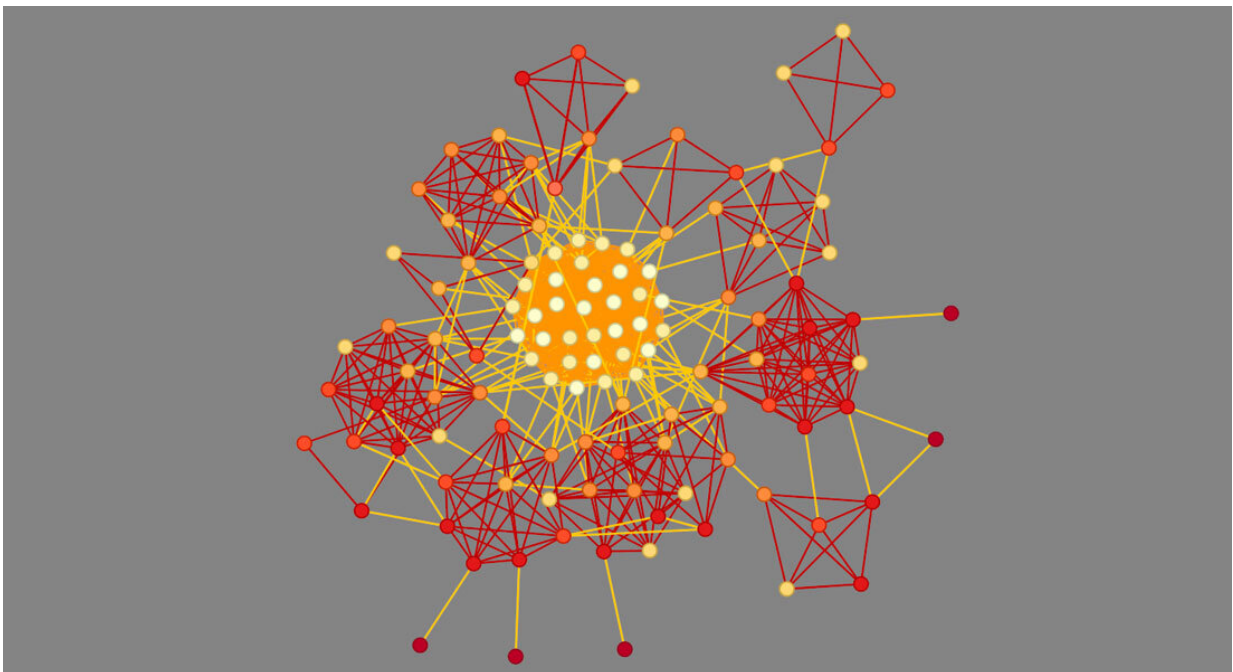# New research into the spreading of infections reveals need for greater collaboration between biology and physics

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Model of a social network. There are 150 individuals (the dots), whose social connections are marked by the lines between them. There are three categories: 1. Close contacts, e.g. household (yellow lines), 2. Regular contacts, e.g. work and adult friends (red lines) and 3. School contacts for children and children's friends (orange lines). The color of the dots marks the age – darker = older. The most important knowledge derived from the research is that un-repeated contacts, e.g. from public transportation, represents a large risk of contamination in super spreader diseases like Covid19. This is why the lockdown tool, which has been widely applied in battling the pandemic, has been extraordinarily efficient.

Researchers at the Niels Bohr Institute, University of Copenhagen, together with epidemiologist Lone Simonsen from Roskilde University form part of the panel advising the Danish government on how to tackle the different infection-spreading situations we have all seen unfold over the past year. Researchers have modeled the spread of infections under a variety of scenarios, and the Coronavirus has proven to not follow the older models of disease spreading.

An increasingly varied picture of its behavior and thus its impact on society has emerged. In several scientific articles, researchers have described the knowledge accrued to date, most recently around the concept of "super-spreaders." It turns out that only approximately 10% of those infected account for roughly 80% of the spread of the infection. The results have been published in the scientific journal *Proceedings of the National Academy of Sciences*, *PNAS*.

Where does our knowledge of infections spreading stem from?

