



## Working Group on Statistical Learning Seminar

**Title:** Assessing epidemic curves for evidence of superspreading

**Speaker:** Joe Meagher (University College Dublin)

**Date:** Mon 11th October 2021 at 12:00PM

**Location:** Online

**Abstract:** The expected number of secondary infections arising from each index case, the reproduction number, or  $R$  number is a vital summary statistic for understanding and managing epidemic diseases. There are many methods for estimating  $R$ ; however, few of these explicitly model heterogeneous disease reproduction, which gives rise to superspreading within the population. Here we propose a parsimonious discrete-time branching process model for epidemic curves that incorporates heterogeneous individual reproduction numbers. Our Bayesian approach to inference illustrates that this heterogeneity results in less certainty on estimates of the time-varying cohort reproduction number  $R_t$ . Leave-future-out cross-validation evaluates the predictive performance of the proposed model, allowing us to assess epidemic curves for evidence of superspreading. We apply these methods to a COVID-19 epidemic curve for the Republic of Ireland and find some support for heterogeneous disease reproduction. We conclude that the 10% most infectious index cases account for approximately 40–80% of the expected secondary infections. Our analysis highlights the difficulties in identifying heterogeneous disease reproduction from epidemic curves and that heterogeneity is a vital consideration when estimating  $R_t$ .

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