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Viral Zoonoses And Human Adaptability - Integrating Multiomic Science With Machine Learning To Track Emergence

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It is widely considered that "new" viruses actually evolve from existing viruses. As with COVID-19, many emerging viral threats have evolved from their counterparts omnipresent in natural animal reservoirs. More recently, investigators have begun to use machine learning algorithms in order to explore viral diversity- a virosphere- that incorporates pathogen genomic information for analysis and study. However, viral evolution and emergence is dictated not only by the genome of the pathogen under consideration, but also a suite of environmental factors and conditions. Together, these factors determine the propensity of the pathogen to cause epidemics of global concern, and this true of natural events or deliberately engineered acts of aggression. Thus, in order to truly assess and understand viral emergence, it is important to to integrate pathogen genotype with phenotype, with structural biology, host-pathogen interactions and dynamics in order to develop a complete and physiologically relevant enterprise. Mechanistic modeling of such an integrated system, rather than a data steam, can potentially allow us to capture processes to target for diagnostics, therapeutics and surveillance development. Incorporating machine learning algorithms on a well curated system can provide predictive power- so as to identify processes of concern for early warning systems. Indeed, because viruses emerge from pre-existing ones, this approach can be streamlined for adaptability and flexibility to different classes of pathogens. Various aspects of this enterprise were exercised by scientists at Lawrence Berkeley National Laboratory during the COVID-19 pandemic, in collaboration with other institutions. Outcomes from these studies will be presented, as will our vision for a biological systems characterization capability which integrates these processes and complex assessments in a seamless manner.