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Using diversity-based methods to estimate true epidemic sizes from sampled outbreaks

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Previous work..

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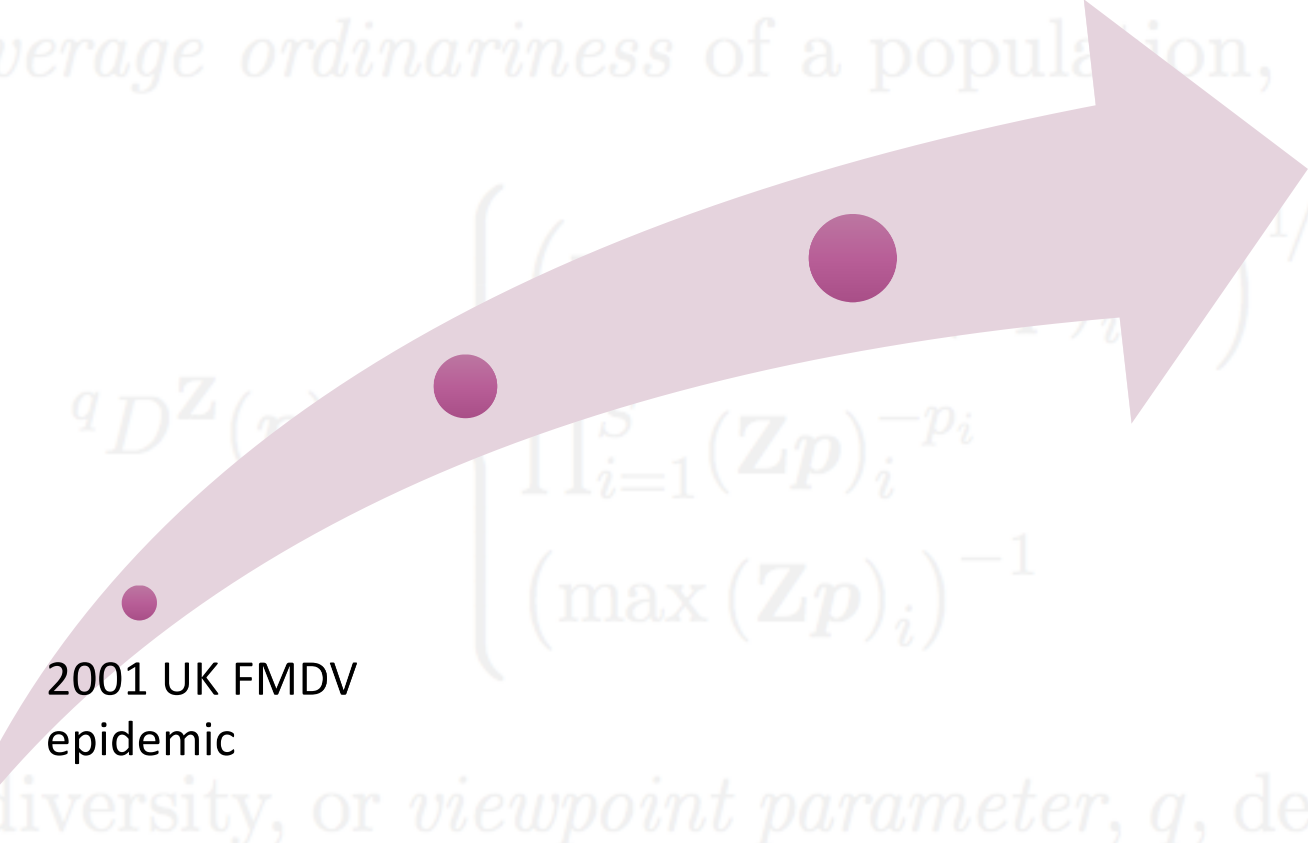
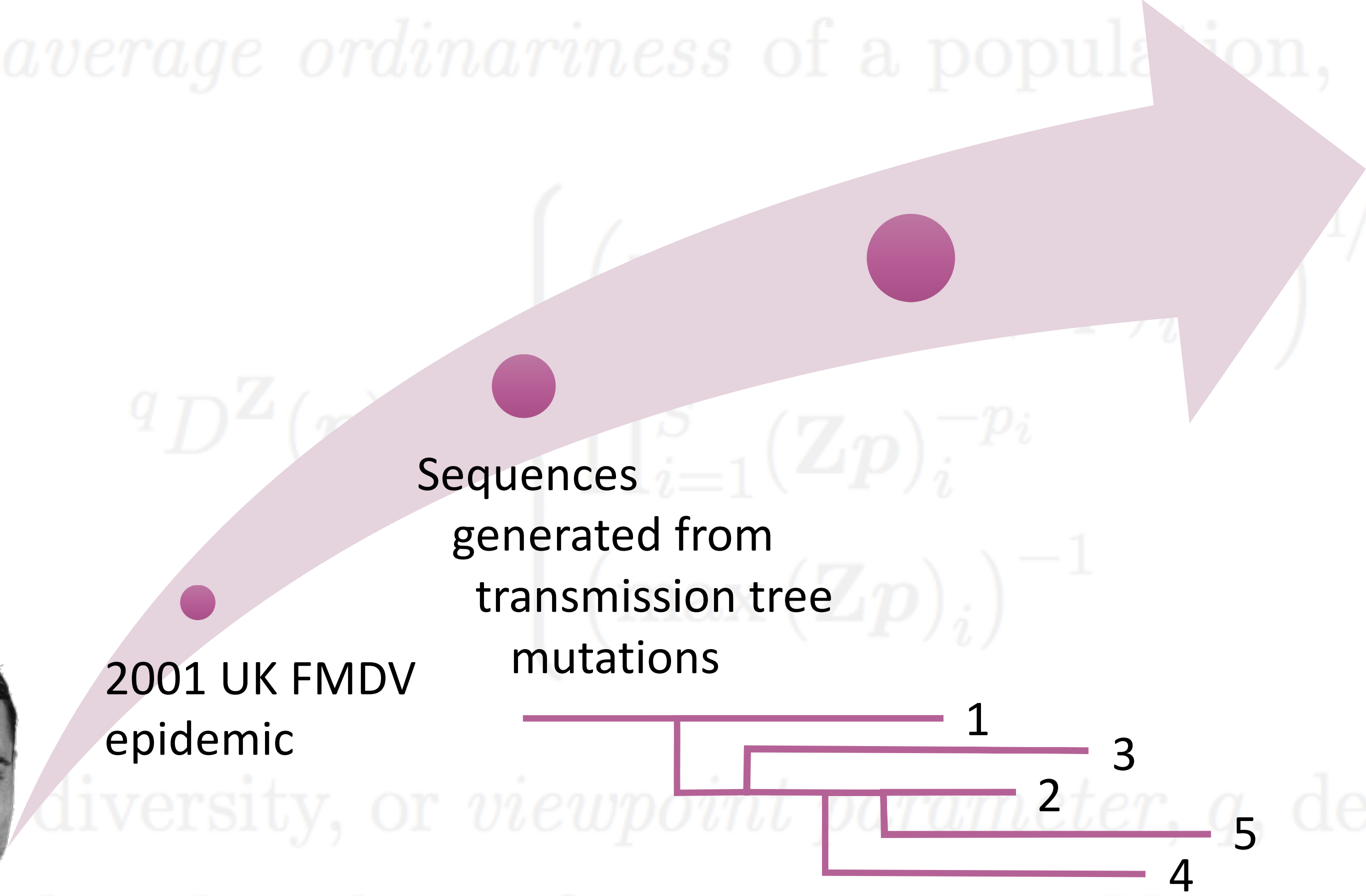


2001 UK FMDV
epidemic

Di Nardo, A. 2016. *Phylodynamic modelling of foot-and-mouth disease virus sequence data*.

