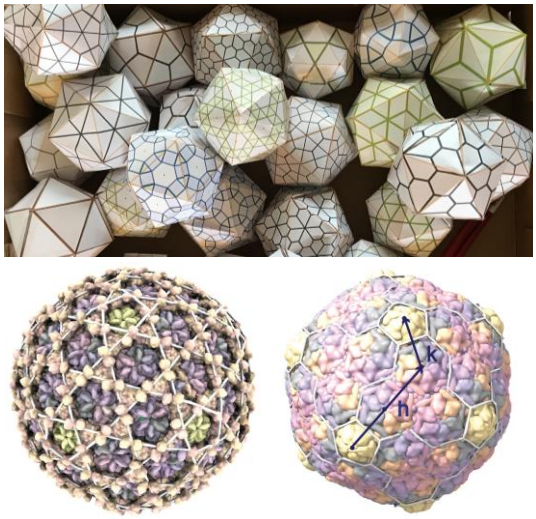
Bridging viral biophysics and evolution

Dr. Antoni Luque

Associate Professor
Department of Mathematics and Statistics
and Viral Information Institute
San Diego State University, CA



Viruses are the most abundant biological entity on Earth and play a pivotal role in regulating the evolution of organisms and the planet's biogeochemistry. Most viruses protect their genome in icosahedral shells made of multiple copies of the same protein. Viral icosahedral shells span two orders of magnitude in size, containing from 60 to several thousand structural proteins. Yet, the physical mechanisms that have evolved such diverse structures are unknown. In this talk, I will share my most recent contributions to this fundamental problem. First, I will introduce the generalized quasi-equivalence theory of icosahedral architectures, which I developed as a framework to investigate viral architectures and their protein components systematically. Second, I will show how my group built on the physical relationship between the protein shell and genome of viruses to predict the existence of unknown viruses from environmental samples. Finally, I will discuss our collaborative efforts to validate our predictions and explore new virus-based biotechnological applications.