The data researchers use to" feed" and develop computer models comes from a wide range of different sources. The Danish municipalities have kept inventories of the spread of the infection, and this data has the advantage that it stems from units that are not overly large. There is a high degree of detail and this means that one can trace local development more clearly and thus construct parameters for super-spreading, which Postdoc Julius Kirkegaard has contributed to. Contact tracing is another source of information. In that case, the focus is on localizing and limiting the individual's transmission of the virus. The third source is

slightly more complicated as it seeks to follow the chain of infections via the gene sequence of the virus.

Who are the super-spreaders?

Regardless of which source researchers examine, the results deliver roughly the same: 10% of all those infected account for as much as 80% of the spread of the infection. It is therefore crucial, in relation to the spread of the virus to locate the so-called super-spreaders and uncover how super-spreading occurs. Researchers stress that, at the moment, we are not quite sure what constitutes a person as a super-spreader. It may purely be down to personal, physiological characteristics. In addition, there are varying degrees of super-spreading in the population, so it is not necessarily just one or the other. Some people simply spread the virus more than others and the variation from persons with almost no transmission to super-spreaders is great.

How do researchers model a population of just under 6 million individuals?

Three basic categories are considered important when modeling the population's behavior, when calculating a scenario for the spread of infection: 1. The family context, 2. Work context and 3. The random contexts people find themselves in—in other words, people in proximity on public transport, at leisure activities etc. The time factor in all three is crucial, as it takes time to infect other people. In terms of time, these three categories are somewhat identical when it comes to common diseases, but not a super-spreader coronavirus variant.

But this is where the individual characteristics of the virus come into play: super-spreaders are quite different when handled in a computer model. Methods known from physics become important here, as it is

necessary to model individuals and their contacts. Researchers have set up computer models both for scenarios with and without super-spreaders, and it transpires that shutting down workspaces as well as sporting events, and public transport has the same effect when the model does not take super-spreaders into account. But when we include super-spreaders, there is a pronounced difference, and the shutdown of public events has a much greater effect.

Disease modeling faces new challenges and strong interdisciplinary collaboration

Diseases can behave very differently and it therefore incredibly important to be both ready and capable of rapid change in relation to the development of new models that reflect the characteristics of different diseases as accurately as possible, if we hope to contain them. Professor Kim Sneppen explains: "The biological variation of different viruses is enormous. SARS-CoV-2 contains a special feature in that it is at its most contagious just before one develops symptoms. This is the exact opposite of an earlier disease that threatened to become a pandemic, namely SARS, which is mostly contagious after one displays symptoms. Viruses are extremely advanced machines that each find specific weak points to exploit. A new field of research is rapidly developing, which examines how viruses attack the cells in our body. COVID-19 has proven to lead to very different sickness progressions for different patients. In that senses, it behaves chaotically, as we say in physics."

Ph.D. student Bjarke Frost Nielsen and Professor Kim Sneppen see a large open field of research within the collaboration between physics and biology. Gathering as much possible information about different viruses is crucial thus enabling physists to deploy this knowledge in mapping scenarios to respond to them.

The potential for research into the spread of infections is great

Bjarke Frost Nielsen says: "We need to create a toolbox that contains a wide variation in the way we tackle the spread of transmission, in our computer programs. This is the immediate perspective we can see in front of us, at the moment. Mathematical disease modeling has been around for almost 100 years, but unfortunately not a lot of headway has been made over that period. To put it bluntly, the same equations from the 1930's are still in use today. In relation to some diseases, they can be correct, but in relation to others they can be way off. This is where, as physicists, we have a completely different approach. There are numerous parameters, i.e., social dynamics and much more varied interactions between individuals that we can build our scenarios upon. This is badly needed, when we see the enormous variations in the different diseases."

More information: Bjarke Frost Nielsen et al, COVID-19 Superspreading Suggests Mitigation by Social Network Modulation, *Physical Review Letters* (2021). [DOI: 10.1103/PhysRevLett.126.118301](#)

Kim Sneppen et al, Overdispersion in COVID-19 increases the effectiveness of limiting nonrepetitive contacts for transmission control, *Proceedings of the National Academy of Sciences* (2021). [DOI: 10.1073/pnas.2016623118](#)

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