Stanford

Alexander Ioannidis

Assistant Professor (Research) of Genetics and of Biomedical Data Science
Institute for Computational and Mathematical Engineering (ICME)

Bio

BIO

Dr. Ioannidis earned his Ph.D. from Stanford University in Computational and Mathematical Engineering together with an M.S. in Management Science and Engineering (Optimization). He graduated summa cum laude from Harvard University in Chemistry and Physics and earned an M.Phil at the University of Cambridge from the Department of Applied Math and Theoretical Physics in Computational Biology. His research focuses on the design of algorithms and application of computational methods for problems in precision health, genomics, clinical data science, and AI in healthcare.

ACADEMIC APPOINTMENTS

- Assistant Professor (Research), Genetics
- Assistant Professor (Research), Department of Biomedical Data Science
- Adjunct Professor, Institute for Computational and Mathematical Engineering (ICME)

BOARDS, ADVISORY COMMITTEES, PROFESSIONAL ORGANIZATIONS

- Editorial Board, Human Genomics

PROFESSIONAL EDUCATION

- Ph.D., Stanford , Computational and Mathematical Engineering
- M.S., Stanford , Management Science and Engineering
- M.Phil, University of Cambridge , Computational Biology
- B.A., summa cum laude, Harvard , Chemistry and Physics

LINKS

- Alexander Ioannidis - website: https://ai-page.org
- spotlight article: https://engineering.stanford.edu/spotlight/alexander-ioannidis
- research highlight: https://engineering.stanford.edu/magazine/researchers-use-genetic-clues-track-and-date-polynesian-exploration
- github: https://github.com/AI-sandbox

Teaching

COURSES

2025-26

- Healthcare Acceleration: Artificial Intelligence: BMDS 272, DESIGN 266 (Aut)

2023-24

- Generative AI in Healthcare: BIODS 295, DESIGN 266 (Spr)

GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Biomedical Data Science (Phd Program)
- Biomedical Data Science (Masters Program)

Publications

PUBLICATIONS

- **Clinical genetic variation across Hispanic populations in the Mexican Biobank.** *Nature medicine*
  Barberena-Jonas, C., Medina-Munoz, S. G., Cedillo-Castelan, V., Sepulveda-Morales, T., Gonzaga-Jauregui, C., ENSA Genomics Consortium, Garcia-Garcia, L., Ioannidis, A. G., Moreno-Estrada, A., Aguilar-Salinas, C., Barberena-Jonas, C., Canizales-Quintero, S., Cruz-Hervert, L. P., et al
  2026
- **Autoencoders for genomic variation analysis.** *Genome research*
  Geleta, M., Montserrat, D. M., Giro-I-Nieto, X., Ioannidis, A. G.
  2026
- **Neural ADMIXTURE for rapid genomic clustering.** *Nature computational science*
  Mantes, A. D., Montserrat, D. M., Bustamante, C. D., Giró-I-Nieto, X., Ioannidis, A. G.
  2023; 3 (7): 621-629
- **Deconvoluting complex correlates of COVID-19 severity with a multi-omic pandemic tracking strategy.** *Nature communications*
  Parikh, V. N., Ioannidis, A. G., Jimenez-Morales, D., Gorzynski, J. E., De Jong, H. N., Liu, X., Roque, J., Cepeda-Espinoza, V. P., Osoegawa, K., Hughes, C., Sutton, S. C., Youlton, N., Joshi, et al
  2022; 13 (1): 5107
- **Archetypal Analysis for population genetics.** *PLoS computational biology*
  Gimbernat-Mayol, J., Dominguez Mantes, A., Bustamante, C. D., Mas Montserrat, D., Ioannidis, A. G.
  2022; 18 (8): e1010301
- **Paths and timings of the peopling of Polynesia inferred from genomic networks.** *Nature*
  Ioannidis, A. G., Blanco-Portillo, J., Sandoval, K., Hagelberg, E., Barberena-Jonas, C., Hill, A. V., Rodriguez-Rodriguez, J. E., Fox, K., Robson, K., Haoa-Cardinali, S., Quinto-Cortes, C. D., Miquel-Poblete, J. F., Auckland, et al
  2021; 597 (7877): 522-526
- **Mapping the human genetic architecture of COVID-19.** *Nature*
  COVID-19 Host Genetics Initiative
  2021
- **Native American gene flow into Polynesia predating Easter Island settlement.** *Nature*
  Ioannidis, A. G., Blanco-Portillo, J., Sandoval, K., Hagelberg, E., Miquel-Poblete, J. F., Moreno-Mayar, J. V., Rodriguez-Rodriguez, J. E., Quinto-Cortes, C. D., Auckland, K., Parks, T., Robson, K., Hill, A. V., Avila-Arcos, et al
  2020
- **Ultra-low-power superconductor logic** *JOURNAL OF APPLIED PHYSICS*
  Herr, Q. P., Herr, A. Y., Oberg, O. T., Ioannidis, A. G.
  2011; 109 (10)
- **The landscape of genomic and socioeconomic variables in colorectal cancer patients based on genetic ancestry.** *Cancer epidemiology, biomarkers & prevention : a publication of the American Association for Cancer Research, cosponsored by the American Society of Preventive Oncology*
  Srinivasan, P., Bristow, S. L., Mendez, F. L., Krinshpun, S., Jurdi, A., Liu, M. C., Rabinowitz, M., Wall, J., Bustamante, C. D., Ioannidis, A. G., De La Vega, F. M., Mitchell, B. L., Aleshin, et al
  2026
- **Signatures of pathogen-driven selection and Austronesian gene flow of Papua New Guinea HLA alleles.** *American journal of human genetics*

