

# Mohammad Ali Nilforooshan

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CONTACT INFORMATION	LIC, Private Bag 3016, Hamilton 3240, New Zealand E-mail: <a href="mailto:mohammad.nilforooshan@lic.co.nz">mohammad.nilforooshan@lic.co.nz</a> Website: <a href="https://nilforooshan.github.io">https://nilforooshan.github.io</a> ORCID: <a href="https://orcid.org/0000-0003-0339-5442">https://orcid.org/0000-0003-0339-5442</a> Google Scholar: <a href="https://goo.gl/iKbCoU">https://goo.gl/iKbCoU</a> GitHub: <a href="https://github.com/nilforooshan">https://github.com/nilforooshan</a>	
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 Traveling	
EDUCATION	<b>Swedish University of Agricultural Sciences, Dept. Animal Breeding and Genetics</b> PhD in Animal Breeding and Genetics – Quantitative Genetics, June 2007 – May 2011	
AWARDS	<ul style="list-style-type: none"> <li>• Grant from Interbull Centre for participation in the 9th World Congress on Genetics Applied to Livestock Production (2010), Leipzig, Germany</li> <li>• 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</li> <li>• Scholarship from the Guest Scholarship Program (2008) of the <a href="#">Swedish Institute</a></li> <li>• 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</li> </ul>	
SKILLS	<b>Scientific:</b> Matrix Algebra, Quantitative Genetics and General Animal Breeding, Statistics, Reviewer for scientific journals <b>Programming:</b> R, SAS, Fortran, Linux Shell scripting (Sed and Awk), Python, Markdown and RMarkdown, Wiki Markup, L <sup>A</sup> T <sub>E</sub> X, Git and GitHub, Docker, Julia, and C (beginner) <b>Analytics:</b> Designing, streamlining and documenting genetic/genomic evaluation pipelines; experienced in several computer packages such as ASReml, DFReml, MiX99 and BLUPF90	
CURRENT POSITION	<b>LIC</b> <i>Scientist – Quantitative Genetics</i>	May 2020 – Present
PREVIOUS POSITIONS	<b>LIC</b> <i>Postdoctoral Research Fellow in Quantitative Genetics</i>	December 2018 – May 2020
	<b>University of Otago, Dept. Mathematics and Statistics</b> <i>Postdoctoral Fellow in Quantitative Genetics</i>	November 2015 – October 2018
	<b>Swedish University of Agricultural Sciences,</b> Dept. Animal Breeding and Genetics, Interbull Centre <i>Geneticist</i>	June 2012 – October 2015
	<b>University of Nebraska-Lincoln, Dept. Statistics</b> <i>Postdoctoral Research Fellow in Computational Biology</i>	September 2011 – May 2012

## TEACHING

- 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.** 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 [gggroups](#): Pedigree and Genetic Groups.

## REVIEW AND EDITORIAL CONTRIBUTIONS

- Acting reviewer for many peer-reviewed journals.
- Frontiers in Genetics – Section Livestock Genomics: [Reducing the Environmental Footprint of Livestock Through Genomic Selection](#)

## PUBLICATIONS

- **Nilforooshan, M.A.** 2023. Technical note: Extension of the reduced animal model to single-step methods. *J. Anim. Sci.* 101: skac272. [doi:10.1093/jas/skac272](#)
- **Nilforooshan, M.A.** 2022. The algorithm for proven and young (APY) from a different perspective. *bioRxiv*. [doi: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. [doi:10.3390/ani12223208](#)
- **Nilforooshan, M.A.**, and A. Ruíz-Flores. 2022. Understanding factors influencing the estimated genetic variance and the distribution of breeding values. *Front. Genet.* 13: 1000228. [doi:10.3389/fgene.2022.1000228](#)
- **Nilforooshan, M.A.** 2022. pedSimulate – An R package for simulating pedigree, genetic merit, phenotype, and genotype data. *R. Bras. Zootec.* 51: e20210131. [doi: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. [doi: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. *Livest. Sci.* 257: 104848. [doi: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. *J. Dairy Sci.* 105(1): 3–21. [doi: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 J. Anim. Sci. Prod.* 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. *Rev. Mex. Cienc. Pec.* 12(3): 878–892. [doi: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. *J. Dairy Sci.* 104(Supplement 1): 356. [S148](#).