Antonello Di Nardo



2001 UK FMDV epidemic

Sequences generated from transmission tree mutations

Di Nardo, A. 2016. *Phylodynamic modelling of foot-and-mouth disease virus sequence data*.

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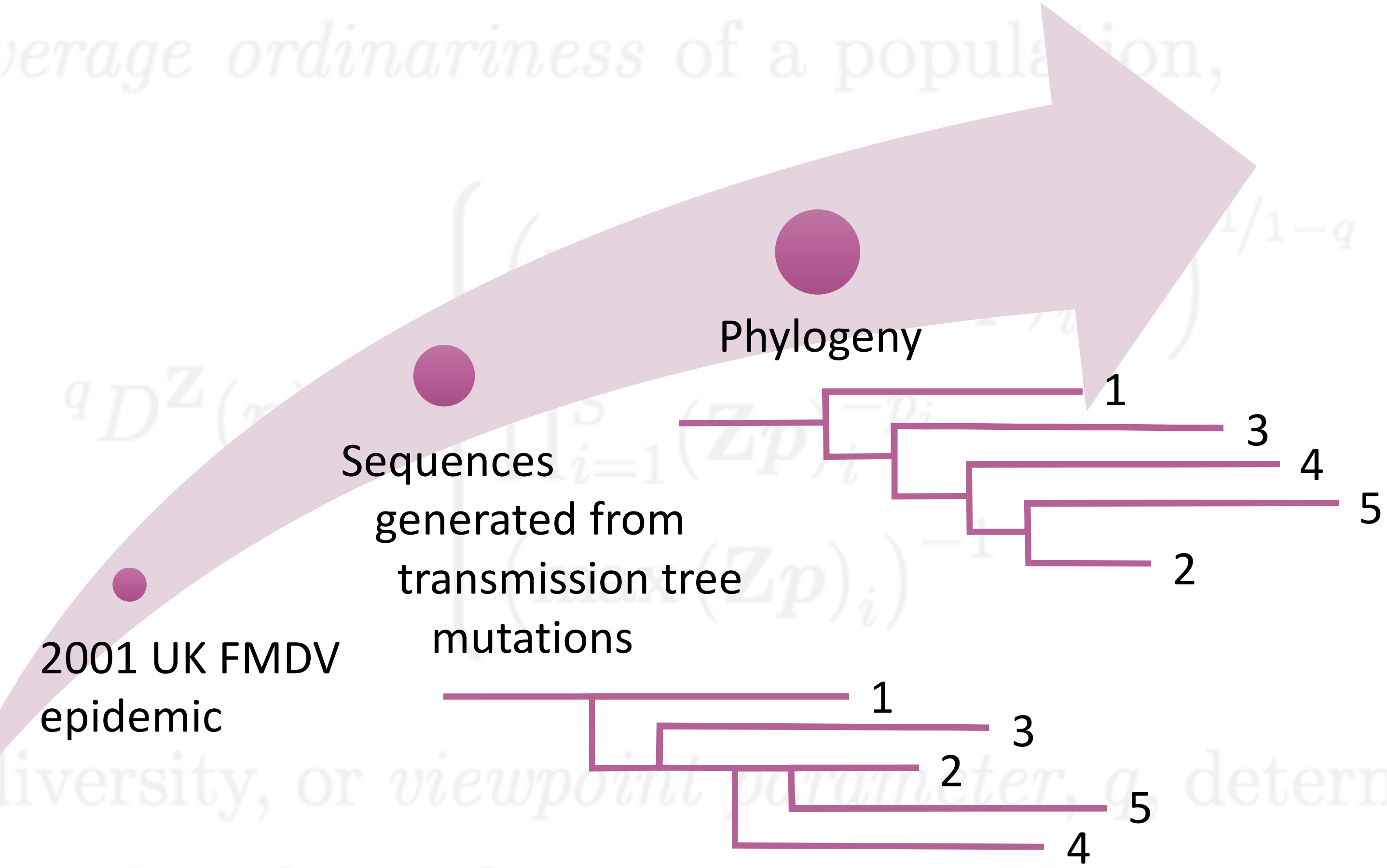

2001 UK FMDV epidemic

Sequences generated from transmission tree mutations

Phylogeny

Di Nardo, A. 2016. *Phylodynamic modelling of foot-and-mouth disease virus sequence data*.

