Mohammad Ali Nilforooshan

CONTACT
INFORMATION

LIC, Private Bag 3016, Hamilton 3240, New Zealand
E-mail: mohammad.nilforooshan@lic.co.nz
Website: https://nilforooshan.github.io
ORCiD: https://orcid.org/0000-0003-0339-5442
Google Scholar: https://goo.gl/iKbCoU
GitHub: https://github.com/nilforooshan

INTERESTS

Matrix Algebra
Statistical methods applied to livestock genetic and genomic evaluation
Putting biology into equations and equations into program codes
Single-step genomic evaluation
Computational biology
Travelling

EDUCATION

Swedish University of Agricultural Sciences, Dept. Animal Breeding and Genetics
PhD in Animal Breeding and Genetics – Quantitative Genetics, June 2007 – May 2011

AWARDS

- Grant from Interbull Centre for participation in the 9th World Congress on Genetics Applied to Livestock Production (2010), Leipzig, Germany
- Grant from FUR foundation (SLU funds for internationalization of postgraduate studies) for participation in the 60th Annual meeting of the European Association for Animal Production (2009), Barcelona, Spain
- Scholarship from the Guest Scholarship Program (2008) of the Swedish Institute
- Grant from FUR foundation (SLU funds for internationalization of postgraduate studies) for participation in the 59th Annual meeting of the European Association for Animal Production (2008), Vilnius, Lithuania

SKILLS

Scientific: Matrix Algebra, Quantitative Genetics and General Animal Breeding, Statistics, Reviewer for scientific journals
Programming: R, SAS, Fortran, Bash, Sed, Awk, Python, Markdown and RMarkdown, Wiki Markup, LaTeX, Git and GitHub, Docker, Julia, and C (beginner)
Analytics: Designing, streamlining and documenting genetic/genomic evaluation pipelines; experienced in several computer packages such as ASReml, DFReml, MiX99 and BLUPF90; experienced in cloud computing (AWS)

POSITIONS

LIC
Scientist – Quantitative Genetics   May 2020 – Present

Postdoctoral Research Fellow in Quantitative Genetics   December 2018 – May 2020

University of Otago, Dept. Mathematics and Statistics
Postdoctoral Fellow in Quantitative Genetics   November 2015 – October 2018

Swedish University of Agricultural Sciences,
Dept. Animal Breeding and Genetics, Interbull Centre
Geneticist   June 2012 – October 2015

University of Nebraska-Lincoln, Dept. Statistics
Postdoctoral Research Fellow in Computational Biology   September 2011 – May 2012

Isfahan Science and Technology Town, Animal Science Core
Research Assistant   September 2004 – June 2006

TEACHING
- Webinar: An introduction to the single-step method for livestock genetic evaluation. Gorgan University of Agricultural Sciences and Natural Resources, Iran, 21 October, 2024.
- Member of an MSc student's advisory panel, University of Texcoco, December, 2023.
- Supervising a visiting PhD student to the Department of Mathematics and Statistics, University of Otago, August – October, 2018.
- Teaching some lectures of the postgraduate course in Quantitative Genetics, held at the University of Otago, Dunedin, New Zealand, July – October, 2018.
- Teaching some lectures of the postgraduate course in Quantitative Genetics, held at the University of Otago, Dunedin, New Zealand, July – October, 2017.
- Teaching R programming, and giving several other talks in the University of Chapingo, Texcoco, Mexico, April 2015.
- Teaching "Dairy Cattle Husbandry" in Kabootar-Abad school of Agriculture, Isfahan, Iran, September 2004 – June 2005.

SOFTWARE
- **Nilforooshan, M.A.** 2024. R package FnR: Inbreeding and Numerator Relationship Coefficients.
- **Nilforooshan, M.A.** 2024. R package pedMermaid: Pedigree Mermaid Syntax.
- **Nilforooshan, M.A.** 2020. R package pedSimulate: Pedigree, Genetic Merit, Phenotype, and Genotype Simulation.
- **Nilforooshan, M.A.** 2019. R package mbend: Matrix Bending.
- **Nilforooshan, M.A.** 2019. R package ggroups: Pedigree and Genetic Groups.

