Aga.PEST.db
 - org.MeSH.Ame.db
 - org.MeSH.Aml.db
 - org.MeSH.Ana.db
 - org.MeSH.Ani.FGSC.db
 - org.MeSH.Ath.db
 - org.MeSH.Atu.K84.db
 - org.MeSH.Bfl.db
 - org.MeSH.Bsu.168.db
 - org.MeSH.Bsu.Bsn5.db
 - org.MeSH.Bsu.RONN1.db
 - org.MeSH.Bsu.TUB10.db
 - org.MeSH.Bsu.W23.db
 - org.MeSH.Bta.db
 - org.MeSH.Cal.SC5314.db
 - org.MeSH.Cbr.db
 - org.MeSH.Cel.db
 - org.MeSH.Cfa.db
 - org.MeSH.Cin.db
 - org.MeSH.Cja.db
 - org.MeSH.Cpo.db
 - org.MeSH.Cre.db
 - org.MeSH.Dan.db
 - org.MeSH.Dda.3937.db
 - org.MeSH.Ddi.AX4.db
 - org.MeSH.Der.db
 - org.MeSH.Dgr.db
 - org.MeSH.Dme.db
 - org.MeSH.Dmo.db
 - org.MeSH.Dpe.db
 - org.MeSH.Dre.db
 - org.MeSH.Dse.db
 - org.MeSH.Dsi.db
 - org.MeSH.Dvi.db
 - org.MeSH.Dya.db
 - org.MeSH.Eco.536.db
 - org.MeSH.Eco.55989.db
 - org.MeSH.Eco.APEC01.db
 - org.MeSH.Eco.B.REL606.db
 - org.MeSH.Eco.BW2952.db
 - org.MeSH.Eco.CFT073.db
 - org.MeSH.Eco.E24377A.db
 - org.MeSH.Eco.ED1a.db
 - org.MeSH.Eco.HS.db
 - org.MeSH.Eco.IAI1.db
 - org.MeSH.Eco.IAI39.db
 - org.MeSH.Eco.K12.DH10B.db
 - org.MeSH.Eco.K12.MG1655.db
 - org.MeSH.Eco.KO11FL.db
 - org.MeSH.Eco.O103.H2.12009.db
 - org.MeSH.Eco.O111.H.11128.db
 - org.MeSH.Eco.O127.H6.E2348.69.db
 - org.MeSH.Eco.O157.H7.EC4115.db
 - org.MeSH.Eco.O157.H7.EDL933.db
 - org.MeSH.Eco.O157.H7.Sakai.db
 - org.MeSH.Eco.O157.H7.TW14359.db
 - org.MeSH.Eco.O26.H11.11368.db
 - org.MeSH.Eco.O26.H7.CB9615.db
 - org.MeSH.Eco.S88.db
 - org.MeSH.Eco.SE11.db
 - org.MeSH.Eco.SMS35.db
 - org.MeSH.Eco.UMN026.db
 - org.MeSH.Eco.UTI89.db
 - org.MeSH.Eqc.db
 - org.MeSH.Gga.db
 - org.MeSH.Gma.db
 - org.MeSH.Hsa.db
 - org.MeSH.Laf.db
 - org.MeSH.Lma.db
 - org.MeSH.Mdo.db
 - org.MeSH.Mes.db
 - org.MeSH.Mga.db
 - org.MeSH.Miy.db
 - org.MeSH.Mml.db
 - org.MeSH.Mmu.db
 - org.MeSH.Mtr.db
 - org.MeSH.Nle.db
 - org.MeSH.Oan.db

- org.MeSH.Ocu.db
- org.MeSH.Oni.db
- org.MeSH.Osa.db
- org.MeSH.Pab.db
- org.MeSH.Pae.LESB58.db
- org.MeSH.Pae.PA14.db
- org.MeSH.Pae.PA7.db
- org.MeSH.Pae.PAO1.db
- org.MeSH.Pfa.3D7.db
- org.MeSH.Pto.db
- org.MeSH.Ptr.db
- org.MeSH.Rno.db
- org.MeSH.Sau.COL.db
- org.MeSH.Sau.ED98.db
- org.MeSH.Sau.M013.db
- org.MeSH.Sau.MRSA252.db
- org.MeSH.Sau.MSHR1132.db
- org.MeSH.Sau.MSSA476.db
- org.MeSH.Sau.Mu3.db
- org.MeSH.Sau.Mu50.db
- org.MeSH.Sau.MW2.db
- org.MeSH.Sau.N315.db
- org.MeSH.Sau.Newman.db
- org.MeSH.Sau.RF122.db
- org.MeSH.Sau.USA300FPR3757.db
- org.MeSH.Sau.USA300TCH1516.db
- org.MeSH.Sau.VC40.db
- org.MeSH.Sce.S288c.db
- org.MeSH.Sco.A32.db
- org.MeSH.Sil.db
- org.MeSH.Spo.972h.db
- org.MeSH.Spu.db
- org.MeSH.Ssc.db
- org.MeSH.Syn.db
- org.MeSH.Tbr.9274.db
- org.MeSH.Tgo.ME49.db
- org.MeSH.Tgu.db
- org.MeSH.Vvi.db
- org.MeSH.Xla.db
- org.MeSH.Xtr.db
- org.MeSH.Zma.db

Github

- <https://github.com/morota>

ADDITIONAL TRAINING

- | | |
|-----------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 2014-2015 | • Participant of the Research Development Fellows Program (RDFP) |
| 2014 | • Participant of Fall 2014 Adopting Research Based Instructional Strategies for Enhancing (ARISE) Professional Development Programs - Just in Time Teaching (JiTT) |

