

Abstract

Event-based dynamic graph drawing can be used to visualise simulated disease spread in a population. Two-dimensional force-directed static graph-drawing algorithms can be extended to 2D + T to draw the temporal network in the space-time cube. In such a way, dynamic graph drawing lets us visualise, for example, a contact tracing simulation [1] of disease spread on such a temporal network. Building on the framework of the DynNoSlice algorithm [2, 3], we propose an extended version of the animation generating software that encodes location of infection spatially. The improvements include a number of functionalities allowing the user to highlight or filter out particular aspects of the disease transmission encoded with a dynamic graph. We test our improved algorithm on Covid-19 contact tracing simulations.

Cluster-specific forces

A cluster is an element type with:

- a *pole node*, positioned in the centre cluster's,
- a *circumference*
- *member nodes* (sharing a commonality we want to make prominent in the drawing)

An edge is inserted between the pole and a member nodes. Members are kept within the cluster's circumference.

A number of *forces* (following the definition in [2] and utilised in DynNoSlice) graphically differentiate the *members* from the rest (other clusters and un-assigned members).

- Node-to-node – attraction between the pole node and the cluster's members nodes.
- Circumference repulsion adapted version of the PrEd algorithm force [4] – the circumference is circumscribed over a polygon (32-degree graph face, nodes placed equidistantly). A member is repelled to the pole from the circumference from each of the face's **abstract** edges:

$$F(v, (a, b)) = \frac{(\gamma - \|p_v - v_e\|)^2}{\|p_v - v_e\|} (p_v - v_e)$$

$$v \in (a, b), a \neq v, b \neq v, \|p_v - v_e\| < \gamma$$

p_x is the position of node x , γ is the desired distance from a node to an edge, and v_e is the position of node v on a line which is defined by the edge (a, b) .

- Pole-to-node repulsion – applied to every non-member node (all nodes that are unassigned to a cluster):

$$F_u^r(v, u) \leftarrow \left(\frac{\gamma}{\|p_v - p_u\|} \right)^8 \hat{vu}$$

p_u and p_v are the positions of the member node and the pole node respectively, and \hat{vu} is the unit vector pointing in the direction from p_v to p_u .

