

Mikel HERNÁEZ

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CURRENT POSITIONS

Center for Applied Medical Research (CIMA) University of Navarra SPAIN
Director, Computational Biology and Translational Genomics Program
Principal Investigator, Machine Learning for Biomedicine Lab

Department of Physics and Applied Mathematics University of Navarra, SPAIN
Adjunct Professor

Institute of Data Science and Artificial Intelligence (DATAI) University of Navarra, SPAIN
Associate Researcher

Navarra Institute for Health Research (IdiSNA) SPAIN
Principal Investigator

EDUCATION

Stanford University CA, USA
Postdoctoral researcher in the Dept. of Electrical Engineering 09/2013–12/2016
o P.I.: Prof. Tsachy Weissman (tsachy@stanford.edu)

TECNUN, University of Navarra SPAIN
PhD in Electrical Engineering, *GPA: Summa Cum Laude* 09/2010–12/2012
o Dissertation: Joint Network-Channel Coding Schemes for Relay Networks
- Advisors: Prof. Pedro Crespo (pcrespo@tecnun.es) and Javier Del Ser (jdelser@tecnalia.es)

TECNUN, University of Navarra SPAIN
Joint BSc/MSc in Telecommunications Engineering, Rank: Top 10 09/2003–02/2009
o Master thesis: Concatenated LDGM Codes for the Transmission of Correlated Sources over Gaussian Broadcast Channels (*GPA: 10/10*)
- Advisor: Prof. Pedro M. Crespo (pcrespo@ceit.es)

Lulea Tekniska Universitet SWEDEN
Erasmus Program 08/2007–01/2008

PAST WORK EXPERIENCE

Carl R. Woese Institute for Genomic Biology, University of Illinois IL, USA
Director of Computational Genomics 2017–2019
Executive Director, CompGen Initiative

Stanford University CA, USA
Postdoctoral Researcher 2013–2016
o Group of Prof. Tsachy Weissman (tsachy@unav.edu)

ENIGMEDIA

Director of Research

- o Supervisor: CEO & Founder Gerard Vidal (gerard@enigmedia.com)

Spain-USA
03/2013 - 09/2013

STANFORD UNIVERSITY-TECNUN

Visiting Researcher

USA-Spain
Summer 2012

TEACHING EXPERIENCE

University of Navarra

Adjunct Professor

SPAIN
01/2020 -

- o Masters in Data Science (School of Sciences)
 - Master's committee member
 - Advance Topics in Machine Learning
 - Deep Learning

University of Illinois at Urbana-Champaign

Lecturer

CA, USA
01/2018 - 12/2019

- o BIOE 383: High-Throughput Genomic Data Analysis (Dept. Bioengineering)
- o ECE 365: Data Science and Engineering (Dept. Electrical and Computer Engineering)

TECNUN School of Engineering, University of Navarra

Lecturer

CA, USA
09/2012 - 01/2013

- o Information Theory and Coding
- o Communication Systems
- o Fundamentals of Computers course

TECNUN School of Engineering, University of Navarra

Teaching Assistant

Spain
2011-2012

- o Information Theory and Coding
- o Communication Systems
 - Set up of a point-to-point wireless communication system for pedagogic purposes

RESEARCH GRANTS

- Awarded a **Marie S. Curie Grant (PI)** from the European Union 2020
- Awarded an **American Department of Defense (DoD) grant (PI)** 2020
- Awarded an **Strategic Research Initiative (SRI) grant (PI)** from the University of Illinois at Urbana-Champaign (UIUC) 2018
- Awarded a **Chan Zuckerberg Initiative (CZI) grant (PI)**, under the Human Cell Atlas 2018
- Awarded a **Mayo Grand Challenge grant (co-PI)**, from Mayo Clinic 2017
- Awarded an **NIH grant**, under the BD2K initiative, in collaboration with the University of Illinois at Urbana-Champaign (UIUC) 2015

