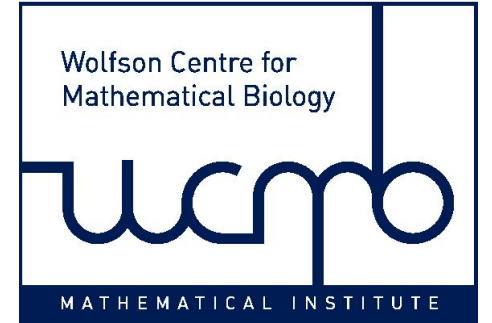




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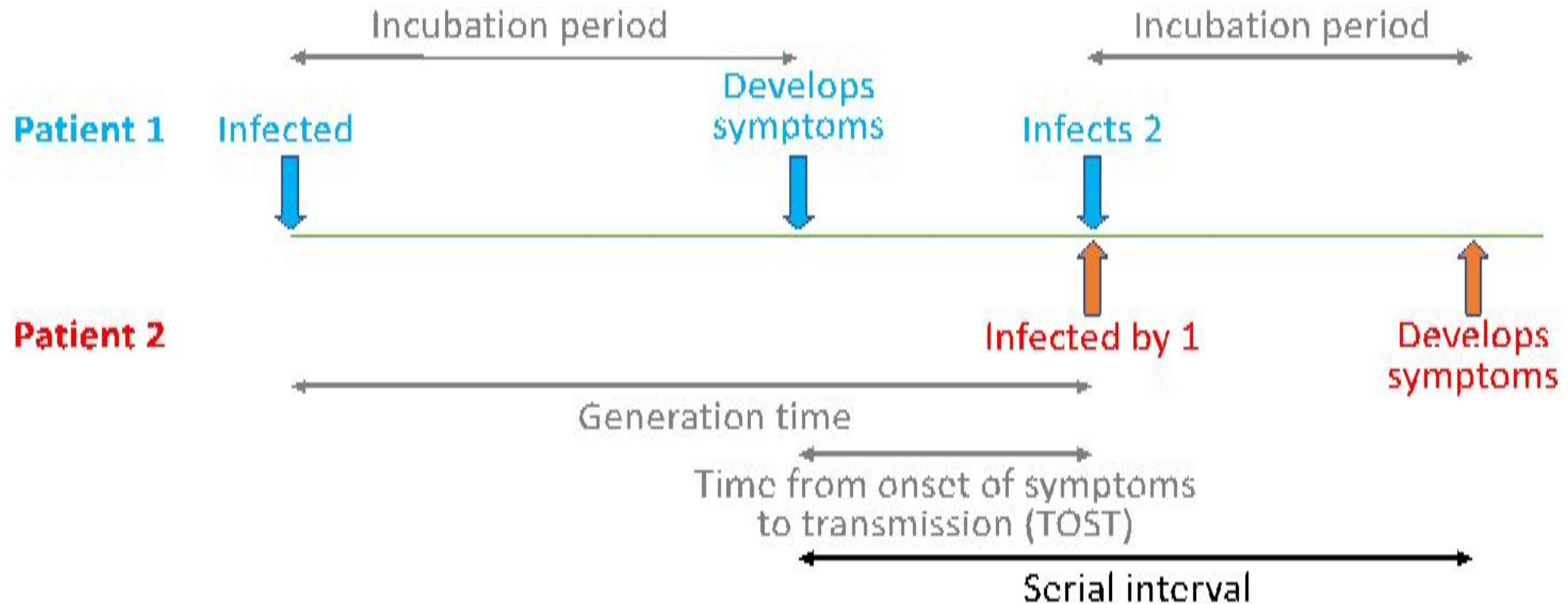
Changes in the SARS-CoV-2 generation time

William Hart
University of Oxford

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1. Estimating the generation time using transmission pair data



