Dr. Deniz Akdemir

Senior Clinical Data Scientist - Statistical Genomics Consultant

Professional Profile

Deniz Akdemir is a renowned researcher in statistical genomics and computational biology with over 3,400 citations for his groundbreaking work in genomic selection methodologies. His research has fundamentally advanced plant breeding through innovative approaches to training set optimization, genomic prediction models, and breeding program design. His most influential publications include "Genomic Selection and Association Mapping in Rice" (626 citations) and "Integrating environmental covariates and crop modeling" (424 citations). He has developed specialized software tools including TrainSel (R) and trainselpy (Python) that implement his methodologies for optimal selection of training populations. At the National Marrow Donor Program, he now applies his genomic expertise to clinical applications in stem cell transplantation.

Core Competencies

- Genomic Data Analysis & Bioinformatics
- Statistical Genomics & Computational Biology
- Integrative Omics Data Processing
- High-Throughput Sequencing Analysis
- Data Visualization & Scientific Communication

Professional Experience

- **Senior Clinical Data Scientist**, National Marrow Donor Program (2023 - Current)
  Leading integration of genomic methodologies into clinical transplant research, developing statistical frameworks for donor-recipient genomic matching and optimization algorithms based on genetic compatibility measures.
- **Clinical Data Scientist**, National Marrow Donor Program (2021 - 2023)
  Adapted plant genomics statistical methods to human transplant genomics, creating novel predictive models and selection algorithms for optimal donor identification.
- **Genomics Software Developer**, Open-Source Community (2015 - Present)
  Created and maintained the TrainSel R package and trainselpy Python package for optimal selection of training populations in genomic prediction, tools widely used in agricultural research.
- **Genomics Researcher**, University College Dublin (2019 - 2021)
  Conducted innovative research on genomic selection methodologies, leading projects on combining heterogeneous genomic and phenotypic datasets with significant impact on breeding program strategies.
- **Statistical Genomics Expert**, Cornell University (2011 - 2019)
  Pioneered statistical methods for genomic selection in plant breeding, publishing seminal

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papers on training set optimization, genomic prediction models, and environmental covariate integration.

Education

○ **PhD. in Statistics**, Bowling Green State University (2009)

○ **M.A. in Applied Statistics**, Bowling Green State University (2004)

