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Anestis Gkanogiannis, Ph.D.

Summary and Research Interests

Senior Bioinformatics & AI Lead with 10+ years delivering large-scale genomics programs across CGIAR, ICBA, and EU research institutes. Proven track record of leading multi-institution projects, defining technical strategy, coordinating cross-functional teams (bioinformatics, wet lab, external providers), and delivering production-grade pipelines, publications, and deployed AI tools. Experienced in technical leadership, mentoring, and infrastructure ownership across HPC and cloud environments.

Professional Experience

December 2022 - September 2025 **Bioinformatics Scientist**, *ICBA*, Dubai, United Arab Emirates

- Scientific and technical lead for national-scale genomics initiatives in the UAE, including population genomics and genetic diversity analysis of 200+ Ghaf tree individuals.
- Owned end-to-end project delivery for long-read genome assembly and annotation projects (PacBio HiFi, Hi-C, Iso-Seq), from experimental design to publication.
- Defined technical roadmaps, selected methods and tools, and coordinated work across bioinformatics, wet-lab scientists, and external collaborators.
- Mentored and supervised junior researchers and collaborators, reviewed analyses, and resolved technical blockers.
- Accountable for reproducible infrastructure, including Nextflow pipelines, Docker/Singularity containers, and HPC operations.
- Led development and release of fastreeR, an open-source phylogenetics toolkit adopted via Bioconductor, Bioconda, PyPI, and DockerHub.
- Delivered applied AI/ML solutions (YOLO, PyTorch, TensorFlow) for plant disease detection and phenotyping.
- Ensured projects resulted in peer-reviewed publications, reusable software, and production-ready pipelines.

April 2022 -November 2022 **Bioinformatician**, *CRG*, Barcelona, Spain

- Core bioinformatics contributor in cancer metabolism projects, supporting RNA-Seq, ATAC-Seq, ChIP-Seq, Nanopore, WGS, CRISPR screens, and SLAM-Seq.
- Led the design and implementation of analysis pipelines using Nextflow and Bioconductor, ensuring reproducibility and scalability.
- Acted as technical reference for experimental scientists, translating biological questions into robust computational workflows.
- Contributed to cross-lab coordination by standardizing analysis practices and documentation.

April 2021 - March 2022 **Career break**, *Personal goal pursuit*, Evia, Greece

- Career break focused on skills refresh, and self-directed training.

January 2017 - March 2021 **Head Bioinformatics Scientist**, *CIAT_CGIAR*, Cali, Colombia

- Led a bioinformatics team (3–5 researchers) supporting multiple CGIAR breeding programs (Cassava, Rice, Bean, Forages).
- Defined analysis strategy and priorities, delegated tasks, reviewed outputs, and ensured delivery across concurrent projects.
- Served as primary interface between bioinformatics, breeders, and program leadership, translating research goals into actionable analytics.
- Led development of AI and machine-learning solutions adopted in breeding and phenotyping workflows, including the PPD Insight mobile app.
- Owned and managed HPC infrastructure, data pipelines, and shared computational resources.

- Contributed to high-impact research including GWAS, genomic selection, population genomics, and domestication studies.
- Delivered challenge-winning ML models (Zindi/CGIAR Wheat Challenge 2020, Syngenta Crop Challenge 2018).

June 2015 - December 2016 **Post-Doctorate Researcher**, *CIRAD*, Montpellier, France

- Led development of web-based tools for analysis and visualization of Cassava NGS data.
- Acted as technical bridge between data producers and end-users.

June 2013 - May 2015 **Post-Doctorate Researcher**, *Genoscope_CEA*, Paris, France

- Designed and implemented novel algorithms for metagenome sequence binning.
- Owned method development, benchmarking, and integration into analysis workflows.

October 2011 - March 2013 **Post-Doctorate Researcher**, *University of New Brunswick*, Fredericton, Canada

- Managed a research team within the I-AID (Intelligent Analysis of Information and Dissemination) project.
- Coordinated ML software development for NLP-based document classification and information extraction.
- Defined project milestones, distributed development tasks, and oversaw delivery of research outputs.
- Contributed to algorithm design and software implementation for large-scale text mining.

Awards

2020 **Zindi/CGIAR Wheat Growth Stage Challenge**
First Place Winner (as CGIAR participant)

- Developed computer vision artificial intelligence model to automate wheat growth stage estimation from farmer-submitted images.

2018 **Syngenta Crop Challenge in Analytics**
First Place Winner

- Participated in developing machine learning models to predict how corn hybrids will perform in untested locations, in an effort to help plant breeders improve hybrid performance predictions.

