Abelardo Aguilar Cámara

PhD Graduate Student

Miami, United States
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Skills

Python

R

Bash Scripting

GitHub

MATLAB Programming

Markdown

Languages

Spanish; Castilian

English

Hobbies

Bird Watching
Nature Photography
Gaming
Linux enthusiast

Profile

Dedicated researcher with experience in **bioinformatics** and **evolution,** with a proven track record**.** Currently a **PhD student** at the **University of Miami**, commited to work hard and serve my institution.

Links

ORCID

- 0000-0003-3133-0590

X (Twitter)

- https://twitter.com/abelardoacm

Github

- https://github.com/abelardoacm
- https://github.com/abelardoaguilar

Education

Biologist, National Autonomous University of Mexico, Mexico City

August 2014 — May 2019

Graduated with honors with the thesis entitled: "Study of the unitary activity of the human oncogenic channel Kv10.1 by noise analysis of its ionic current"

Master of Science, National Autonomous University of Mexico, Mexico City

January 2020 — March 2023

Graduated with honors with the thesis entitled: "Pangenomic study of single-stranded DNA viruses". Candidate for the Alfonso Caso.

PhD, University of Miami, Miami

August 2023 — Present

Engaging in advanced research focusing on the biophysics of viral capsids, seeking to understand their structural complexities.

Research Articles

A Note on the Potential Clinical Use of Sofosbuvir to Treat COVID-19: The Importance of Protease Inhibitors, SSRN Electronic Journal

January 2020

- *10.2139/ssrn.3653571*

Two short low complexity regions (LCRs) are hallmark sequences of the Delta SARS-CoV-2 variant spike protein, Scientific Reports 12, 938

January 2022

Becerra, A., Muñoz-Velasco, I., **Aguilar-Cámara, A. et al.**

- In charge of the bioinformatics process for the detection of low complexity regions in SARS-CoV-2 genomes (- *https://github.com/abelardoacm/SARS-COV2_LCRs)*
- *10.1038/s41598-022-04976-8*

Big impacts with small efforts: A spatial prioritization for amphibian conservation in the Sierra Madre del Sur, Mexico, Animal Conservation

January 2024

Fuentes, D., **Aguilar-Cámara, A. et al.**

- accepted in "Animal Conservation", in publication process

Participation in congresses

Analysis of metagenomes reveals potential ancestral candidates of tailed phages (Poster), Princeton University

January 2024

Bacteria versus Phage: the Main Event

Simplifying the enigma: Archaeal phylogenomics through a pangenomic approach and discrete characters (Talk), San Miguel de Allende

October 2023

VII Congress of Biochemistry and Molecular Biology of Bacteria

*awarded for outstanding talk

On ssDNA viral evolution: Insights from pangenomic analysis (Poster), Montpellier

September 2022

International Symposium on ssDNA Viruses (IS3DV)

Bayesian Phylogenetic Inference In Viral Evolution (Talk), Guanajuato

July 2023

Bioinformatics and Complex Networks Retreat

Low complexity regions detection in SARS CoV-2 variants (Talk), Tlaxcala

November 2021

2nd Colloquium on Applications of Molecular Biology

Pangenomic analysis of ssDNA viruses (Talk), National Autonomous University of Mexico

December 2021

PUMAVIR symposium

Research Internships

Institute for Integrative Systems Biology, Evolutionary Genetics Lab, Valencia

October 2018 — February 2019

Employed Big Data tools to assess genomic complexity metrics across more than 10,000 viral reference genomes and metagenomes.

Faculty of Sciencies (UNAM), Laboratory of Protists, Mexico City

August 2015 — August 2016

Preparation of ciliates samples for electron and bright field microscopy

Employment History

Lecturer, National Autonomous University of Mexico, Mexico City

August 2022 — July 2023

- Designed and delivered physics lessons tailored for Biology students, promoting active participation and discussions on current biological research topics, ensuring deep understanding.

Online course tutor, ATGenomics, Mexico City

January 2022 — Present

- Led R and Python classes tailored for biological science professionals leveraging my expertise in statistics and bioinformatics.

Research Assistant, University of Miami, Miami

August 2023 — Present

- Actively developing and refining bioinformatics tools tailored to model the distinct biophysical properties of viral capsids, drawing insights from genomic data.

Specialized courses

Finding Hidden Messages in DNA (Bioinformatics I), University of California San Diego in Coursera

November 2017

Genome Sequencing (Bioinformatics II), University of California San Diego in Coursera

December 2017

Comparing Genes, Proteins and Genomes (Bioinformatics III), University of California San Diego in Coursera

March 2018

Python Bioinformatics, ATGenomics

November 2021

References

Dr. Antoni Luque from University of Miami
antoni.luque@miami.edu

Dr. Arturo Carlos II Becerra Bracho from Faculty of Science (UNAM)
abb@ciencias.unam.mx

Dr. Arturo Picones Medina from Cell Physiology Institute (UNAM)
arturopicones@ciencias.unam.mx