Font-Porterias, N., Nemat-Gorgani, N., Kichula, K. M., Al-Hindi, D. R., Harrison, G. F., Tao, S., Zhu, F., Montero-Martin, G., Fernández-Viña, M. A., Guethlein, L. A., Parham, P., Oppenheimer, S. J., Ioannidis, et al

2026

- **Analysis of a deeply-phenotyped familial hypercholesterolemia cohort from Mexico shows a role for both rare and common alleles across known dyslipidemia genes and reveals structural variation in a novel locus.** *Human genomics*

  Katsanis, N., Mourtzi, N., Quinto-Cortés, C. D., Martagon, A. J., Ioannidis, A. G., De La Vega, F. M., Gulcher, J., Lee, M. T., Faghihi, M. A., Lopez-Pineda, A., Moreno-Grau, S., Montserrat, D. M., Barrabés, et al

  2025; 19 (1): 141

- **Advances in Biomedical Missing Data Imputation: A Survey** *IEEE ACCESS*

  Barrabes, M., Perera, M., Novelle Moriano, V., Giro-I-Nieto, X., Mas Montserrat, D., Ioannidis, A. G.

  2025; 13: 16918-16932

- **Feature Shift Localization Network**

  Barrabes, M., Montserrat, D., Dev, K., Ioannidis, A. G.

  edited by Singh, A., Fazel, M., Hsu, D., Lacoste-Julien, S., Berkenkamp, F., Maharaj, T., Wagstaff, K., Zhu, J.

  JMLR-JOURNAL MACHINE LEARNING RESEARCH.2025

- **Compressive Meta-Learning**

  Montserrat, D., Bonet, D., Perera, M., Giro-I-Nieto, X., Ioannidis, A. G., ACM

  ASSOC COMPUTING MACHINERY.2025: 2102-2113

- **An archaic HLA class I receptor allele diversifies natural killer cell-driven immunity in First Nations peoples of Oceania.** *Cell*

  Loh, L., Saunders, P. M., Faoro, C., Font-Porterias, N., Nemat-Gorgani, N., Harrison, G. F., Sadeeq, S., Hensen, L., Wong, S. C., Widjaja, J., Clemens, E. B., Zhu, S., Kichula, et al

  2024

- **Polygenic risk score portability for common diseases across genetically diverse populations.** *Human genomics*

  Moreno-Grau, S., Vernekar, M., Lopez-Pineda, A., Mas-Montserrat, D., Barrabés, M., Quinto-Cortés, C. D., Moatamed, B., Lee, M. T., Yu, Z., Numakura, K., Matsuda, Y., Wall, J. D., Ioannidis, et al

  2024; 18 (1): 93

- **Genetic Signatures of Positive Selection in Human Populations Adapted to High Altitude in Papua New Guinea.** *Genome biology and evolution*

  Gonzalez-Buenfil, R., Vieyra-Sanchez, S., Quinto-Cortes, C. D., Oppenheimer, S. J., Pomat, W., Laman, M., Cervantes-Hernandez, M. C., Barberena-Jonas, C., Auckland, K., Allen, A., Allen, S., Phipps, M. E., Huerta-Sanchez, et al

  2024; 16 (8)

- **Evaluating disparities in receptor status, overall survival, and time to hormone therapy among women with breast cancer**

  Taparra, K. A., DeVille, N. V., Melendez-Ramos, A., Blanco-Portillo, J., Ioannidis, A., Patel, M. I., Pollom, E. L., Horst, K. C.

  LIPPINCOTT WILLIAMS & WILKINS.2024

- **Genetic landscape of colorectal cancer (CRC) across genetic ancestries: Implications for early cancer detection (ECD).**

  Ioannidis, A., Srinivasan, P., Bristow, S. L., Krinshpun, S., Solari, O., Rivero-Hinojosa, S., Aushev, V. N., Jurdi, A. A., Liu, M. C., Mitchell, B., Aleshin, A., Reiter, J. G., Nakamura, et al

  LIPPINCOTT WILLIAMS & WILKINS.2024

- **Deep history of cultural and linguistic evolution among Central African hunter-gatherers.** *Nature human behaviour*

  Padilla-Iglesias, C., Blanco-Portillo, J., Pricop, B., Ioannidis, A. G., Bickel, B., Manica, A., Vinicius, L., Migliano, A. B.