Figure 1. Cluster with pole p and m_i member nodes

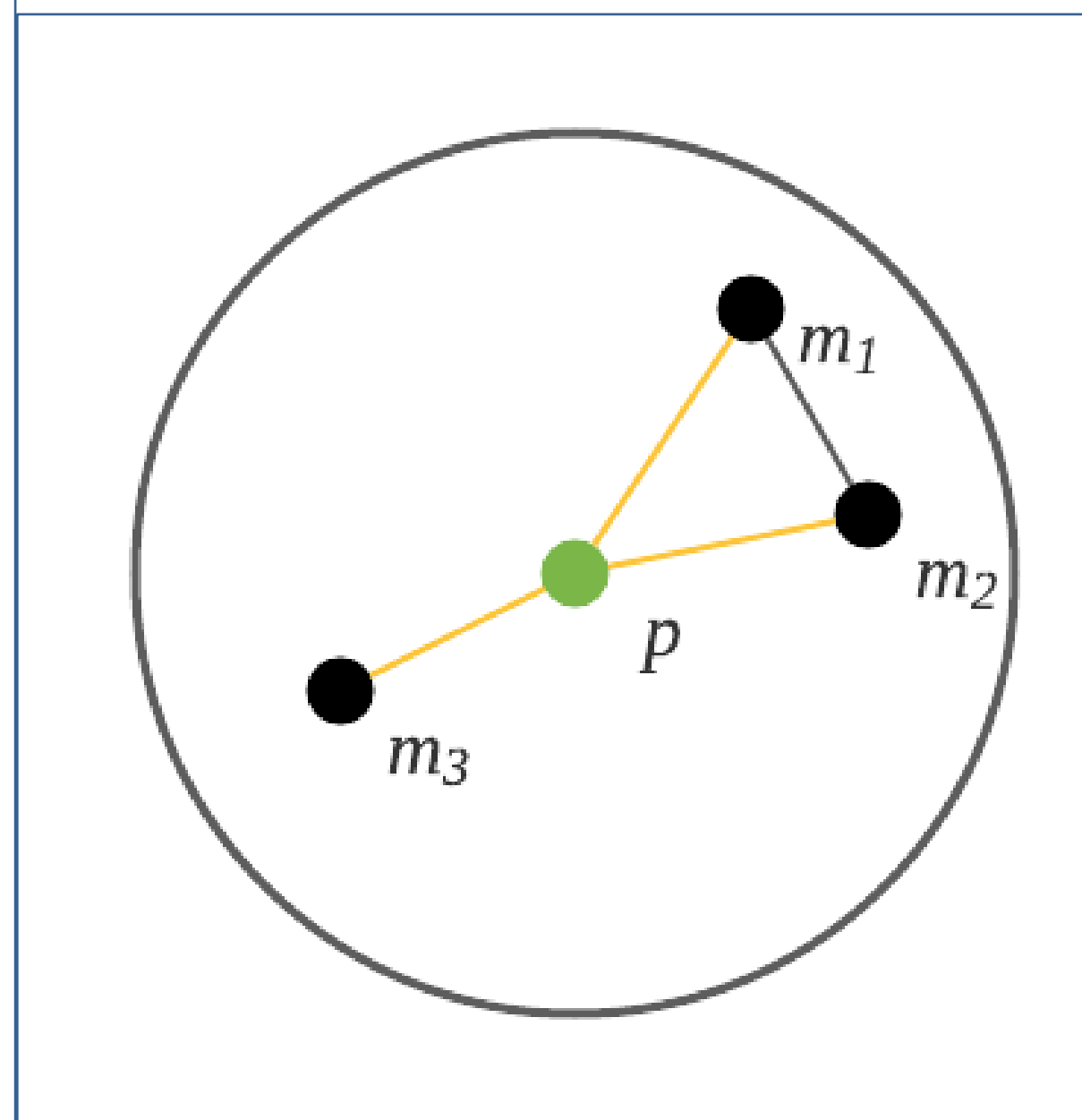


Figure 2. Pole-to-node repulsion