PARTICIPATION IN MEETINGS, SYMPOSIUMS AND WORKSHOPS

- | | |
|------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 2014 | <ul style="list-style-type: none"> • Sheep Genomics Workshop. University of Nebraska-Lincoln. November 13-14. • NCERA-225. Implementation and Strategies for National Beef Cattle Genetic Evaluation. Bozeman, Montana. October 23-24. |
|------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|

- 19th Summer Institute in Statistical Genetics: “Module 23: Advanced Quantitative Genetics ”. University of Washington. July 23-25. Taught by Mike Goddard and Peter Visscher.
 - 19th Summer Institute in Statistical Genetics: “Module 19: Statistical & Quantitative Genetics of Disease”. University of Washington. July 21-23. Taught by John Witte and Naomi Wray.
 - UC Davis Bioinformatics Training Program: “Using Galaxy for Analysis of High Throughput Sequence Data”. University of California, Davis. June 16-20. Taught by the Bioinformatics Core.
 - Short course: “Evolutionary Quantitative Genetics”. University of Wisconsin-Madison. May 19-23. Taught by Bruce Walsh.
- 2013
- Short course: “Statistical methods for prediction of complex traits using whole-genome molecular markers”. University of Wisconsin-Madison. May 27-31. Taught by Daniel Gianola and Gustavo de los Campos.
- 2012
- Short course: “Introduction to genome-enabled selection & Inferring causal phenotype networks using structural equation models”. Kyoto University. August 31. Taught by Guilherme J.M. Rosa.
 - Short course: “Identifying Genes for Complex and Mendelian Traits Using Next Generation Sequence Data”. 26th International Biometric Conference. August 26. Taught by Suzanne Leal.
 - Short course: “Programming and computer algorithms with focus on genomic selection in animal breeding”. University of Georgia. May 15 - June 1. Taught by Ignacy Misztal, Shogo Tsuruta, Ignacio Aguilar, Zulma Vitezica, and Andres Legarra.
- 2009
- Symposium: “Statistical Genetics of Livestock for the Post-Genomic Era (SGLPGE)”. University of Wisconsin-Madison. May 4-6.
- 2006
- Short course: “Estimation of Variance Components in Animal Breeding”. Obihiro University of Agriculture and Veterinary Medicine. November. Taught by Shogo Tsuruta.
- COMPUTER SKILLS
- Programming Languages: Python, Fortran
 - Statistical/Numerical Computational Tools: R, Octave
 - Content-description Languages: XML, XHTML, CSS, \LaTeX
 - Operating Systems: Linux and Mac OS X
- MISCELLANEOUS
- Languages: English and Japanese
 - Courses taken for credits at the University of Wisconsin-Madison
 - Spring 2012
 - Animal Sciences 875-004: Topics in Analysis of Quantitative Genomic Data (Daniel Gianola)

- Dairy Science 875-005: Parallel Programming & High Performance Computing (Xiao-Lin Nick Wu)
- Fall 2011
 - Dairy Science 875-005: Molecular Aspects of Animal Breeding (Hasan Khatib)
 - Statistics 840: Statistical Model Building and Learning (Grace Wahba)
- Spring 2011
 - Mathematics 609: Mathematical Methods in Systems Biology (Gheorghe Craciun)
 - Statistics 610: Introduction to Statistical Inference (Chunming Zhang)
 - Statistics 992-001: Statistical Methods for QTL Mapping (Karl Broman)
- Fall 2010
 - Statistics 609: Mathematical Statistics I (Chunming Zhang)
 - Statistics 701: Applied Time Series Analysis, Forecasting & Control I (Yazhen Wang)
 - Statistics 775: Introduction to Bayesian Decision & Control (Kam-Wah Tsui)
- Summer 2010
 - Population Health Sciences 904: Analytic Methods in Genetic Epidemiology (Corinne Engelman, Karl Broman, Bret Payseur, Kristin Meyers)
- Spring 2010
 - Animal Sciences 875: Linear Models with Applications in Biology and Agriculture (Daniel Gianola)
 - Statistics 850: Theory & Application of Regression and Analysis of Variance II (Wei-Yin Loh)
- Fall 2009
 - Computer Science 576: Introduction to Bioinformatics (Colin Dewey)
 - Dairy Science 875-006: Design & Analysis of Microarray Experiments in Agriculture (Guilherme J. M. Rosa)
 - Dairy Science 875-011: Introduction to Bayesian Data Analysis with R (Xiao-Lin Nick Wu)
 - Genetics 629: Evolutionary Genetics (John Doebley, Bret Larget, Bret Payseur)
 - Statistics 849: Theory & Application of Regression and Analysis of Variance I (Sunduz Keles)
- Summer 2009
 - Computer Science 367: Introduction to Data Structure
- Spring 2009
 - Agronomy 771: Experimental Design (Mike Casler)
 - Agronomy 772: Applications in ANOVA (Mike Casler)
 - Mathematics 222: Calculus and Analytic Geometry
 - Statistics 771: Statistical Computing (Michael Newton)
- Fall 2008
 - Statistics 424: Statistical Experimental Design for Engineers (Peter Z. G. Qian)
 - Statistics 541: Introduction to Biostatistics (Ismael Fischer)
 - Zoology 645: Modeling in Population Genetics & Evolution (Andrew Peters)
- Summer 2008
 - Computer Science 302: Introduction to Programming
 - Mathematics 431: Introduction to the Theory of Probability