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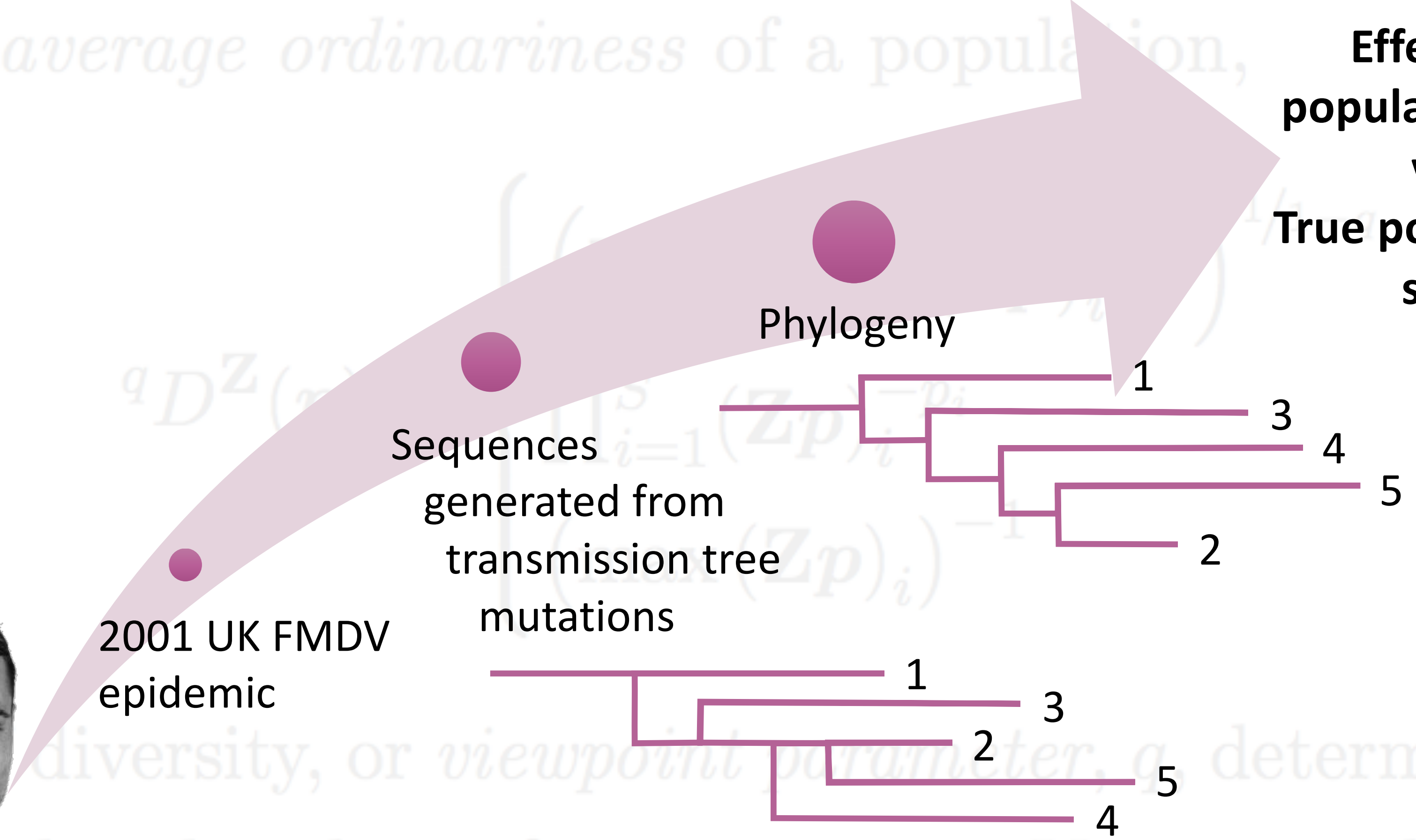

2001 UK FMDV epidemic

Sequences generated from transmission tree mutations

Phylogeny

Effective population size vs. True population size

Di Nardo, A. 2016. *Phylodynamic modelling of foot-and-mouth disease virus sequence data*.

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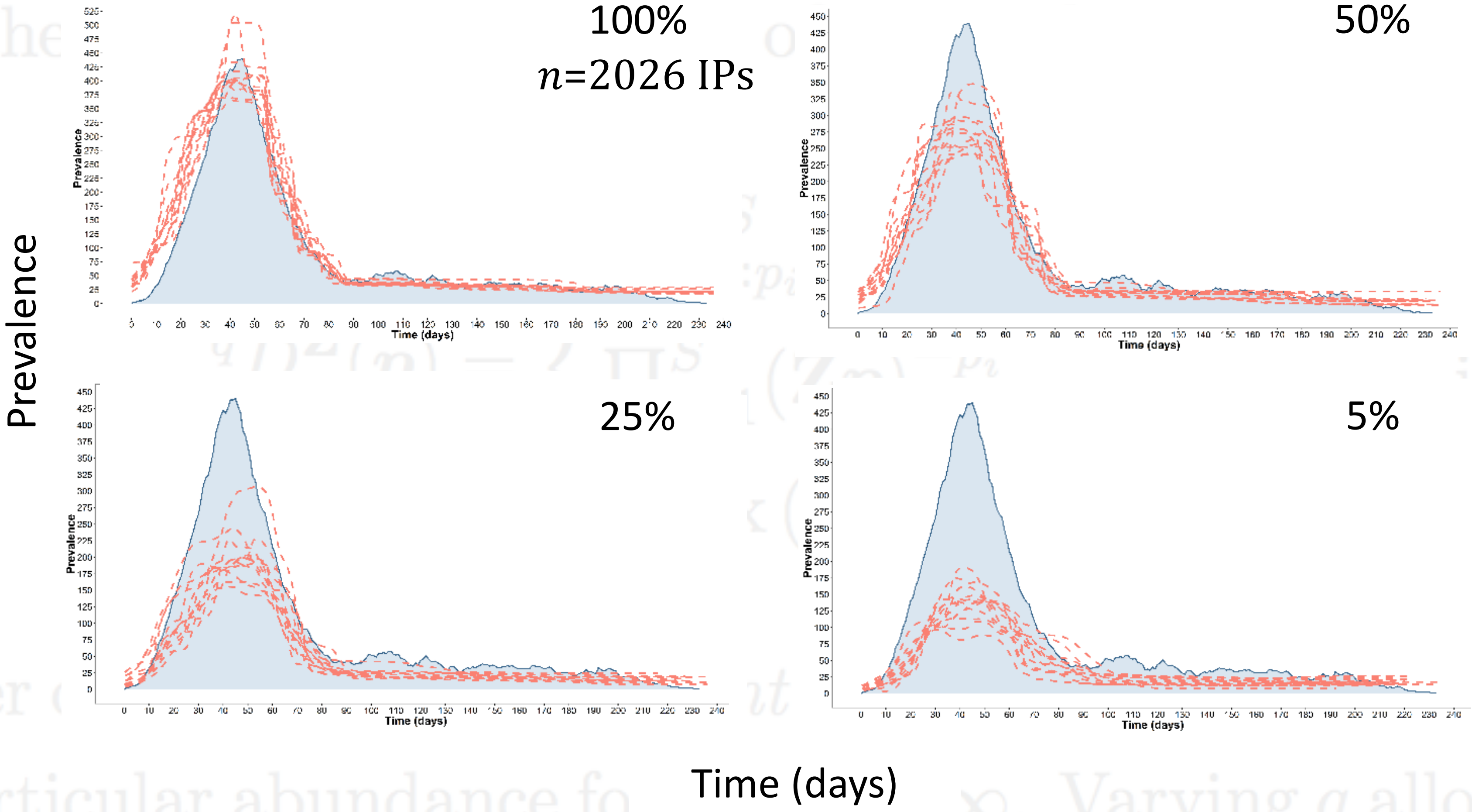

Di Nardo, A. 2016. *Phylodynamic modelling of foot-and-mouth disease virus sequence data*: Figure 5-2.