  2024

- **Comparison of colorectal cancer (CRC) characteristics across genetic ancestries: Implications for early cancer detection (ECD).**

  Myer, P., Srinivasan, P., Bristow, S. L., Krinshpun, S., Solari, O., Aushev, V. N., Jurdi, A. A., Liu, M. C., Mitchell, B. L., Aleshin, A., Reiter, J. G., Weitzel, J. N., Nakamura, et al

  LIPPINCOTT WILLIAMS & WILKINS.2024: 164

- **Machine Learning Strategies for Improved Phenotype Prediction in Underrepresented Populations.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*

  Bonet, D., Levin, M., Montserrat, D. M., Ioannidis, A. G.

  2024; 29: 404-418

- **HyperFast: Instant Classification for Tabular Data**
  Bonet, D., Montserrat, D., Giro-i-Nieto, X., Ioannidis, A. G.
  edited by Wooldridge, M., Dy, J., Natarajan, S.
  ASSOC ADVANCEMENT ARTIFICIAL INTELLIGENCE.2024: 11114-11123

- **Overcoming health disparities in precision medicine**
  De la Vega, F. M., Barnes, K. C., Fox, K., Ioannidis, A., Kenny, E., Mathias, R. A., Pasaniuc, B.
  edited by Hunter, L., Altman, R. B., Ritchie, M. D., Murray, T., Klein, T. E.
  WORLD SCIENTIFIC PUBL CO PTE LTD.2024: 322-326

- **PopGenAdapt: Semi-Supervised Domain Adaptation for Genotype-to-Phenotype Prediction in Underrepresented Populations.** *Pacific Symposium on Biocomputing. Pacific Symposium on Biocomputing*
  Comajoan Cara, M., Mas Montserrat, D., Ioannidis, A. G.
  2024; 29: 327-340

- **Machine Learning Strategies for Improved Phenotype Prediction in Underrepresented Populations.** *bioRxiv : the preprint server for biology*
  Bonet, D., Levin, M., Montserrat, D. M., Ioannidis, A. G.
  2023

- **Mexican Biobank advances population and medical genomics of diverse ancestries.** *Nature*
  Sohail, M., Palma-Martínez, M. J., Chong, A. Y., Quinto-Cortés, C. D., Barberena-Jonas, C., Medina-Muñoz, S. G., Ragsdale, A., Delgado-Sánchez, G., Cruz-Hervert, L. P., Ferreyra-Reyes, L., Ferreira-Guerrero, E., Mongua-Rodríguez, N., Canizales-Quintero, et al
  2023

- **PopGenAdapt: Semi-Supervised Domain Adaptation for Genotype-to-Phenotype Prediction in Underrepresented Populations.** *bioRxiv : the preprint server for biology*
  Cara, M. C., Montserrat, D. M., Ioannidis, A. G.
  2023

- **Demographic history and genetic structure in pre-Hispanic Central Mexico.** *Science (New York, N.Y.)*
  Villa-Islas, V., Izarraras-Gomez, A., Larena, M., Campos, E. M., Sandoval-Velasco, M., Rodríguez-Rodríguez, J. E., Bravo-Lopez, M., Moguel, B., Fregel, R., Garfias-Morales, E., Medina Tretmanis, J., Velázquez-Ramírez, D. A., Herrera-Muñóz, et al
  2023; 380 (6645): eadd6142

- **Global Biobank Meta-analysis Initiative: Powering genetic discovery across human disease.** *Cell genomics*
  Zhou, W., Kanai, M., Wu, K. H., Rasheed, H., Tsuo, K., Hirbo, J. B., Wang, Y., Bhattacharya, A., Zhao, H., Namba, S., Surakka, I., Wolford, B. N., Lo Faro, et al
  2022; 2 (10): 100192

- **SALAI-Net: species-agnostic local ancestry inference network.** *Bioinformatics (Oxford, England)*
  Oriol Sabat, B., Mas Montserrat, D., Giro-I-Nieto, X., Ioannidis, A. G.
  2022; 38 (Supplement_2): ii27-ii33

- **Validating and automating learning of cardiometabolic polygenic risk scores from direct-to-consumer genetic and phenotypic data: implications for scaling precision health research.** *Human genomics*
  Lopez-Pineda, A., Vernekar, M., Moreno-Grau, S., Rojas-Munoz, A., Moatamed, B., Lee, M. T., Nava-Aguilar, M. A., Gonzalez-Arroyo, G., Numakura, K., Matsuda, Y., Ioannidis, A., Katsanis, N., Takano, et al
  2022; 16 (1): 37

