Hugo Armando GUILLEN-RAMIREZ
PhD in Computer Science

Contents

Education

2018 PhD in Computer Science
Specialization: Machine Learning applied to biological datasets
CICESE Research Center, Mexico

2014 MSc in Computer Science
Specialization: Theoretical models of computation
CICESE Research Center, Mexico

2011 Bachelor’s in Computer Systems Engineering
Specialization: Distributed applications and systems
Instituto Tecnológico de Tepic, México

Articles in peer-reviewed journals

2026
Guillen-Ramirez, H., … , Beldi, G., & Endrich, O. (2026). LLM-augmented semantic embeddings enable Cross-Lingual mapping of medical procedure terms. *Scientific Reports*. https://doi.org/10.1038/s41598-025-34778-7

2025
Guillen-Ramirez, H., Sanchez-Taltavull, D., Perrodin, S., Peisl, S., Triep, K., Gaudet-Blavignac, C., ... & Beldi, G. (2025). Prediction of postoperative infections by strategic data imputation and explainable machine learning. Journal of the American Medical Informatics Association, 32(11), 1706-1717. https://doi.org/10.1093/jamia/ocaf145

Zwicky, S. N., Spari, D., Rodjakovic, D., **Guillen-Ramirez, H.**, Yilmaz, B., & Beldi, G. (2025). Preoperative Enterosignatures Predict Surgical Site Infections After Abdominal Surgery. In Open Forum Infectious Diseases (Vol. 12, No. 9, p. ofaf549). US: Oxford University Press. https://doi.org/10.1093/ofid/ofaf549

2024
Peisl, S., Sánchez-Taltavull, D., **Guillen-Ramirez, H.**, Tschan, F., Semmer, N. K., Hübner, M., ... & Keller, S. (2024). Noise in the operating room coincides with surgical difficulty. BJS open, 8(5), zrae098. https://doi.org/10.1093/bjsopen/zrae098

Peisl, S., **Guillen-Ramirez, H.**, Sánchez-Taltavull, D., Widmer, A., Sommerstein, R., & Beldi, G. (2024). Influence of patient characteristics on microbial composition in surgical-site infections: insights from national surveillance study. British Journal of Surgery, 111(6), znae138. https://doi.org/10.1093/bjs/znae138

Dhaka, B., Zimmerli, M., Hanhart, D., Moser, M. B., **Guillen-Ramirez, H.**, Mishra, S., ... & Johnson, R. (2024). Functional identification of cis-regulatory long noncoding RNAs at controlled false discovery rates. Nucleic Acids Research, 52(6), 2821-2835. https://doi.org/10.1093/nar/gkae075

2023 and earlier

Esposito, R., …, **Guillen-Ramirez, H.,** ... & Johnson, R. (2023). Tumour mutations in long noncoding RNAs enhance cell fitness. Nature communications, 14(1), 3342. https://doi.org/10.1038/s41467-023-39160-7

Esposito, R., …, **Guillen-Ramirez, H.A.**, …, & Johnson, R. (2022). Multi-hallmark long noncoding RNA maps reveal non-small cell lung cancer vulnerabilities. Cell genomics, 2(9), p.100171. https://doi.org/10.1016/j.xgen.2022.100171

Bosch-Guiteras, N., Uroda, T., **Guillen-Ramirez, H.A.**, Riedo, R., Gazdhar, A., Esposito, R., Pulido-Quetglas, C., Zimmer, Y., Medová, M. & Johnson, R. (2021). Enhancing CRISPR deletion via pharmacological delay of DNA-PKcs. Genome Research. https://doi.org/10.1101/gr. 265736.120

Aguilera-Mendoza, L., Marrero-Ponce, Y., García-Jacas, C. R., Chavez, E., Beltran, J. A., **Guillen-Ramirez, H. A.**, & Brizuela, C. A. (2020). Automatic construction of molecular similarity networks for visual graph mining in chemical space of bioactive peptides: an unsupervised learning approach. Scientific reports, 10(1), 1-23. https://doi.org/10.1038/s41598-020-75029-1

Calvillo-Vázquez, J. G., **Guillén-Ramírez, H. A.**, DiazDuarte-Rodríguez, M., Licea-Claverie, A., & Méndez, E. R. (2019). Particle size distribution from extinction and absorption data of metallic nanoparticles. Applied optics, 58(36), 9955-9966. https://doi.org/10.1364/AO.58.009955