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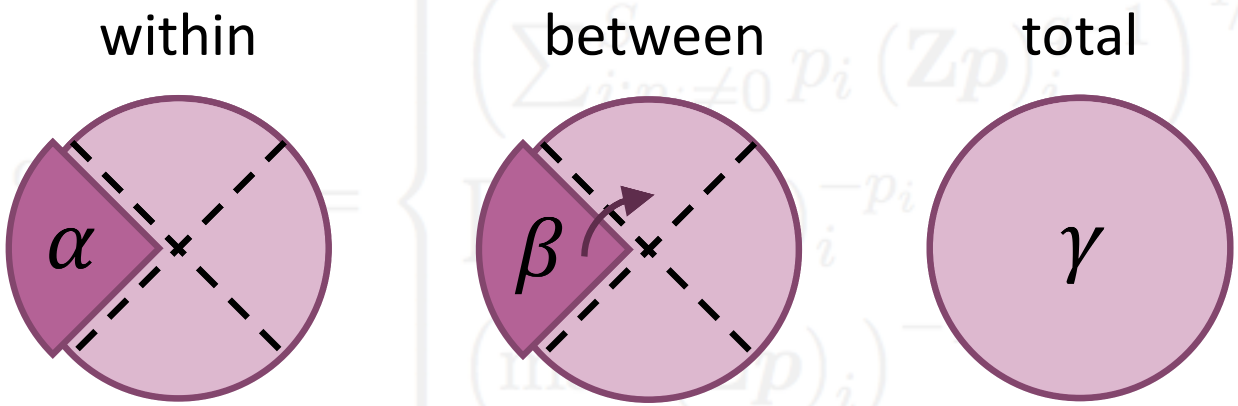
Incomplete surveillance data may cause a mismatch between N_e and N such that..

$$N_e \ll N$$

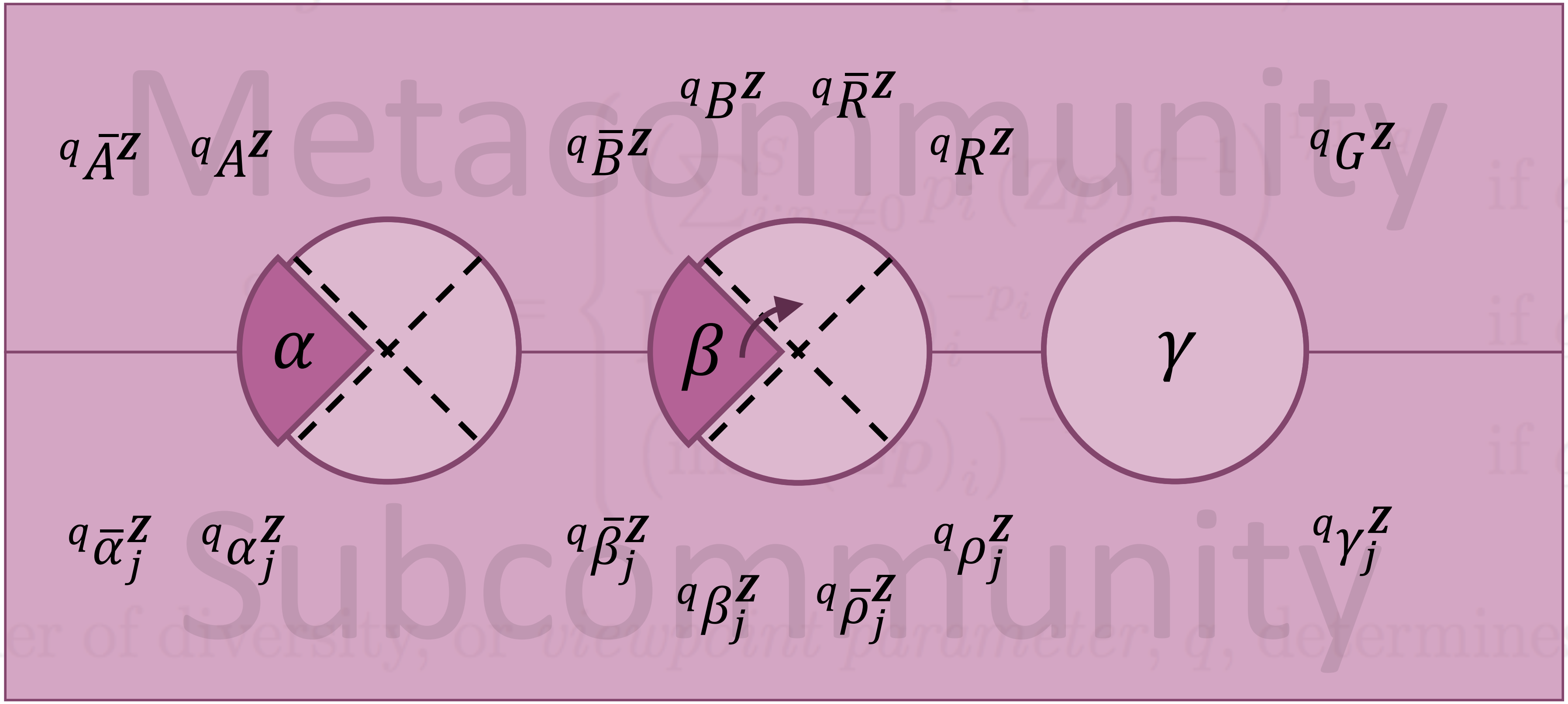
Di Nardo, A. 2016. *Phylodynamic modelling of foot-and-mouth disease virus sequence data*: Figure 5-2.

We propose a new method..

Framework for Partitioning Diversity



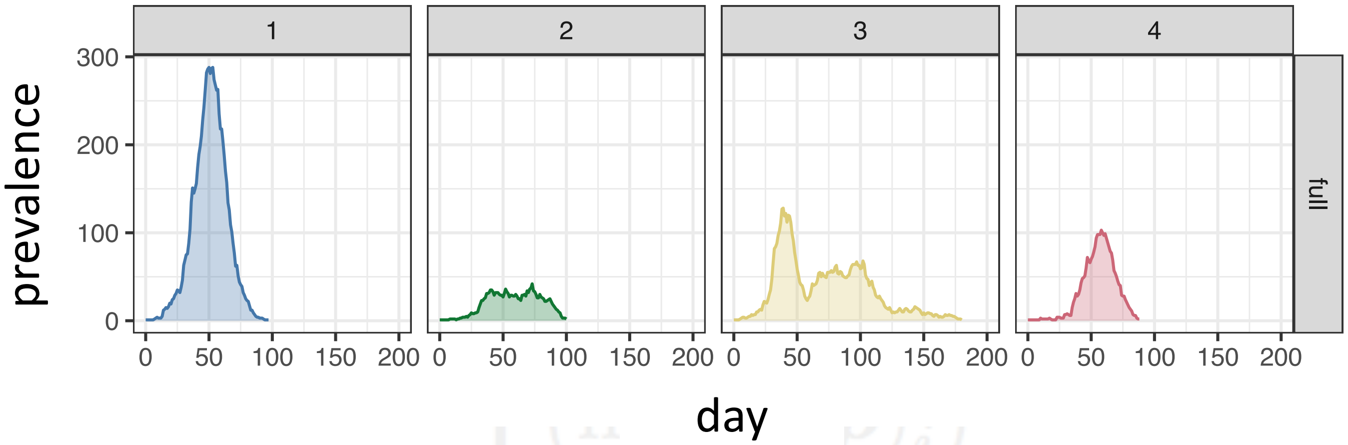
Framework for Partitioning Diversity



Reeve, R., et al. 2016. *How to partition diversity*. arXiv 1404.6520:1–9.