REVIEW AND EDITORIAL CONTRIBUTIONS
- Acting reviewer for many peer-reviewed journals.
- Associate Editor of the *New Zealand Journal of Agricultural Research*.
- Topic Editor of the special issue "Reducing the Environmental Footprint of Livestock Through Genomic Selection" in *Frontiers in Genetics – Section Livestock Genomics*.

PUBLICATIONS
- Velez Labrada, J.L., P. Pérez-Rodríguez, **M.A. Nilforooshan**, A. Ruíz-Flores. 2025. Comparison of machine learning methods for predicting genomic breeding values for growth traits in Braunvieh cattle. *Revista Mexicana de Ciencias Pecuarias* 16(1): 179–193. https://doi.org/10.22319/rmcp.v16i1.6616
- **Nilforooshan, M.A.**, A. Ruíz-Flores, P. Pérez-Rodríguez, T. Pabiou, L.A. Saavedra-Jiménez, and J.E. Valerio-Hernández. 2025. Multitrait analysis of growth traits for the optimization of breeding value prediction in Braunvieh cattle. *Revista Mexicana de Ciencias Pecuarias* 16(1): 55–68. https://doi.org/10.22319/rmcp.v16i1.6648
- **Nilforooshan, M.A.** 2024. FnR: R package for computing inbreeding and numerator relationship coefficients. *BMC Ecology and Evolution* 24: 99. https://doi.org/10.1186/s12862-024-02285-4
- **Nilforooshan, M.A.** 2024. Short Communication: Reduced GBLUP equations to core animals in the algorithm for proven and young (APY). *Veterinary and Animal Science* 23: 100334. https://doi.org/10.1016/j.vas.2024.100334
- Valerio-Hernández, J.E., P. Pérez-Rodríguez, **M.A. Nilforooshan**, and A. Ruíz-Flores. 2023. Single-step genomic evaluation for growth traits in a Mexican Braunvieh cattle population. *Animal Bioscience* 36(7): 1003–1009. https://doi.org/10.5713/ab.22.0158
- **Nilforooshan, M.A.** 2023. Technical note: Extension of the reduced animal model to single-step methods. *Journal of Animal Science* 101: skac272. https://doi.org/10.1093/jas/skac272