Aguilera-Mendoza, L., Marrero-Ponce, Y., Beltran, J. A., Tellez Ibarra, R., **Guillen-Ramirez, H. A.**, & Brizuela, C. A. (2019). "Graph-based data integration from bioactive peptide databases of pharmaceutical interest: toward an organized collection enabling visual network analysis." Bioinformatics. https://doi.org/10.1093/bioinformatics/btz260

Guillen-Ramirez, H. A., & Martínez-Pérez, I. M. (2018). "Classification of riboswitch sequences using k-mer frequencies". Biosystems, 174, 63-76. https://doi.org/10.1016/j.biosystems. 2018.09.001

Articles in proceedings

2018: Ibarra-Hernández, R. F., Bertin, N., Alonso-Arévalo, M. A., & **Guillén-Ramírez, H. A.** (2018). "A benchmark of heart sound classification systems based on sparse decompositions". In Society of Photo-Optical Instrumentation Engineers (SPIE) Conference Series (Vol. 10975). https://doi.org/10.1117/12.2506758

2017: Guillen-Ramirez, H. A., Colbes, J., Brizuela, C. A., & Martinez-Perez, I. M. (2017). "Accurate classification of immunomodulatory RNA sequences". In 2017 International Joint Conference on Neural Networks (IJCNN) (pp. 236-241). IEEE. https://doi.org/10.1109/IJCNN.2017.7965860

2013: Brizuela, C. A., Luna-Taylor, J. E., Martinez-Perez, I., **Guillen, H. A.,** Rodriguez, D. O., & Beltran-Verdugo, A. (2013). "Improving an evolutionary multi-objective algorithm for the biclustering of gene expression data". In 2013 IEEE Congress on Evolutionary Computation (pp. 221-228). IEEE. https://doi.org/10.1109/CEC.2013.6557574

Preprints

Guillen-Ramirez, H., Triep, K., Gaudet-Blavignac, C., Phull, B., Beldi, G., & Endrich, O. (2025). MAP-CARE: Enhancing Cross-Lingual Medical Intervention Terms Analysis Through LLM-supported Semantic Embeddings. https://doi.org/10.21203/rs.3.rs-6848278/v1

Conference presentations and posters

[TO ADD: day of clinical research 2024 2025]

Poster: *Intraoperative Vital Sign Variability as Early Warning Signals of Postoperative Infection.*
Blatter T., Wintsch Y., Triep K., Endrich O., Guillen-Ramirez H.A., Beldi G.
MCID Annual Event 2025, Switzerland.

Poster: *MAP-CARE: Advancing International Healthcare Through Enhanced Multilingual Medical Terminology Analysis.*
Guillen-Ramirez H., Triep K., Beldi G., Endrich O.
Precision Health Day 2025, USI–SUPSI, Switzerland.

Talk: *Implementing Semantic Search for Cohort Selection Using Procedure-Based CHOP Codes.*
Guillen-Ramirez H., Triep K., Endrich O., Beldi G.
Annual Meeting of SGG-SGVC-SASL & SVEP 2024, Switzerland.

Talk: *Prediction of Postsurgical Infection by Explainable AI and Strategic Data Imputation.*
Guillen-Ramirez H., Sanchez-Taltavull D., Peisl S., Perrodin S., Triep K., Endrich O., Beldi G.
Annual Meeting of SGG-SGVC-SASL & SVEP 2024, Switzerland.

Talk: *Early Prediction of Postsurgical Infections Using a Bayesian Approach.*
Guillen-Ramirez H., Sanchez-Taltavull D., Peisl S., Perrodin S., Triep K., Endrich O., Beldi G.
Annual Meeting of SGG-SGVC-SASL & SVEP 2023, Switzerland.

Talk: *Age Is an Independent Predictor for the Shift From Skin to Intestinal Microbes in Surgical Site Infections Across Different Types of Procedures.*
Peisl S., Guillen-Ramirez H., Sanchez-Taltavull D., Sommerstein R., Beldi G.
Annual Meeting of SGG-SGVC-SASL & SVEP 2023, Switzerland.

Poster: *GeneHTracker: Improving Reproducibility and Reusability of Datasets Based on Gene Identifiers.*
Guillen-Ramirez H.A., Johnson R.
21st European Conference on Computational Biology (ECCB 2022), Sitges, Barcelona.

Poster: *Transposable Elements as Functional Domains of Long Noncoding RNAs.*
Guillen-Ramirez H.A., Johnson R.
2020 Virtual Meeting on Transposable Elements, Cold Spring Harbor Laboratory.