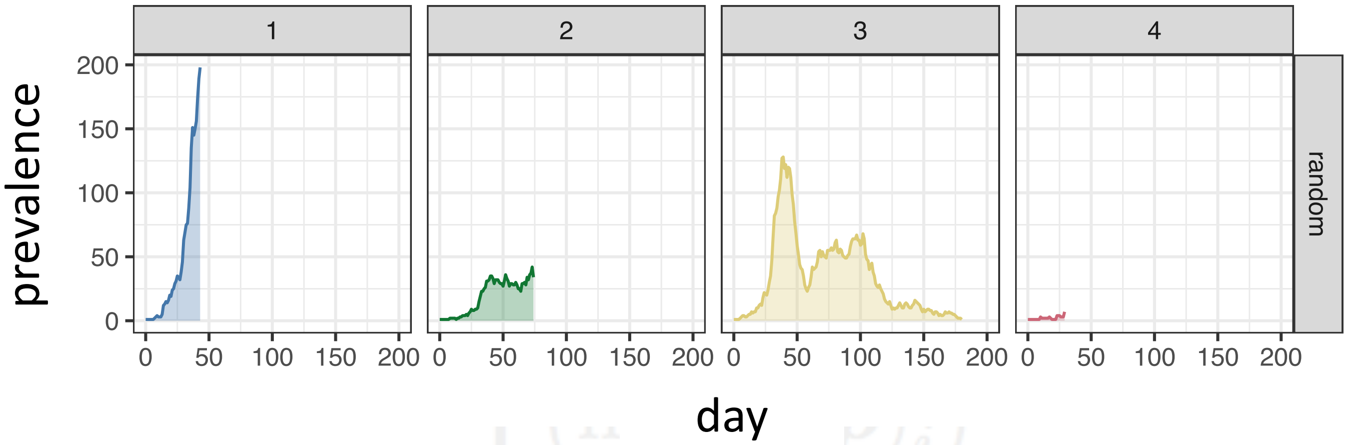
Methods

- Simulate outbreaks



Methods

- Simulate outbreaks (truncated)



Methods

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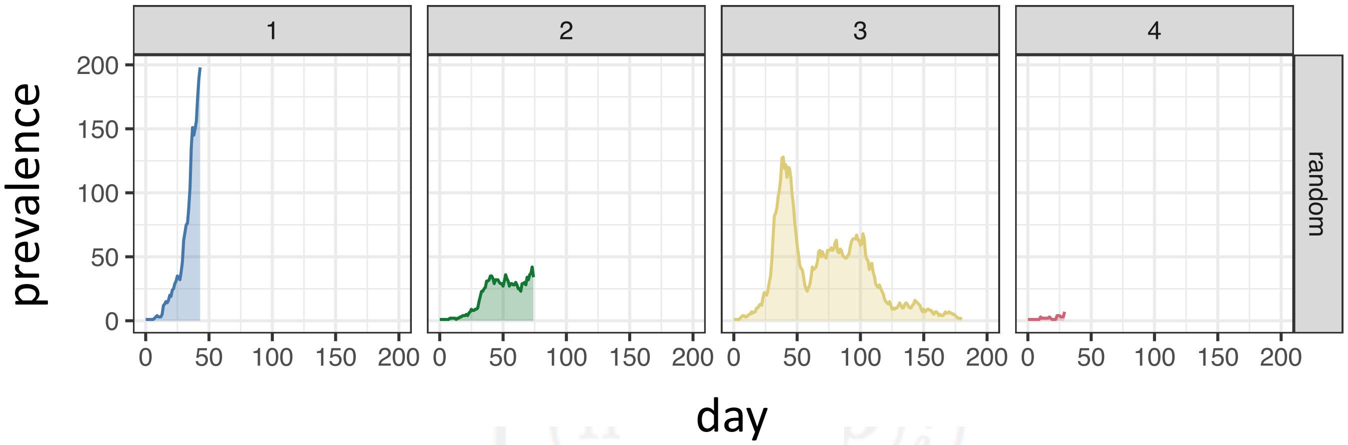
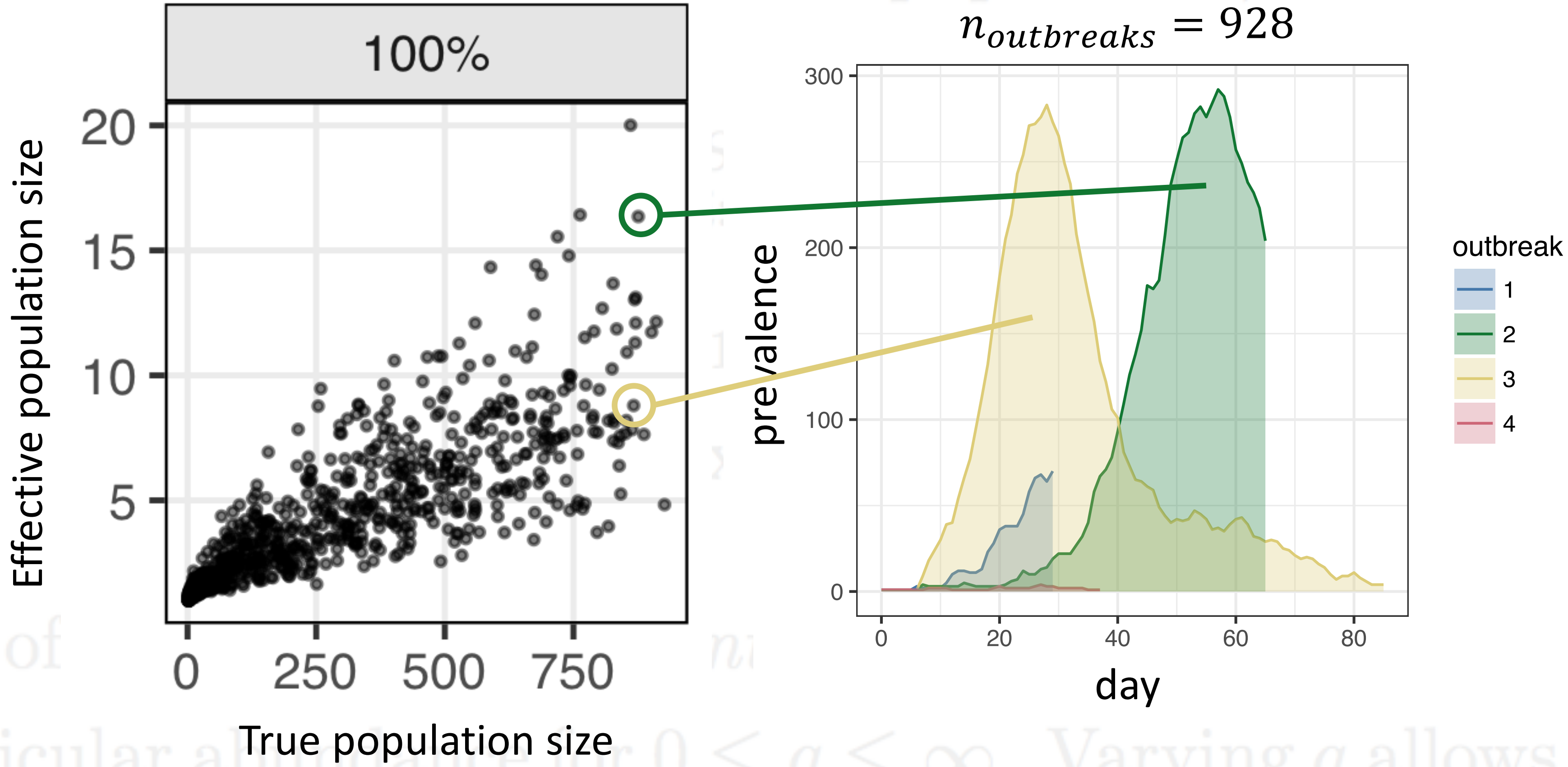
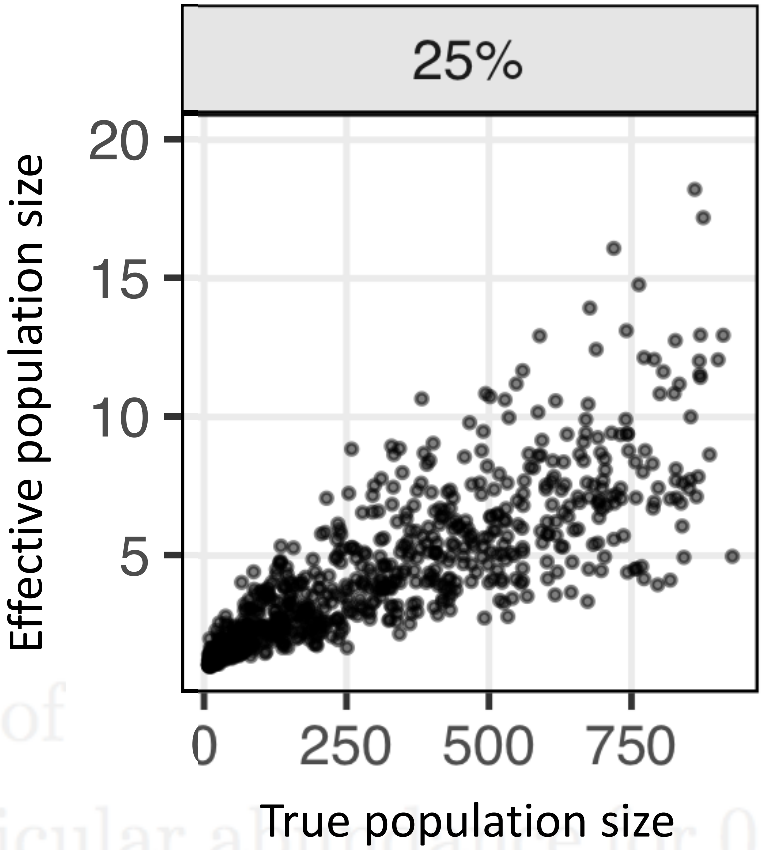