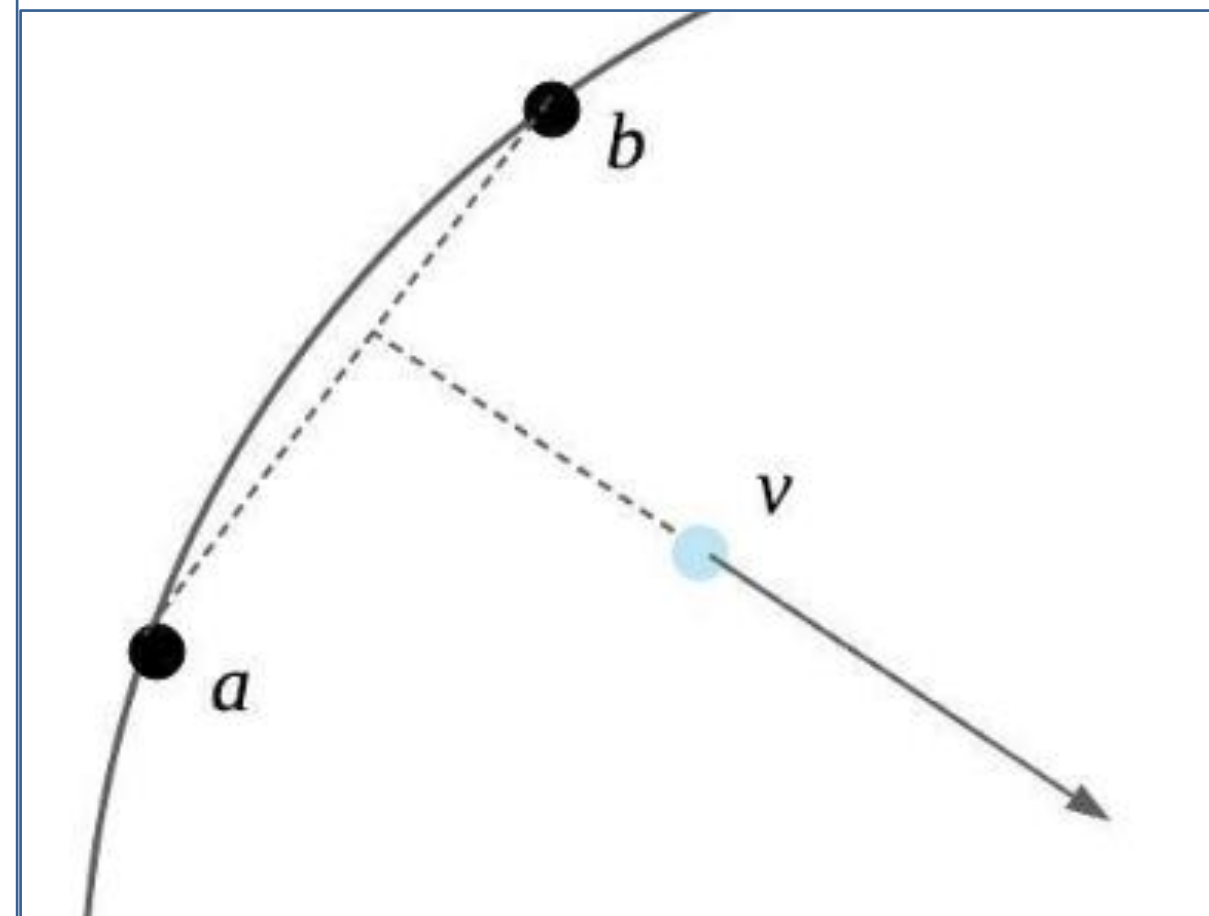
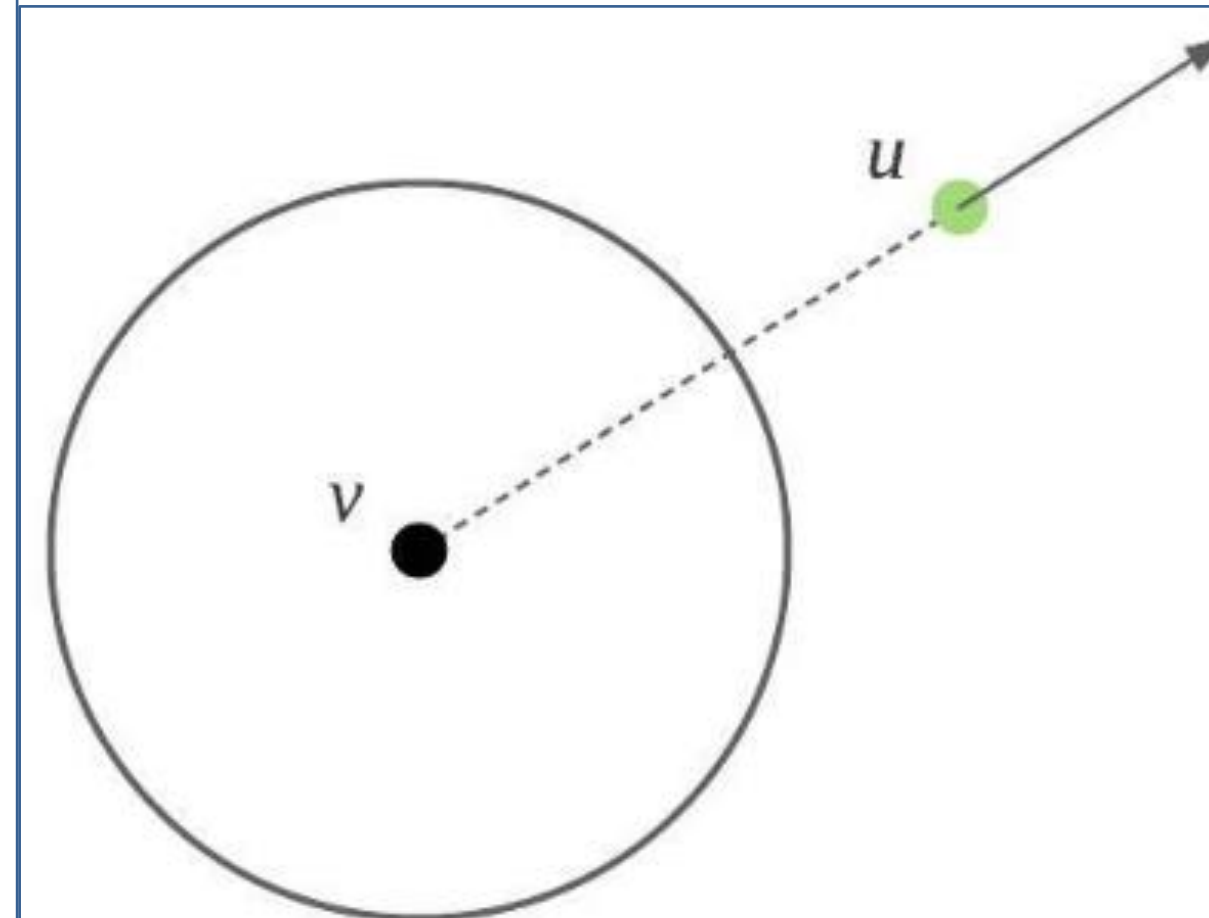


