

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	<ul style="list-style-type: none"> 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, L ^A T _E X, 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, DFRe ml, MiX99 and BLUPF90; experienced in cloud computing (AWS)
POSITIONS	LIC <i>Scientist – Quantitative Genetics</i> May 2020 – Present <i>Postdoctoral Research Fellow in Quantitative Genetics</i> December 2018 – May 2020 University of Otago , Dept. Mathematics and Statistics <i>Postdoctoral Fellow in Quantitative Genetics</i> November 2015 – October 2018 Swedish University of Agricultural Sciences , Dept. Animal Breeding and Genetics, Interbull Centre <i>Geneticist</i> June 2012 – October 2015 University of Nebraska-Lincoln , Dept. Statistics <i>Postdoctoral Research Fellow in Computational Biology</i> September 2011 – May 2012

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 [gggroups](#): 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](https://doi.org/10.3168/jds.2021-20927).
- **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. gggroups: 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 lantbruksuniversitet, *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. Khazaali, 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. Hosseini, 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>
- Hosseini, 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](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 – 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>
- **Nilforooshan, M.A.** 2022. Reduced Animal Model for ssGBLUP. *figshare*. <https://doi.org/10.6084/m9.figshare.20539650.v3>

[6084/m9.figshare.16455681.v2](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}](#)