

Supplementary information for “Visualizing the network structure of Covid-19 in Singapore”

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1 The Singaporean context

Singapore is an interesting case in which to examine SARS-CoV-2 transmission networks because of interaction patterns in the population and seemingly unique pandemic dynamics. The first case of Covid-19 in Singapore was identified on January 23, 2020. Local spread of SARS-CoV-2 was slow for two months, but a substantial outbreak began in late March. While viral spread during February and early March occurred in Singaporean society at large (termed ‘community transmission’ by local public health authorities), the later outbreak between April and September 2020 occurred primarily among work permit holders (guest workers) residing in dormitory settings. Bangladesh and India are the two most common national origins of guest workers. These settings are highly densely occupied, with as many as twenty workers occupying a single room, creating a context where viral transmission was difficult to control. As of September 15, 54,248 Covid-19 cases were identified in dormitory settings, amounting to 94% of all cases in Singapore.¹ Numerous international media reports drew attention to the inequalities of the guest worker system and the plight of workers confined to cramped settings (Stack, 2020; Tan, 2020). Remarkably, as of December 1, 2020 Singapore had seen only 29 Covid-19 deaths.²

2 Data sources and network construction

From the first detected case of Covid-19 infection through April 19, 2020 the Singapore Ministry of Health (MoH) provided daily press releases with anonymized case-level information, including links between individuals and infection clusters (press releases are available from moh.gov.sg/covid-19).

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These data are derived from the MoH contact tracing program. Information on links and cluster associations was frequently updated after initial announcements. I include all cases, link and cluster updates through April 19, 2020. Subsequent to April 19, public individual-level information is more limited and does not permit identification of links between cases and clusters. Individual-level variables include test date, gender, nationality, migration status, and travel history. In addition to individual cases, MoH officials identified 79 clusters prior to April 19: clusters are multiple infections associated with a location or event. About one third of clusters are dormitories.

MoH press releases and accompanying appendices provide two sources of network data: links between individuals (i.e. known social contacts) and associations of individuals with clusters. A link between individuals means that this pair are identified as contacts through the MoH contact tracing program (though we cannot know with certainty that infection occurred through this contact). A link between an individual and a cluster means that MoH officials determined that an individual was physically present at a location or event determined to constitute a cluster. Visualizations adopt the Kamada-Kawai layout.

For visual clarity, figure 1 omits all individuals whose only known tie is to a cluster. These individuals are represented by the scaling of cluster diameter to (log of) cluster size. In other words, infected individuals are represented as nodes only if they have ties to two individuals, two clusters, or one individual and one cluster. The reason for this choice is illustrated in supplementary figure S1, which shows the main component represented in figure 1b retaining all individuals as nodes. Visual clarity is reduced and these nodes are largely redundant to the scaling of cluster size. (Figure S1 scales cluster diameter to the square root of cluster size rather than the logarithm for reasons for visual clarity).

3 Network meso-structure

As noted in the main document, previous research examines network properties in order to understand the dynamics of disease spread. For example, sociological research has examined the structure of romantic networks in order to draw inferences about the spread of sexually transmitted diseases (Bearman et al., 2004). But most epidemiological research focuses on local network properties such

