Mikel HERNAEZ

CIMA University of Navarra, Pio XII, 55, 31008, Pamplona, Spain
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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***

- 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***

- Dissertation: Joint Network-Channel Coding Schemes for Relay Networks
  - Advisors: Prof. Pedro Crespo (pcrespo@tecnun.es) and Javier Del Ser (jdelser@tecnalia.es)

Stanford University *CA, USA*
Visiting Researcher ***Summer 2012***

TECNUN, University of Navarra *SPAIN*
Joint BSc/MSc in Telecommunications Engineering, Rank: Top 10 ***09/2003–02/2009***

- Master thesis: Concatenated LDGM Codes for the Transmission of Correlated Sources over Gaussian Broadcast Channels *(GPA: 10/10)*
  - Advisor: Prof. Pedro M. Crespo (pcrespo@tecnun.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***

- Group of Prof. Tsachy Weissman (tsachy@stanford.edu)

ENIGMEDIA *SPAIN-USA*
Director of Research ***03/2013 - 09/2013***

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

Teaching experience

University of Navarra *SPAIN*
Adjunct Professor ***01/2020 -***

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

University of Illinois at Urbana-Champaign *CA, USA*
Lecturer ***01/2018 - 12/2019***

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

TECNUN School of Engineering, University of Navarra *CA, USA*
Lecturer ***09/2012 - 01/2013***

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

TECNUN School of Engineering, University of Navarra *SPAIN*
Teaching Assistant ***2011–2012***

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

Research Grants

Ramon y Cajal Fellowship (National Career award) *2022-2027*
Spanish Ministry of Science and Innovation, PI ***220,000€***
Machine Learning methods for translational biomedicine.

CRCNS US-Spain Research Proposal *2022-2027*
NIH (USA) / ISCIII (Spain), co-PI ***$1,500,000***
Deep Learning Methods to Discover Molecular Determinants of Neurovascular Coupling in Health and Disease.

Spanish National Research Project *2024-2027*
Spanish Ministry of Science and Innovation, PI ***180,000€***
Explainable Deep Learning for tailored therapeutics to overcome drug resistance in cancer.

Jose Castillejo Mobility grant *2025*
Spanish Ministry of Education, PI ***12,000€***
Research stay at New York University (NYU).

La Caixa Health Research grant *2025-2027*
La Caixa Foundation, Senior Researcher ***1,000,000€***
Uncovering resistance mechanism to CAR-T cells via deep learning in scRNA-seq for improved therapies.

Spanish Digital and Ecological Transition grant *2022-2025*
Spanish Ministry of Science and Innovation, co-PI ***187,000€***
Non-invasive cancer diagnosis using machine learning based characterization of circulating tumor cells.

Congressionally-directed medical research program (CDMRP) grant *2020-2024*
US Department of Defense, co-PI ***$750,000***
Novel Methods to Elucidate Abiraterone Resistance Mechanisms Using RNASeq Data and Xenograft Models from CRPC Patients.

Spanish National Research Project *2021-2024*
Spanish Ministry of Science and Innovation, PI ***39,680 €***
Tools and mechanisms for secure compression and management of genomic information for clinical laboratories: Translational aspects.

Marie S. Curie - Individual Fellowships *2020-2022*
European Research Council, PI ***175,000€***
Elucidating Transcriptional Rewiring on Hematological Malignancies via Computational Methods.

CZI single-cell grant *2018-2019*
SVSF (Chan-Zuckerberg Initiative), PI ***$105,000***
Quantization and Compressive Learning Methods for Omics Data.

College of Engineering Intramural grant *2018-2019*
University of Illinois, co-PI ***$150,000***
Bringing digital era formats to genomic information.