Figure 3. Circumference repulsion



PrEd adaptation

A force described by this node-to-pole repulsion formula, rather than the one included in the PrEd algorithm [4], provides a more stable layout with graphs of composed of above ca. 30 nodes.

New functionalities

Figure 4. Continuous with Location Highlight

- Highlights infection location / setting

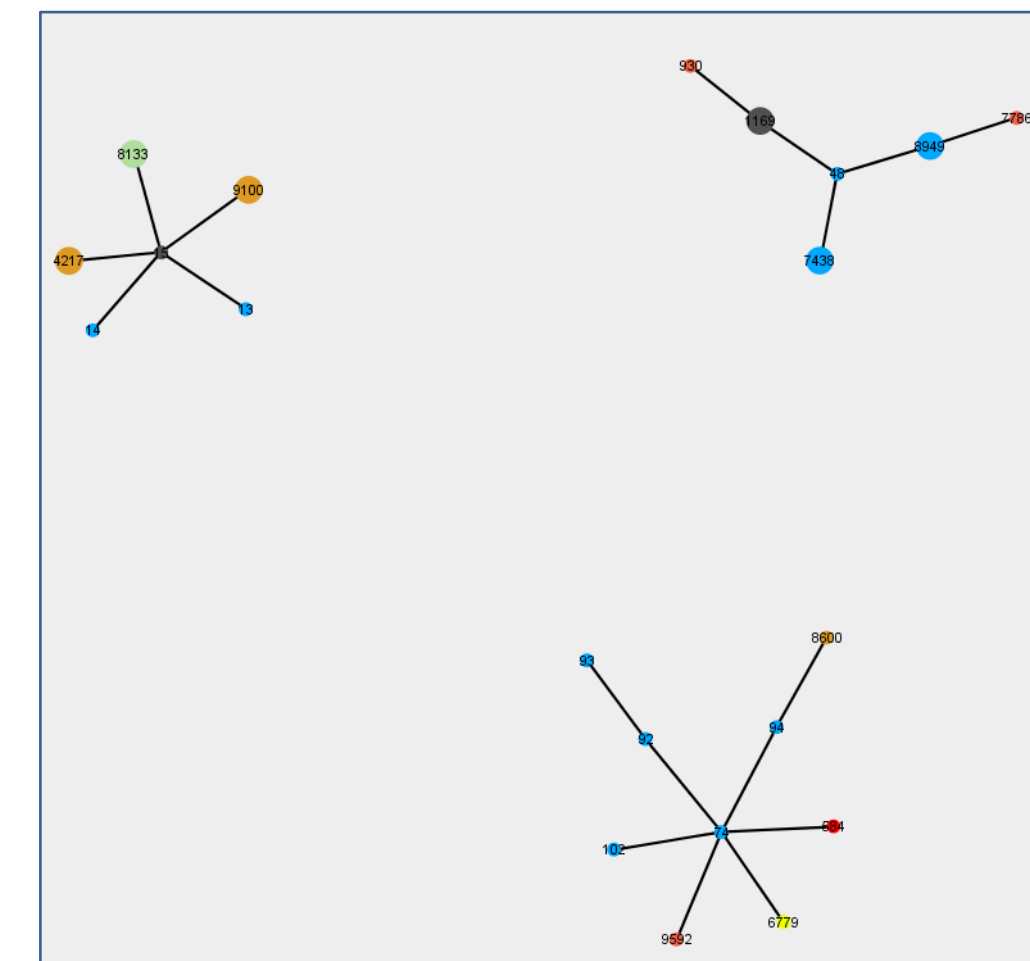


Figure 6. Continuous with Transmission Highlight

- Pick two locations / settings.
- Highlights edge e , if node n_{source} was infected in the first location, and n_{target} was infected in the second

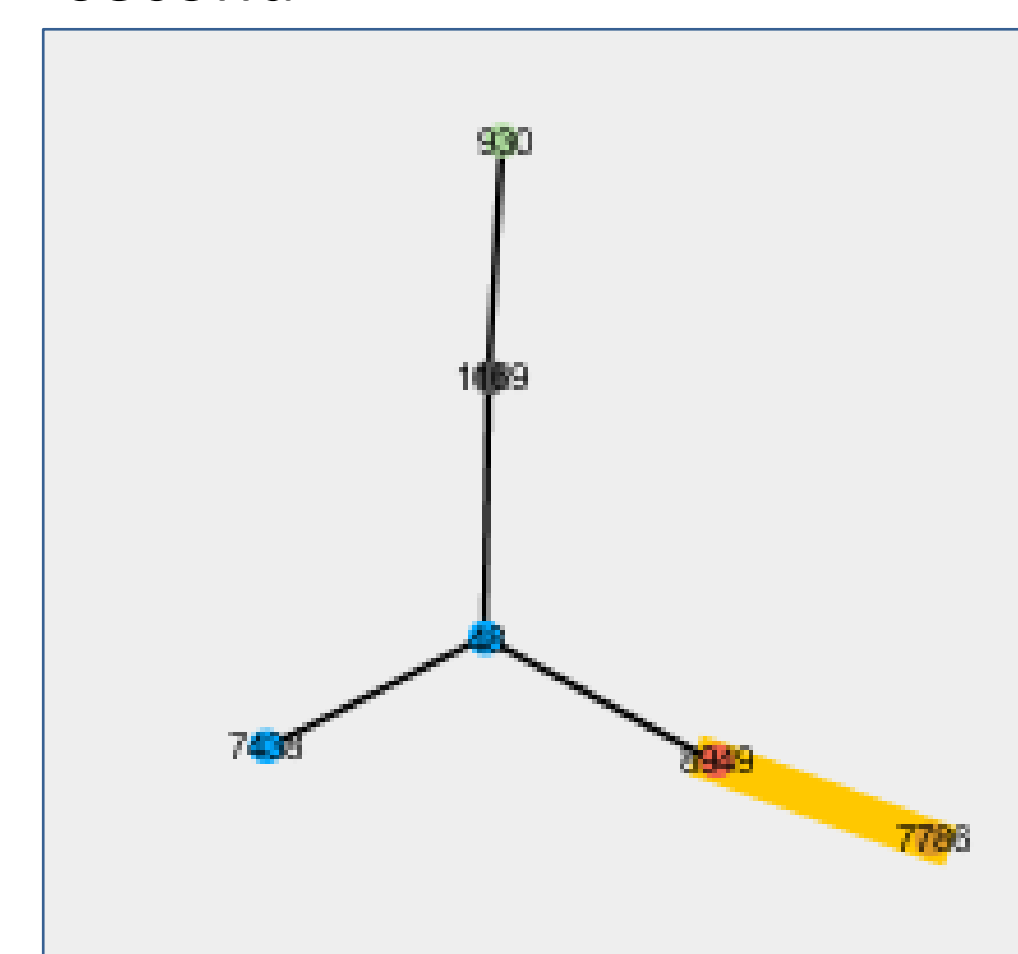


Figure 8. Continuous with Multiple Locations Attraction

- A version of Continuous with Location Attraction
- Pick multiple locations, each represented as a cluster (pole labelled as a location name)
- Nodes infected in *location* will be encouraged to stay within *cluster_i* circumference.

