Mohammad Ali Nilforooshan

Quantitative Geneticist
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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, Department of Animal Breeding and Genetics
PhD in Animal Breeding and Genetics – Quantitative Genetics June 2007 – May 2011

AWARDS

- Travel grant from Interbull Centre for participation in the 9th World Congress on Genetics Applied to Livestock Production (2010), Leipzig, Germany
- Travel 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
- PhD scholarship from the Guest Scholarship Program (2008) of the Swedish Institute
- Travel 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, Git, GitHub, Docker, and Julia
- **Analytics:** Designing, streamlining and documenting genetic/genomic evaluation pipelines; experienced in several computer packages such as ASReml, DFReml, MiX99, BLUPF90, and APEX; experienced in cloud computing (AWS)
- **Typesetting & documentation:** Markdown, RMarkdown, Wiki Markup, LaTeX, and Typst

POSITIONS

LIC, Hamilton, New Zealand
R&D Division
Scientist – Quantitative Genetics May 2020 – Present
Postdoctoral Research Fellow in Quantitative Genetics December 2018 – May 2020

University of Otago, Dunedin, New Zealand
Department of Mathematics and Statistics
Postdoctoral Fellow in Quantitative Genetics November 2015 – October 2018

Swedish University of Agricultural Sciences, Uppsala, Sweden
Interbull Centre, Department of Animal Breeding and Genetics
Geneticist June 2012 – October 2015

University of Nebraska-Lincoln, NE, USA
Department of Statistics
Postdoctoral Research Fellow in Computational Biology September 2011 – May 2012

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

TEACHING

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

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*.

SOFTWARE

Nilforooshan, M. A. (2024a). R package FnR: Inbreeding and Numerator Relationship Coefficients. https://CRAN.R-project.org/package=FnR

Nilforooshan, M. A. (2024b). R package pedMermaid: Pedigree Mermaid Syntax. https://CRAN.R-project.org/package=pedMermaid

Nilforooshan, M. A. (2020). R package pedSimulate: Pedigree, Genetic Merit, Phenotype, and Genotype Simulation. https://CRAN.R-project.org/package=pedSimulate

Nilforooshan, M. A. (2019a). R package mbend: Matrix Bending. https://CRAN.R-project.org/package=mbend

Nilforooshan, M. A. (2019b). R package ggroups: Pedigree and Genetic Groups. https://CRAN.R-project.org/package=ggroups

PUBLICATIONS

Vélez, J. L., Pérez-Rodríguez, P., **Nilforooshan, M. A.**, & Ruíz Flores, A. (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., Ruíz-Flores, A., Pérez-Rodríguez, P., Pabiou, T., Saavedra-Jiménez, L. A., & Valerio-Hernández, J. E. (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. (2024a). FnR: R package for computing inbreeding and numerator relationship coefficients. *BMC Ecology and Evolution*, *24*(1), 99. https://doi.org/10.1186/s12862-024-02285-4

Nilforooshan, M. A. (2024b). 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., Ruíz-Flores, A., **Nilforooshan, M. A.**, & Pérez-Rodríguez, P. (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. (2023a). 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. (2023b). The algorithm for proven and young (APY) from a different perspective. *bioRxiv*, 2022.11.23.517757. https://doi.org/10.1101/2022.11.23.517757

Nilforooshan, M. A. (2022a). A note on the conditioning of the H^{-1} matrix used in single-step GBLUP. *Animals*, *12*(22), 3208. https://doi.org/10.3390/ani12223208

Nilforooshan, M. A. & Ruíz-Flores, A. (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. (2022b). 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. (2022c). 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. (2022d). 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. & Jorjani, H. (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, M. A., Newman, S.-A., Dodds, K. G., **Nilforooshan, M. A.**, Auvray, B., McIntyre, S., & Campbell, D. (2021). Genomic evaluations of sheep in New Zealand. *New Zealand Journal of Animal Science and Production*, *81*, 106–111. http://www.nzsap.org/proceedings/genomic-evaluations-sheep-new-zealand

Saavedra-Jiménez, L. A., Ramírez-Valverde, R., Núñez-Domínguez, R., Ruíz-Flores, A., García-Muñiz, J. G., & **Nilforooshan, M. A.** (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., Reynolds, E., Couldrey, C., **Nilforooshan, M. A.**, Winklm, A., & Sherlock, R. (2021). Genomic evaluations for crossbreed dairy cattle. *Journal of Dairy Science*, *104*(Supplement 1), 356. https://www.adsa.org/Portals/0/SiteContent/Docs/Meetings/2021ADSA/ADSA2021_Abstracts.pdf

Nilforooshan, M. A., Garrick, D., & Harris, B. (2021a). Alternative ways of computing the numerator relationship matrix. *Frontiers in Genetics*, *12*, 1236. https://doi.org/10.3389/fgene.2021.655638

