

## Infographic: Fighting the coronavirus pandemic with collaborative science and data sharing

On February 27, a teenager in the Seattle area was diagnosed with [Covid-19](#). Shortly after, researchers at the Seattle Flu Study shared [genomic](#) data about his strain of the virus with other researchers on an “open science” site.

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[Researchers] determined that the teenager’s strain was a direct descendent of a strain of [Covid-19](#) found in an unrelated patient in the Seattle area on January 20. The discovery was a key link in concluding that the virus had been spreading in the Seattle area for weeks.

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Credit: Nextstrain

The way researchers connected those dots highlights the role of open science projects in tracking the evolution of Covid-19 and other diseases. Sharing data and working collaboratively across the web, scientists are quickly analyzing genetic samples, helping to shape the public response. But the rush to interpret the data also creates new risks.

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Nextstrain cofounder Trevor Bedford, a researcher at the Fred Hutchinson Cancer Research Center in Seattle, [wrote](#) on Twitter that a strain circulating in Lombardy, Italy, was related to one found in Munich, Germany, that public health officials had said was contained.

Other scientists disagreed with Bedford’s analysis, as noted by [Science magazine](#).

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Nextstrain is an important tool, but genetic data has to be considered alongside other data as well.

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