- **Ancient DNA reveals five streams of migration into Micronesia and matrilocality in early Pacific seafarers.** *Science (New York, N.Y.)*
  Liu, Y. C., Hunter-Anderson, R., Cheronet, O., Eakin, J., Camacho, F., Pietrusewsky, M., Rohland, N., Ioannidis, A., Athens, J. S., Douglas, M. T., Ikehara-Quebral, R. M., Bernardos, R., Culleton, et al
  2022; 377 (6601): 72-79

- **Predicting Dog Phenotypes from Genotypes.** *Annual International Conference of the IEEE Engineering in Medicine and Biology Society. IEEE Engineering in Medicine and Biology Society. Annual International Conference*
  Bartusiak, E. R., Barrabes, M., Rymbekova, A., Gimbernat-Mayol, J., Lopez, C., Barberis, L., Montserrat, D. M., Giro-I-Nieto, X., Ioannidis, A. G.
  2022; 2022: 3558-3562

- **Generative Moment Matching Networks for Genotype Simulation.** *Annual International Conference of the IEEE Engineering in Medicine and Biology Society. IEEE Engineering in Medicine and Biology Society. Annual International Conference*

Perera, M., Montserrat, D. M., Barrabes, M., Geleta, M., Giro-I-Nieto, X., Ioannidis, A. G.
2022; 2022: 1379-1383

- **The genetic legacy of the Manila galleon trade in Mexico.** *Philosophical transactions of the Royal Society of London. Series B, Biological sciences*
  Rodriguez-Rodriguez, J. E., Ioannidis, A. G., Medina-Munoz, S. G., Barberena-Jonas, C., Blanco-Portillo, J., Quinto-Cortes, C. D., Moreno-Estrada, A.
  2022; 377 (1852): 20200419
- **Opportunities and challenges for the use of common controls in sequencing studies.** *Nature reviews. Genetics*
  Wojcik, G. L., Murphy, J., Edelson, J. L., Gignoux, C. R., Ioannidis, A. G., Manning, A., Rivas, M. A., Buyske, S., Hendricks, A. E.
  2022
- **Bayesian model comparison for rare-variant association studies.** *American journal of human genetics*
  Venkataraman, G. R., DeBoever, C., Tanigawa, Y., Aguirre, M., Ioannidis, A. G., Mostafavi, H., Spencer, C. C., Poterba, T., Bustamante, C. D., Daly, M. J., Pirinen, M., Rivas, M. A.
  2021
- **High Resolution Ancestry Deconvolution for Next Generation Genomic Data** *bioRxiv*
  Hilmarsson, H., Kumar, A. S., Rastogi, R., Bustamante, C. D., Mas Montserrat, D., Ioannidis, A. G.
  2021
- **Neural ADMIXTURE: rapid population clustering with autoencoders** *bioRxiv*
  Dominguez Mantes, A., Mas Montserrat, D., Bustamante, C., Giró-i-Nieto, X., Ioannidis, A. G.
  2021
- **Discovering prescription patterns in pediatric acute-onset neuropsychiatric syndrome patients.** *Journal of biomedical informatics*
  Lopez Pineda, A., Pourshafeie, A., Ioannidis, A., McCloskey Leibold, C., Chan, A. L., Bustamante, C. D., Frankovich, J., Wojcik, G. L.
  2020: 103664
- **LAI-NET: LOCAL-ANCESTRY INFERENCE WITH NEURAL NETWORKS**
  Montserrat, D., Bustamante, C., Ioannidis, A., IEEE
  IEEE.2020: 1314–18
- **Class-Conditional VAE-GAN for Local-Ancestry Simulation** *MLCB Proceedings*
  Mas Montserrat, D., Bustamante, C., Ioannidis, A. G.
  2019
- **Reconstructing admixture and migration dynamics of post-contact Mexico**
  Esteban Rodriguez-Rodriguez, J., Blanco-Portillo, J., Ioannidis, A., Moreno-Estrada, A.
  WILEY.2018: 228
- **Integrated Power Divider for Superconducting Digital Circuits** *IEEE TRANSACTIONS ON APPLIED SUPERCONDUCTIVITY*
  Oberg, O. T., Herr, Q. P., Ioannidis, A. G., Herr, A. Y.
  2011; 21 (3): 571–74
- **Digital circuits using self-shunted Nb/NbxSi1-x/Nb Josephson junctions** *APPLIED PHYSICS LETTERS*
  Olaya, D., Dresselhaus, P. D., Benz, S. P., Herr, A., Herr, Q. P., Ioannidis, A. G., Miller, D. L., Kleinsasser, A. W.
  2010; 96 (21)