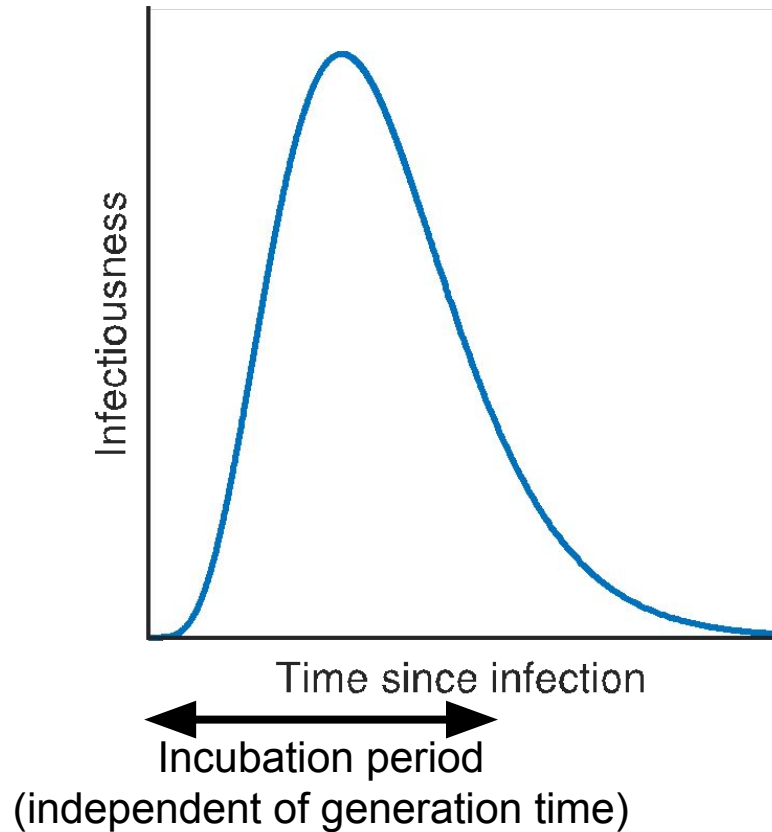
(Hart *et al.* "High infectiousness immediately before COVID-19 symptom onset highlights the importance of contact tracing". *eLife*, 2021, <https://doi.org/10.7554/eLife.65534>)

1. Estimating the generation time using transmission pair data

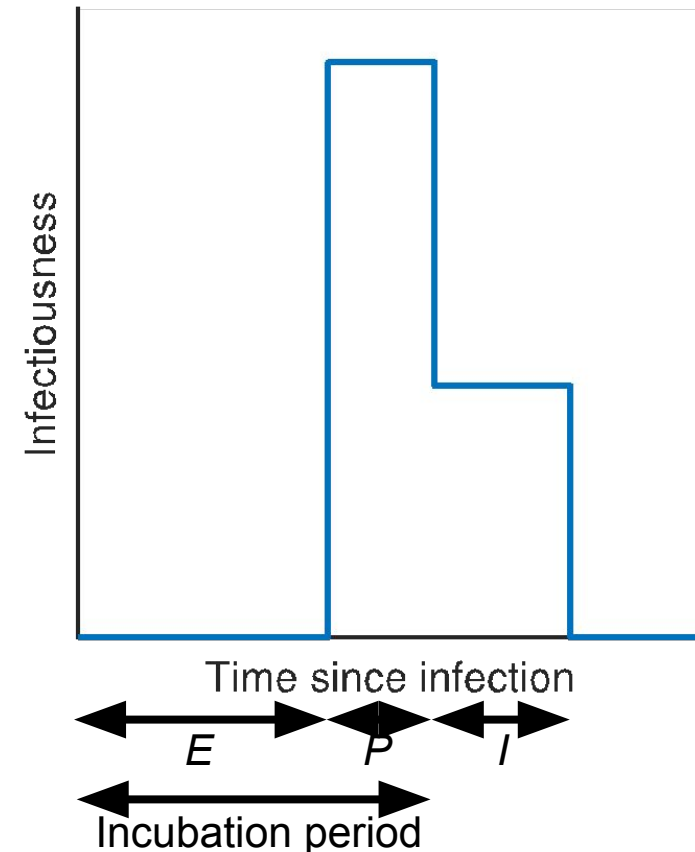
- Often only the dates on which the infector and infectee developed symptoms are known (so the serial interval is known, but not the generation time).
- May also have partial information about when the infector and/or infectee became infected (intervals of possible exposure dates).
- In order to infer the generation time, we need to make an assumption about the relationship between infectiousness and symptoms.