2008 **Discovery Challenge, European Conference on Machine Learning (ECML)**
First prize, Spam Detection Task

2005 - 2008 **Greek General Secreteriat for Research and Technology**
PENED Scholarship

1995 **Greek Mathematic Society**
Regional Award

Education

December 2005 - May 2011 **Ph.D., Computer Science**, *AUEB*, Athens, Greece

Thesis	*Information Retrieval and Text Classification. Linear Classifiers and Modified Perceptron.*
Research	Machine Learning, Artificial Intelligence, Information Retrieval, Text Classification

October 2003 - June 2005 **M.Sc., Computer Science**, *AUEB*, Athens, Greece

Thesis	*Text Classification with k-NN.*
Research	Machine Learning, Artificial Intelligence, Information Retrieval, Text Classification

October 1998 - June 2003 **B.Sc., Physics**, *University of Crete*, Heraklion, Greece

Research	Lasers specialization (emphasis on laser-superconductor interaction)
Extra	Computer programming and algorithms

Skills & Core Strengths

Technical Leadership & Delivery

- Technical leadership of genomics and AI projects from concept to publication and deployment
- Project ownership, roadmap definition, prioritization, and delivery under real constraints

- Mentoring and technical supervision of junior researchers and cross-functional collaborators
- Translating scientific goals into scalable, reproducible computational solutions

Bioinformatics & Genomics

- Genome assembly and annotation (PacBio HiFi, Hi-C, Iso-Seq, ONT)
- Population genomics, genetic diversity, GWAS, LD analysis, PCA, ADMIXTURE
- Variant calling, QC, and large-scale NGS data processing
- Metagenomics and comparative genomics

AI & Machine Learning (Applied)

- Machine learning and deep learning for genomics and phenotyping
- Computer vision (YOLO), NLP, and predictive modeling
- Frameworks: TensorFlow, PyTorch, scikit-learn, HuggingFace
- Proven record of production and challenge-winning models

Software Engineering & Infrastructure

- Reproducible pipelines: Nextflow, Docker, Singularity
- Linux, HPC (Slurm, SGE), cloud environments (AWS, GCP, Azure)
- Open-source development and maintenance (fastreeR, production pipelines)
- Version control, CI/CD, collaborative development practices

Programming

- Python, R (Bioconductor), Bash
- Java, C/C++ (performance-critical tools, long-term codebases)
- Scientific software prototyping and production deployment

Publications

[1] **Anestis Gkanogiannis**, Salama Rashed Almansoori, Maher Kabshawi, Mohammad Shahid, Saif Almansoori, Hifzur Rahman, and Augusto Becerra Lopez-Lavalle. Population genomics and genetic diversity of prosopis cineraria in the united arab emirates: Insights for conservation in arid ecosystems. *Plants*, 14(19), 2025.

[2] Srinivasan Samineni, Sridhar Gummadi, Sumitha Thushar, Dil Nawaz Khan, **Anestis Gkanogiannis**, Luis Augusto Becerra Lopez-Lavalle, and Rakesh Kumar Singh. Exploring proso millet resilience to abiotic stresses: High-yield potential in desert environments of the middle east. *Agronomy*, 15(1), 2025.

[3] Tom Brown, Kathleen Collier, Fernando Cruz, **Anestis Gkanogiannis**, Sagane Joye-Dind, Yannis Nevers, Stepan Saenko, Tyler Alioto, Anthony Bretaudeau, Michael Charleston, Phuong Duy Doan, Christoph Hahn, Thomas Harrop, Katie Herron, Fredrick Kebaso, Romane Libouban, Locedi Mansueto, Shivakumara Manu, Asime Oba, David Swarbreck, Anna Syme, Fabio Zanarello, Jean-Marc Aury, Jèssica Gómez-Garrido, and Alice Dennis. Genome annotation and other post-assembly workflows for the tree of life, 2024.

[4] **Anestis Gkanogiannis**, Hifzur Rahman, Rakesh Kumar Singh, and Augusto Becerra Lopez-Lavalle. Chromosome-level genome assembly and functional annotation of citrullus colocynthis: unlocking genetic resources for drought-resilient crop development. *Planta*, 260(6):124, 2024.

[5] Natalia Pardo-Lorente, **Anestis Gkanogiannis**, Luca Cozzuto, Antoni Gañez Zapater, Lorena Espinar, Ritobrata Ghose, Jacqueline Severino, Laura García-López, Rabia Gül Aydin, Laura Martin, Maria Victoria Neguembor, Evangelia Darai, Maria Pia Cosma, Laura Batlle-Morera, Julia Ponomarenko, and Sara Sdelci. Nuclear localization of mthfd2 is required for correct mitosis progression. *Nature Communications*, 15(1):9529, 2024.