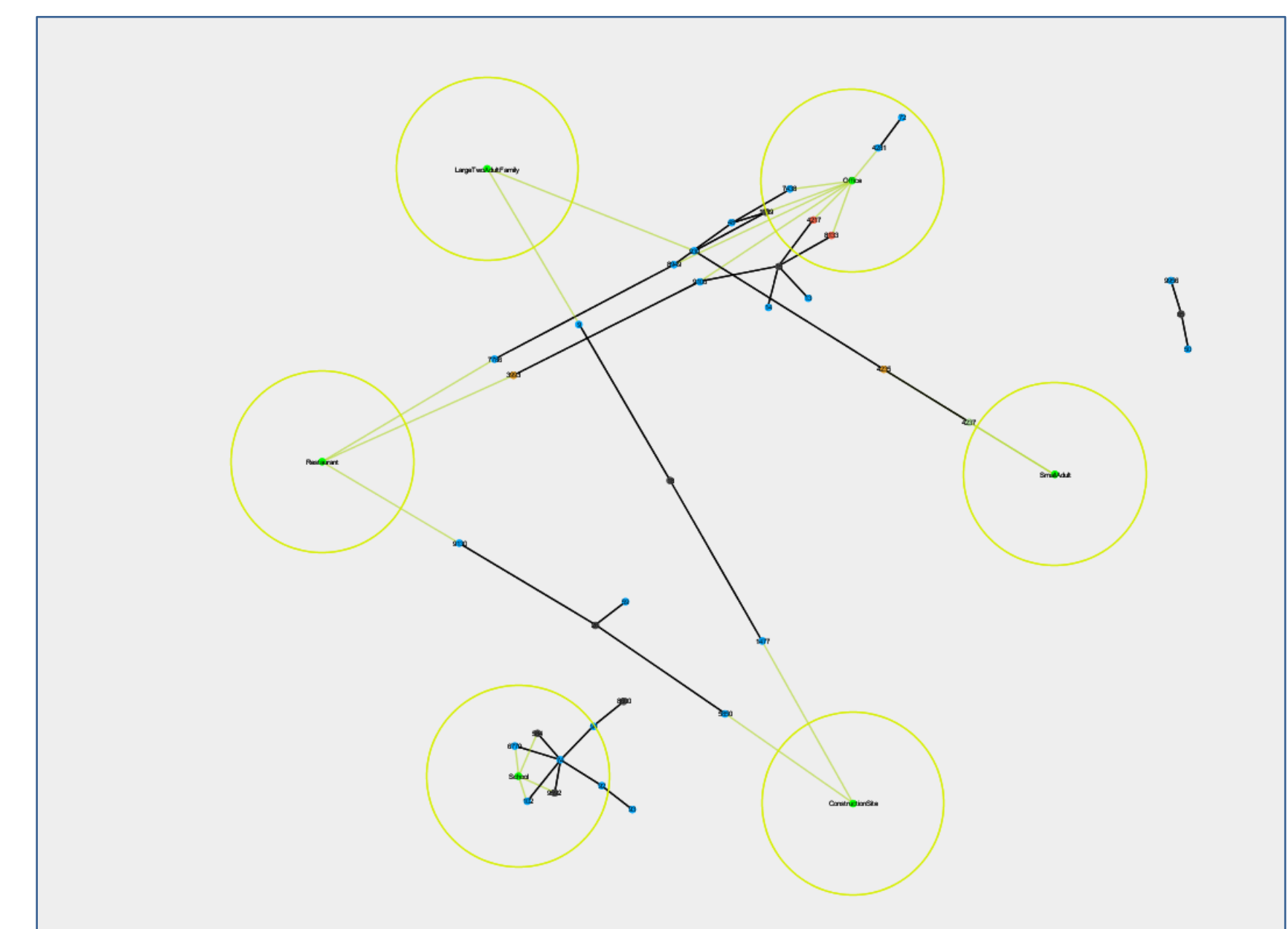


Figure 9. Node colour-encoding scheme

Infection status	Colour encoding
Exposed	Green
Asymptomatic	Yellow
Presymptomatic	Orange
Symptomatic	Red
Severely symptomatic	Dark Red
Recovered	Blue
Dead	Grey