PREPRINTS AND UNDER REVIEW

*: Contacting author and/or (joint) first author

- M. Goyal, G. Serrano, Ilan Shomorony, I. Ochoa, and **M. Hernaez**, *JIND: Joint Integration and Discrimination for Automated Single-Cell Annotation*, Bioarxiv, 2020.
- J. Peng, U. V. Chembazhi, S. Bangru, I. M. Traniello, A. Kalsotra, I. Ochoa, and **M. Hernaez**, *SimiC: A Single Cell Gene Regulatory Network Inference method with Similarity Constraints*, Bioarxiv, 2020.
- U. Chembazhi, S. Bangru, **M. Hernaez**, A. Kalsotra, *Cellular plasticity balances the metabolic and proliferation dynamics of a regenerating liver*, Bioarxiv, 2020.
- C. Alberti, T. Paridaens, J. Voges, D. Naro, J. J. Ahmad, M. Ravasi, D. Renzi, P. Ribeca, G. Zoia, I. Ochoa, M. Mattavelli, J. Delgado, **M. Hernaez***, *An introduction to MPEG-G, the new ISO standard for genomic information representation*, Biorxiv, 2018.

JOURNAL PAPERS AND CONFERENCE PROCEEDINGS

*: Contacting author and/or (joint) first author

- A. No, **M. Hernaez***, I. Ochoa, CROMqs: An Infinitesimal SuccessiveRefinement Lossy Compressor for the Quality Scores, *Journal of Bioinformatics and Computational Biology*, 2020
- Q. Meng, I. Ochoa, **M. Hernaez***, *GPress: a framework for querying General Feature Format (GFF) files and expression files in a compressed form*, *Bioinformatics*, in press 2020.
- J. Voges, T. Paridaens, F. Muntefering, L. S.Mainzer, B. Bliss, M. Yang, I. Ochoa, J. Fostier, J. Ostermann, and **M. Hernaez***. GABAC: an arithmetic coding solution for genomic data, *Bioinformatics*, 2019.
- O. Gevaert,..., **M. Hernaez**,..., N. Pochet. *Imaging-AMARETTO: a radiogenomics software tool for interpreting multi-omics networks for relevance to radiographic and histopathology imaging-derived biomarkers of clinical outcomes with application to studies of brain tumors*, <https://doi.org/10.1101/2020.10.06.327601>JCO Clinical Cancer Informatics, 2020.
- I. Fisher-Hwang, I. Ochoa, T. Weissman, **M. Hernaez***, *Denoising of Aligned Genomic Data*, **Nature Scientific Reports**, 2019.
- **M. Hernaez***, C. Blatti, O. Gevaert, *Comparison of single gene and module-based methods for modeling gene regulatory networks*, **Bioinformatics**, 2019.
- H. Zheng, K. Brennan, **M. Hernaez**, O. Gevaert, *Benchmark of lncRNA Quantification for RNA-Seq of Cancer Samples*, **GigaScience**, 2019.
- **M. Hernaez***, D. Pavlichin, and T. Weissman, I. Ochoa, *Genomic Data Compression*, **Annual**

Review of Biomedical Data Science, 2019.