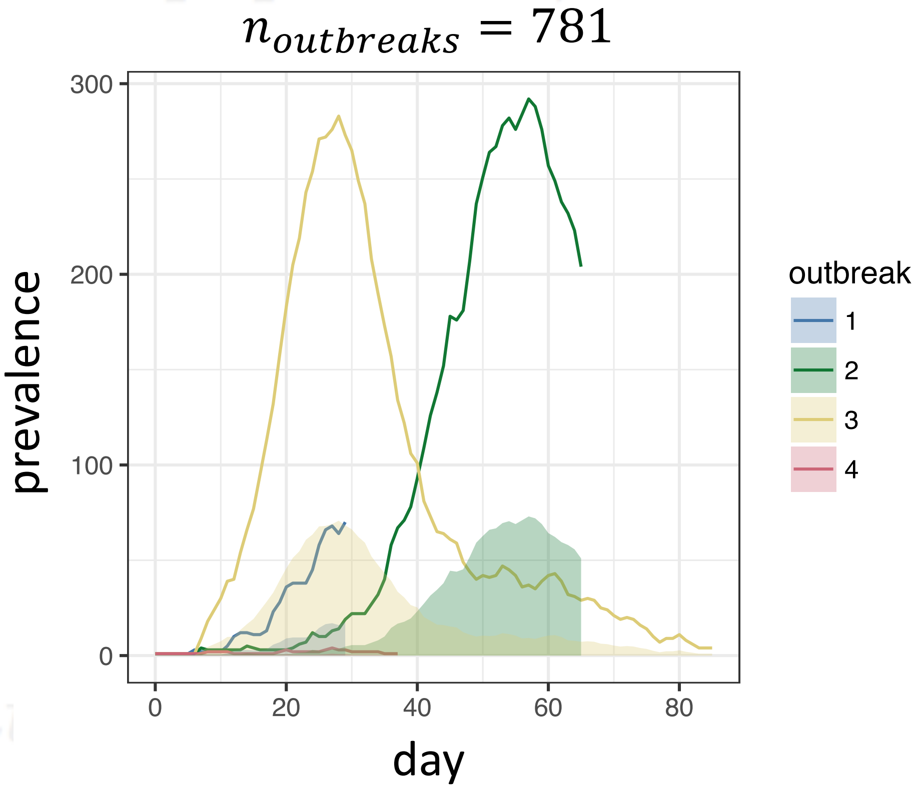
- Viral genetic diversity of the 2001 FMDV outbreak
- Calculate ${}^{q}G^{\boldsymbol{Z}}$ (Effective number of sequences / infected premises)