- **Nilforooshan, M.A.** 2022. The algorithm for proven and young (APY) from a different perspective. *bioRxiv.* https://doi.org/10.1101/2022.11.23.517757
- **Nilforooshan, M.A.** 2022. A note on the conditioning of the $\mathbf{H}^{-1}$ matrix used in single-step GBLUP. *Animals* 12: 3208. https://doi.org/10.3390/ani12223208
- **Nilforooshan, M.A.**, and A. Ruíz-Flores. 2022. Understanding factors influencing the estimated genetic variance and the distribution of breeding values. *Frontiers in Genetics* 13: 1000228. https://doi.org/10.3389/fgene.2022.1000228
- **Nilforooshan, M.A.** 2022. pedSimulate – An R package for simulating pedigree, genetic merit, phenotype, and genotype data. *Revista Brasileira de Zootecnia* 51: e20210131. https://doi.org/10.37496/rbz5120210131
- **Nilforooshan, M.A.** 2022. Compensating for the increase in the sum of eigenvalues and monitoring the bending performance for conditioning covariance matrices in multi-trait livestock evaluations. *animal - Open Space* 1(1): 100005. https://doi.org/10.1016/j.anopes.2022.100005
- **Nilforooshan, M.A.** 2022. A new computational approach to Henderson's method of computing the inverse of a numerator relationship matrix. *Livestock Science* 257: 104848. https://doi.org/10.1016/j.livsci.2022.104848
- **Nilforooshan, M.A.**, and H. Jorjani. 2022. INVITED REVIEW: A quarter of a century—International genetic evaluation of dairy sires using MACE methodology. *Journal of Dairy Science* 105(1): 3–21. https://doi.org/10.3168/jds.2021-20927
- Lee, A.M., S-A. Newman, K.G. Dodds, **M.A. Nilforooshan**, B. Auvray, S. McIntyre, and D. Campbell. 2021. Genomic evaluations of sheep in New Zealand. *New Zealand Journal of Animal Science and Production* 81: 106–111.
- Saavedra-Jiménez, L.A., R. Ramírez-Valverde, R. Núñez-Domínguez, A. Ruíz-Flores, J.G. García-Muñiz, and **M.A. Nilforooshan**. 2021. Effect of two phantom parent grouping strategies on the genetic evaluation of growth traits in Mexican Braunvieh cattle. *Revista Mexicana de Ciencias Pecuarias* 12(3): 878–892. https://doi.org/10.22319/rmcp.v12i3.5562
- Harris, B., E. Reynolds, C. Couldrey, **M.A. Nilforooshan**, A. Winkelman, and R. Sherlock. 2021. Genomic evaluations for crossbreed dairy cattle. *Journal of Dairy Science* 104(Supplement 1): 356. S148.
- **Nilforooshan, M.A.**, D. Garrick, and B. Harris. 2021. Alternative ways of computing the numerator relationship matrix. *Frontiers in Genetics* 12: 1236. https://doi.org/10.3389/fgene.2021.655638
- **Nilforooshan, M.A.**, and D. Garrick. 2021. Reduced animal models fitting only equations for phenotyped animals. *Frontiers in Genetics* 12: 372. https://doi.org/10.3389/fgene.2021.637626
- **Nilforooshan, M.A.** 2020. mbend: An R package for bending non-positive-definite symmetric matrices to positive-definite. *BMC Genetics* 21: 97. https://doi.org/10.1186/s12863-020-00881-z
- **Nilforooshan, M.A.**, and L.A. Saavedra-Jiménez. 2020. ggroups: An R package for pedigree and genetic groups data. *Hereditas* 157: 17. https://doi.org/10.1186/s41065-020-00124-2
- **Nilforooshan, M.A.** 2020. Memory-efficient self-cross-product for large matrices using R and Python. *Journal of Mathematical and Computational Science* 10(3): 497–506. https://doi.org/10.28919/jmcs/4457
- **Nilforooshan, M.A.** 2020. Updating genetic relationship matrices and their inverses: A methodology note. *Canadian Journal of Animal Science* 100(2): 292–298. https://doi.org/10.1139/CJAS-2019-0106
- **Nilforooshan, M.A.** 2020. Application of single-step GBLUP in New Zealand Romney sheep. *Animal Production Science* 60(9): 1136–1144. https://doi.org/10.1071/AN19315
- **Nilforooshan, M.A.**, and M. Lee. 2019. The quality of the algorithm for proven and young with various sets of core animals in a multibreed sheep population. *Journal of Animal Science* 97(3): 1090–1100. https://doi.org/10.1093/jas/skz010
- **Nilforooshan, M.A.**, J.H. Jakobsen, W.F. Fikse, B. Berglund, and H. Jorjani. 2014. Multiple-trait multiple-country genetic evaluation of Holstein bulls for female fertility and milk production traits. *animal* 8(6): 887–894. https://doi.org/10.1017/S1751731114000895
- Behdad, S., M.A. Edriss, **M.A. Nilforooshan**, and A.H. Movassagh. 2013. Wool characteristics of Bakhtiari sheep and the correlated responses to selection for pre-weaning daily gain. *Indian*

Journal of Animal Science 83(1): 82–85.

- **Nilforooshan, M.A.** 2011. Multiple-trait multiple country genetic evaluation of fertility traits in dairy cattle. Uppsala : Sveriges lantbruksuniv., *Acta Universitatis Agriculturae Sueciae*, 1652-6880; 2011:31. ISBN 978-91-576-7566-8. Doctoral thesis.

