

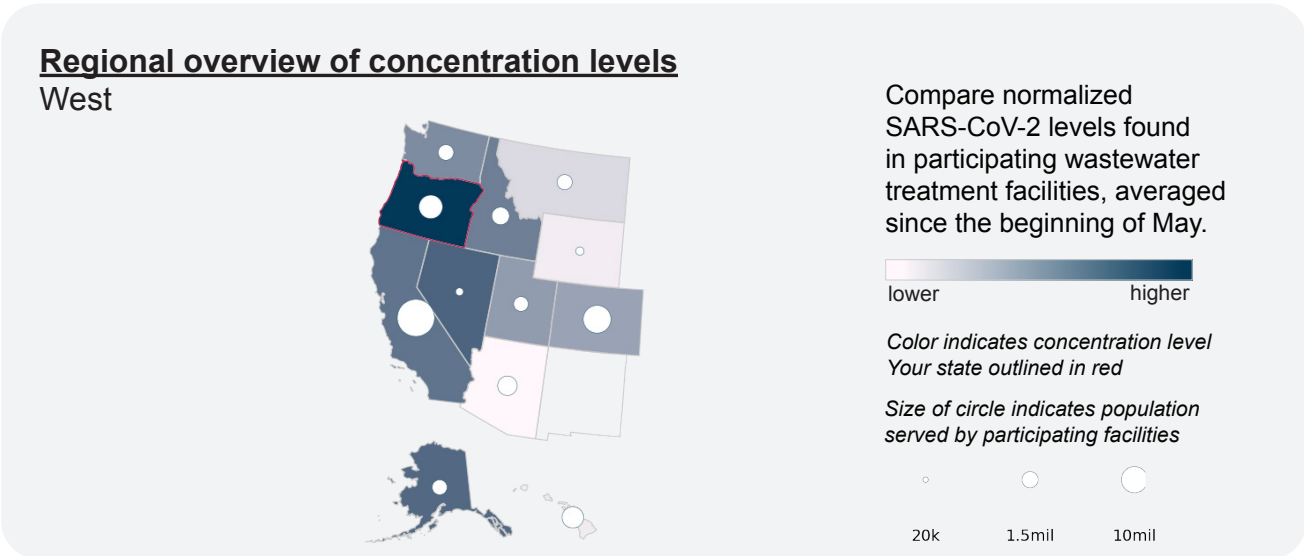
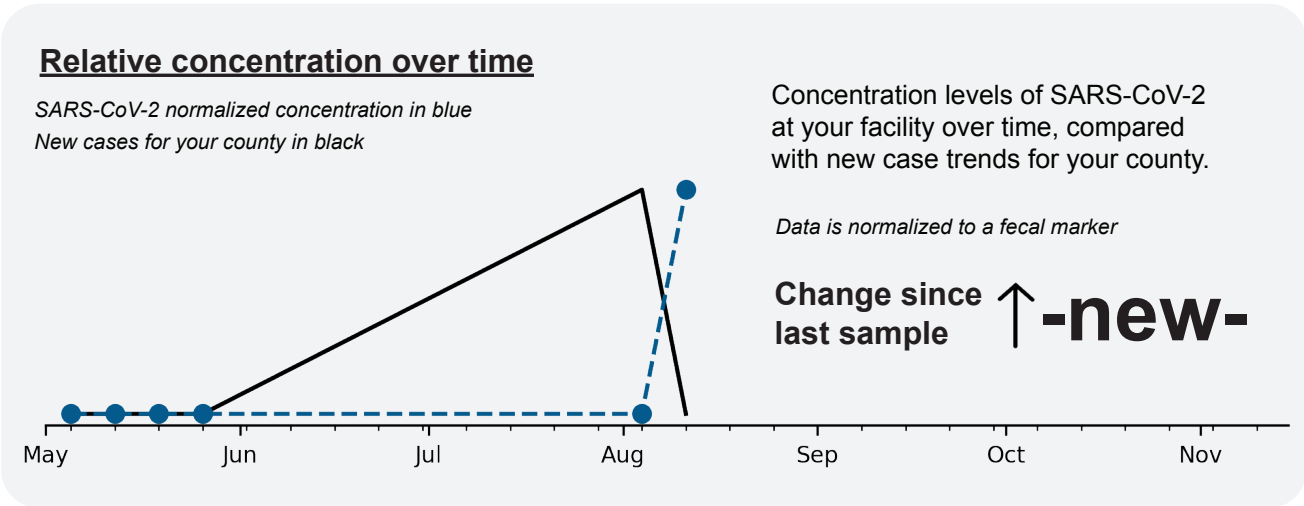
Nehalem Bay WATP Influent (OR)