[6] Hifzur Rahman, Prashant Vikram, Yulan Hu, Sugandha Asthana, Abhinav Tanaji, Padmaktshni Suryanarayanan, Chris Quadros, Lovely Mehta, Mohammed Shahid, **Anestis Gkanogiannis**,

Sumitha Thushar, Salma Balazadeh, Bernd Mueller-Roeber, Luis Augusto Becerra Lopez-Lavalle, Tong Wei, and Rakesh Kumar Singh. Mining genomic regions associated with agronomic and biochemical traits in quinoa through gwas. *Scientific Reports*, 14(1), 2024.

[7] Cécile Triay, Alice Boizet, Christopher Fragoso, **Anestis Gkanogiannis**, Jean-François Rami, and Mathias Lorieux. Fast and accurate imputation of genotypes from noisy low-coverage sequencing data in bi-parental populations, 2024.

[8] María Alejandra Ospina, **Anestis Gkanogiannis**, Luis Londoño, Thierry Tran, Sandra Salazar, Johanatan Newby, Luis Augusto, and Becerra Lopez-Lavalle. Estudio de asociación del genoma completo para contenido de cianuro en clones de yuca. *Biotecnología Productiva y Sostenible*, page 73, 2023.

[9] Laura Pascual-Reguant, Queralt Serra-Camprubí, Debayan Datta, Damiano Cianferoni, Savvas Kourtis, Antoni Gañez Zapater, Chiara Cannatá, Lorena Espinar, Jessica Querol, Laura García-López, Sara Musa-Afaneh, Maria Guirola, **Anestis Gkanogiannis**, Andrea Miró Canturri, Marta Guzman, Olga Rodríguez, Andrea Herencia-Ropero, Joaquin Arribas, Violeta Serra, Luis Serrano, Tian V Tian, Sandra Peiró, and Sara Sdelci. Interactions between brd4s, loxl2, and med1 drive cell cycle transcription in triple-negative breast cancer. *EMBO Molecular Medicine*, 15(12):e18459, 2023.

[10] Laura Perez-Fons, Tatiana Maria Ovalle, Margit Drapal, Maria Alejandra Ospina, **Anestis Gkanogiannis**, Adriana Bohorquez-Chaux, Luis Augusto Becerra Lopez-Lavalle, and Paul David Fraser. Integrated genetic and metabolic characterization of latin american cassava (manihot esculenta) germplasm. *Plant Physiology*, 05 2023. kiad269.

[11] Mauricio Peñuela, Camila Riccio-Rengifo, Jorge Finke, Camilo Rocha, **Anestis Gkanogiannis**, Rod A. Wing, and Mathias Lorieux. Prediction of crossover recombination using parental genomes. *PLOS ONE*, 18(2):1–21, 02 2023.

[12] Angélica M. Jaramillo, Santiago Sierra, Paul Chavarriaga-Aguirre, Diana Katherine Castillo, **Anestis Gkanogiannis**, Luis Augusto Becerra López-Lavalle, Juan Pablo Arciniegas, Tianhu Sun, Li Li, Ralf Welsch, Erick Boy, and Daniel Álvarez. Characterization of cassava orange proteins and their capability to increase provitamin a carotenoids accumulation. *PLOS ONE*, 17(1):1–24, 01 2022.

[13] Mauricio Peñuela, Jenny Johana Gallo-Franco, Jorge Finke, Camilo Rocha, **Anestis Gkanogiannis**, Thaura Ghneim-Herrera, and Mathias Lorieux. Methylation in the chh context allows to predict recombination in rice. *International Journal of Molecular Sciences*, 23(20), 2022.

[14] Mario Caccamo, Bruno A Santos, Faraz Khan, Andy Powell, Monica Carvajal-Yepes, **Anestis Gkanogiannis**, L Augusto Becerra Lopez-Lavalle, Joe Tohme, Peter Wenzl, and Sarah C Dyer. Developing a natural variation platform for pest-resistant cassava breeding. In *Plant and Animal Genome XXVII Conference (January 12-16, 2019)*. PAG, 2019.

[15] David Johnston-Monje, Janneth Guittierrez, Tatiana Ovalle, **Anestis Gkanogiannis**, and Luis Augusto Becerra Lopez-Lavalle. Provenance, transmission and dynamics of bacteriomes and mycobiomes in arabidopsis, brachypodium, maize, wheat, rice, tomato, soy, cassava and 9 other important species of angiosperm plant. In *Molecular Plant-Microbe Interactions*, volume 32, pages 211–211, 2019.