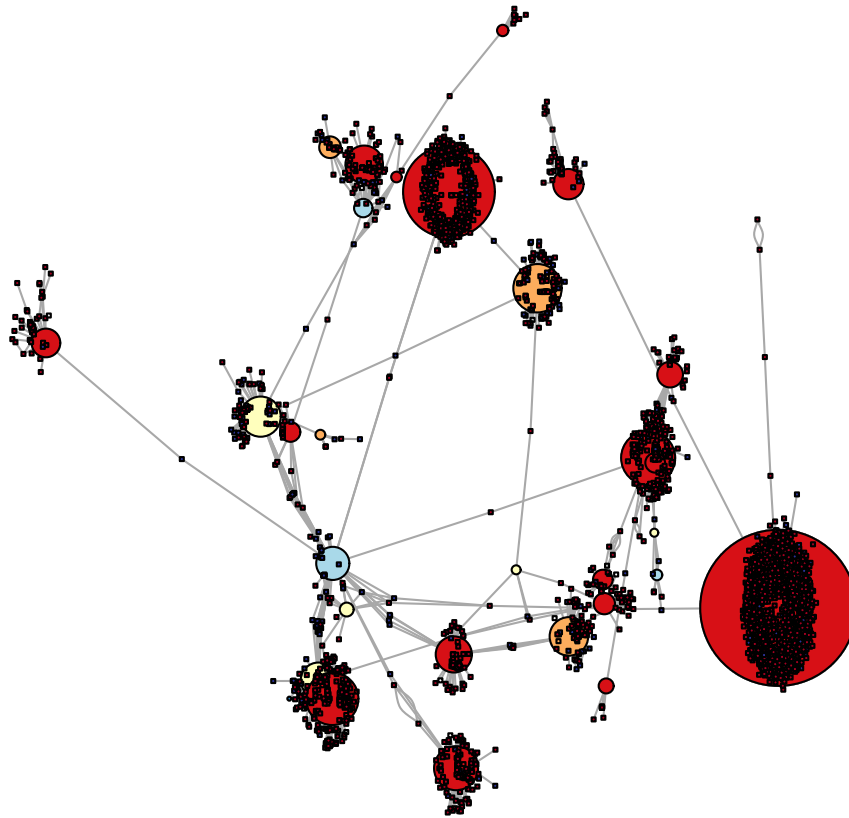


Figure S1: Main component of transmission network, without removal of individuals connected to only one cluster

as the degree distribution. Epidemiologists stress that the reproduction number r_t (the number of infections resulting from a source) likely varies widely, with the tail of the distribution reflecting ‘super-spreading’ events: individuals who transmit the virus to many others (Adam et al., 2020). Less is known about the number of infection chains resulting from such events and the length of chains between clusters. I conceptualize this meso-structure as the pattern of infection relations between clusters, including both clusters themselves and the infection chains between them. This meso structure is not a feature of virus biology, but rather of the social interactions, mobility patterns and physical proximity that create the potential for virus transmission. Meso structure is also distinct from macro structure, which involves the still higher level of aggregation of transmission between cities, regions and countries (e.g. Chinazzi et al., 2020).

One possible model of transmission meso-structure is a multiple hub-and-spoke model, according to which each infection cluster generates a varying number of infection chains (i.e. the cluster-level degree distribution), each of which generates additional clusters which in turn seed further chains. This model of spread could arise if local network properties (e.g. heterogeneous degree distribution and clustering) affect transmission locally, but spread between clusters is not substantially constrained by meso-level social interaction patterns. Notably figure 1 does not conform to this model: rather, while cluster 1 generated 7–8 infection chains, other clusters only generated 1–2 infection chains. This observation is supported by an inter-cluster reduction of the network. This network consists of all clusters in the main component; ties between clusters are infection chains through individuals of any length (supplement figure S2). This meso-structure may reflect interaction patterns between these apparently later clusters, for example, the relative infrequency of interactions between individuals in different dormitory settings. It is beyond the scope of this paper to account for this network structure; rather the goal is to draw attention to the social interaction patterns at higher levels of aggregation that may impact infectious disease spread.

4 Broader network context

It is important to emphasize that the network represented in figure 1 consists of the largest connected components within the transmission network, *not* the universe of all connected individuals,