Nilforooshan, M. A. & Garrick, D. (2021a). 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. (2020a). 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. & Saavedra-Jiménez, L. A. (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. (2020b). 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. (2020c). 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. (2020d). 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. & Lee, M. (2019). The quality of the algorithm for proven and young with various sets of core animals in a multi-breed sheep population. *Journal of Animal Science*, *97*(3), 1090–110. https://doi.org/10.1093/jas/skz010

Nilforooshan, M. A., Jakobsen, J. H., Fikse, W. F., Berglund, B., & Jorjani, H. (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., Edriss, M. A., **Nilforooshan, M. A.**, & Movassagh, A. H. (2013). Wool characteristics of Bakhtiari sheep and the correlated responses to selection for pre-weaning daily gain. *Indian Journal of Animal Sciences*, *83*(1), 82–85. http://epubs.icar.org.in/ejournal/index.php/IJAnS/article/view/26453

Nilforooshan, M. A. (2011). *Multiple-trait multiple country genetic evaluation of fertility traits in dairy cattle* (Publication No. 2011:31) [Doctoral dissertation, Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala]. https://res.slu.se/id/publ/33755

Nilforooshan, M. A., Fikse, W. F., Berglund, B., Jakobsen, J. H., & Jorjani, H. (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., Jakobsen, J. H., Fikse, W. F., Berglund, B., & Jorjani, H. (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 and Animal Sciences*, *34*(2), 129–135. https://doi.org/10.3906/vet-0710-18

Nilforooshan, M. A., Khazaeli, A., & Edriss, M. A. (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., Hosseinnia, P., Edrisi, M., Rahmani, H. R., & **Nilforooshan, M. A.** (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., Edrisi, M., Edriss, M. A., & **Nilforooshan, M. A.** (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., Dashab, G., Ghareh Aghaji, A. A., **Nilforooshan, M. A.**, & Movassagh, H. (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. & Edriss, M. A. (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., **Nilforooshan, M. A.**, & Sadeghi, J. M. (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., Edriss, M. A., Ghare Aghaji, A. A., Movasagh, H., & **Nilforooshan, M. A.** (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. & Edriss, M. A. (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* [Master's thesis, Isfahan (Khorasgan) Azad University, Isfahan]. https://doi.org/10.5281/zenodo.4297235

DATA AND CODE

Nilforooshan, M. A. (2025). Code & Data – A GBLUP to produce ssGBLUP solutions for genotyped animals. *figshare*. https://doi.org/10.6084/m9.figshare.28502144

Nilforooshan, M. A. (2023c). 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. (2022e). Code & Data – A note on the conditioning of the H^{-1} matrix used in single-step GBLUP. *Mendeley Data*. https://doi.org/10.17632/cn9jzpj7fg.1

Nilforooshan, M. A. (2022f). 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. (2022g). Reduced animal model for ssGBLUP. *figshare*. https://doi.org/10.6084/m9.figshare.16455681.v2

Nilforooshan, M. A. (2022h). Code & Data — Further improvement of bending performance for conditioning covariance matrices. *Mendeley Data*. https://doi.org/10.17632/gnyrym4mv4.3

Nilforooshan, M. A. (2022i). 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., Garrick, D., & Harris, B. (2021b). Code & Data – Alternative ways of computing the numerator relationship matrix. *figshare*. https://doi.org/10.6084/m9.figshare.13497939.v1

Nilforooshan, M. A. & Garrick, D. (2021b). R examples – Reduced animal models fitting only equations for phenotyped animals. *figshare*. https://doi.org/10.6084/m9.figshare.13369607.v1

Nilforooshan, M. A. (2020e). 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., Tiplady, K. M., Reynolds, E. G. M., **Nilforooshan, M. A.**, Couldrey, C., & Harris, B. L. (2023, August 26–September 1). Genomic prediction with selected sequence variants in gestation length of New Zealand dairy cattle [Slides file, Abstract file]. In *Proceedings of the 74th Annual meeting of the European Association for Animal Production, Lyon, France* (p. 164, Vol. 29).

Harris, B. L., Sherlock, R. G., & **Nilforooshan, M. A.** (2022, July 3–8). Large-scale multiple-trait single-step marker model implementation. In *Proceeding of the 12th World Congress on Genetics Applied to Livestock Production, Rotterdam, The Netherlands* (pp. 1360–1363). https://doi.org/10.3920/978-90-8686-940-4_324

Nilforooshan, M. A., Auvray, B., & Lee, M. (2018, February 11–16). Animal-specific combining of the GRM and the NRM in single-step GBLUP [Poster file, Paper file]. In *Proceeding of the 11th World Congress on Genetics Applied to Livestock Production, Auckland, New Zealand* (pp. 1360–1363).