Journal Papers and Conference Proceedings

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

2025

- de la Fuente J, Serrano G, Veleiro U, Casals M, Vera L, Pizurica M, Gómez-Cebrián N, Puchades-Carrasco L, Pineda-Lucena A, Ochoa I, Vicent S, Gevaert O* and **Hernaez M***, *Towards an*

inductive world for drug repurposing approaches. **Nature Machine Intelligence**, 2025.
In press

2024

- Goñi E, Mas AM, Gonzalez J, Abad A, Santisteban M, Fortes P, Huarte M*, **Hernaez M***, *Uncovering functional lncRNAs by scRNA-seq with ELATUS*, **Nature Communications**, 2024.
  doi: 10.1038/s41467-024-54005-7

- Serrano G, Berastegui N, Díaz-Mazkiaran A, García-Olloqui P, Rodriguez-Res C, Huerga-Dominguez S, Ainciburu M, Vilas-Zornoza A, Martin-Uriz PS, Aguirre-Ruiz P, Ullate-Agote A, Ariceta B, Lamo-Espinosa JM, Acha P, Calvete O, Jimenez T, Molero A, Montoro MJ, Díez-Campelo M, Valcarcel D, Solé F, Alfonso-Pierola A, Ochoa I, Prosper F*, Ezponda T*, **Hernaez M***, *Single-cell transcriptional profile of CD34+ hematopoietic progenitor cells from del (5q) myelodysplastic syndromes and impact of lenalidomide*, **Nature Communications**, 2024.
  doi: 10.1038/s41467-024-49529-x

- Ruiz-Arenas C, Marin I, Wang L, Ochoa I, Perez-Jurado JL, **Hernaez M***, *NetActivity enhances transcriptional signals by combining gene expression into robust gene set activity scores through interpretable autoencoders*, **Nucleic Acids Research**, 2024.
  doi: 10.1093/nar/gkae197

- Veleiro U, de la Fuente J, Serrano G, Pizurica M, Casals M, Pineda-Lucena A, Vicent S, Ochoa I, Gevaert G*, **Hernaez M***, *GeNNius: An ultrafast drug-target interaction inference method based on graph neural networks*, **Bioinformatics**, 2024.
  doi: 10.1093/bioinformatics/btad774

- Munterferring F, Chandak S, Adhisantoso Y, Ostermann J, **Hernaez M***, Voges J*, *Genie: The First Open-Source ISO/IEC Encoder for Genomic Data*, **Communications Biology**, 2024.
  doi: 10.1038/s42003-024-06249-8

- Palacios-Berraquero ML, Rodriguez-Marquez P, Calleja-Cervantes ME, Berastegui N, Zabaleta A, Burgos L, Alignani D, San Martin-Uriz P, Vilas-Zornoza A, Rodriguez-Diaz S, Inoges S, Lopez-Diaz de Cerio A, Huerga S, Tamariz E, Rifon J, Alfonso-Pierola A, Lasarte JJ, Paiva B, **Hernaez M**, Rodriguez-Otero P, San-Miguel J, Ezponda T*, Rodriguez-Madoz JR*, Prosper F*. *Molecular mechanisms promoting long-term cytopenia after BCMA CAR-T therapy in Multiple Myeloma*, **Blood Advances**, 2024.
  doi: 10.1182/bloodadvances.2023012522

- de la Nava D, Ausejo-Mauleon I, Laspidea V, Gonzalez-Huarriz M, Lacalle A, Casares N, Zalacain M, Marrodan L, García-Moure M, Ochoa MC, Tallon-Cobos AC, Hernandez-Osuna R, Marco-Sanz J, Dhandapani L, Hervás-Corpión I, Becher OJ, Nazarian J, Mueller S., Phoenix TN, van der Lugt J, **Hernaez M**, Guruceaga E, Koschmann C, Venneti S, Allen JE, Dun MD, Fueyo J, Gomez-Manzano C, Gallego Perez-Larraya J, Patiño-García A, Labiano S, Alonso MM*, *The oncolytic adenovirus Delta-24-RGD in combination with ONC201 induces a potent antitumor response in pediatric high-grade and diffuse midline glioma models*, **Neuro-oncology**, 2024.