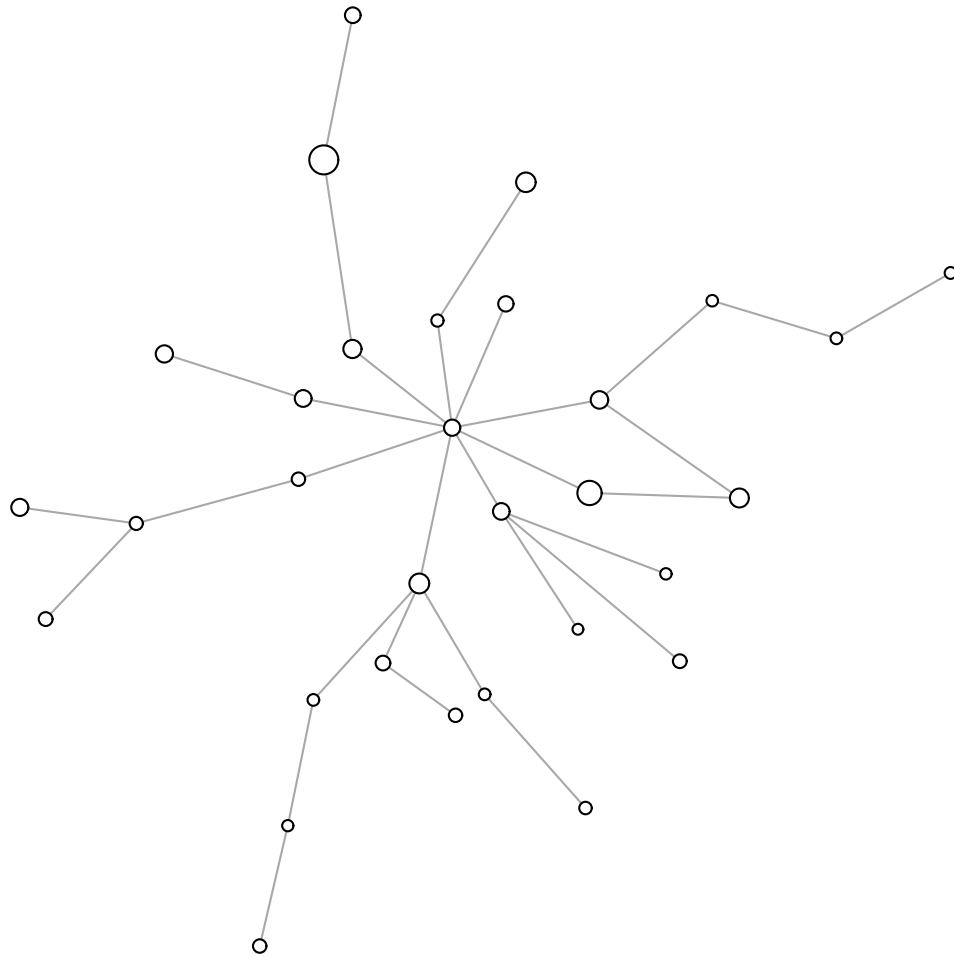


Figure S2: Inter-cluster reduction of main component (see main text for explanation). Position of clusters corresponds to position in main text figure 1, panel A.

Table S1: Distribution of network connectivity

Type	Main component		Component n \geq 10		Whole network	
	N	%	N	%	N	%
	Jan 23, 2020 - Apr. 19, 2020					
Imported	1	0%	17	3%	173	31%
Local linked	3010	73%	3801	92%	4118	100%
Local unlinked	457	24%	739	39%	898	47%
All local	3466	57%	4539	75%	5015	83%
	Mar 25, 2020 - April 19, 2020					
Imported	1	1%	10	6%	48	27%
Local linked	3010	76%	3679	93%	3932	100%
Local unlinked	456	25%	726	40%	854	47%
All local	3465	60%	4404	77%	4785	83%

or all individuals with a positive Covid-19 test. MoH assigned one of three statuses to each case: imported (i.e. an individual appeared to have contracted Covid-19 abroad), linked (an individual had social contact with another infected individual, or was associated with a cluster) or unlinked (no known connections to other cases and clusters. Appendix table 1 provides a summary of this broader network context.

Overall, a very high-proportion of cases are linked to 6 network components (including the largest component) — 92% of cases initially classified as ‘local linked’ by MoH and 75% of all local cases. (The discrepancy is due to cases initially classified ‘unlinked’ by MoH but for which links were later identified). This has two main implications. First, it suggests that MoH contact tracing was highly effective at detecting contacts between cases and clusters. Second, the fact that such a high percentage of linked cases are connected in just six components suggests that these data are informative about transmission meso-structure. Furthermore, 76% of cases occurring between the first case associated with the main component (detected March 25) and the end of the data on April 19 are associated with the main component. This suggests that the main component is a reliable representation of the meso-structure of Covid-19 transmission during this period. Figure S2 shows the network including all connected nodes to illustrate this broad network context.