Effective number of sequences, $^{1}G^{\mathbf{Z}}$

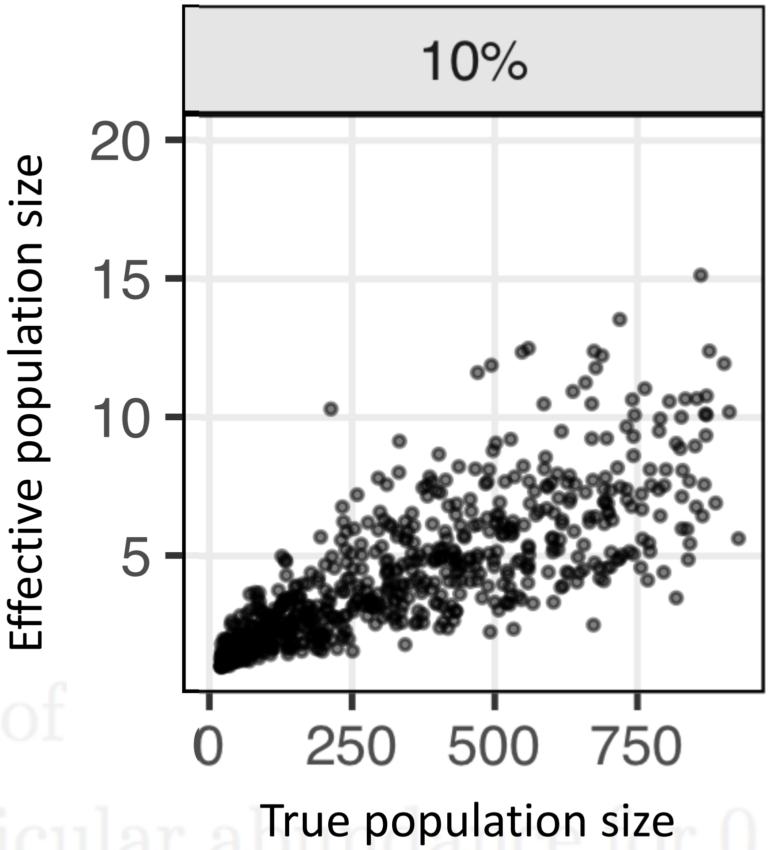


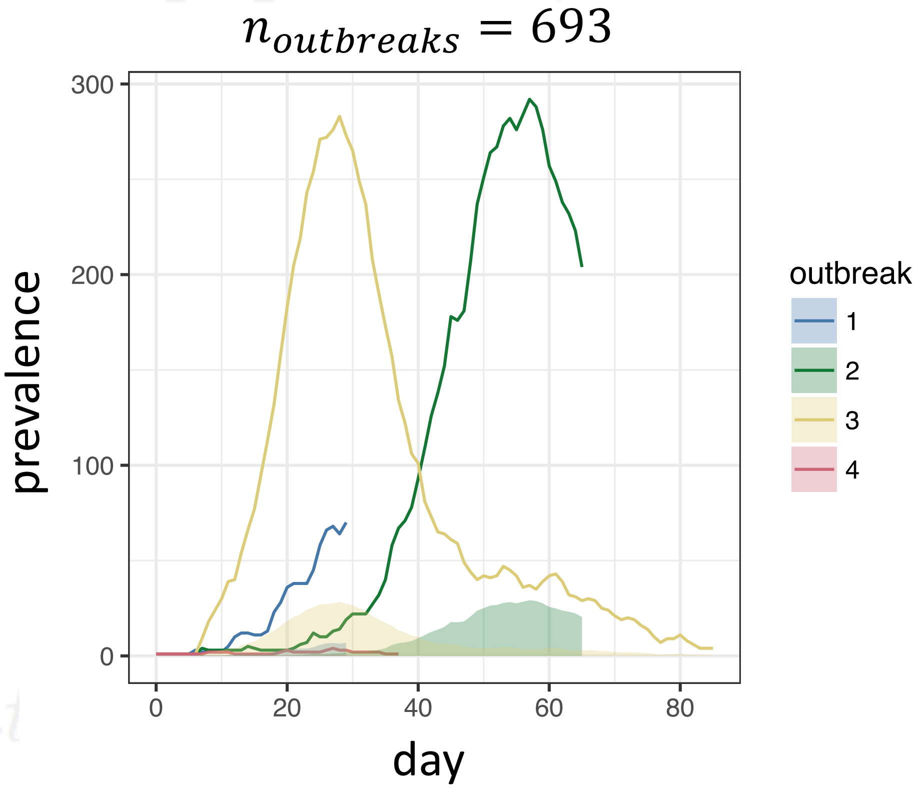
Effective number of sequences, ${}^{1}G^{\mathbf{Z}}$