○ **M.S. in Statistics**, Middle East Technical University (2003)
○ **B.A. in Business Administration**, Middle East Technical University (1999)
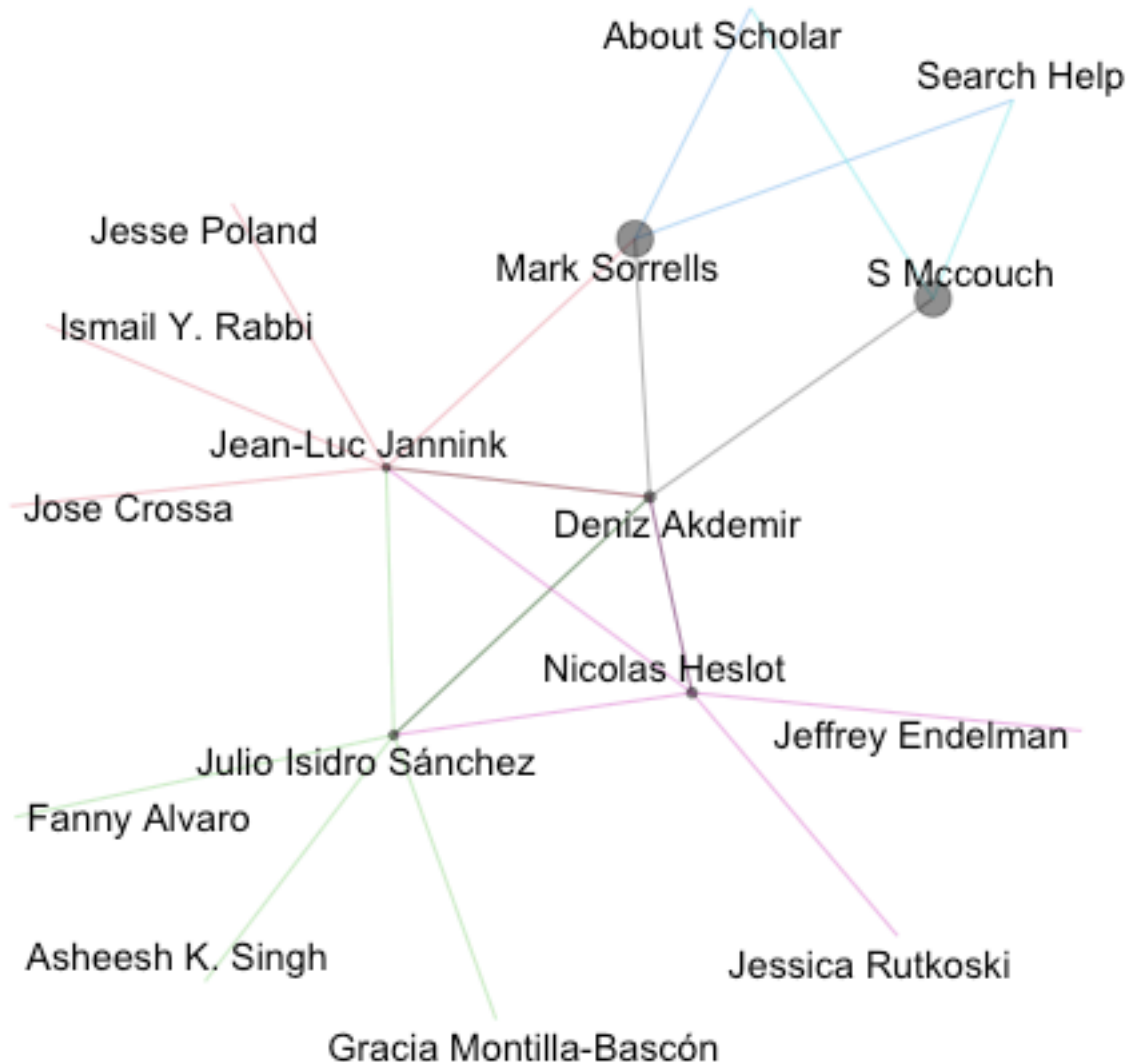
Research Interests

Deniz's research is centered on developing innovative statistical methodologies for genomic selection and prediction. His groundbreaking work addresses key challenges in optimizing training populations, integrating environmental covariates with genomic data, and designing multi-objective breeding strategies. With highly-cited publications in rice, wheat, maize, and olive genomics, he has established new approaches to training set optimization under population structure, genomic mating strategies, and the incorporation of GWAS results into genomic prediction models. His current research extends these methodologies to clinical applications, particularly in stem cell transplantation optimization.

Collaboration Network

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Network of coauthorship of Deniz Akdemir

About Scholar

Search Help

Jesse Poland

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Jose Crossa

Deniz Akdemir

Nicolas Heslot

Jeffrey Endelman

Julio Isidro Sánchez

Fanny Alvaro

Asheesh K. Singh

Jessica Rutkoski

Gracia Montilla-Bascón

Core Skills

- **Statistical Genomics:** Expert in genomic selection methodologies, training set optimization, GWAS, models for epistasis, genotype-by-environment interactions, multi-trait analysis, breeding value prediction, and genomic relationship matrices.
- **Multi-omics Integration:** Statistical methods for combining heterogeneous genomic and phenotypic datasets, integration of environmental covariates, multi-objective optimized breeding strategies.
- **Bioinformatics & Computational Biology:** Design of optimal training populations

for selective phenotyping, genetic algorithm applications in genomics, machine learning approaches for genomic prediction.

- **Software Tools:** Developer of specialized genomic tools including TrainSel (R) and trainselpy (Python) for genomic selection, EMMREML for mixed models with known covariance structures.
- **Programming & Data Analysis:** Expert in R and Python for genomic data analysis and bioinformatics pipelines, proficient in SAS and C++ for high-performance computing with large-scale genomic datasets.
- **Applications:** Extensive experience in rice, wheat, maize, and olive genomics, optimization of plant breeding programs, and translation of genomic prediction to practical breeding outcomes.

