The early visualizations provided an overview of the simulations without any aggregation on the components, nodes, or edges. Although our end users found this useful for getting an initial overview of the simulations, the large number of components made it very difficult to visualize data and policy results associated with the spread of the disease beyond the number of components and the number of nodes/edges.
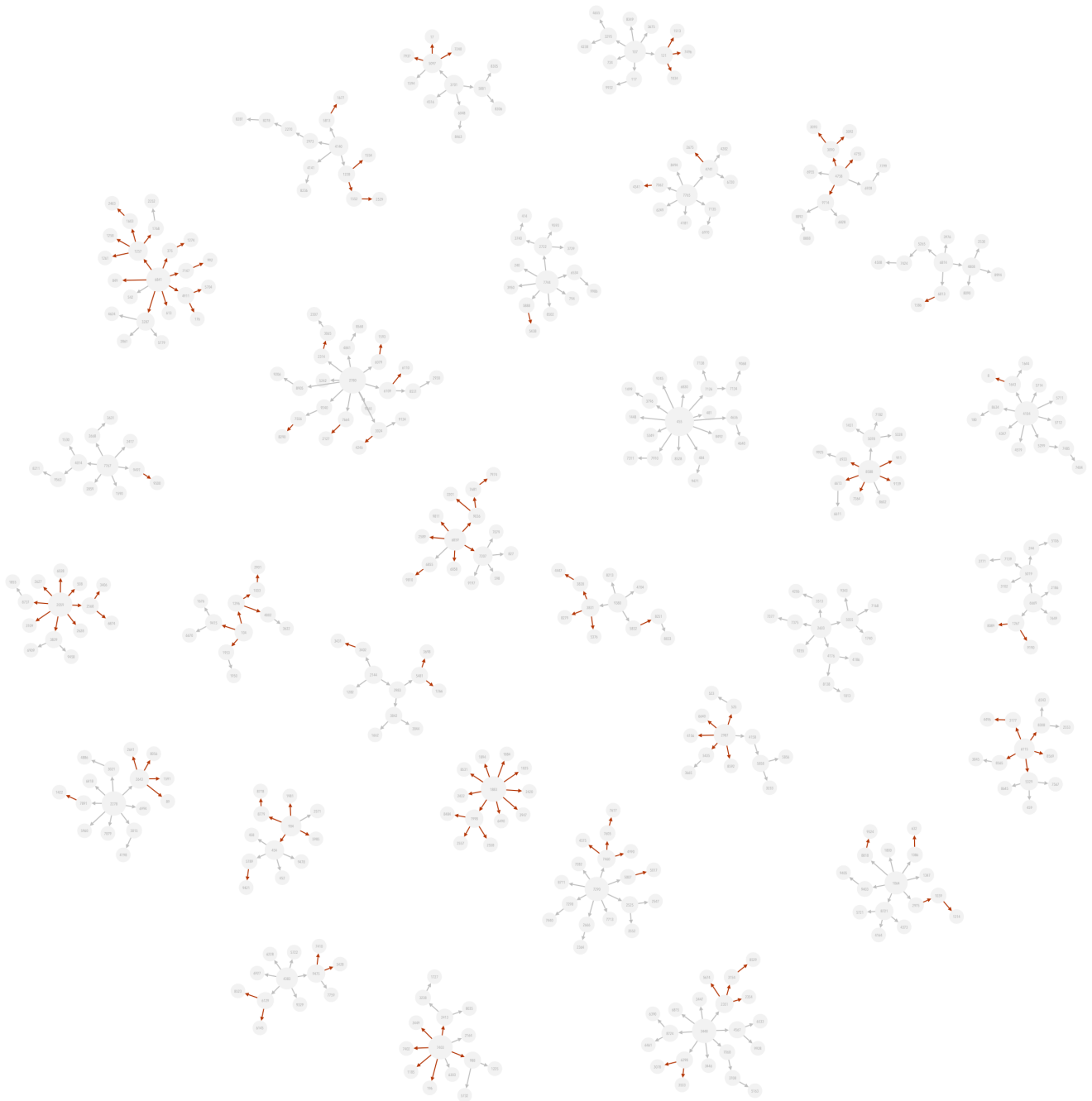

Figure 1: A static network visualization where the largest 30 transmission chains are visualized with asymptomatic transmission events highlighted with red color. The visualization indicates long chains (red) where asymptomatic spread plays an important role in spreading the simulated disease which was of interest to the epidemiologists.
