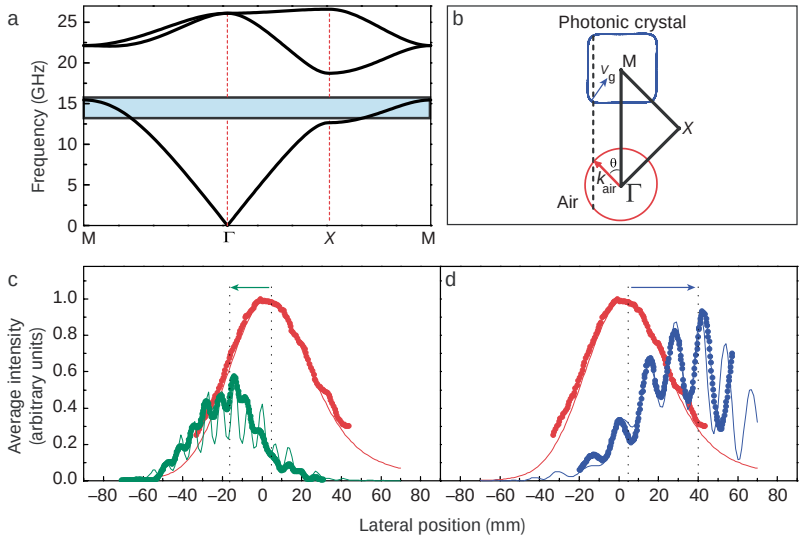

Figure 1 Comparison of positive and negative refraction. **a,** Band diagram for our structure for transverse magnetic polarization. Shading denotes the frequency range in which negative refraction occurs. **b,** Equal-frequency contours in *k* space of air and of the photonic crystal at 13.7 GHz. θ is the angle of incidence from the air to the crystal; v_g is the group velocity inside the photonic crystal. **c,** Negative refraction. Average intensities were calculated at the second interface with the photonic crystal (green) and at the first interface without the photonic crystal (red), and corresponding power distributions were measured. **d,** Positive refraction. Average intensities were calculated at the second interface with a slab containing polystyrene pellets (blue) and at the first interface without the slab (red), and the corresponding power distributions were measured. Arrows in **c** and **d** indicate the refracted beam's direction of divergence from the incident beam.

to confirm our structure's predicted negative refraction, using the interfaces of the photonic crystal in the Γ–M direction. The electric field was kept parallel to the rods for all measurements and calculations; the horn antenna was orientated so that the incident waves make an angle of 45° with the normal of the Γ–M interface. Our structure exhibits the maximum angular range of negative refraction at an operating frequency of 13.7 gigahertz (GHz). In simulations using the finite-difference time-domain method (FDTD), the incident gaussian beam width was set at 6 cm, which is equal to the width of the horn antenna.

The centre of the outgoing gaussian beam is shifted to the left of the centre of the incident gaussian beam (Fig. 1c), which corresponds to negative refraction[7]. The negative index of refraction was determined to be -1.94, which is close to the theoretical value of -2.06 calculated by the FDTD method. For comparison, we repeated the measurements and simulations with a slab containing only polystyrene pellets, which has a refractive index of 1.46, and found the refracted beam to be on the right of the incident beam, corresponding to a positive index of 1.52 (Fig. 1d).

The advantage of negative refraction in the valence band is that there is no Bragg reflection; such reflections occur in higher bands of the photonic crystal, and we have a well-defined, single-beam propagation that is negatively refracted. Another advantage of operating in the valence band is that the transmission efficiency at this frequency is 63%, which is almost three orders of magnitude larger than the typical transmission efficiency in a left-handed material[2,3]. The negative-refraction effect that we describe depends only on the refractive index of the dielectric material and on the geometric factors used in two-dimensional photonic crystals. This effect can therefore also be observed at optical wavelengths, at which it is possible to obtain similar refractive indices by using transparent semiconductors.

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COMMUNICATIONS ARISING

Social networks

Sexual contacts and epidemic thresholds

Distributions of the number of sexual partners reported in surveys show a pronounced skew, with most people having had one or no partners in the past year and a small fraction having had many[1,2]. Liljeros and colleagues[3] infer from the results of a Swedish survey that there is a "scale-free" population distribution of sexual contacts, consistent with a preferential-attachment model[3,4], in which "the rich get richer" and epidemics are driven by extremely promiscuous individuals. Here we reanalyse the data from Sweden and from other countries, using more appropriate statistical tools. Our findings support the conventional wisdom that epidemic thresholds exist in these populations, and indicate that current public-health strategies to reduce the spread of HIV and other sexually transmitted infections do not need to be radically refocused.

An important epidemiological question for highly skewed partnership distributions is whether their variance is finite[5,6]. As the reproduction number of a pathogen increases linearly with the variance in the level of sexual activity[7,8], populations with infinite variance lack epidemic thresholds. In these populations, a sexually transmitted infection could persist regardless of its transmissibility, and interventions such as vaccines or barrier contraceptives would be ineffective for eradicating it.

Liljeros *et al.* estimate the scaling exponent for Sweden by fitting a line to the apparently linear region of the upper tail of the logged sexual-contact distribution. This approach is not statistically appropriate, for several reasons[9]. Inference on the basis of the distribution's extreme upper tail yields wildly increasing confidence intervals because there is little empirical information in this region (Fig. 1). Estimates based on partial lifetime contacts (as in Fig. 2b of ref. 3) are a source of further difficulties, including temporal confounding and censoring.

