

Coronavirus evolutionary tree can illuminate pandemic's 'past, present and possible future'

For anyone who knows how to look, the past, present, and possible futures of the new coronavirus can be found in its evolutionary tree. We are uncovering the tree now, bit by bit.

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The question now is: Can we read it fast enough to make a difference as we race to limit the virus's spread?

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It may already have made a difference in Seattle, where genome sequencing of the first two known Washington cases alerted researchers to weeks of silent viral spread, an insight impossible from positive tests alone. It was, in part, these clues about a larger, hidden outbreak that prompted swift social-distancing measures, long before test results began to catch up.

For now, during this period of extreme social distancing, a major priority is to implement [widespread diagnostic testing](#) to learn where and how quickly the virus is spreading. Eventually, [expanded testing and contact tracing](#) may tell us who should stay home and who might safely go back to work, letting the economy restart. But the case of Seattle points toward a more distant future [in which](#) routine genome sequencing can also [guide our public-health response](#).

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