

J. Cesar Ignacio Espinoza Ph.D.

(520) 270-2926 | e-mail: j.cesar.ignacio<at>gmail.com | **TN-Eligible**

Accomplished and energetic bioinformatics-trained biologist with a solid track of achievements in genomic and metagenomic research. Passionate and motivated, with an ample background in biological sciences, statistics, and scientific computing. Areas of expertise include next-generation sequencing analysis, genomics, microbiology, virus-host interactions, and molecular biology

Experience:

Jan 2018-Present **Research Laboratory Specialist.** Marine Environmental Biology, University of Southern California, PI: Jed A. Fuhrman. (Duties are a mix of lab manager and researcher)

- Led the development of a novel methodological technique to investigate virus-host interactions.
- Led the bioinformatic analyses built specifically for our experimental set up (above).
- Contributed with my virus expertise to the development of bioinformatic tools that identify putative hosts to environmental viruses.
- Analyze, summarize, and communicate research results in specialized meetings and symposia.
- Train undergraduate students and junior graduate students on the correct use of laboratory equipment.
- Monitor and enforce safety regulations.
- Schedule equipment and time for junior staff.
- Document and monitor sample collection and storage.
- Purchase laboratory supplies and kept ordering logs.
- Function as a system administrator of a small ubuntu-linux computing cluster providing technical support and mentorship to 15 researchers.

Sep 2015-Dec 2017 **Postdoctoral Research Fellow.** Marine Environmental Biology, University of Southern California, PI: Jed A. Fuhrman

- Led a meta transcriptomic project of a marine community looking to identify different patterns of viral expression.
- Led the metagenomic sequencing of a marine viral community over multiple time points spanning multiple years that showed the basic evolutionary principles that govern virus-host coevolution.
- Analyzed, summarized, and communicated research results in specialized meetings, symposia and publications.
- Assisted and mentored junior lab members.

Feb 2015-Sep 2015 **Postdoctoral Research Associate I.** Department of soil water and environmental science, University of Arizona, PI: Virginia I. Rich

- Contributed to the genome annotation of a novel genome of the phylum OP5.
- Developed the bioinformatic pipeline used to identify ecological clusters of the OP5 clade in permafrost samples.

Aug 2008-Jan 2015 **Graduate Research Assistant.** Department of molecular and cellular biology, University of Arizona, PI: Matthew B. Sullivan **(2008-2010: Fulbright Fellow)**

- Developed new software applications or customized existing applications to meet specific scientific project needs.
- Created novel computation approaches and visualization tools as required by research goals, this was a result of the novelty of the experimental molecular techniques used.
- Analyzed large molecular datasets such as genomic sequence data and proteomics to understand the biogeography and evolution of marine viruses.

Education:

- University of Arizona, Tucson, AZ. **Ph.D. Molecular and Cellular Biology**, December 2014.
- University of Arizona, Tucson, AZ. **M.Sc. Ecology and Evolutionary Biology**, August 2010.
- Tecnológico del Valle de Oaxaca, México. **B.Sc. Biology**, June 2007.

Awards and Scholarships:

- **Young Scientist Award**, International Conference on Genomics – Ocean, Qingdao, China, October 2018. 120,000 RMB (16,800 USD)
- **ISME17 Travel Award**, ISME17 Leipzig Germany, August 2018. 800 EUR (910 USD)
- **USC-CONACyT Provost Postdoctoral Fellowship**, Los Angeles CA, 2015-2017 136,000 USD
- **Galileo Circle Scholarship**, University of Arizona College of Science, April 2014. 1,000 USD
- **Complemento Scholarship**, Ministry of Public Education, Mexico, 2013-2014. 5,000 USD
- **IRES-SBR**, International Research Experience for Students, Station Biologique de Roscoff (SBR). 2009
- **Fulbright Scholarship**, University of Arizona. Ecology and evolutionary biology, 2008-2010. 43,000 USD
- **CONACyT Scholarship**, National Council for Science and Technology, Mexico, 2002-2007 60,000 MXN (~6,000) USD

Selected Publications:

Full list at google scholar: <https://tinyurl.com/yyzur6vv>

18 publications with 1918 citations; h-index: 13

Ignacio-Espinoza J.C., N. Ahlgren & J.A. Fuhrman (2019) [Long-term stability and Red Queen-like strain dynamics in marine viruses](#). *Nature Microbiology* 5:265-271

Brum*, J.R., **Ignacio-Espinoza***, J.C., Kim*, E.H., G. Trubl, R.M. Jones, S. Roux, N.C. VerBerkmoes, V.I. Rich, M.B. Sullivan. [Illuminating structural proteins in viral “dark matter” with metaproteomics](#). *PNAS* 113: 2436-2441

Deng, L. *, **Ignacio-Espinoza***, J.C., A. Gregory, B.T. Poulos, P. Hugenholtz & M.B. Sullivan. [Viral tagging reveals discrete populations in Synechococcus viral genome sequence space](#). *Nature* 513: 242–245.

Ignacio-Espinoza J.C. & M.B. Sullivan. [Phylogenomics of T4 cyanophages: lateral gene transfer in the 'core' and origins of host genes](#). *Environmental Microbiology* 14:2113-26.

**Equal contribution, strict alphabetical order*

Relevant Skills:

- Fully proficient in Perl.
- Working knowledge of R and shell scripting.
- Comfortable managing large datasets, often involving more than one type of data.
- Experienced developing novel molecular methodological techniques and building bioinformatic pipelines to analyze the results of these novel assays.
- 3+ years of experience as a systems administrator managing and maintaining an Ubuntu/Linux cluster, providing technical support, training, and mentorship to 14 researchers.
- 6+ years of experience working with metagenomics, proteomics and metatranscriptomics datasets in the context of virus-host interactions.
- Extensive experience developing bioinformatics pipelines, with emphasis in genomics and metagenomics and more recently RNA-RNA interactions.
- Well trained in molecular biology and microbiology techniques: PCR, DNA extraction, Cloning, RNA extraction, retro transcription, protein extraction, DNA-RNA-Protein quantification, agarose gels, western blots, sterile technique, next gen seq library preparation (all steps).
- Multivariate statistics.
- Familiar with the API workflows for most common bioinformatics public databases.
- Experience in writing grants and scientific communication, involving preparing manuscripts and giving invited talks.
- Spanish, native speaker.
- English, full professional proficiency.