

# A comprehensive study of the early phylodynamics of SARS-CoV-2 in Europe

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## Abstract

This project will focus on the spatial dynamics of the early spread of SARS-CoV-2 in Europe. We will apply a novel approach based on the Multi-type Birth Death phylodynamic model to infer structured population dynamics jointly with between-subpopulation transmission rates from viral genome sequences. The inferred epidemic trajectories for the combined outbreak responsible for the observed sequence data will allow us to better understand the entry into and early spread of SARS-CoV-2 in Europe.

## 1 Results

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