Sample collection date: **August 11, 2020**

SARS-CoV-2 virus in sewage

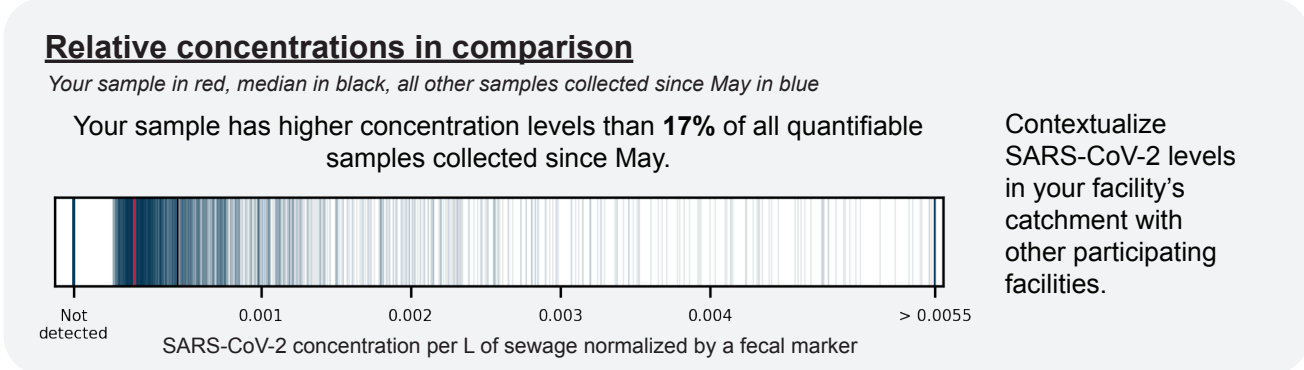
DETECTED

Virus concentration per liter of sewage
11,613 copies



About the data

Our methods for detecting SARS-CoV-2 in sewage are adapted from CDC protocols and available at www.biobot.io/covid19. Our approach relies on detecting genetic fragments of the virus that are excreted in stool, which does not determine if the virus is dead or active.



Case Estimates Reflect Active R&D

Evaluate as beta results when comparing to reported Covid19 cases

For more information, <https://doi.org/10.1101/2020.04.05.20051540>
read the whitepapers: <https://doi.org/10.1101/2020.06.15.20117747>

Reported COVID19 cases in Tillamook County, OR

New cases	Cumulative cases
0	34

On August 11, 2020, as reported by USAfacts.org

Biobot COVID19 case estimate

20 cases
(0.55% incidence rate)

Using a reported flow rate of 0.34 MGD

Biobot's wastewater testing protocols

We are continuously working to improve our protocols to increase the sensitivity of our measurements and reduce variability. We use a qPCR-based method to detect and quantify the SARS-CoV-2 virus and an associated fecal normalization control.

The RNA extraction method changed between protocols v1 and v2 to improve the sensitivity of our measurements. Protocols v2.1-v2.3 reflect changes in our quantification method to further improve the precision of our analysis and reduce variability. Internal tests have been conducted to assure data integrity. The SARS-CoV-2 viral titers that we report may be affected by slight batch effects between these protocol versions.

The sensitivity of our assay varies slightly between these protocols. The exact limit of detection (LOD) that applies to your sample can vary. Generally, the LOD for each protocol is: v1: 6,400 copies/L; v2: 34,000 copies/L; v2.1: 1,700 copies/L; v2.2: 2,100 copies/L; v2.3: 3,600 copies/L.

Why normalize with a fecal marker?

We normalize SARS-CoV-2 viral titers to account for differences in the total people contributing to each sample. We use PMMV as this internal control, which is an RNA virus that is excreted in stool.

Biobot's COVID19 case estimate

We measure the concentration of SARS-CoV-2 in sewage. We convert our measurements into a COVID19 case estimate using the following basic equation:

$$\text{Number of infected people} = \frac{\text{total amount of virus per day}}{\text{virus shed per infected person per day}}$$

Comparing with confirmed clinical cases

Our COVID19 case estimates may not match the confirmed case numbers in the community for a variety of reasons. Clinical testing may not represent the entire infected population. The SARS-CoV-2 virus may start being shed before patients develop symptoms and seek testing.

We encourage you to share these reports with your local public health officials to compare our case estimates with the number of confirmed cases in your local community.

Data use

The Biobot COVID19 case estimates provide an alternative metric to guide responses to the outbreak. We recommend that you share this information with local public health officials. We believe this work will have the greatest impact on a statewide level, and hope that you will reach out to your state officials and encourage the expansion of our partnership across your state.

Pioneering a better way to track Covid-19

We are the nation's leader in wastewater epidemiology. We analyze sewage to determine the presence of infected individuals and estimate the number of Covid-19 cases, providing:

- **Trend analysis**: Determine when to safely re-open, and keep open, our communities and businesses through frequent sampling.
- **Early warning**: Detect the re-emergence of Covid-19 in a population to rapidly take action and contain new outbreaks.
- **Testing at scale**: For a fraction of the cost of mass individual testing, get an overview of the scope of the outbreak.

For questions, email support@biobot.io