

Dr. Deniz Akdemir

STATISTICAL GENOMICS AND GENOMIC ASSISTED BREEDING

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Core Skills

- **Statistical Genomics:** Genomic selection, multi-trait methodologies, genomic prediction, GWAS, models for epistasis and genotype by environment interactions, optimization of plant and animal breeding programs.
- **Statistics:** Multivariate analysis, high-dimensional data modeling, Bayesian methods, machine learning, deep learning, data science, biostatistics.
- **Statistical Computation:** Proficient in R, SAS, Python and C++ for statistical programming and analysis.
- **Software Development:** Development of research and commercial grade software.
- **Management and administration:** Strategic planning, project management, team leadership, grant/patent writing, budgeting, accounting.
- **Languages:** English (fluent), Turkish (native).

Career Summary

- **Senior Clinical Data Scientist, National Marrow Donor Program, Minneapolis, USA (2023 - Current):** Engaged in statistical and machine learning analysis of stem cell transplant data, focusing on research into donor optimization. Applied for grants and submitted manuscripts to peer-reviewed journals. Wrote patent applications.
- **Clinical Data Scientist, National Marrow Donor Program, Minneapolis, USA (2021 - 2023):** Engaged in statistical and machine learning analysis of stem cell transplant data, focusing on research into donor optimization.
- **Postdoctoral Research Associate, School of Agriculture and Food Science, University College Dublin, Dublin, Ireland (2019 - 2021):** Conducted research on methods for combining heterogeneous genomic and phenotypic datasets and prepared statistical software for data analysis.
- **Statistical Consultant, Cornell Statistical Consulting Unit, Cornell University, Ithaca, NY, USA (2017 - 2019):** Provided statistical consulting services for researchers at Cornell University, including the preparation and presentation of statistics workshops.
- **Postdoctoral Research Associate, Department of Plant Breeding and Genetics, Cornell University, Ithaca, NY, USA (2011 - 2017):** Focused on research developing new methodologies in genomic selection and prediction, mixed models, and machine learning, advising graduate students and preparing statistical software.
- **Visiting Assistant Professor, Department of Statistics and Actuarial Science, University of Central Florida, Orlando, FL, USA (2010 - 2011):** Responsibilities included teaching Data Mining Methodology, Theoretical Statistics, Applied Time Series Analysis, and Nonparametric Statistics.
- **Visiting Assistant Professor, Department of Mathematics and Statistics, Ohio Northern University, Ada, OH, USA (2009 - 2010):** Taught Statistics for Professionals, Statistics for Engineers, and Statistical Computing, catering to various undergraduate levels.

Workshops and Training Sessions

- **Genomic Assisted Breeding Workshops:** Conducted workshops in the USA, Ireland, Spain, and Belgium, educating the agricultural community on genomic technologies.
- **Public Speaking:** Presented at various international conferences including EFI conference in Geneva and ASHI Annual Meeting in San Antonio.

Publications

Akdemir, D., Auletta, J. J., Bupp, C., Maier, M., & Bolon, Y.-T. (2025). Establishment of a machine learning-based prediction framework to assess trade-offs in decisions that affect post-HCT outcomes. *Computers in Biology and Medicine*, 191, 110113.