$n_{outbreaks} = 781$

Effective number of sequences, $^1G^{\mathbf{Z}}$

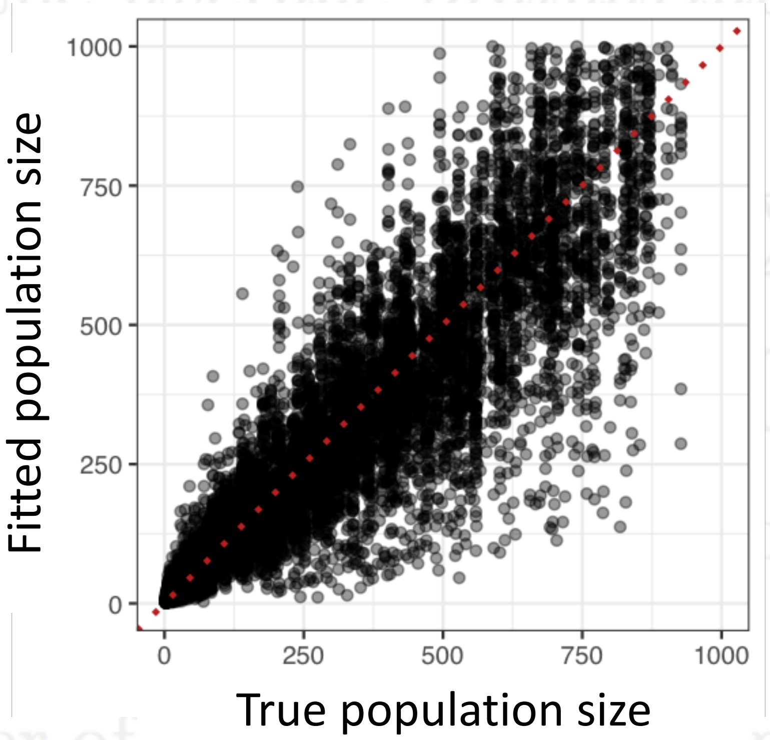




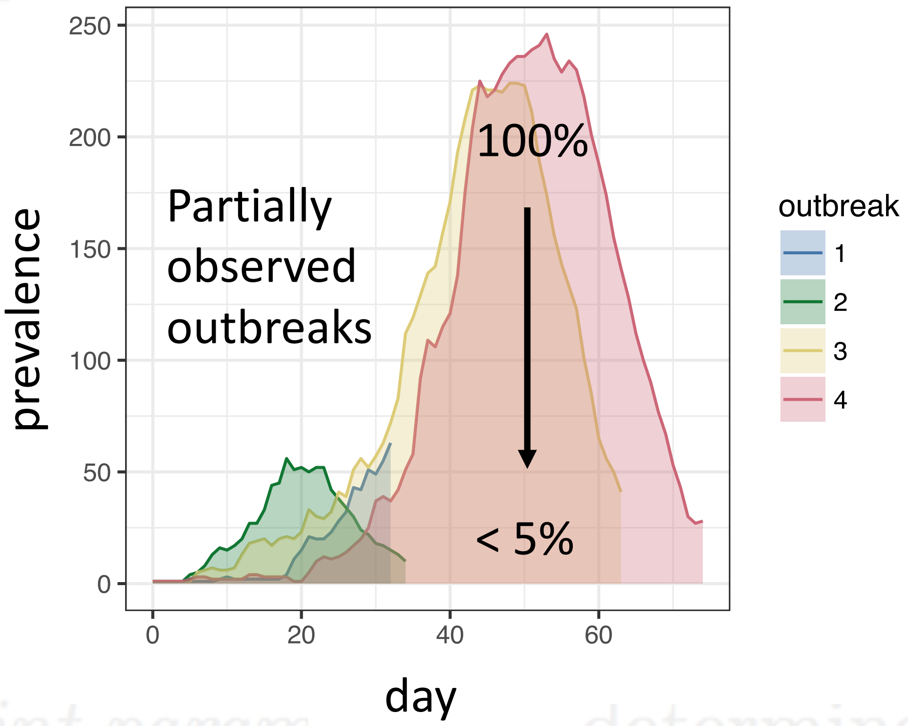
Next, we use ${}^{q}G^{\mathbf{Z}}$ with other simple summary statistics..

..to fit a linear model.

Model fit



Adjusted $R^2 = 0.9001$



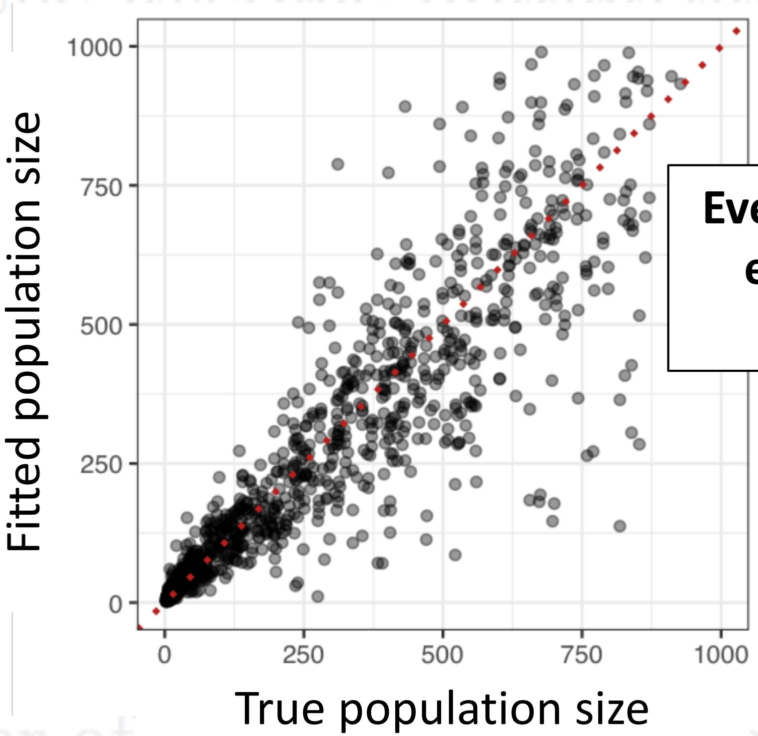
$n_{outbreaks} = 10759$

100%

Partially observed outbreaks

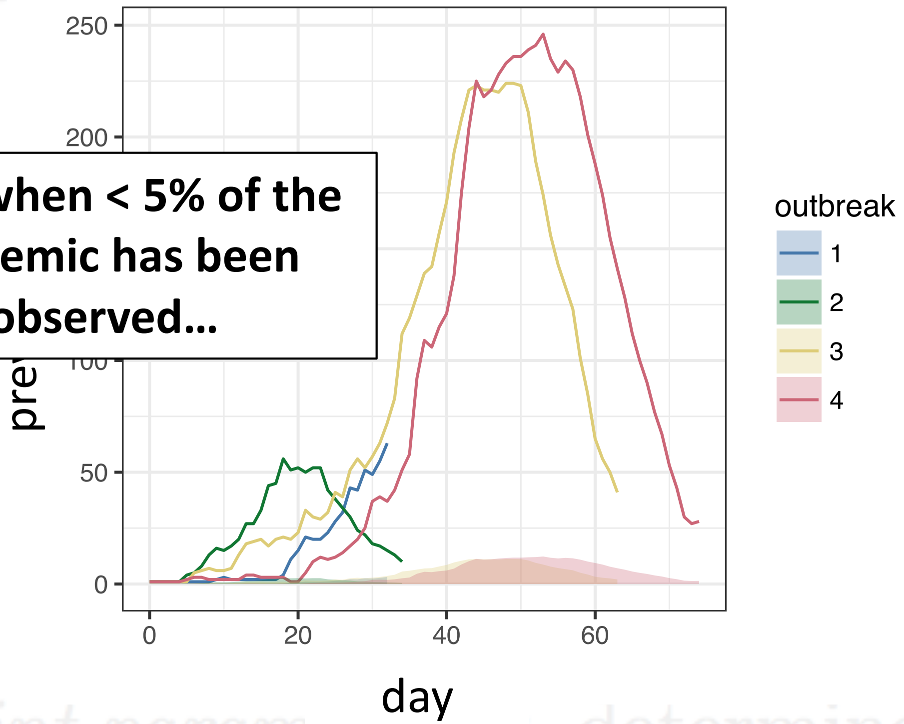
< 5%

Model fit



Even when < 5% of the epidemic has been observed…

$n_{outbreaks} = 4038$



Conclusion

- We can infer epidemic size from partially observed outbreaks
- These methods are more accurate than existing techniques

WHAT NEXT?

- Incorporate measures of β-diversity
- Apply more advanced machine learning techniques, *e.g.* Google's TensorFlow

https://www.tensorflow.org

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- From the R console: `install.packages('rdiversity')`
- Reeve, R. et al. (2016). *How to partition diversity*. arXiv:1404.6520 [q-bio.QM].
- Di Nardo, A. 2016. *Phylodynamic modelling of foot-and-mouth disease virus sequence data*. [PhD Thesis]

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