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## **Estimating the basic reproduction number at the beginning of an outbreak**

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The basic reproduction number,  $R_0$ , is a key quantity allowing public health officials to track how quickly an outbreak spreads through a population. In this talk, we compare several different estimators of  $R_0$  assuming that only weekly data is available, with a focus on the early stages of an outbreak. We compare four estimators: a variant on maximum likelihood, incidence decay, incidence decay with exponential adjustment, and partially observed Markov process approaches. Our simulations concentrate on a flu epidemic, and several different scenarios are considered. In particular, we study also the setting of model misspecification, when one model structure is fit to data generated by a different model. Benefits and drawbacks of each  $R_0$  estimator will be discussed.

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