



# Mpox

[Mpox Home](#)



CDC is updating webpages with the term "mpox" to reduce stigma and other issues associated with prior terminology. This change is aligned with the recent [World Health Organization](#) decision.

## Outbreak Reproduction Number Estimates

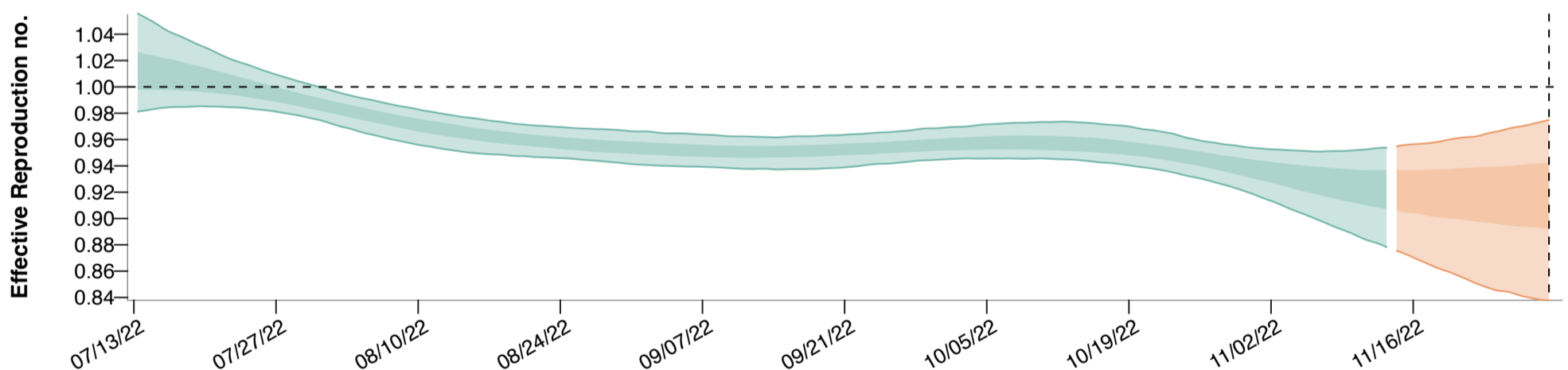
Data as of December 5, 2022

CDC is using a model to estimate the effective reproduction number (Rt) for the mpox outbreak in the US. Rt is used to understand the trajectory of an epidemic up to the current time (where we are now). Each week, CDC will update this website with the most recent estimates.

### Outbreak Reproduction Number Estimates

#### VIEW DATA BY:

- ESTIMATE
- ESTIMATE BASED ON PARTIAL DATA



[Data Table](#)

[Download "Rt Data" \(CSV\)](#)

The graph shows the effective reproduction number (Rt) estimation over time based on complete data (green) or partial data (orange). The most recent data are considered incomplete due to delays in reporting mpox cases. As a result, there is more uncertainty associated with the most recent Rt estimates.

- $R_t > 1$  means the epidemic is **growing**
- $R_t < 1$  means the epidemic is **shrinking**
- Shading represents the 50% and 90% credible intervals (uncertainty in the estimates)

This plot uses the EpiNow2 package (<https://cran.r-project.org/web/packages/EpiNow2/index.html>) to estimate the time-varying reproduction number on cases by date of report. The time-varying reproduction number is the average number of secondary cases infected by a single primary case in a large population.

The package requires three distributions:

- **Generation time:** the time between infection of a primary and secondary case
- **Incubation period:** the time between infection and symptom onset in a case
- **Any other delays:** for example, delays from symptom onset to reporting

We approximated the generation time using an estimate of the serial interval (rash onset to rash onset) with mean of 7.0 days (95% CrI 5.8 – 8.4) and standard deviation of 4.2 (95% CrI: 3.2 – 5.6) from 40 case pairs (primary-secondary) across 12 U.S. jurisdictions. Determining case pairs (primary-secondary) has been a challenge in the current outbreak, as information on specific contacts is missing for many cases; in addition, many cases report multiple anonymous sex partners or attendance at large events, such as festivals, in the three weeks prior to symptom onset. We only included cases if there was a high degree of certainty that the secondary case was infected by the primary case. Days between onset of any monkeypox symptom and days between rash onset in the primary and secondary cases were calculated for each case pair. The EpiEstim package in R software was used to estimate the distribution of the serial interval for known primary and secondary cases in case pairs using Bayesian methods for both symptom and rash onset.

For the incubation period, we used estimates for rash onset from this preprint: [Estimating the incubation period of mpox virus during the 2022 multi-national outbreak | medRxiv](#) and updated the analysis to include data from the case pairs for which exposure information was available (14 cases). The updated estimate for 35 cases had mean 7.5 (95% CrI: 6.0 – 9.8) and standard deviation 4.9 (95% CrI: 3.2 – 8.8).

The model assumes that testing procedures and surveillance effort remain constant over the estimation period. The method does not distinguish between imported vs. locally acquired infections and does not account for under-ascertainment.

More information about this analysis can be found in the [Mpox Technical Reports](#).

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