1. Estimating the generation time using transmission pair data

i. “Independent transmission and symptoms model”



ii. “Mechanistic model”

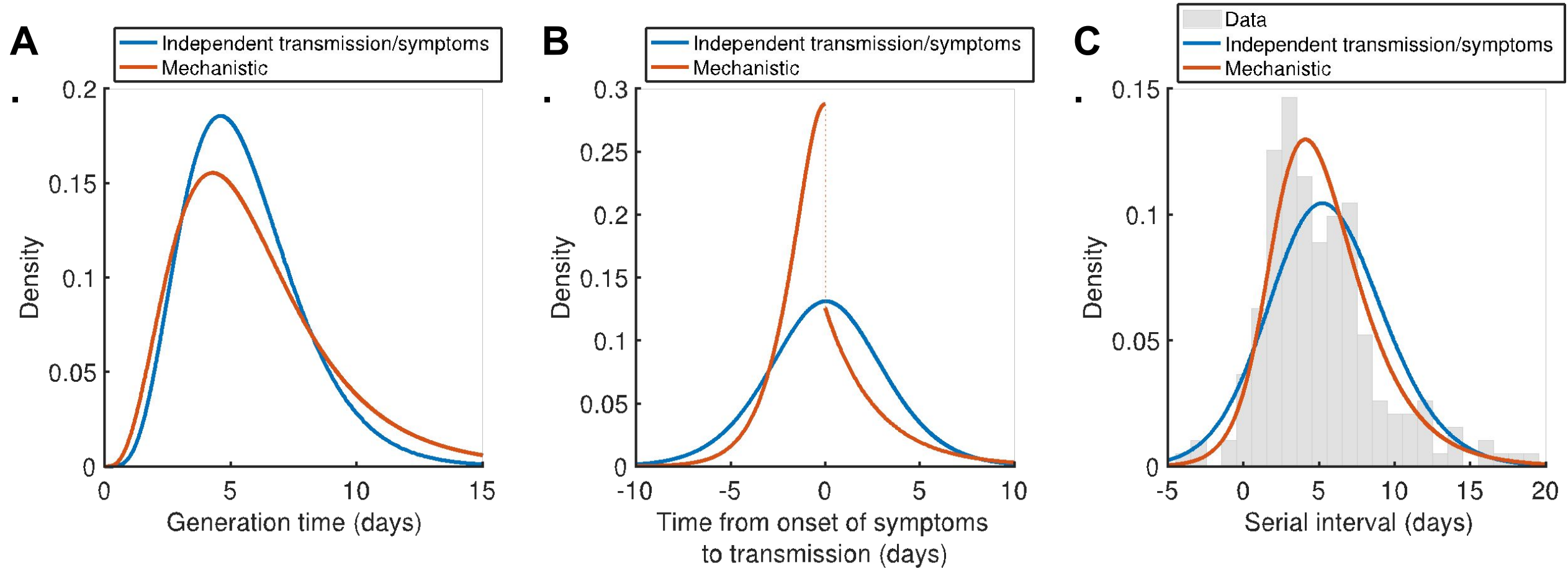


(Hart *et al.* “High infectiousness immediately before COVID-19 symptom onset highlights the importance of contact tracing”. *eLife*, 2021, <https://doi.org/10.7554/eLife.65534>)

2. Application to early-pandemic data

- We fitted the two models to data from 191 infector-infectee transmission pairs, collected between December 2019 and March 2020, mostly from Asia.
- These data were initially collated by Ferretti *et al.* (<https://doi.org/10.1101/2020.09.04.20188516>) from five separate studies.