- o I. Ochoa, H. Li, F. Baumgarte, C. Hergenrother, J. Voges, **M. Hernaez*** *AliCo: A New Efficient Representation for SAM Files*, **Data Compression Conference (DCC)**, 2019.
- o J. Seimetz, W. Arif, S. Bangru, **M. Hernaez**, A. Kalsotra, *Cell-type specific polysome profiling from mammalian tissues*, **Methods**, 155, 2019.
- o K. Kendig, S. Baheti, M. Bockol , T. Drucker, S. Hart, J. Heldenbrand , **M. Hernaez**, M. Hudson, M. Kalmbach, E. Klee , N. Mattson, C. Ross, M. Taschuk, E. Wieben, M. Wiefert, D. Wildman and L. Mainzer, *Sentieon DNaseq variant calling workflow demonstrates strong computational performance and accuracy*, **Frontiers in Genetics**, 2019.
- o S. Chandak, I. Ochoa, T. Weissman, **M. Hernaez***, *SPRING: a next-generation compressor for FASTQ data*, **Bioinformatics**, 2018.
- o L. Rogusky, I. Ochoa, **M. Hernaez**, S. Deorowicz, *FaStore - a space-saving solution for raw sequencing data*, **Bioinformatics**, 2018.
- o J. Voges, J. Oesterman, **M. Hernaez***, *CALQ: compression of quality values of aligned sequencing data*, **Bioinformatics**, 2018.
- o R Long, **M Hernaez***, I Ochoa, T Weissman, *GeneComp, a new reference-based compressor for SAM files*, *Data Compression Conference (DCC)*, 2017
- o K. Tatwawadi, **M. Hernaez***, I. Ochoa, and T. Weissman, *GTRAC: fast retrieval from compressed collections of genomic variants*, **Bioinformatics**, btw437, 2016.
- o C. Alberti, N. Daniels, **M. Hernaez***, J. Voges, R. L. Goldfeder, A. A. Hernandez-Lopez, M. Mattavelli, B. Berger, *An Evaluation Framework for Lossy Compression of Genome Sequencing Quality Values*, **Data Compression Conference (DCC)**, 2016.
- o I. Ochoa, **M. Hernaez***, R. Goldfeder, T. Weissman and E. Ashley, *Denoising of Quality Scores for Boosted Inference and Reduced Storage*, **Data Compression Conference (DCC)**, 2016.
- o **M. Hernaez***, I. Ochoa and T. Weissman, *A cluster-based approach to compression of Quality Scores*, **Data Compression Conference (DCC)**, 2016.
- o I. Ochoa, **M. Hernaez***, R. Goldfeder, T. Weissman and E. Ashley, *Effect of lossy compression of quality scores on variant calling*, **Briefings in Bioinformatics**, 2016.
- o S. Deorowicz, S. Grabowski, I. Ochoa, **M. Hernaez** and T. Weissman, *Comment on: "ERGC: An efficient referential genome compression algorithm"*, **Bioinformatics**, btw704, 2015.
- o G. Malysa, **M. Hernaez***, I. Ochoa, M. Rao, K. Ganesan and T. Weissman, *QVZ: lossy compression of quality values*, **Bioinformatics**, btw330, 2015.