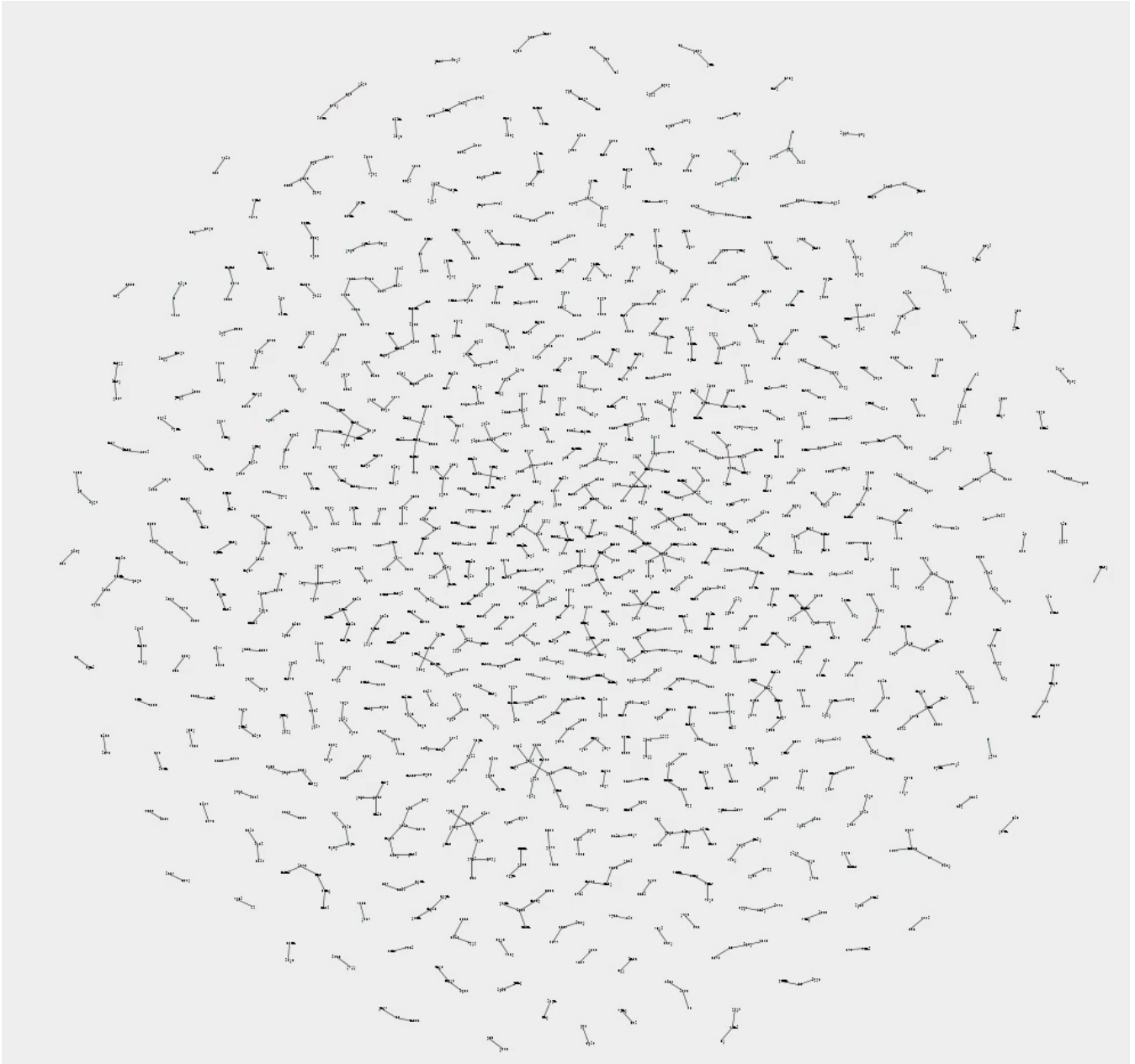
Figure 2: Dynamic graph animations showing the result of a smaller-scale simulation. No transmission chains were filtered out. The dynamic graph was drawn with a multilevel, event-based dynamic graph drawing algorithm (see [AMA21] in main paper references). The final animation frame (shown here) shows the full extent of the simulation. The visualization provides an overview of the entire simulation, providing all details. This gives an overall impression of the reach of the disease and how the disease spreads over time.