doi: 10.1093/neuonc/noae066

- Patiño-García A*, Guruceaga E, Andueza MP, Ocón M, Fodop Sokoudjou JJ, de Villalonga Zornoza N, Alkorta-Aranburu G, Tamayo I, Gurpide A, Camps C, Jantus-Lewintre E, Navamuel-Andueza M, Sanmamed MF, Melero I, Elgendy M, Fusco JP, Zulueta JJ, de-Torres JP, Bastarrika G, Seijo L, Pio R, Montuenga LM, **Hernaez M**, Ochoa I, Perez-Gracia JL*, *Whole exome sequencing and machine learning germline analysis of individuals presenting with extreme phenotypes of high and low risk of developing tobacco-associated lung adenocarcinoma*, **EBioMedicine**, 2024.
  doi: 10.1016/j.ebiom.2024.105048

- Barace S, Santamaría E, Infante S, Arcelus S, De La Fuente J, Goñi E, Tamayo I, Ochoa I, Sogbe M, Sangro B, **Hernaez M**, Avila MA*, Argemi J*, *Application of Graph Models to the Identification of Transcriptomic Oncometabolic Pathways in Human Hepatocellular Carcinoma. Biomolecules*, 2024.
  doi: 10.3390/biom14060653.

- Naro D, Delgado J, Llorente S, **Hernaez M**, *Use of Beacon v2 for Improving Genomics Based Research in a Clinical Setting*, **Studies in Health Technology and Informatics**, 2024.
  doi: 10.3233/SHTI240636

- Torella L, Klermund J, Bilbao-Arribas M, Tamayo I, Andrieux G, Chmielewski KO, Vales A., Olagüe C, Moreno-Luqui D, Raimondi I, Abad A, Torrens-Baile J, Salido E, Huarte M, **Hernaez M**, Boerries M, Cathomen T, Zabaleta N, Gonzalez-Aseguinolaza G*, *Efficient and Safe Therapeutic Use of Paired Cas9-Nickases for Primary Hyperoxaluria Type 1*, **EMBO Molecular Medicine**, 2024.
  doi: 10.1038/s44321-023-00008-8

2023

- Blatti C, de la Fuente J, Gao H, Marín-Goñi I, Chen Z, Zhao SD, Tan W, Weinshilboum R, Kalari KR, Wang L*, **Hernaez M***, *Bayesian Machine Learning Enables Identification of Transcriptional Network Disruptions Associated with Drug-Resistant Prostate Cancer*. **Cancer Research**, 2023.
  doi: 10.1158/0008-5472.CAN-22-1910.

- Bakr S, Brennan K, Mukherjee P, Argemi J, **Hernaez M***, Gevaert O*, *Identifying key multi-functional components shared by critical cancer and normal liver pathways via SparseGMM*, **Cell Reports Methods**, 2023
  doi: 10.1016/j.crmeth.2022.100392.

- Calviño C, Ceballos C, Alfonso A, Jauregui P, Calleja-Cervantes ME, San Martin-Uriz P, Rodriguez-Marquez P, Martin-Mallo A, Iglesias E, Abizanda G, Rodriguez-Diaz S, Martinez-Turrillas R, Illarramendi J, Viguria MC, Redondo M, Rifon J, Villar S, Lasarte JJ, Inoges S, Lopez-Diaz de Cerio A, **Hernaez M***, Prosper F*, Rodriguez-Madoz JR*, *Optimization of universal allogeneic CAR-T cells combining CRISPR and transposon-based technologies for treatment of acute myeloid leukemia*. **Frontiers in Immunology**, 2023.
  doi: 10.3389/fimmu.2023.1270843.

- Traniello IM, Bukhari SA, Dibaeinia P, Serrano G, Avalos A, Ahmed AC, Sankey AL, **Hernaez M**, Sinha S, Zhao SD, Catchen J, Robinson GE*. *Single-cell dissection of aggression in honeybee colonies*, **Nature Ecology and Evolution**, 2023.
  doi: 10.1038/s41559-023-02090-0.

