CONTACT INFORMATION

A218f Animal Science Building
Department of Animal Science
University of Nebraska-Lincoln
Lincoln, NE 68583-0908 USA

E-mail: morota@unl.edu
Phone: TBA
WWW: 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.

PROFESSIONAL POSITIONS

Department of Animal Science
University of Nebraska-Lincoln, Lincoln, Nebraska USA

Assistant Professor (70% Research & 30% Teaching)   **Start date: 08/2014**

WORK EXPERIENCE

Department of Animal Sciences
University of Wisconsin-Madison, Madison, Wisconsin USA

Graduate Research Assistant   **06/2011 - 05/2014**

Animal Genetics Research & Development Group
Zoetis, Inc., Kalamazoo, Michigan USA

Quantitative Geneticist (student internship)   **06/2013 - 11/2013**

EDUCATION

University of Wisconsin-Madison, Madison, Wisconsin USA

Ph.D., Animal Sciences, May 2014

- 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

- 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

- Thesis: "Genetic Analysis of Threshold Traits."
- Advisor: Prof. Dr. Mitsuyoshi Suzuki

Professional society memberships	• American Society of Animal Science 2014 - Present • Japanese Society of Animal Breeding and Genetics 2013 - Present • The International Biometric Society (ENAR) 2012 - Present
Editorial Activities	Ad hoc Reviewer for: Computers and Electronics in Agriculture, DNA Research, Scientia Agricola Number of reviewed papers: 2012 (1), 2013 (1), 2014 (1)
Manuscripts in review	**9**. **Morota G** and Gianola D. Kernel-based whole-genome prediction of complex traits: a review. **8**. Valente BD, **Morota G**, Peñagaricano F, Rosa GJM, Gianola D, and Weigel KA. The causal meaning of genomic predictors and how it affects construction and comparison of genome-enabled selection models. *BioRxiv doi: 10.1101/001511* , *arXiv: http://arxiv.org/abs/1401.1165*
Peer reviewed journal papers	As of August 2014, 13 citations total, h-index of 2, i10-index of 0 on Google Scholar and 6 citations total, h-index of 2 according to Web of Science.
2014	**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 ⋆ **Highly accessed.** **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.* doi: 10.1111/jbg.12079 **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.* doi: 10.1111/jbg.12075
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. ⋆ **Highly accessed.** **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**(8):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**(6):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.
	2. Valente BD, **Morota G**, Rosa GJM and Gianola D and Weigel KA (2014) The causal meaning of genomic predictors and how it affects the construction and comparison of genome-enabled selection models. Proceedings, 10th World Congress of Genetics Applied to Livestock Production. August 17-22, Vancouver, BC, Canada.
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	My PDF presentation slides are available on SlideShare (http://www.slideshare.net/chikudaisei/).
2013	**2.** Department of Animal Science, University of Nebraska-Lincoln, Nebraska, USA.
2011	**1.** OBIHIRO GCOE Animal Global Health Seminar. Obihiro University of Agriculture and Veterinary Medicine, Obihiro, Hokkaido Japan
CONFERENCE ABSTRACTS	
<u>Contributed</u>	
2012	• **Morota G**, Rosa GJM, Weigel KA, and Gianola D. (2012) Application of Bayesian and Sparse Network Models for Assessing Linkage Disequilibrium in Animals and Plants. 26th International Biometric Conference. August 26-31, Kobe, Japan. http://secretariat.ne.jp/ibc2012/30Aug.html#aug-30-14:00-Contributed36. ⋆ **Second Oral Prize Winners.**
<u>Posters</u>	
2013	• **Morota G**, Tsuyuzaki K, and Nikaido I. (2013) 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**. (2013) 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.
DEPARTMENTAL SEMINARS	
2014	• Ph.D. Thesis Defense. University of Wisconsin-Madison.
	• Dairy Science Graduate Seminar. University of Wisconsin-Madison.

2013	• Special Seminar. Zoetis, Inc., Kalamazoo, Michigan USA.
2012	• Animal Breeding & Genomics Seminar. University of Wisconsin-Madison.
2011	• Master's Thesis Defense. University of Wisconsin-Madison.
2010	• Animal Breeding & Genomics Seminar. University of Wisconsin-Madison.
2008	• Animal Breeding & Genomics Seminar. University of Wisconsin-Madison.

PARTICIPATION IN SYMPOSIUMS AND WORKSHOPS

2014
- 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 Conponents in Animal Breeding". Obihiro University of Agriculture and Veterinary Medicine. November. Taught by Shogo Tsuruta.

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**

R packages
- dkDNA: 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.Ddi.AX4.db
- org.MeSH.Aga.PEST.db	- org.MeSH.Der.db
- org.MeSH.Ame.db	- org.MeSH.Dgr.db
- org.MeSH.Aml.db	- org.MeSH.Dme.db
- org.MeSH.Ana.db	- org.MeSH.Dmo.db
- org.MeSH.Ani.FGSC.db	- org.MeSH.Dpe.db
- org.MeSH.Ath.db	- org.MeSH.Dre.db
- org.MeSH.Atu.K84.db	- org.MeSH.Dse.db
- org.MeSH.Bfl.db	- org.MeSH.Dsi.db
- org.MeSH.Bsu.168.db	- org.MeSH.Dvi.db
- org.MeSH.Bsu.Bsn5.db	- org.MeSH.Dya.db
- org.MeSH.Bsu.RONN1.db	- org.MeSH.Eco.536.db
- org.MeSH.Bsu.TUB10.db	- org.MeSH.Eco.55989.db
- org.MeSH.Bsu.W23.db	- org.MeSH.Eco.APEC01.db
- org.MeSH.Bta.db	- org.MeSH.Eco.B.REL606.db
- org.MeSH.Cal.SC5314.db	- org.MeSH.Eco.BW2952.db
- org.MeSH.Cbr.db	- org.MeSH.Eco.CFT073.db
- org.MeSH.Cel.db	- org.MeSH.Eco.E24377A.db
- org.MeSH.Cfa.db	- org.MeSH.Eco.ED1a.db
- org.MeSH.Cin.db	- org.MeSH.Eco.HS.db
- org.MeSH.Cja.db	- org.MeSH.Eco.IAI1.db
- org.MeSH.Cpo.db	- org.MeSH.Eco.IAI39.db
- org.MeSH.Cre.db	- org.MeSH.Eco.K12.DH10B.db
- org.MeSH.Dan.db	- org.MeSH.Eco.K12.MG1655.db
- org.MeSH.Dda.3937.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

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 (Ismor 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

REFERENCES   References and additional information available upon request.