Figure 5. Continuous with Location Attraction

- Pick a location / setting, (invisible node $n_{location}$)
- Nodes infected in *location* are attracted to $n_{location}$

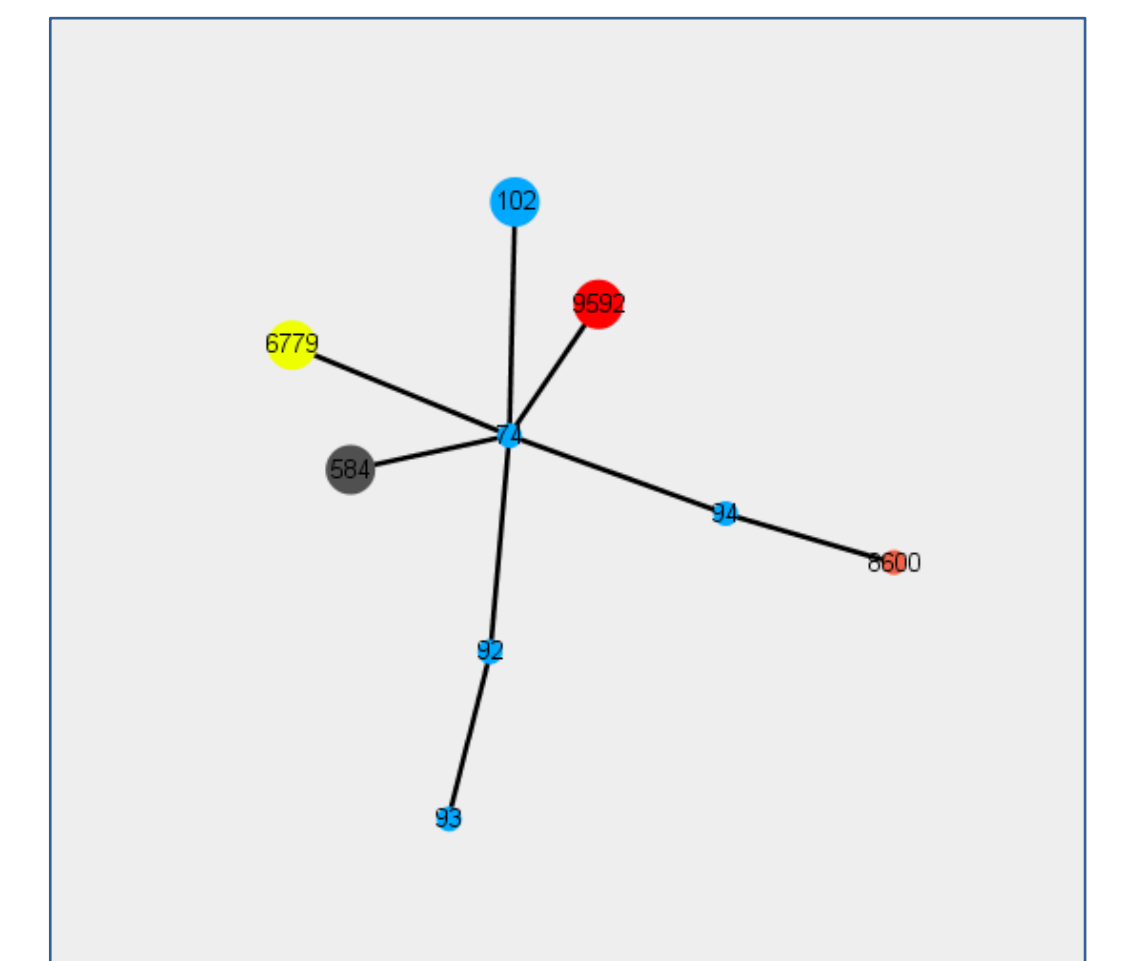
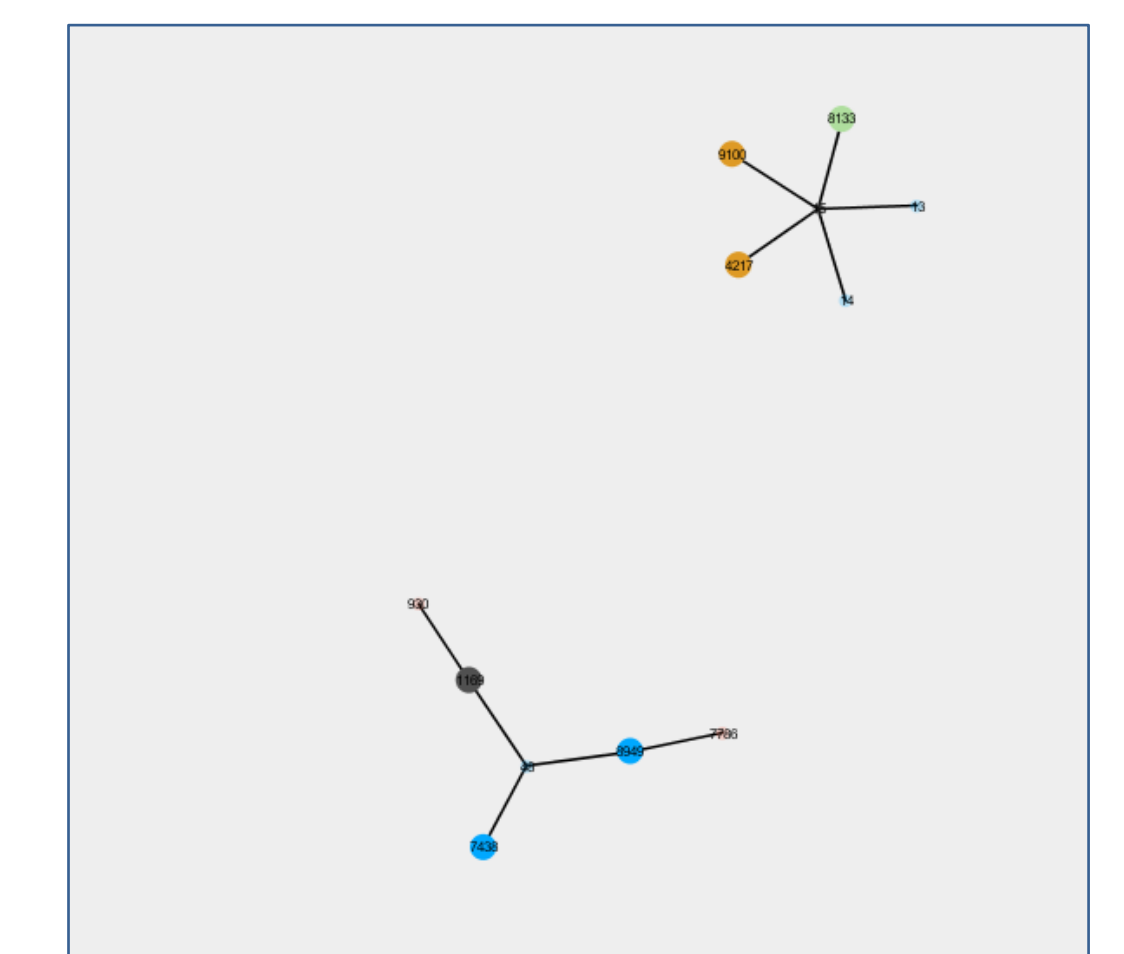


Figure 7. Continuous with Location Filter

- Filter out components with fewer than a given share of infections in *location*
- Highlight nodes matching the location



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References

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