- **Nilforooshan, M.A.**, W.F. Fikse, B. Berglund, J.H. Jakobsen, and H. Jorjani. 2011. Short communication: Quantifying bias in a single-trait international model ignoring covariances from multiple-trait national models. *Journal of Dairy Science* 94(5): 2631–2636. https://doi.org/10.3168/jds.2010-3863

- **Nilforooshan, M.A.**, J.H. Jakobsen, W.F. Fikse, B. Berglund, and H. Jorjani. 2010. Application of a multiple-trait, multiple-country genetic evaluation model for female fertility traits. *Journal of Dairy Science* 93(12): 5977–5986. https://doi.org/10.3168/jds.2010-3437

- **Nilforooshan, M.A.** 2010. Contemporary grouping in mixed-size dairy herds experiencing four seasons. *Turkish Journal of Veterinary & Animal Sciences* 34(2): 129–135. https://doi.org/10.3906/vet-0710-18

- **Nilforooshan, M.A.**, A. Khazaeli, and M.A. Edriss. 2008. Effects of missing pedigree information on dairy cattle genetic evaluations (short communication). *Archives Animal Breeding* 51(2): 99–110. https://doi.org/10.5194/aab-51-99-2008

- Edriss, M.A., P. Hosseinia, M. Edrisi, H.R. Rahmani, and **M.A. Nilforooshan**. 2008. Prediction of second parity milk performance of dairy cows from first parity information using artificial neural network and multiple linear regression methods. *Asian Journal of Animal and Veterinary Advances* 3(4): 222–229. https://doi.org/10.3923/ajava.2008.222.229

- Hosseinia, P., M. Edrisi, M.A. Edriss, and **M.A. Nilforooshan**. 2007. Prediction of second parity milk yield and fat percentage of dairy cows based on first parity information using neural network system. *Journal of Applied Sciences* 7(21): 3274–3279. https://doi.org/10.3923/jas.2007.3274.3279

- Edriss, M.A., G. Dashab, A.A. Ghare Aghaji, **M.A. Nilforooshan**, and H. Movasagh. 2007. A study on some physical attributes of Naeini sheep wool for textile industry. *Pakistan Journal of Biological Sciences* 10(3): 415–420. https://doi.org/10.3923/pjbs.2007.415.420

- **Nilforooshan, M.A.**, and M.A. Edriss. 2007. Comparison of Holstein bull semen sources on milk traits in Isfahan province in Iran. *Archives Animal Breeding* 50(1): 71–83. https://doi.org/10.5194/aab-50-71-2007

- Edriss, M.A., **M.A. Nilforooshan**, and J.M. Sadeghi. 2006. Estimation of direct genetic and maternal effects for production traits of Iranian Holstein cows using different animal models. *Pakistan Journal of Biological Sciences* 9(4): 636–640. https://doi.org/10.3923/pjbs.2006.636.640

- Dashab, G., M.A. Edriss, A.A. Ghare Aghaji, H. Movasagh, and **M.A. Nilforooshan**. 2006. Wool fiber quality of Naeini sheep. *Pakistan Journal of Biological Sciences* 9(2): 270–276. https://doi.org/10.3923/pjbs.2006.270.276

- **Nilforooshan, M.A.**, and M.A. Edriss. 2004. Effect of age at first calving on some productive and longevity traits in Iranian Holsteins of the Isfahan province. *Journal of Dairy Science* 87(7): 2130–2135. https://doi.org/10.3168/jds.S0022-0302(04)70032-6

- **Nilforooshan, M.A.** 2003. Genetic Evaluation and Comparison between Domestic and Imported (Canada, USA, Europe) Sperms for Milk Yield, Fat Yield, and Fat Percentage in Some Dairy Farms of Isfahan Province. MSc thesis. https://doi.org/10.5281/zenodo.4297235

DATA AND CODE

- **Nilforooshan, M.A.** 2023. Code & Data – A GBLUP to produce ssGBLUP solutions for genotyped animals. *figshare.* https://doi.org/10.6084/m9.figshare.28502144.v1

- **Nilforooshan, M.A.** 2023. Code & Data – Genomic evaluations reduced to equations for core animals in the algorithm for proven and young (APY). *figshare.* https://doi.org/10.6084/m9.figshare.20539650.v3

- **Nilforooshan, M.A.** 2022. Code & Data – A note on the conditioning of the $\mathbf{H}^{-1}$ matrix used in single-step GBLUP. *Mendeley Data.* https://doi.org/10.17632/cn9jzpj7fg.1

- **Nilforooshan, M.A.** 2022. Code & Data – Understanding factors influencing the estimated genetic variance and the distribution of breeding values. *Mendeley Data.* https://doi.org/10.

