Owing to rapid mutation, the evolution of RNA viruses such as influenza, Ebola and Zika occurs on a human timescale; rather than being forced to infer past evolutionary events, we can observe them in near real-time. In these cases of pathogens of intense public health relevance, an accurate and timely picture of ongoing evolution is especially important. The rapid antigenic evolution of influenza demands that the World Health Organization (WHO) issue twice-yearly recommendations for influenza vaccine strain choice. In the Northern Hemisphere, the February recommendation is used in the following winter’s vaccine, and thus vaccine choice amounts to forecasting the makeup of the viral population ~10 months in advance. While in the cases of Ebola and Zika, desired inferences are more epidemiological in nature, involving transmission chains and geographic spread. Here, I present tools that continually ingest publicly available sequence data to give a near real-time view of viral evolutionary dynamics. I also present methods to visualize ongoing virus evolution and to forecast future strain turnover. These methods are applicable to an increasing array of pathogens as sequencing becomes increasingly rapid and accessible.