We take a more principled statistical approach, using a stochastic mechanism for the underlying preferential-attachment process. This yields a Yule distribution[10], and infinite variance when the single scaling parameter $\rho \leqslant 3$. (Details of the Yule model and the statistical estimation procedure are presented elsewhere[9].) We generalize the simple Yule model to allow for a mixture of distributions — a process for the lower tail, and a preferential-attachment-type process for the upper tail. Assuming the Yule form, we can estimate the model parameter using maximum

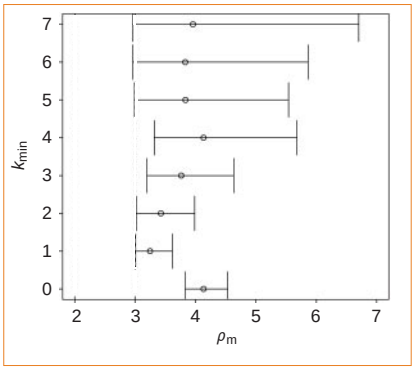

Figure 1 Interval estimates of the scaling parameter, ρ, for the generalized Yule probability mass function for Swedish males and females. Data show the sensitivity of the 95% bootstrap confidence intervals to the upper tail of the partnership distribution, defined as $k > k_{min}$, where k is the number of sexual partners in the previous 12 months. For both males and females, the best-fitting model has $k_{min} = 1$. By contrast, Liljeros *et al.*[3] used $k_{min} = 5$ for males and $k_{min} = 4$ for females. For these values, our estimates of parameter uncertainty are six times greater than the intervals reported by Liljeros *et al.*[3].

likelihood, and base our model selection on the bayesian information criterion[9].

The 95% bootstrap confidence-interval estimates of the scaling parameters fall above the infinite-variance range (females, 3.60–5.21; males, 3.01–3.63). Our results are similar when we analyse two further data sets from Uganda and the United States (both based on representative samples with substantially higher response rates than in the Swedish survey). Thus, there seems to be consistent evidence that sexual-contact distributions are characterized by finite variance[9].

Our findings suggest that sexual-contact distributions, although strongly right-skewed, are characterized by finite variance. This implies that interventions aimed at reducing transmissibility have the potential to reduce the reproductive number of sexually transmitted infections below the epidemic threshold.

To justify using "radically different" prevention strategies for sexually transmitted infections, strong evidence is needed that current strategies will be ineffective. Results based on unverified mathematical assumptions about network structure do not come close to meeting this standard[11]. Such data provide no new insight for epidemiology[7,8], and conclusions drawn from them could jeopardize campaigns to eliminate sexually transmitted infections worldwide.

It has been suggested in the media that 'eliminating' highly promiscuous nodes could be more effective than reducing their probability of transmission, but this overlooks the remarkable progress in preventing mother-to-child infection, the difficulty in identifying highly active individuals, and the growing evidence of the importance of other behavioural patterns, such as differential assortative mixing[1] and concurrency[12,13]. The high stakes in the battle against HIV and AIDS call for a broad perspective.

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Liljeros et al. *reply* — Jones and Handcock have reanalysed two of our four data sets of the number of different sexual partners for Swedish men and women. Specifically, they analyse the probability-distribution function $p(k)$, which yields less reliable information than the cumulative distribution,

$$P(\geq k) = \sum_{k' \geq k} p(k')$$

that we used in our analysis, and they propose that the tails of $p(k)$ decay with a power-law exponent $\rho > \rho_c = 3$, which is larger than the threshold value above which the variance of the distribution is finite. They also question whether public-health strategies need to be refocused in view of their inferred existence of epidemic thresholds.

We argue that these claims are misleading. Jones and Handcock's point that the tail exponent $\rho > \rho_c = 3$, the threshold for finite variance, is not a new one. Their estimates, in fact, agree with ours[1], which indicate that the tails of the distributions of the number of sexual partners decay asymptotically as power laws with $\rho_c > 3$: the apparent discrepancy arises because Jones and Handcock use the probability-distribution function, $p(k)$, whereas we studied the cumulative distribution, $P(\geq k)$. The exponent ρ is related to the exponent α by the equation $\rho = \alpha + 1$; hence, our values of α are the same as those that Jones and Handcock derive for ρ.

Jones and Handcock ignore two of our data sets[1], in which we analyse the number of lifetime sexual partners. This is important in view of the duration of the infectious period of some sexually transmitted pathogens such as HIV. When we re-analyse the data sets for the number of lifetime partners using the Yule distribution, we obtain exactly the same result as for a power-law fit because the Yule distribution closely resembles a power law in the interval analysed (further details are available from the authors).

Jones and Handcock argue that if the variance of the distribution of sexual partners is finite, then interventions aimed at reducing disease transmissibility have the potential to eradicate sexually transmitted infections. The two data sets that they analysed pertain to the number of different sexual partners during the previous year, rendering any discussion about the existence of epidemic thresholds speculative (because other factors besides the distribution of the number of partners in the previous year influence the existence of an epidemic threshold for infinitely large networks[2–5]). For finite networks, the variance of these distributions must be finite, as we are analysing finite populations of individuals who are sexually active for finite periods of time[6]. We did not, therefore, raise the issue of infinitely low thresholds in our communication[1].

We contend that Jones and Handcock's conclusion is premature, given that contagious processes differ fundamentally for scale-free and single-scale networks[4,5] and that, if a threshold were to exist, it would be very low, as the variance of the distribution of the number of sexual partners is much larger than the mean[5,7,8].

Jones and Handcock claim that there is no need for a radical refocusing of current public-health strategies[9]. We agree, as targeting high-risk sexual behaviour and carrying out contact-tracing routines — the strategies best suited to scale-free networks — are well established practices in many countries.

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