Talk: *Accurate Classification of Immunomodulatory RNA Sequences.*
Guillen-Ramirez H.A., Colbes J., Brizuela C.A., Martinez-Perez I.M.
International Joint Conference on Neural Networks (IJCNN 2017), Anchorage, Alaska, USA.

Poster: *Simulation of a Programmable Molecular Computer.*
Guillen H.A., Martinez-Perez I.
21st International Conference on DNA Computing and Molecular Programming (DNA 2015), Boston, USA.

Talk: *Challenges in the Prediction of Non-Coding RNA Genes* (translated from Spanish).
Guillen H.A., Martinez-Perez I.
National Meeting on Computer Science (Encuentro Nacional de Ciencias de la Computación, ENC 2014), Mexico.

Poster: *Design of a Tissue P-System for Solving the MAX-CLIQUE Problem* (translated from Spanish).
Guillen H.A., Martinez-Perez I.
6th International Congress on Computer Science (CiComp 2013), Mexico.

Grants and awards

[TO ADD: SHINE]

2025-2029: Digitalization Commission of the University of Bern (DigiK UniBE) "Secure International Collaboration: Advancing Medical AI with Federated Learning and Synthetic Data" (**500'000.00 CHF**) (Switzerland)

2021 – 2023: Marie Skłodowska-Curie Individual Fellowship, European Commission "Computational genomics of long noncoding RNA domains across metazoans" (**€196,590.72**) (Ireland)

2011 – 2018: CONACYT National Scholarship for master and doctoral studies (Mexico).

Thesis supervision

2021 – 2022: Co-supervised two master's theses: **Mateusz Brodzik** (Universitat Pompeu Fabra (UPF), Spain) and **Jules Montuelle** (Université de Fribourg, Switzerland).

Teaching

2025

- *Introduction to R* — Faculty of Medicine, University of Bern, Switzerland. **Graduate level**.
- *Introduction to Clinics* — Artificial Intelligence in Medicine Master's Program, University of Bern, Switzerland. **Graduate level**.
- *Medical Informatics* — Biomedical Engineering Master's Program, University of Bern, Switzerland. **Graduate level**.

2024

- *Introduction to Clinics* — Artificial Intelligence in Medicine Master's Program, University of Bern, Switzerland. **Graduate level**.

2023

- *Introduction to Clinics* — Artificial Intelligence in Medicine Master's Program, University of Bern, Switzerland. **Graduate level**.

2022 and earlier

2022

- *The RNA World* — University College Dublin, Ireland. **Graduate level**.

2019

- *Cancer Genomics* — University of Bern, Switzerland. **Graduate level**.
- *Computational Biology (Genome Indexing Algorithms)* — CICESE Research Center, Mexico. **Graduate level**.

2017–2019

- *Artificial Intelligence*, *Advanced Mathematics for Engineering*, *Evolutionary Computing*, and *Assembly Language* — Autonomous University of Baja California, Mexico. **Undergraduate level**.

2017–2018

- *Mathematics II, IV, V*, *Intermediate Algebra I & II*, and *Mathematical Reasoning V & VI* — Xochicalco High School, Mexico. **High school level**.

Invited talks

[TO ADD: Mexico, 2025]

2020, Oct “Discrete mathematics and the design of CRISPR-Cas9 genome editing libraries" at Instituto Tecnológico de Tepic, Mexico.

2017, Mar “Score functions for discriminant k-mers and their application in ncRNA classification" (translated from Spanish) at CICESE Research Center, Mexico.

2016, Oct “Methods for ncRNA gene prediction: RNA secondary structure alternative graph representations" (translated from Spanish) in the XII National Meeting on Mathematical Biology (Center of Mathematical Sciences, UNAM Campus Morelia), Mexico.

2016, Oct “Bio-computing: RNA, BioPython, and Graphs" (translated from Spanish) in the Computer Science Fall School at CICESE Research Center, Mexico.

Attended courses

2025 Supervising Master's Theses and Doctoral Dissertations. University of Bern, Switzerland.

2025 From Idea to Impact: Crafting Successful Grant Proposals. University of Bern, Switzerland.

2025 Missing Data and Imputation Methods (Swiss Institute of Bioinformatics), Lausanne, Switzerland.

2025 Causal Inference (Swiss Institute of Bioinformatics), Basel, Switzerland.

2025 Federated Learning in Bioinformatics (Swiss Institute of Bioinformatics), Lugano, Switzerland.

2023 Bayesian Statistics with R (Swiss Institute of Bioinformatics), Basel, Switzerland.

2023 How to illustrate your research results: Creating advanced vector graphics in Adobe Illustrator CC. University of Bern, Switzerland.