Pabiou, T., **Nilforooshan, M. A.**, Venot, E., & Moore, K. (2015, January 19–21). Interbeef presents new opportunities for beef farmers [Paper file]. In *British Cattle Conference, Telford, England* (pp. 15–18).

Pabiou, T., **Nilforooshan, M. A.**, Laloe, D., Hjerpe, E., & Venot, E. (2014, August 17–22). Across-country genetic parameters in beef cattle for Interbeef weaning weight genetic evaluation [Poster file, Paper file]. In *Proceeding of the 10th World Congress on Genetics Applied to Livestock Production, Vancouver, Canada.*

Venot, E., Pabiou, T., Hjerpe, E., **Nilforooshan, M. A.**, Launay, A., & Wickham, B. (2014, August 17–22). Benefits of Interbeef international genetic evaluations for weaning weight [Paper file]. In *Proceeding of the 10th World Congress on Genetics Applied to Livestock Production, Vancouver, Canada.*

Mäntysaari, E., & **Nilforooshan, M. A.** (2014, May 20–21). Effect of the size of the reference population on the validation reliability of national genomic evaluations [Slides file]. In *Interbull Meeting, Berlin, Germany.*

Nilforooshan, M. A. (2014, May 20–21). A review of the validation of national genomic evaluations [Slides file, Paper file]. In *Interbull Bulletin, Berlin, Germany* (pp. 111–117, Vol. 48).

Nilforooshan, M. A. & Hjerpe, E. (2014, March 10). Interbeef report on weaning genetic evaluation performed in March 2014 for Charolais and Limousin. In *Interbeef Technical Meeting, Uppsala, Sweden.*

Braillon, L., & **Nilforooshan, M. A.** (2013, August 27). Review of the Interbeef proof publication proposal [Slides file]. In *Interbeef Technical Meeting, Nantes, France.*

Nilforooshan, M. A., Hjerpe, E., Palucci, V., & Dürr, J. (2013, March 27–28). Interbeef report on weaning genetic evaluation for Charolais and Limousin [Slides file]. In *Interbeef Technical Meeting, Aarhus, Denmark.*

Nilforooshan, M. A. (2012, December 6–7). Report on the weaning weight phenotypic data editing for Charolais and Limousin [Slides file]. In *Interbeef Technical Meeting, Uppsala, Sweden.*

Jorjani, H., Jakobsen, J., **Nilforooshan, M. A.**, Hjerpe, E., Zumbach, B., Palucci, V., & Dürr, J. (2011, February 27–28). Genomic evaluation of BSW populations. InterGenomics: Results and deliverables [Slides file, Paper file]. In *Interbull Bulletin, Guelph, Ontario, Canada* (pp. 5–8, Vol. 43).

Nilforooshan, M. A., Rönnegård, L., & Jorjani, H. (2010, August 1–6). Various statistical models for prediction of SNP effects from a multi-national/breed reference population [Poster file, Paper file]. In *Proceeding of the 9th World Congress on Genetics Applied to Livestock Production, Leipzig, Germany.*

Nilforooshan, M. A., Zumbach, B., Jakobsen, J., Loberg, A., Jorjani, H., & Dürr, J. (2010, May 31–June 4). Validation of national genomic evaluations [Slides file, Paper file]. In *Interbull Bulletin, Riga, Latvia* (pp. 56–61, Vol. 42).

Nilforooshan, M. A., Jakobsen, J., Fikse, F., Berglund, B., & Jorjani, H. (2009, August 21–24). MT-MACE for female fertility and milk yield [Slides file, Paper file]. In *Interbull Bulletin, Barcelona, Spain* (pp. 68–71, Vol. 40).

Nilforooshan, M. A. (2009a, December 7). International genetic evaluations of fertility traits using MT-MACE [Poster file]. In *Faculty research day, Faculty of Veterinary Medicine and Animal Science, Swedish University of Agricultural Sciences, Uppsala, Sweden.*

Nilforooshan, M. A. (2009b, June 4). International genetic evaluations of fertility traits using MT-MACE [Poster file]. In *The 80th Anniversary of the Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Uppsala, Sweden.*

Nilforooshan, M. A., Jakobsen, J., Fikse, F. W., Berglund, B., & Jorjani, H. (2009, January 26–29). International genetic evaluations for female fertility traits using multi-trait MACE [Slides file, Paper file]. In *Interbull Bulletin, Uppsala, Sweden* (pp. 99–102, Vol. 39).

Nilforooshan, M. A., Fikse, F. W., & Jorjani, H. (2008, August 24–27). International genetic evaluations of fertility traits considering more than one trait per country [Slides file, Abstract file]. In *Proceeding of the 59th Annual meeting of the European Association for Animal Production, Vilnius, Lithuania* (p. 268, Vol. 14).

EXTENSION

Papers in Farsi