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**Sample-size estimation**

* You should state whether an appropriate sample size was computed when the study was being designed
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* If no explicit power analysis was used, you should describe how you decided what sample (replicate) size (number) to use

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No sample size calculation was performed since this study did not include the collection of data.

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* High-throughput sequence data should be uploaded before submission, with a private link for reviewers provided (these are available from both GEO and ArrayExpress)

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Biological replication: this does not apply since this study did not include the collection of data.

Technical replication: the number of steps used in our Markov chain Monte Carlo model fitting procedure is given in the Materials and Methods (“Parameter estimation”). This fitting procedure was also tested using simulated data to ensure convergence in these test cases.

**Statistical reporting**

* Statistical analysis methods should be described and justified
* Raw data should be presented in figures whenever informative to do so (typically when N per group is less than 10)
* For each experiment, you should identify the statistical tests used, exact values of N, definitions of center, methods of multiple test correction, and dispersion and precision measures (e.g., mean, median, SD, SEM, confidence intervals; and, for the major substantive results, a measure of effect size (e.g., Pearson's r, Cohen's d)
* Report exact p-values wherever possible alongside the summary statistics and 95% confidence intervals. These should be reported for all key questions and not only when the p-value is less than 0.05.

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No statistical analyses were performed on raw data. Bayesian (Markov chain Monte Carlo) methods were used to fit the models. The fitting procedure for the independent transmission and symptoms model is described in the Materials and Methods (“Parameter estimation”), and the equivalent procedure for the mechanistic model in the Appendix. Prior and posterior distributions of fitted parameters are shown in Figure 1-figure supplement 1 and Figure 1-figure supplement 2, and central estimates and credible intervals are given in Appendix 1-table 2 and Appendix 1-table 3.

(For large datasets, or papers with a very large number of statistical tests, you may upload a single table file with tests, Ns, etc., with reference to sections in the manuscript.)

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* Indicate how samples were allocated into experimental groups (in the case of clinical studies, please specify allocation to treatment method); if randomization was used, please also state if restricted randomization was applied
* Indicate if masking was used during group allocation, data collection and/or data analysis

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* Where provided, these should be in the most useful format, and they can be uploaded as “Source data” files linked to a main figure or table
* Include model definition files including the full list of parameters used
* Include code used for data analysis (e.g., R, MatLab)
* Avoid stating that data files are “available upon request”

Please indicate the figures or tables for which source data files have been provided:

The household transmission data used in our analyses are included in our submission (Figure 1-Source Data 1). Code for reproducing our results is available at https://github.com/will-s-hart/UK-generation-times.