- Ainciburu M, Ezponda T, Berastegui N, Alfonso-Pierola A, Vilas-Zornoza A, San Martin-Uriz P, Alignani D, Lamo-Espinosa J, San-Julian M, Jiménez-Solas T, Lopez F, Muntion S, Sanchez-Guijo F, Molero A, Montoro J, Serrano G, Diaz-Mazkiaran A, Lasaga M, Gomez-Cabrero D, Diez-Campelo M, Valcarcel D, **Hernaez M**, Romero JP*, Prosper F*. *Uncovering perturbations in human hematopoiesis associated with healthy aging and myeloid malignancies at single-cell resolution*, **Elife**, 2023.
  doi: 10.7554/eLife.79363.

- Basurco L, Abellanas MA, Ayerra L, Conde E, Vinueza-Gavilanes R, Luquin E, Vales A, Vilas A, Martin-Uriz PS, Tamayo I, Alonso MM, **Hernaez M**, Gonzalez-Aseguinolaza G, Clavero P, Mengual E, Arrasate M, Hervás-Stubbs S, Aymerich MS*, *Microglia and astrocyte activation is region-dependent in the α-synuclein mouse model of Parkinson's disease*, **Glia**, 2023.
  doi: 10.1002/glia.24295.

2022

- Rodriguez-Marquez P, Calleja-Cervantes ME, Serrano G, Oliver-Caldes A, Palacios-Berraquero ML, Martin-Mallo A, Calviño C, Español-Rego M, Ceballos C, Lozano T, San Martin-Uriz P, Vilas-Zornoza A, Rodriguez-Diaz S, Martinez-Turrillas R, Jauregui P, Alignani D, Viguria MC, Redondo M, Pascal M, Martin-Antonio B, Juan M, Urbano-Ispizua A, Rodriguez-Otero P, Alfonso-Pierola A, Paiva B, Lasarte JJ, Inoges S, Lopez-Diaz de Cerio A, San-Miguel J, Fernandez de Larrea C, **Hernaez M***, Rodriguez-Madoz JR*, Prosper F*. CAR density influences antitumoral efficacy of BCMA CAR T cells and correlates with clinical outcome. **Science Advances**. 2022.
  doi: 10.1126/sciadv.abo0514.

- Goyal M, Serrano G, Argemi J, Shomorony I, **Hernaez M***, Ochoa I*, *JIND: joint integration and discrimination for automated single-cell annotation*, **Bioinformatics**. 2022
  doi: 10.1093/bioinformatics/btac140.

- Peng J, Serrano G, Traniello IM, Calleja-Cervantes ME, Chembazhi UV, Bangru S, Ezponda T, Rodriguez-Madoz JR, Kalsotra A, Prosper F, Ochoa I*, **Hernaez M***, *SimiC enables the inference of complex gene regulatory dynamics across cell phenotypes*. **Communications Biology**. 2022
  doi: 10.1038/s42003-022-03319-7.

- Berastegui N, Ainciburu M, Romero JP, Garcia-Olloqui P, Alfonso-Pierola A, Philippe C, Vilas-Zornoza A, San Martin-Uriz P, Ruiz-Hernández R, Abarrategi A, Ordoñez R, Alignani D, Sarvide S, Castro-Labrador L, Lamo-Espinosa JM, San-Julian M, Jimenez T, López-Cadenas F, Muntion S, Sanchez-Guijo F, Molero A, Montoro MJ, Tazón B, Serrano G, Diaz-Mazkiaran A, **Hernaez M**, Huerga S, Bewicke-Copley F, Rio-Machin A, Maurano MT, Díez-Campelo M, Valcarcel D, Rouault-Pierre K, Lara-Astiaso D, Ezponda T*, Prosper F*, *The transcription factor DDIT3 is a*

potential driver of dyserythropoiesis in myelodysplastic syndromes. **Nature Communications**, 2022.
doi: 10.1038/s41467-022-35192-7.

2021

- **Hernaez M***. *Towards scalable genomic data access*. **Nature Computational Science**. 2021
doi: 10.1038/s43588-021-00089-w.