- I. Alustiza, **M. Hernaez**, P. Crespo, *Design of a new scheme for multi-hop wireless networks using decode-and-forward strategy*, **EURASIP Journal on Wireless Communications and Networking**, (1), 1-8, 2015
- I. Ochoa, **M. Hernaez** and T. Weissman, *Aligned genomic data compression via improved modeling*, **Journal of bioinformatics and computational biology**, Vol. 12, No. 6, 2014.
- I. Ochoa, **M. Hernaez*** and T. Weissman, *iDoComp: a compression scheme for assembled genomes*, **Bioinformatics**, btu698, 2014.
- **M. Hernaez***, P.M. Crespo, J. Del Ser, *On the Design of a Novel Joint Network-Channel Coding Scheme for the Multiple Access Relay Channel*, **IEEE Journal on Selected Areas in Communications**, Vol. 31, No. 8, 1157-1167, August 2013.
- **M. Hernaez***, P.M. Crespo, J. Del Ser, *A Decode-and-Forward Scheme for Multihop Wireless Networks*, **IEEE Vehicular Technology Conference (VTC2013-Fall)**, Las Vegas, Sept. 2013
- I. Alustiza, **M. Hernaez**, X. Insasusti and P.M. Crespo, *Teaching Information Theory via a Simulation Tool for Communications Systems*, **IEEE Collaborative Learning & New Pedagogic Approaches in Engineering Education (IEEE EDUCON)**, Berlin (Germany), March 2013.
- **M. Hernaez***, P.M. Crespo, J. Del Ser *A Flexible Channel Coding Approach for Short-Length Codewords*, **IEEE Communications Letters**, Vol. 16, No. 9, 1508-1511, September 2012.
- **M. Hernaez***, P.M. Crespo, *A novel Scheme for Message-Forwarding in Ad-Hoc Wireless Networks*, **IEEE Vehicular Technology Conference (VTC2011-Spring)**, Budapest (Hungary), May 2011
- **M. Hernaez***, P.M. Crespo, J. del Ser, *Joint Non-Binary LDPC-BICM and Network Coding with Iterative Decoding for the Multiple Access Relay Channel*, **IEEE Vehicular Technology Conference (VTC2011-Spring)**, Budapest (Hungary), May 2011
- I. Ochoa, P. Crespo and **M. Hernaez***, *LDPC Codes for Non-Uniform Memoryless Sources and Unequal Energy Allocation*, **IEEE Communications Letters**, Vol. 14, No. 9, 2010.
- **M. Hernaez***, P. M. Crespo, J. Del Ser, J. Garcia-Frias, *Serially-Concatenated LDGM Codes for Correlated Sources over Gaussian Broadcast Channels*, **IEEE Communications Letters**, Vol 13, No. 10, 788-790, October 2009.
- I. Ochoa, P. Crespo, J. Del Ser and **M. Hernaez**, *Turbo Joint Source-Channel Coding of Non-Uniform Memoryless Sources in the Bandwidth-Limited Regime*, **IEEE Communications Letters**, Vol. 14, No. 4, 2010.

SCHOLARSHIPS AND AWARDS

- Awarded an **NIH grant**, under the BD2K initiative, in collaboration with the University of Illinois at Urbana-Champaign (UIUC) 2015
- Postdoctoral research funded by the **Stanford Data Science Initiative** 2015-2016
- Enigmmedia named the best new company of the Basque Country (Spain) 2013
- University of Navarra Fellowship** for graduate studies 2009-2011
- Master Thesis funded by **Telefonica Fellowship**. 2008

US PATENTS

- o I. Ochoa and **M. Hernaez**, *A Universal Compressor for Genomic Re-Sequencing Data*, Provisional US patent filled by Stanford's OTL - The Office of Technology Licensing, June 2014.
- o S.Chandak, K. Tatwawadi, T. Weissman, I. Ochoa, and **M. Hernaez**, *Systems and Methods for Compressing Genetic Sequencing Data*, Submitted to Stanford's OTL - The Office of Technology Licensing - and UIUC's OTM - Office of Technology Management, 2018.

SERVICE ACTIVITIES

Workshop Organization Committees:

- o Chair of special session on "Omics Data Compression and Storage: Present and Future" at ISMB/ECCB, Basel, 2019 (acceptance rate 15%).
- o Chair of special session on "Omics Data Compression and Storage: Present and Future" at ISMB (International Society for Computational Biology), Chicago, 2018 (acceptance rate 20%).
- o Chair of special session on "Bioinformatics" at the 56th Annual Allerton Conference on Communication, Control, and Computing (Allerton), October, 2018.
- o Chair of special session on "Bioinformatics" at the 55th Annual Allerton Conference on Communication, Control, and Computing (Allerton), October, 2017.

Professional Organizations:

- o International Society of Computational Biology (ISCB): Member
- o Stanford Compression Forum: Organizer of the first and second edition (2015 - 2016)
- o International Organization for Standardization (ISO): Active participant in the initiative to define and establish a compression standard for genomic data (under the MPEG working group).
- o Stanford Data Science Initiative (SDSI): Active member and grantee (2014 - 2016)
- o Center for Science of Information (CSol), NSF Science and Technology Center: Active member and grantee (2013-2015)

ADDITIONAL INFORMATION

Reviewer: Bioinformatics, Nature Technical Reports, Nature Biotechnology, BMC Bioinformatics, IEEE Communications Letters, several conference proceedings.