[16] Mathias Lorieux, **Anestis Gkanogiannis**, Christopher Fragoso, and Jean-François Rami. Noisymputer: genotype imputation in bi-parental populations for noisy low-coverage next-generation sequencing data. In *bioRxiv 658237*, 2019.

[17] Luis Augusto Becerra López-Lavalle, Fausto Villafrade Rodriguez Zapata, Tatiana Ovalle, Manuel Ruiz, **Anestis Gkanogiannis**, and Joe Tohmé. Capturing next-generation genome wide molecular markers in cassava helps to untangle the crop's genetic improvement history. In *Proceedings Plant and Animal Genome XXVI Conference, 2018 PAG, San Diego*, 2018.

[18] **Anestis Gkanogiannis**, Alexis Dereeper, Boris Szurek, Carlos Zarate, Camilo López, Luis Augusto Becerra López-Lavalle, and Manuel Ruiz. The cassava genome hub. In *Proceedings Plant and Animal Genome XXVI Conference, 2018 PAG, San Diego*, 2018.

[19] Fausto Villafrade Rodriguez Zapata, Tatiana Ovalle, Manuel Ruiz, **Anestis Gkanogiannis**, and Luis Augusto Becerra López-Lavalle. Population structure of wild and cultivated plants shows hierarchical organization of cassava germplasm diversity. In *Proceedings Plant and Animal Genome XXVI Conference, 2018 PAG, San Diego*, 2018.

[20] Stéphanie Bocs, David Couvin, Frédéric De Lamotte, Alexis Dereeper, Gaëtan Droc, Jean François Dufayard, Nordine El Hassouni, Cédric Farcy, **Anestis Gkanogiannis**, Valentin Guignon, and others. South green bioinformatics platform: Plateforme collaborative de bioinformatique verte héraultaise. CIRAD, 2017.

[21] **Anestis Gkanogiannis** and Brüls Thomas. A scalable assembly-free variable selection algorithm for biomarker discovery from metagenomes. *BMC Bioinformatics*, Aug 19;17(1):311, 2016.

[22] **Anestis Gkanogiannis** and Theodore Kalamboukis. A perceptron-like linear supervised algorithm for text classification. In *Advanced Data Mining and Applications (ADMA), Lecture Notes in Computer Science, 2010, Volume 6440/2010, 86-97, Chongqing, China*, 2010.

[23] **Anestis Gkanogiannis** and Theodore Kalamboukis. A modified and fast perceptron learning rule and its use for tag recommendations in social bookmarking systems. In *ECML PKDD Discovery Challenge 2009 (DC09), International Workshop at the ECML/PKDD in Bled, Slovenia, September 7th, 2009*, 2009.

[24] **Anestis Gkanogiannis** and Theodore Kalamboukis. An algorithm for text categorization. In *The 31st Annual International ACM SIGIR Conference, 20-24 July, Singapore*, 2008.

[25] **Anestis Gkanogiannis** and Theodore Kalamboukis. A novel supervised learning algorithm and its use for spam detection in social bookmarking systems. In *Winner of ECML PKDD Discovery Challenge 2008 (DC08), task 1: Spam Detection in Social Bookmarking Systems, Adwerp, Belgium, 2008*, 2008.

[26] Vaggelis Kotsonis, **Anestis Gkanogiannis**, Theodore Kalamboukis, and Stelios Eliakis. A greek-english cross language medical information retrieval system. In *Conference on Medical Imaging and Informatics, MIMI 2007, Beijing*, 2008.

Teaching & Mentorship

Jan 2025 **Mentorship Program**, *Plant and Animal Genome*, San Diego, USA

- Mentor to 3 early-career researchers in genomics and bioinformatics.

Sep 2005 - Jul 2010 **Teaching Assistant**, *AUEB*, Athens, Greece

- Supervised and mentored undergraduate and graduate students in programming, statistics, and information retrieval
- Designed and led hands-on laboratory sessions and project-based coursework

Workshops

- ELIXIR BioHackathon Europe: BUSCO genes for phylogenomics (2025)
- EMBL-EBI: Plant genomes: from data to discovery (2024)
- ELIXIR BioHackathon Europe: Genome annotation workflows (2023)
- EiB: AI & ML for Genomic Selection (2019)
- Cornell / BTI / IRRI / NIAB (2017–2018)

Languages

English	Professional / Working proficiency. Working experience since 2011
French	Intermediate level. Working experience since 2013
Spanish	Intermediate level. Working experience since 2016
Greek	Mother tongue

Interests

Building practical IoT / ML prototypes (Raspberry Pi, sensors, applied AI)

Travel and expedition planning (road trips, scuba diving)

References

References available upon request