- Voges J, **Hernaez M**, Mattavelli M, Ostermann J*. *An introduction to mpeg-g: the first open iso/iec standard for the compression and exchange of genomic sequencing data*. **Proceedings of the IEEE**. 2021.
doi: 10.1109/JPROC.2021.3082027

- Chembazhi UV, Bangru S, **Hernaez M**, Kalsotra A*. *Cellular plasticity balances the metabolic and proliferation dynamics of a regenerating liver*. **Genome Research**. 2021
doi: 10.1101/gr.267013.120.

2020

- **Hernaez M***, Blatti C, Gevaert O, *Comparison of single gene and module-based methods for modeling gene regulatory networks*, **Bioinformatics**, 2020.
doi: 10.1093/bioinformatics/btz549

- Meng Q, Ochoa I, **Hernaez M***, *GPress: a framework for querying General Feature Format (GFF) files and expression files in a compressed form*, **Bioinformatics**, 2020.
doi: 10.1093/bioinformatics/btaa604

- Voges J, Paridaens T, Müntefering F, Mainzer LS, Bliss B, Yang M, Ochoa I, Fostier J, Ostermann J*, **Hernaez M***. *GABAC: an arithmetic coding solution for genomic data*. **Bioinformatics**. 2020
doi: 10.1093/bioinformatics/btz922.

- No A, **Hernaez M***, Ochoa I*. *CROMqs: An infinitesimal successive refinement lossy compressor for the quality scores*. **Journal of Bioinformatics and Computational Biology**. 2020
doi: 10.1142/S0219720020500316.

- Gevaert O*, Nabian M, Bakr S, Everaert C, Shinde J, Manukyan A, Liefeld T, Tabor T, Xu J, Lupberger J, Haas BJ, Baumert TF, **Hernaez M**, Reich M, Quintana FJ, Uhlmann EJ, Krichevsky AM, Mesirov JP, Carey V, Pochet N*. *Imaging-AMARETTO: An Imaging Genomics Software Tool to Interrogate Multiomics Networks for Relevance to Radiography and Histopathology Imaging Biomarkers of Clinical Outcomes*. **JCO Clinical Cancer Informatics**. 2020
doi: 10.1200/CCI.19.00125.

2019

- Chandak S*, Ochoa I, **Hernaez M***, Weissman T, *SPRING: a next-generation compressor for FASTQ data*, **Bioinformatics**, 2019.
  doi: 10.1093/bioinformatics/bty1015.

- **Hernaez M***, Pavlichin D, and Weissman T, Ochoa I*, *Genomic Data Compression*, **Annual Review of Biomedical Data Science**, 2019.
  doi: 10.1146/annurev-biodatasci-072018-021229

- Fisher-Hwang I, Ochoa I, Weissman T, **Hernaez M***, *Denoising of Aligned Genomic Data*, **Scientific Reports**, 2019.
  doi: 10.1038/s41598-019-51418-z

- Ochoa I, Li H, Baumgarte F, Hergenrother C, Voges J, **Hernaez M**, *AliCo: A New Efficient Representation for SAM Files*, **Proceedings of the Data Compression Conference (DCC)**, 2019.
  doi: 10.1109/DCC.2019.00017.

- Zheng H, Brennan K, **Hernaez M**, Gevaert O*, *Benchmark of lncRNA Quantification for RNA-Seq of Cancer Samples*, **GigaScience**, 2019.
  doi: 10.1093/gigascience/giz145.

- Kendig KI, Baheti S, Bockol MA, Drucker TM, Hart SN, Heldenbrand JR, **Hernaez M**, Hudson ME, Kalmbach MT, Klee EW, Mattson NR, Ross CA, Taschuk M, Wieben ED, Wiepert M, Wildman DE, Mainzer LS*. *Sentieon DNASeq Variant Calling Workflow Demonstrates Strong Computational Performance and Accuracy*. **Frontiers in Genetics**. 2019
  doi: 10.3389/fgene.2019.00736.