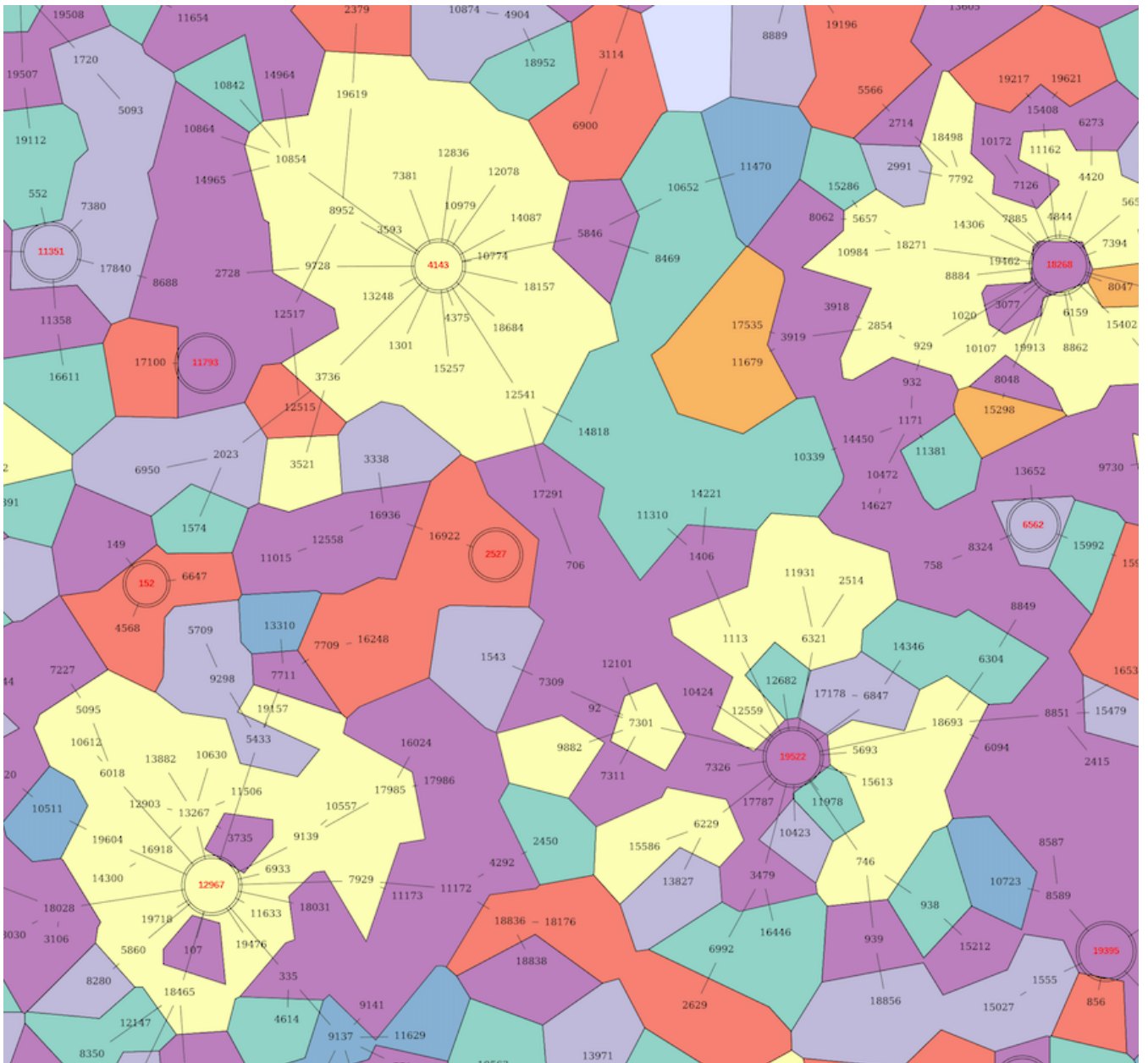
Figure 3: A heavily zoomed in section of the GMap (see [GHK10] in the main paper references]) visualization of a simulation: nodes with the same "location" property have the same background color (such as yellow). The contiguous areas indicate that infections often spread within a single location.