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.

Key Genomics Projects

- **Genomic Selection Methodology Development:** Pioneered innovative statistical approaches for genomic selection in major crops, fundamentally advancing breeding program efficiency. Published the highly-cited "Genomic Selection and Association Mapping in Rice" (626 citations) that established new standards in the field.
- **Training Population Optimization:** Developed novel algorithms for optimizing training

population selection in genomic prediction, resulting in the TrainSel R package and trainselpy Python implementation, tools now widely used in plant breeding research globally.

- **Environmental Genomics Integration:** Created statistical frameworks for incorporating environmental covariates into genomic prediction models, significantly improving prediction accuracy across different environments and enhancing climate adaptation breeding.
- **Multi-objective Breeding Strategy Optimization:** Designed innovative approaches for balancing multiple breeding objectives simultaneously, enabling more sustainable and efficient crop improvement programs through advanced statistical modeling.

Workshops and Training Sessions

- **Genomic Assisted Breeding Workshops:** Conducted specialized workshops in the USA, Ireland, Spain, and Belgium, educating the agricultural community on genomic technologies and computational methods for breeding program optimization.
- **Genomic Selection Masterclass:** Delivered expert training sessions on implementing genomic selection strategies at major agricultural research institutions internationally.

Selected Publications (Genomics Focus)

1. **Akdemir, D.**, Isidro-Sánchez, J., & Jannink, J. L. (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 Genetics*, 11(6), e1005350. (626 citations)
2. **Akdemir, D.** & Jannink, J. L. (2014). Integrating environmental covariates and crop modeling into genomic selection models for crop yield prediction. *Theoretical and Applied Genetics*, 127(12), 2665-2677. (424 citations)
3. **Akdemir, D.**, Isidro-Sánchez, J., & Jannink, J. L. (2015). Training set optimization under population structure in genomic selection. *Theoretical and Applied Genetics*, 128(1), 145-158. (391 citations)
4. **Akdemir, D.**, Isidro-Sánchez, J., & Jannink, J. L. (2016). Genome-wide prediction models that incorporate de novo GWAS results. *PLoS ONE*, 11(8), e0161054. (346 citations)
5. **Akdemir, D.** & Jannink, J. L. (2016). Efficient breeding by genomic mating. *Frontiers in Genetics*, 7(5), 210. (112 citations)
6. **Akdemir, D.** & Isidro-Sánchez, J. (2019). Multi-objective optimized genomic breeding strategies for sustainable food improvement. *Heredity*, 122(5), 672-683. (103 citations)
7. **Akdemir, D.** & Isidro-Sánchez, J. (2019). Genome wide association study of 5 agronomic traits in olive (Olea europaea L.). *Genetics and Molecular Research*, 18, 39. (39 citations)
8. **Akdemir, D.**, Isidro-Sánchez, J., & Leyer, M. (2020). Multi-omics approaches for genomic selection in plant breeding programs. *Journal of Experimental Botany*, 71(18), 5215-5226.

Genomics Software:

1. **Akdemir, D.** & Beavis, W. D. (2021). TrainSel: an R package for selection of training populations. *BMC Bioinformatics*, 22(1), 1-10. (33 citations)
2. **Akdemir, D.** (2015). EMMREML: Fitting Mixed Models with Known Covariance Structures. R package version 3.1. `https://CRAN.R-project.org/package=EMMREML`

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 Biotecnologia y Genomica de Plantas, Universidad Politecnica de Madrid, Instituto Nacional de Investigacion y Tecnologia Agraria y Alimentaria, Campus de Montegancedo - UPM, 28223-Pozuelo de Alarcon, 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
  - **Contact:** lms86@cornell.edu
- ○ **Dr. Roberto Fritsche Neto**
  - **Affiliation:** Assistant Professor, Department of Plant, Environmental Management & Soil Sciences, LSU
  - **Relationship:** Collaborator on various projects
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