- Seimetz J, Arif W, Bangru B, **Hernaez M**, Kalsotra A, *Cell-type specific polysome profiling from mammalian tissues*, **Methods**, 155, 2019.
  doi: 10.1016/j.ymeth.2018.11.015

2018

- Rogusky L, Ochoa I, **Hernaez M**, Deorowicz S*, *FaStore - a space-saving solution for raw sequencing data*, **Bioinformatics**, 2018.
  doi: 10.1093/bioinformatics/bty205

- Voges J, Oesterman J, **Hernaez M***, *CALQ: compression of quality values of aligned sequencing data*, **Bioinformatics**, 2018.
  doi: 10.1093/bioinformatics/btx737

2017

- Long R, **Hernaez M**, I Ochoa, T Weissman, *GeneComp, a new reference-based compressor for SAM files*, **Proceedings of the Data Compression Conference (DCC)**, 2017.

doi: 10.1109/DCC.2017.76.

- Ochoa I*, **Hernaez M**, Goldfeder R, Weissman T, Ashley E. *Effect of lossy compression of quality scores on variant calling*. **Briefings in Bioinformatics**. 2017.
  doi: 10.1093/bib/bbw011.

2016

- Tatwawadi T.*, **Hernaez M**, Ochoa I, and Weissman T, *GTRAC: fast retrieval from compressed collections of genomic variants*, **Bioinformatics**, 2016.
  doi: 10.1093/bioinformatics/btw437.

- Alberti C, Daniels , **Hernaez M**, Voges J, Goldfeder RL, Hernandez-Lopez AA, Mattavelli M, Berger B, *An Evaluation Framework for Lossy Compression of Genome Sequencing Quality Values*, **Proceedings of the Data Compression Conference (DCC)**, 2016.
  doi: 10.1109/DCC.2016.39.

- Ochoa I, **Hernaez M**, Goldfeder RL, Weissman T, Ashley E, *Denoising of Quality Scores for Boosted Inference and Reduced Storage*, **Proceedings of the Data Compression Conference (DCC)**, 2016.
  doi: 10.1109/DCC.2016.92.

- **Hernaez M**, Ochoa I, Weissman T, *A cluster-based approach to compression of Quality Scores*, **Proceedings of the Data Compression Conference (DCC)**, 2016.
  doi: 10.1109/DCC.2016.49

- Deorowicz S*, Grabowski S, Ochoa I*, **Hernaez M**, Weissman T. *Comment on: 'ERGC: an efficient referential genome compression algorithm'*. **Bioinformatics**. 2016.
  doi: 10.1093/bioinformatics/btv704.

2015

- Malysa G, **Hernaez M***, Ochoa I*, Rao M, Ganesan K, Weissman T, *QVZ: lossy compression of quality values*, **Bioinformatics**, 2015.
  doi: 10.1093/bioinformatics/btv330.

- Alustiza I, **Hernaez M**, Crespo P,*Design of a new scheme for multi-hop wireless networks using decode-and-forward strategy*, **EURASIP Journal on Wireless Communications and Networking**. 2015.
  doi: 10.1186/s13638-015-0372-8.

2014

- Ochoa I, **Hernaez M** and Weissman T, *Aligned genomic data compression via improved modeling*, **Journal of bioinformatics and computational biology**, 2014.
  doi: 10.1142/S0219720014420025.

- Ochoa I*, **Hernaez M** and T. Weissman, *iDoComp: a compression scheme for assembled genomes*, **Bioinformatics**, 2014.
  doi: 10.1093/bioinformatics/btu698

2013

- **Hernaez M**, Crespo PM, Del Ser J, *On the Design of a Novel Joint Network-Channel Coding Scheme for the Multiple Access Relay Channel*, **IEEE Journal on Selected Areas in Communications**, 2013.
  doi: 10.1109/JSAC.2013.130802

- **Hernaez M**, Crespo PM, Del Ser J, *A Decode-and-Forward Scheme for Multihop Wireless Networks*, **Proceedings of the IEEE Vehicular Technology Conference (VTC2013-Fall)**, 2013
  doi: 10.1109/VTCFall.2013.6692030.