- Akdemir, D., Knox, R., & Isidro y Sanchez, J. (2020). Combining partially overlapping multi-omics data in databases using relationship matrices. *Frontiers in Plant Science*, 11, 947. <https://doi.org/10.3389/fpls.2020.00947>
- Pinho Morais, P. P., Akdemir, D., Braatz de Andrade, L. R., Jannink, J.-L., Fritsche-Neto, R., Borem, A., ... Granato, I. S. C. (2020). Using public databases for genomic prediction of tropical maize lines. *Plant Breeding*, 139(4), 697–707. <https://doi.org/10.1111/pbr.12827>
- Akdemir, D., Beavis, W., Fritsche-Neto, R., Singh, A. K., & Isidro-Sanchez, J. (2019). Multi-objective optimized genomic breeding strategies for sustainable food improvement. *Heredity*, 122(5), 672–683. <https://doi.org/10.1038/s41598-018-38081-6>
- Akdemir, D., & Isidro-Sanchez, J. (2019). Design of training populations for selective phenotyping in genomic prediction. *Scientific Reports*, 9(1), 1–15. <https://doi.org/10.1038/s41598-018-38081-6>
- Ikeogu, U. N., Akdemir, D., Wolfe, M. D., Okeke, U. G., Chinedozi, A., Jannink, J.-L., & Egesi, C. N. (2019). Genetic correlation, genome-wide association and genomic prediction of portable NIRS predicted carotenoids in cassava roots. *Frontiers in Plant Science*, 10, 1570. <https://doi.org/10.3389/fpls.2019.01570>
- Kaya, H. B., Akdemir, D., Lozano, R., Cetin, O., Kaya, H. S., Sahin, M., ... Jannink, J.-L. (2019). Genome wide association study of 5 agronomic traits in olive (*olea europaea* l.). *Scientific Reports*, 9(1), 1–14. <https://doi.org/10.1038/s41598-019-55338-w>
- Fristche-Neto, R., Akdemir, D., & Jannink, J.-L. (2018). Accuracy of genomic selection to predict maize single-crosses obtained through different mating designs. *Theoretical and Applied Genetics*, 131(5), 1153–1162. <https://doi.org/10.1007/s00122-018-3068-8>
- Horn, L., Shimelis, H., Kariaga, M., Onamu, R., Wakhungu, J., Were, H., et al.others. (2018). Importance of cowpea production, breeding and production constrains under dry areas in africa. *RUFORUM Working Document Series*, 17(1), 499–514. <https://doi.org/10.1016/j.aoas.2020.03.002>
- Okeke, U. G., Akdemir, D., Rabbi, I., Kulakow, P., & Jannink, J.-L. (2018). Regional heritability mapping provides insights into dry matter content in african white and yellow cassava populations. *The Plant Genome*, 11(1), 170050. <https://doi.org/10.3835/plantgenome2017.06.0050>
- Akdemir, D., Jannink, J.-L., & Isidro-Sanchez, J. (2017). Locally epistatic models for genome-wide prediction and association by importance sampling. *Genetics Selection Evolution*, 49(1), 1–14. <https://doi.org/10.1186/s12711-017-0348-8>
- Isidro-Sanchez, J., Akdemir, D., & Montilla-Bascon, G. (2017). Genome-wide association analysis using r. In *Oat* (pp. 189–207). https://doi.org/10.1007/978-1-4939-6682-0_14
- Okeke, U. G., Akdemir, D., Rabbi, I., Kulakow, P., & Jannink, J.-L. (2017). Accuracies of univariate and multivariate genomic prediction models in african cassava. *Genetics Selection Evolution*, 49(1), 1–10. <https://doi.org/10.1101/116301>
- Stansell, Z., Akdemir, D., & Bjorkman. (2017). Use of a quality trait index to increase the reliability of phenotypic evaluations. *HortScience*, 52, 1490.
- Akdemir, D. (2016). Array normal model and incomplete array variate observations. In *Applied matrix and tensor variate data analysis* (pp. 93–122). https://doi.org/10.1007/978-4-431-55387-8_5
- Akdemir, D., & Sanchez, J. I. (2016). Efficient breeding by genomic mating. *Frontiers in Genetics*, 7, 210. <https://doi.org/10.3389/fgene.2016.00210>
- Ashraf, B., Edriss, V., Akdemir, D., Autrique, E., Bonnett, D., Crossa, J., ... Jannink, J.-L. (2016). Genomic prediction using phenotypes from pedigreed lines with no marker data. *Crop Science*, 56(3), 957–964. <https://doi.org/10.2135/cropsci2015.02.0111>
- Crossa, J., Jarquin, D., Franco, J., Perez-Rodriguez, P., Burgueno, J., Saint-Pierre, C., et al.others. (2016). Genomic prediction of gene bank wheat landraces. *G3: Genes, Genomes, Genetics*, 6(7), 1819–1834.
- Jafarzadeh, J., Bonnett, D., Jannink, J.-L., Akdemir, D., Dreisigacker, S., & Sorrells, M. E. (2016). Breeding value of primary synthetic wheat genotypes for grain yield. *PloS One*, 11(9), e0162860. <https://doi.org/10.1371/journal.pone.0162860>
- Jafarzadeh, J., Bonnett, D., Jannink, J.-L., Akdemir, D., & Sorrells, M. E. (2016). Determining the breeding value of primary synthetic wheats for increased grain yield. *PLOS ONE*, 11(9), e0162860. <https://doi.org/10.1371/journal.pone.0162860>
- Spindel, J., Begum, H., Akdemir, D., Collard, B., Redona, E., Jannink, J., & McCouch, S. (2016). Genome-wide prediction models that incorporate de novo GWAS are a powerful new tool for tropical rice improvement. *Heredity*, 116(4), 395–408. <https://doi.org/10.1038/hdy.2015.113>
- Akdemir, D., & Jannink, J.-L. (2015). Locally epistatic genomic relationship matrices for genomic association and prediction. *Genetics*, 199(3), 857–871. <https://doi.org/10.1534/genetics.114.173658>
- Akdemir, D., Sanchez, J. I., & Jannink, J.-L. (2015). Optimization of genomic selection training populations with a ge-