2. Application to early-pandemic data

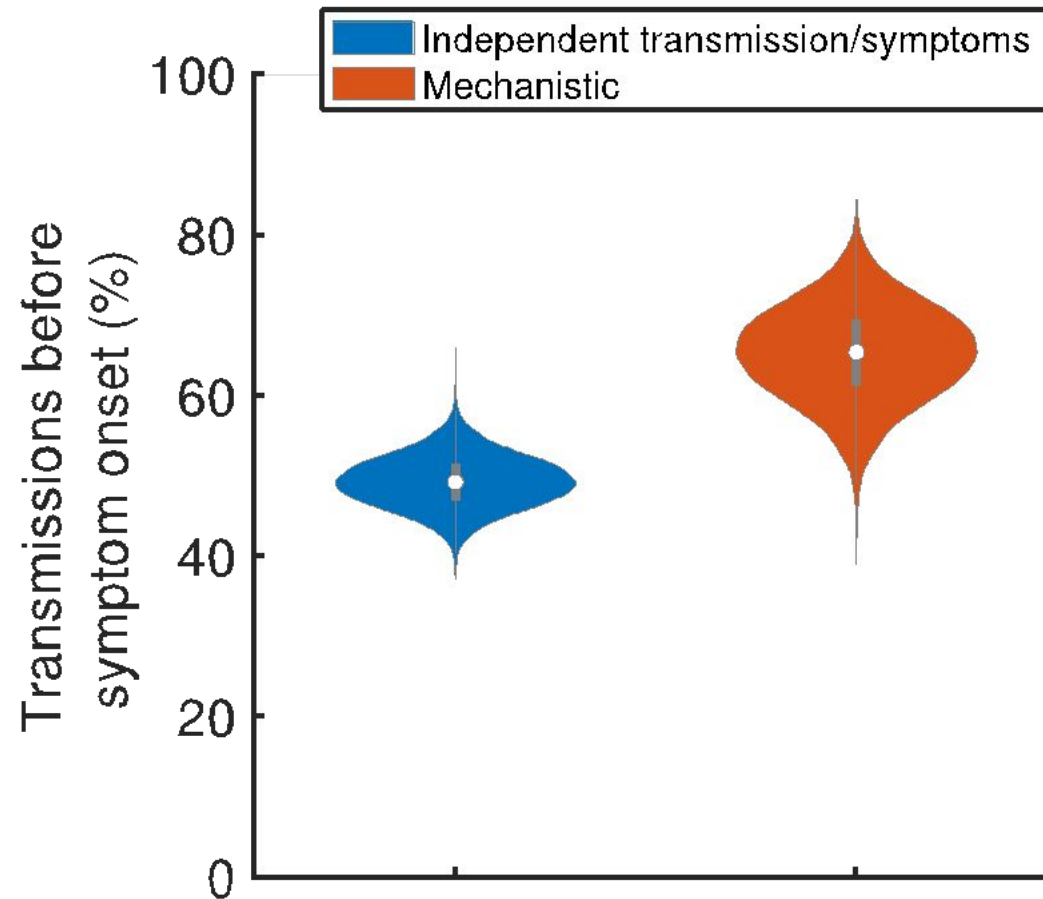


(Hart *et al.* "High infectiousness immediately before COVID-19 symptom onset highlights the importance of contact tracing". *eLife*, 2021, <https://doi.org/10.7554/eLife.65534>)

2. Application to early-pandemic data

- Point estimates for the mean and standard deviation of the generation time were:
 - i. Independent transmission and symptoms model – mean 5.6 days, standard deviation 2.3 days.
(Consistent with other estimates obtained under the same assumption and using data from the same time period).
 - ii. Mechanistic model – mean 6.0 days, standard deviation 3.2 days
(Slightly higher mean and higher standard deviation compared to model (i)).