- Alustiza I, **Hernaez M**, Insasusti X, Crespo PM, *Teaching Information Theory via a Simulation Tool for Communications Systems*, **IEEE Collaborative Learning & New Pedagogic Approaches in Engineering Education (IEEE EDUCON)**, 2013.
  doi: 10.1109/EduCon.2013.6530098

2012

- **Hernaez M**, Crespo PM, Del Ser J, *A Flexible Channel Coding Approach for Short-Length Codewords*, **IEEE Communications Letters**, 2012.
  doi: 10.1109/LCOMM.2012.073112.121295.

2011

- **Hernaez M**, Crespo PM, *A novel Scheme for Message-Forwarding in Ad-Hoc Wireless Networks*, **Proceedings of the IEEE Vehicular Technology Conference (VTC2011-Spring)**, 2011.
  doi: 10.1109/VETECS.2011.5956446.

- **Hernaez M**, Crespo PM, Del Ser J, *Joint Non-Binary LDPC-BICM and Network Coding with Iterative Decoding for the Multiple Access Relay Channel*, **Proceedings of the IEEE Vehicular Technology Conference (VTC2011-Spring)**, 2011.
  doi: 10.1109/VETECS.2011.5956367.

2010

- Ochoa I, Crespo P, **Hernaez M**, *LDPC Codes for Non-Uniform Memoryless Sources and Unequal Energy Allocation*, **IEEE Communications Letters**, 2010.
  doi: 10.1109/LCOMM.2010.09.100662.

- Ochoa I, Crespo P, Del Ser J, **Hernaez M**, *Turbo Joint Source-Channel Coding of Non-Uniform*

Memoryless Sources in the Bandwidth-Limited Regime, **IEEE Communications Letters**, 2010. doi: 10.1109/LCOMM.2010.04.092462

- Ochoa I, Crespo PM, Del Ser J, **Hernaez M**. *Joint Turbo Coding and Source-Controlled Modulation of Cycle-Stationary Sources in the Bandwidth-Limited Regime.* **Mobile Lightweight Wireless Systems**, 2010. doi: 10.1007/978-3-642-16644-0_53.

2009

- **Hernaez M***, Crespo PM, Del Ser J, Garcia-Frias J, *Serially-Concatenated LDGM Codes for Correlated Sources over Gaussian Broadcast Channels*, **IEEE Communications Letters**, 2009. doi: 10.1109/LCOMM.2009.091289

Patents

- Voges J, **Hernaez M**, Ostermann J, *Method for encoding and decoding of quality values of a data structure*, US Patent App. 16/341,307, 2021.

- Chandak S, Tatwawadi K, Weissman T, Ochoa I, **Hernaez M**, *Systems and Methods for Compressing Genetic Sequencing Data and Uses Thereof* , US Patent App. 16/545,751, 2020

Scholarships and Awards

ISO/IEC Excellence Award	*2023*
Ramon y Cajal Fellowship, Spanish Ministry of Science (Spanish National Career Award)	*2023*
Marie S. Curie fellowship, ERC (European Pathway to Independence Award)	*2020*
Stanford Data Science Initiative Postdoctoral Fellowship	*2015-2016*
Enigmedia, inc. named "Best New Company of the Basque Country" (Spain)	*2013*
University of Navarra Fellowship for PhD program	*2009–2011*
Telefonica Fellowship for Master's thesis (largest Teleco. operator in Spain)	*2008*

Service Activities

Workshop Organization Committees:

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

Professional Organizations:

- International Society of Computational Biology (ISCB): Member

- Stanford Compression Forum: Organizer of the first and second edition (2015 - 2016)
- 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).
- Stanford Data Science Initiative (SDSI): Active member and grantee (2014 - 2016)
- Center for Science of Information (CSoI), 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.