- netic algorithm. *Genetics Selection Evolution*, 47(1), 1–10. <https://doi.org/10.1186/s12711-015-0116-6>
- Isidro, J., Jannink, J.-L., Akdemir, D., Poland, J., Heslot, N., & Sorrells, M. E. (2015). Training set optimization under population structure in genomic selection. *Theoretical and Applied Genetics*, 128(1), 145–158. <https://doi.org/10.1186/s12711-015-0116-6>
- Spindel, J., Begum, H., Akdemir, D., Virk, P., Collard, B., Redona, E., ... McCouch, S. R. (2015). Genomic selection and association mapping in rice (*Oryza sativa*): Effect of trait genetic architecture, training population composition, marker number and statistical model on accuracy of rice genomic selection in elite, tropical rice breeding lines. *PLoS Genet*, 11(2), e1004982. <https://doi.org/10.1371/journal.pgen.1005350>
- Heslot, N., Akdemir, D., Sorrells, M. E., & Jannink, J.-L. (2014). Integrating environmental covariates and crop modeling into the genomic selection framework to predict genotype by environment interactions. *Theoretical and Applied Genetics*, 127(2), 463–480. <https://doi.org/10.2135/cropsci2014.03.0249>
- Yan, A., Edwards, J. D., Menda, N., Tecle, I. Y., Akdemir, D., Tiede, T., ... Jannink, J.-L. (2014). Zeabase: A data retrieval web-portal and bioinformatics platform for maize genomic selection. *BMC Bioinformatics*, 15(1). <https://doi.org/10.1186/s12859-014-0398-7>
- Akdemir, D., & Gupta, A. K. (2011). Array variate random variables with multiway kronecker delta covariance matrix structure. *Journal of Algebraic Statistics*, 2(1). <https://doi.org/10.18409/jas.v2i1.12>
- Roa, J. C., Tapia, O., Cakir, A., Basturk, O., Dursun, N., Akdemir, D., ... Adsay, N. V. (2011). Squamous cell and adenosquamous carcinomas of the gallbladder: Clinicopathological analysis of 34 cases identified in 606 carcinomas. *Modern Pathology*, 24(8), 1069–1078. <https://doi.org/10.1038/modpathol.2011.68>
- Akdemir, D., & Gupta, A. K. (2010). A matrix variate skew distribution. *European Journal of Pure and Applied Mathematics*, 3(2), 128–140. <https://doi.org/10.18409/jas.v2i1.12>
- Dursun, N., Roa, J., Tapia, O., Cakir, A., Coban, I., Basturk, O., ... Adsay, N. (2010). Intravesicular papillary-tubular neoplasm (IVPN) as a unifying category for mass-forming preinvasive neoplasms of the gallbladder: An analysis of 87 cases: Clinicopathologic and immunohistochemical analysis of 123 cases. *LABORATORY INVESTIGATION*, 90, 144A–144A. <https://doi.org/10.1097/pas.0b013e318262787c>
- Akdemir, D. (2003). *Components of response variance for cluster samples* (Master's thesis, Middle East Technical University; Vol. 37, pp. 9–12). <https://doi.org/10.5152/tpd.2013.03>

Education

- **PhD. in Statistics**, Bowling Green State University, Bowling Green, OH, USA, 2009.
- **M.A. in Applied Statistics**, Bowling Green State University, Bowling Green, OH, USA, 2004.
- **M.S. in Statistics**, Middle East Technical University, Ankara, Turkey, 2003.
- **B.A. in Business Administration**, Middle East Technical University, Ankara, Turkey, 1999.

Professional References

- **Dr. Yung-Tsi Bolon**
 - **Affiliation:** Director, Immunobiology & Bioinformatics Research, NMDP, Minneapolis, Minnesota, United States
 - **Relationship:** Supervisor at the National Marrow Donor Program
 - **Contact:** ybolon@nmdp.org
- **Dr. Julio Isidro-Sanchez**
 - **Affiliation:** Associate Professor: Centro de Biotecnología y Genómica de Plantas, Universidad Politécnica de Madrid, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria, Campus de Montegancedo - UPM, 28223-Pozuelo de Alarcón, Madrid, Spain
 - **Relationship:** Expert in plant breeding and genetics, collaborator on various projects
 - **Contact:** j.isidro@upm.es
- **Dr. Jhonathan Pedroso**
 - **Affiliation:** Research Scientist at Corteva Agriscience, Corteva, Johnston, Iowa, USA
 - **Relationship:** Industry partner in genomic tool development, contributed to software enhancements
 - **Contact:** jhowpd@gmail.com
- **Dr. Lynn Johnson**
 - **Affiliation:** Interim Director and Statistical Consultant, Cornell Statistical Consulting Unit, Cornell University, Ithaca, NY, USA
 - **Relationship:** Coworker at the Cornell Statistical Consulting Unit
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- **Dr. Roberto Fritsche Neto**

- **Affiliation:** Assistant Professor, Department of Plant, Environmental Management & Soil Sciences, LSU
- **Relationship:** Collaborator on various projects
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