2. Application to early-pandemic data

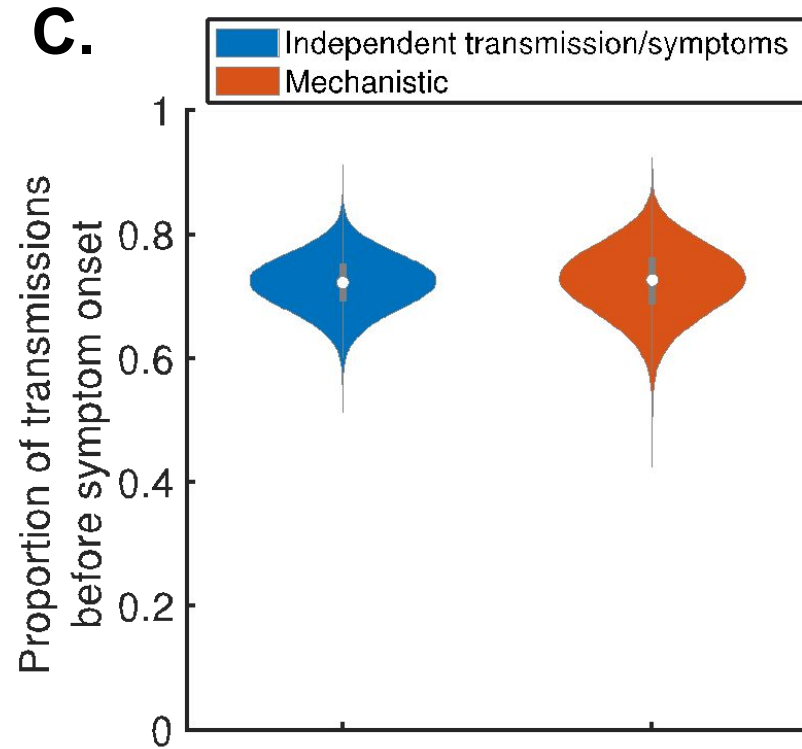
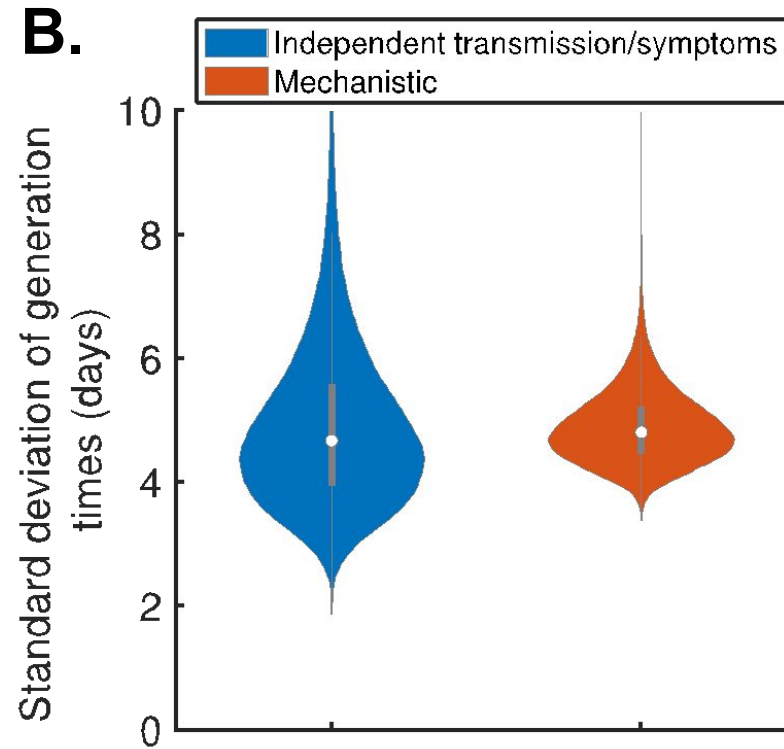
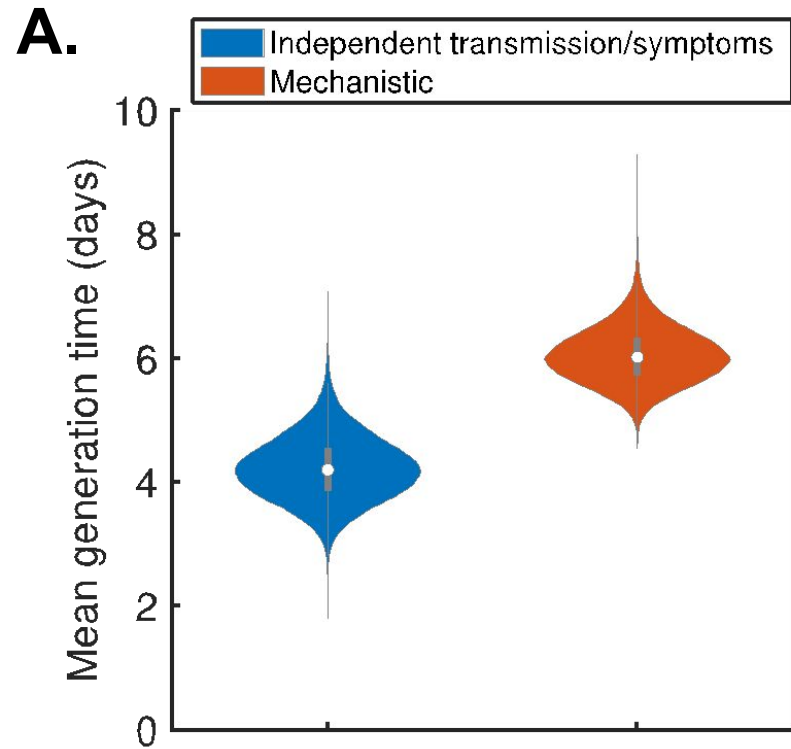


(Hart *et al.* “High infectiousness immediately before COVID-19 symptom onset highlights the importance of contact tracing”. *eLife*, 2021, <https://doi.org/10.7554/eLife.65534>)

3. Application to UK household data

- We then used the two models to estimate the generation time using data from 172 UK households, collected by Public Health England between March and November 2020.
- Some adaptations to methodology needed to fit the models to household data (e.g., need to account for uncertainty in who infected whom within each household, as well as the regularity of household contacts).