- **Nilforooshan, M.A.**, D. Garrick, and B. Harris. 2021. Alternative ways of computing the numerator relationship matrix. *Front. Genet.* 12: 1236. doi:10.3389/fgene.2021.655638
- **Nilforooshan, M.A.**, and D. Garrick. 2021. Reduced animal models fitting only equations for phenotyped animals. *Front. Genet.* 12: 372. doi:10.3389/fgene.2021.637626
- **Nilforooshan, M.A.** 2020. mbend: An R package for bending non-positive-definite symmetric matrices to positive-definite. *BMC Genet.* 21: 97. doi:10.1186/s12863-020-00881-z
- **Nilforooshan, M.A.**, and L.A. Saavedra-Jiménez. 2020. gggroups: An R package for pedigree and genetic groups data. *Hereditas* 157: 17. doi:10.1186/s41065-020-00124-2
- **Nilforooshan, M.A.** 2020. Memory-efficient self-cross-product for large matrices using R and Python. *J. Math. Comput. Sci.* 10(3): 497–506. doi:10.28919/jmcs/4457
- **Nilforooshan, M.A.** 2020. Updating genetic relationship matrices and their inverses: A methodology note. *Can. J. Anim. Sci.* 100(2): 292–298. doi:10.1139/CJAS-2019-0106
- **Nilforooshan, M.A.** 2020. Application of single-step GBLUP in New Zealand Romney sheep. *Anim. Prod. Sci.* 60(9): 1136–1144. doi: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. *J. Anim. Sci.* 97(3): 1090–1100. doi: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. doi: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 J. Anim. Sci.* 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. *J. Dairy Sci.* 94(5): 2631–2636. doi: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. *J. Dairy Sci.* 93(12): 5977–5986. doi:10.3168/jds.2010-3437
- **Nilforooshan, M.A.** 2010. Contemporary grouping in mixed-size dairy herds experiencing four seasons. *Turk. J. Vet. Anim. Sci.* 34(2): 129–135. doi: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). *Arch. Tierz., Dummerstorf* 51(2): 99–110. doi: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 J. Anim. Vet. Adv.* 3(4): 222–229. doi: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. *J. Applied Sci.* 7(21): 3274–3279. doi: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. *Pak. J. Biol. Sci.* 10(3): 415–420. doi: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. *Arch. Tierz., Dummerstorf* 50(1): 71–83. doi: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. *Pak. J. Biol. Sci.* 9(4): 636–640. doi: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. *Pak. J. Biol. Sci.* 9(2): 270–276. doi: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. *J. Dairy Sci.* 87(7): 2130–2135. doi: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. doi:10.5281/zenodo.4297235

#### DATA AND CODE

- **Nilforooshan, M.A.** 2022. Code & Data – A note on the conditioning of the  $\mathbf{H}^{-1}$  matrix used in single-step GBLUP. *Mendeley Data*. doi: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*. doi:10.17632/zd3xx54j62.3
- **Nilforooshan, M.A.** 2022. Code & Data – Genomic evaluations reduced to equations for core animals in the algorithm for proven and young (APY). *figshare*. doi:10.6084/m9.figshare.20539650.v2
- **Nilforooshan, M.A.** 2022. Reduced Animal Model for ssGBLUP. *figshare*. doi:10.6084/m9.figshare.1645568
- **Nilforooshan, M.A.** 2021. Code & data — Further improvement of bending performance for conditioning covariance matrices. *Mendeley Data*. doi:10.17632/gnyrym4mv4.3
- **Nilforooshan, M.A.** 2021. Code – A new computational approach to Henderson’s method for computing the inverse of a numerator relationship matrix. *Mendeley Data*. doi:10.17632/db9pd7ns6d.2
- **Nilforooshan, M.A.** 2021. Twenty simulated pedigrees with different combinations of three parameters using R package pedSimulate. *Mendeley Data*. doi:10.17632/c4pv8w8pmp.2
- **Nilforooshan, M.A.**, D. Garrick, and B. Harris. 2021. Code & Data – Alternative Ways of Computing the Numerator Relationship Matrix. *figshare*. doi: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*. doi:10.6084/m9.figshare.13369607.v1
- **Nilforooshan, M.A.** 2021. mbend: Data, Code & Results. *Mendeley Data*. doi:10.17632/kf3d8v8939.1
- **Nilforooshan, M.A.** 2021. Benchmarking matrix self-cross-products, using R and Python functions. *Mendeley Data*. doi:10.17632/vk8vy7ghnf.1

#### PROCEEDINGS

- Harris, B.L., R.G. Sherlock, and **M.A. Nilforooshan**. 2022. Large-scale multiple-trait single-step marker model implementation. *12th World Congress on Genetics Applied to Livestock Production*, Rotterdam, The Netherlands. July, 3–8, 2022.
- **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}](#)