Nevertheless, due to unobserved transmission events, this network is necessarily an approximation. Approximately 6% of cases with known connections are located in small disconnected

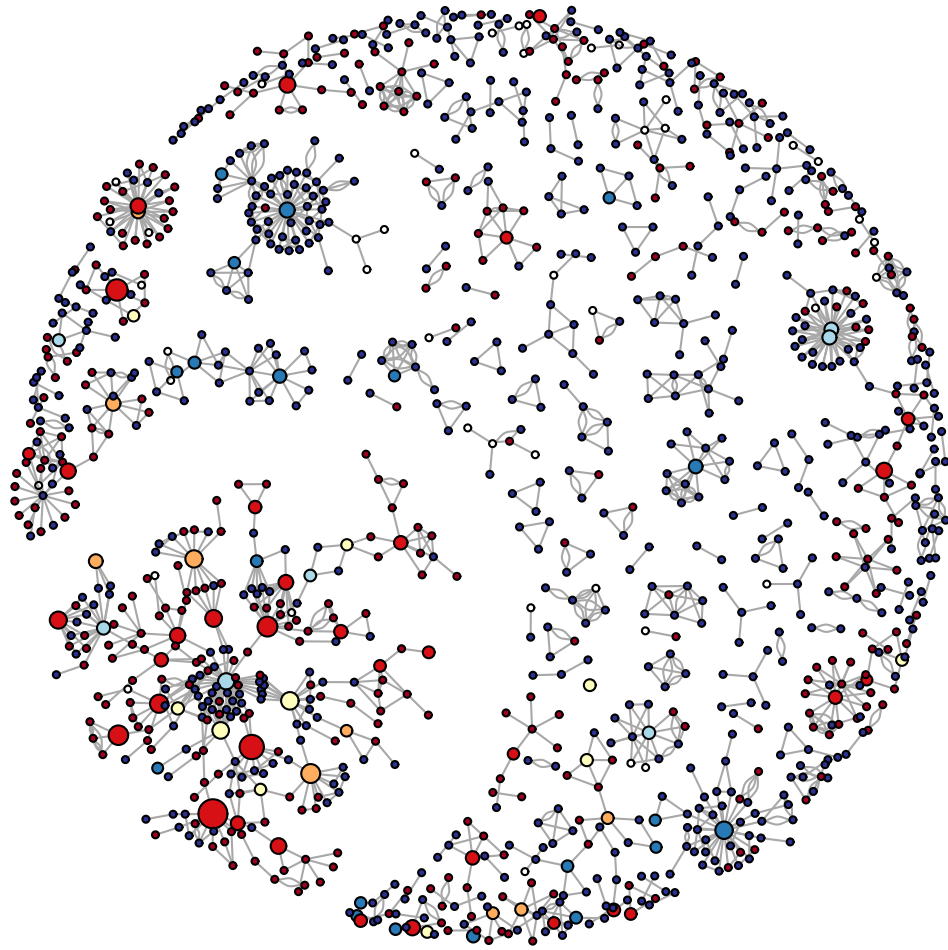


Figure S3: Representation of all connected individuals and clusters

components (e.g. dyads), and 20% of non-imported cases have no known connections to other cases or clusters. Assuming that SARS-CoV-2 transmission always occurs between specific individuals (even if in fleeting interactions), these cases represent missing ties (unobserved transmission events) in the network. However, inclusion of these unobserved events in the network is unlikely to have a substantial impact on the observed meso-structure.

In order for these unobserved transmission events to substantially alter the network meso-structure, unobserved ties would have to exhibit a very high level of network autocorrelation: multiple disconnected nodes would need to be extremely likely to have connections to other nodes in order for these to amount to a structurally meaningful effect. This level of autocorrelation is unlikely to exist in practice.

For example, according to media reports, MoH officials believed that a cluster in panel B — localized in a mall — was the source for cluster 1 (panel A), with transmission moving from mall employees to workers (Lai, 2020). While this transmission chain is not observed in the network data (likely due to undetected transmission), the structure of transmission within the main component suggests that this is likely a short path through a small number of individuals. This would not alter the overall picture of Covid-19 meso-structure in panel A.

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