3. Application to UK household data



3. Application to UK household data

- Point estimates for the mean and standard deviation of the generation time were:

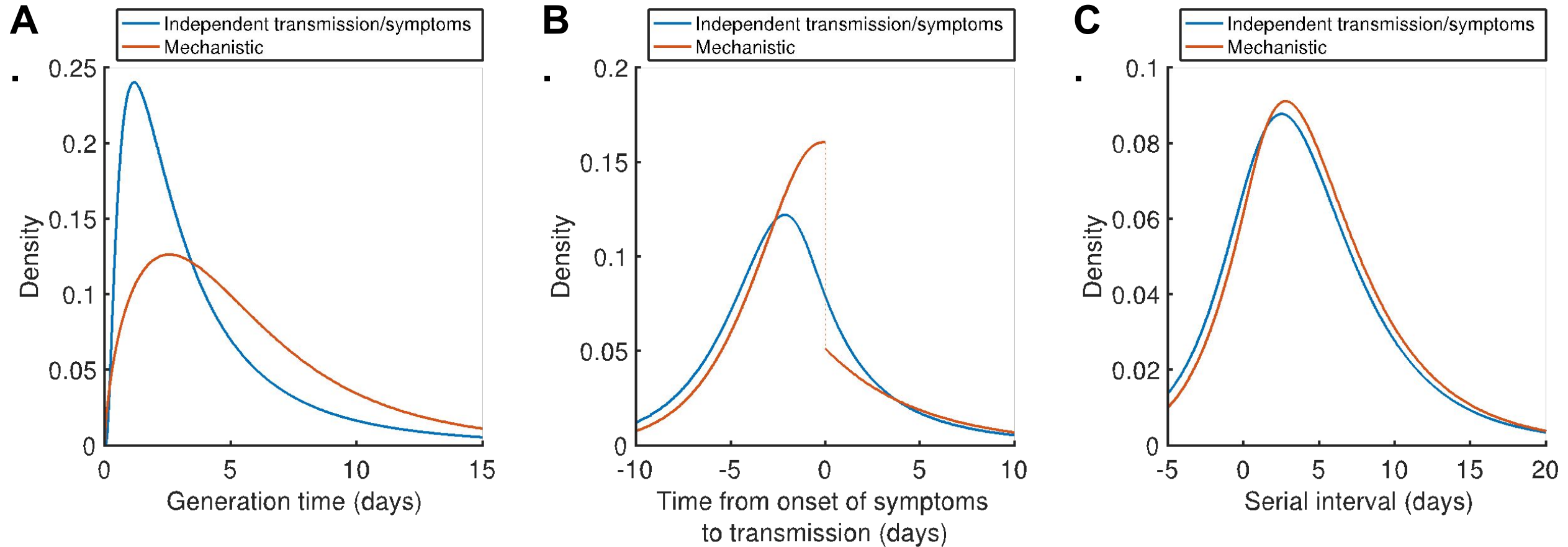
- i. Independent transmission and symptoms model – mean 4.2 days, standard deviation 4.9 days.

- (Similar mean to earlier estimates, but higher standard deviation).