[17632/zd3xx54j62.3](https://doi.org/10.17632/zd3xx54j62.3)

- **Nilforooshan, M.A.** 2022. Reduced Animal Model for ssGBLUP. *figshare.* https://doi.org/10.6084/m9.figshare.16455681.v2
- **Nilforooshan, M.A.** 2022. Code & data — Further improvement of bending performance for conditioning covariance matrices. *Mendeley Data.* https://doi.org/10.17632/gnyrym4mv4.3
- **Nilforooshan, M.A.** 2022. Twenty simulated pedigrees with different combinations of three parameters using R package pedSimulate. *Mendeley Data.* https://doi.org/10.17632/c4pv8w8pmp.2
- **Nilforooshan, M.A.** 2021. Code – A new computational approach to Henderson's method for computing the inverse of a numerator relationship matrix. *Mendeley Data.* https://doi.org/10.17632/db9pd7ns6d.2
- **Nilforooshan, M.A.**, D. Garrick, and B. Harris. 2021. Code & Data – Alternative Ways of Computing the Numerator Relationship Matrix. *figshare.* https://doi.org/10.6084/m9.figshare.13497939.v1
- **Nilforooshan, M.A.**, and D. Garrick. 2021. R examples – Reduced Animal Models Fitting Only Equations for Phenotyped Animals. *figshare.* https://doi.org/10.6084/m9.figshare.13369607.v1
- **Nilforooshan, M.A.** 2020. mbend: Data, Code & Results. *Mendeley Data.* https://doi.org/10.17632/kf3d8v8939.1
- **Nilforooshan, M.A.** 2019. Benchmarking matrix self-cross-products, using R and Python functions. *Mendeley Data.* https://doi.org/10.17632/vk8vy7ghnf.1

PROCEEDINGS

- Wang, Y., K.M. Tiplady, E.G.M. Reynolds, **M.A. Nilforooshan**, C. Couldrey, and B.L. Harris. 2023. Genomic prediction with selected sequence variants in gestation length of New Zealand dairy cattle. *74th Annual meeting of the European Association for Animal Production*, Lyon, France. August 26 – September 1, 2023. Book of Abstracts No. 29. {slides file}
- Harris, B.L., R.G. Sherlock, and **M.A. Nilforooshan**. 2022. Large-scale multiple-trait single-step marker model implementation. *Proceeding of 12th World Congress on Genetics Applied to Livestock Production (WCGALP)*, Rotterdam, The Netherlands. July, 3–8, 2022. pp. 1360–1363. https://doi.org/10.3920/978-90-8686-940-4_324
- **Nilforooshan, M.A.**, B. Auvray, and M. Lee. 2018. Animal-specific combining of the GRM and the NRM in single-step GBLUP. *11th World Congress on Genetics Applied to Livestock Production*, Auckland, New Zealand. February, 11–16, 2018. {poster file}
- Pabiou, T., **M.A. Nilforooshan**, E. Venot, and K. Moore. 2015. Interbeef presents new opportunities for beef farmers. *British Cattle Conference*, Telford, England. January 19–21, 2015.
- Pabiou, T., **M.A. Nilforooshan**, D. Laloe, E. Hjerpe, and E. Venot. 2014. Across-Country Genetic Parameters in Beef Cattle for Interbeef Weaning Weight Genetic Evaluation. *10th World Congress on Genetics Applied to Livestock Production*, Vancouver, Canada. August, 17–22, 2014. {poster file}
- Venot, E., T. Pabiou, E. Hjerpe, **M.A. Nilforooshan**, A. Launay, and B. Wickham. 2014. Benefits of Interbeef International Genetic Evaluations for Weaning Weight. *10th World Congress on Genetics Applied to Livestock Production*, Vancouver, Canada. August, 17–22, 2014.
- Mäntysaari, E., and **M.A. Nilforooshan**. 2014. Effect of the size of the reference population on the validation reliability of national genomic evaluations. *Interbull Meeting*, Berlin, Germany. May 20–21, 2014.
- **Nilforooshan, M.A.** 2014. A review of the validation of national genomic evaluations. *Interbull Bulletin.* 48: 111–117. *Interbull Meeting*, Berlin, Germany. May 20–21, 2014. {slides file}
- **Nilforooshan, M.A.**, and E. Hjerpe. 2014. Interbeef report on weaning genetic evaluation, performed in March 2014 for Charolais and Limousin. *Interbeef Technical Meeting*, Uppsala, Sweden. March 10, 2014.
- Braillon, L., and **M.A. Nilforooshan**. 2013. Review of the Interbeef proof publication proposal. *Interbeef Technical Meeting*, Nantes, France. August 27, 2013.
- **Nilforooshan, M.A.**, E. Hjerpe, V. Palucci, and J. Dürr. 2013. Interbeef report on weaning genetic evaluation for Charolais and Limousin. *Interbeef Technical Meeting*, Aarhus, Denmark.