2022 EMBO Lab Leadership Postdoc Course (EMBO Laboratory Management Courses), streamed from Heidelberg, Germany.

2022 Networking For Postdocs - A Strategic Approach (University College Dublin), Ireland. 2022 Promoting Yourself And Your Research (University College Dublin), Ireland.

2022 Preparing Academic Applications And Interviews For Postdocs (University College Dublin), Ireland.

2022 Get That Paper Written And Published (University College Dublin), Ireland.

2022 Online Interview Skills For Postdocs (University College Dublin), Ireland.

2021 Single-cell Transcriptomics (Swiss Institute of Bioinformatics), streamed from Lausanne, Switzerland.

2021 Reproducible research and data analysis using Nextflow pipelines (Swiss Institute of Bioinformatics), streamed from Lausanne and Barcelona.

2021 Data Management Plan (Swiss Institute of Bioinformatics), streamed from Lausanne, Switzerland.

2020 Enrichment Analysis, (Swiss Institute of Bioinformatics), streamed from Lausanne, Switzerland.

2020 Advanced statistics: statistical modelling, (Swiss Institute of Bioinformatics), Lausanne, Switzerland.

2016 XVIII Fall School on Mathematical Biology (Center of Mathematical Sciences, UNAM Campus Morelia), Michoacán, Mexico.

2016 NGS Data Analysis and Informatics Conference, San Diego, USA.

2015 Applications of Artificial Organic Networks (National Meeting on Computer Science 2015), Baja California, Mexico.

Job descriptions

Job Title: Advanced Postdoctoral Researcher
Company: University of Bern
Location: Bern, Switzerland
From: 2023 – March
To: I currently work here
I am developing Machine Learning models trained on Real-World Data (RWD) and Real-World Evidence (RWE) for predicting clinical outcomes using human clinical data from the University Hospital. Additionally, I am researching the use of Deep Learning, Generative AI, and Large Language Models for sensitive data.

Job Title: MSCA Postdoctoral Fellow
Company: University College Dublin
Location: Dublin, Ireland
From: 2021 - July
To: 2023 - February
I held a Marie Skłodowska-Curie Individual Fellowship (H2020-MSCA-IF-2019) awarded by the European Commission for the project “Computational genomics of long noncoding RNA domains across metazoans". I routinely applied machine learning algorithms to several types of genomic data (genomic annotations, RNA-Seq, CRISPR screening readouts) and I also implemented my own pipelines in Python and R. Additionally, I designed and implemented structured databases to store my output data.

Job Title: Postdoctoral Researcher
Company: University of Bern
Location: Bern, Switzerland
From: 2019 - March
To: 2021 - July
I worked in the project: “Identification and functional prediction of lncRNA elements.” I implemented my own pipelines in Python and R to process genomics annotations and get insight into the functional regions of long noncoding RNAs. Additionally, I performed machine learning and feature engineering on biological data to predict long noncoding RNA molecules properties such as subcellular localisation.

I worked in the project: “Identification and functional prediction of lncRNA elements.” I developed Python scripts for feature engineering, automatic machine learning, network visualization, statistical testing on genomic regions, and pipelines for designing and processing CRISPR deletion libraries in bash, awk, Python and R.

Job Title: Postdoctoral Researcher
Company: CICESE Research Center
Location: Ensenada, Mexico
From: 2019 - January
To: 2019 - March
I worked in the project: “Finding research opportunities in Artificial Intelligence for the public health of the Mexican population.” I wrote a literature review on possible venues for applying NLP onto health records.

Job Title: Part-time Professor
Company: Autonomous University of Baja California
Location: Ensenada, Mexico
From: 2017 - August

To: 2019 - March
I taught the courses Artificial Intelligence, Advanced Mathematics for Engineering, Evolutionary Computing, and Assembly Language.

PhD Student
Company: CICESE Research Center
Location: Ensenada, Mexico
From: 2014 – January
To: 2018 – November
I developed a non-coding RNA (ncRNA) gene predictor based in homology search on known sequences supported by machine learning, meta-heuristics, and state-of-the-art biological information. I implemented my own visualisations for features derived from RNA secondary structures, pinpointing sites of interest within the RNA molecules.