- ii. Mechanistic model – mean 6.0 days, standard deviation 4.9 days

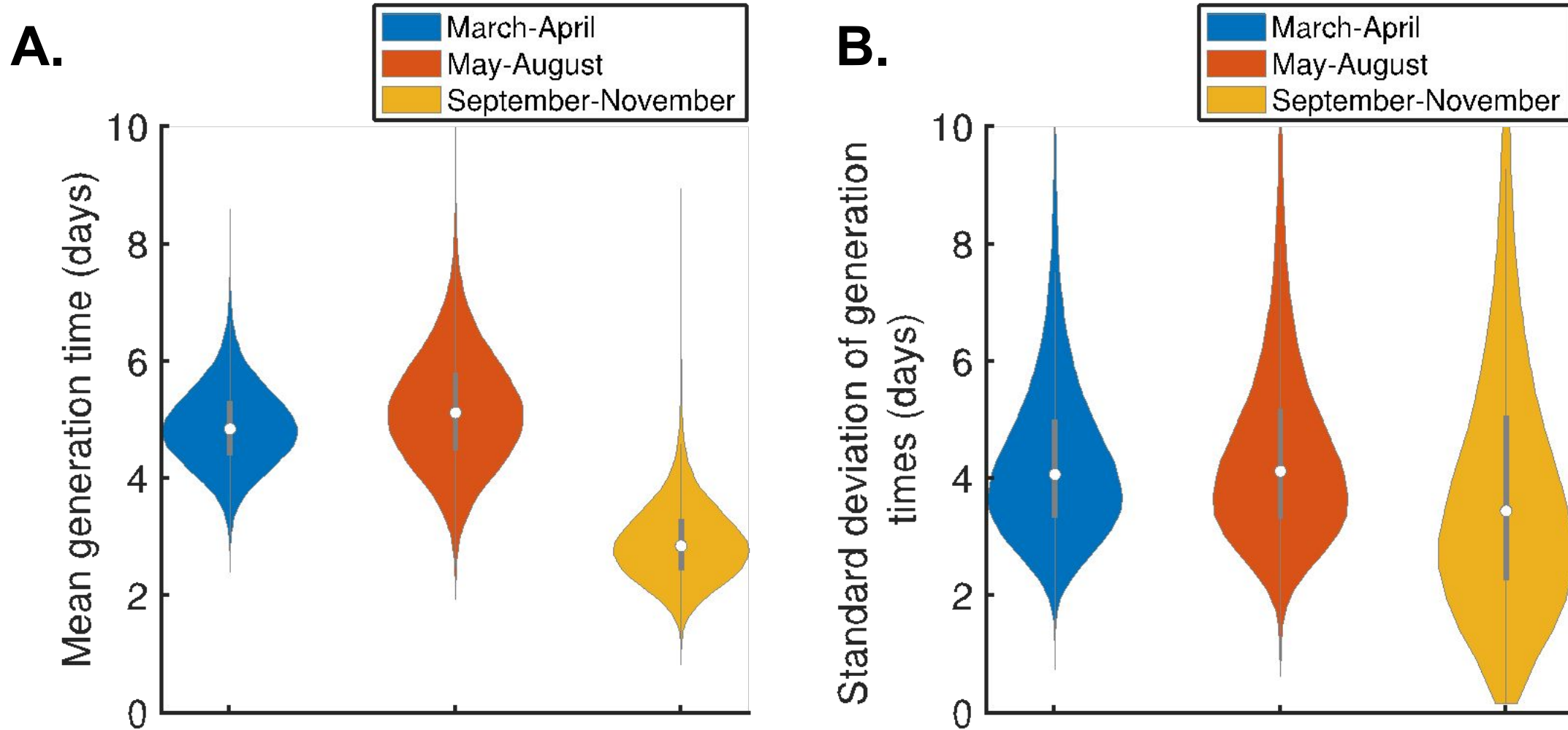
- (Higher mean and similar standard deviation compared to model (i)).

3. Application to UK household data



(Hart *et al.* “High infectiousness immediately before COVID-19 symptom onset highlights the importance of contact tracing”. *eLife*, 2021, <https://doi.org/10.7554/eLife.65534>)

3. Application to UK household data



(Hart *et al.* "Inference of SARS-CoV-2 generation times using UK household data". *medRxiv*, 2021, <https://doi.org/10.1101/2021.05.27.21257936>)

3. Application to UK household data

- Both models indicated a lower generation time in September-November 2020 compared to earlier months.

4. Conclusions

- Estimates of the generation time can be sensitive to modelling assumptions. Several factors need to be considered when deciding which of our estimates to use, for example:
 - i. Epidemiological plausibility of the different models.
 - ii. The assumptions underlying models in which estimates of the generation time are used (e.g., models for estimating the reproduction number).

4. Conclusions

- Estimates of the generation time can be sensitive to modelling assumptions. Several factors need to be considered when deciding which of our estimates to use, for example:
 - i. Epidemiological plausibility of the different models.
 - ii. The assumptions underlying models in which estimates of the generation time are used (e.g., models for estimating the reproduction number).
- Our results indicate a temporal decrease in the generation time. Continued data collection and analysis is necessary to ensure up-to-date estimation in light of (e.g.) variants, behavioural changes, vaccination.

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