March 27–28, 2013.

- **Nilforooshan, M.A.** 2012. Report on the weaning weight phenotypic data editing for Charolais and Limousin. *Interbeef Technical Meeting*, Uppsala, Sweden. December 6–7, 2012.
- Jorjani, H., J. Jakobsen, **M.A. Nilforooshan**, E. Hjerpe, B. Zumbach, V. Palucci, and J. Dürr. 2011. Genomic Evaluation of BSW Populations. InterGenomics: Results and Deliverables. *Interbull Bulletin.* 43: 5–8. *Interbull Technical Workshop*, Guelph, Ontario, Canada. February 27–28, 2011. {slides file}
- **Nilforooshan, M.A.**, L. Rönnegård, and H. Jorjani. 2010. Various statistical models for prediction of SNP effects from a multi-national/breed reference population. *9th World Congress on Genetics Applied to Livestock Production*, Leipzig, Germany. August 1–6, 2010. {poster file}
- **Nilforooshan, M.A.**, B. Zumbach, J. Jakobsen, A. Loberg, H. Jorjani, and J. Dürr. 2010. Validation of national genomic evaluations. *Interbull Bulletin.* 42: 56–61. *Interbull Meeting*, Riga, Latvia. May 31 to June 4, 2010. {slides file}
- **Nilforooshan, M.A.** 2009. Developing the method of estimating genetic similarity between populations. *60th Annual meeting of the European Association for Animal Production*, Barcelona, Spain. August 21–24, 2009. Book of Abstracts No. 15: 610. {poster file}
- **Nilforooshan, M.A.**, J. Jakobsen, F. Fikse, B. Berglund, and H. Jorjani. 2009. MT–MACE for female fertility and milk yield. *Interbull Bulletin.* 40: 68–71. *Interbull Meeting*, Barcelona, Spain. August 21–24, 2009. {slides file}
- **Nilforooshan, M.A.** 2009. International genetic evaluations of fertility traits using MT–MACE. Faculty research day, Faculty of Veterinary Medicine and Animal Science, Swedish University of Agricultural Sciences, Uppsala, Sweden. December 7, 2009.
- **Nilforooshan, M.A.** 2009. International genetic evaluations of fertility traits using MT–MACE. 80th Anniversary of the Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden, June 4, 2009.
- **Nilforooshan, M.A.**, J. Jakobsen, F.W. Fikse, B. Berglund, and H. Jorjani. 2009. International genetic evaluations for female fertility traits using multi-trait MACE. *Interbull Bulletin.* 39:99–102. Interbull Workshop on Genomic Information in Genetic Evaluations, Uppsala, Sweden. January 26–29, 2009. {slides file}
- **Nilforooshan, M.A.**, F.W. Fikse, and H. Jorjani. 2008. International genetic evaluations of fertility traits considering more than one trait per country. *59th Annual meeting of the European Association for Animal Production*, Vilnius, Lithuania. August 24–27, 2008. Book of Abstracts No. 14: 268. {slides file}

EXTENSION   Papers in Farsi