Unravelling the chains of transmission of the 9th Ebola outbreak in DRC, 2018

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Context

From 8 May to 25 July 2018, the Democratic Republic of Congo faced its ninth outbreak of Ebola virus disease (EVD) in Equateur province, with a total of 54 cases reported. As part of the response to control the outbreak, field epidemiology teams from Médecins Sans Frontières (MSF), the Center for Disease Control (CDC) and the World Health Organization (WHO) have been monitoring cases and their contacts. Using temporal and contact information, MSF and CDC teams have independently and manually reconstructed the outbreak's chain of transmission. Although these chains provide a better understanding of how EVD spread within the population, they also differ in some of the links between who infected whom.

At the same time, in order to rapidly confirm EVD in suspected cases, the Institut National de Recherche Biomédicale (INRB) and the Institut Pasteur de Dakar (IPD) have carried out laboratory diagnostic activities, including the genetic sequencing of viral strains. Can this genetic information help us to better understand who has infected whom and to reconcile both transmission chains?

In order to answer this question, we will use a Bayesian statistical framework to infer transmission chains using temporal, geographic, contact and genetic data synergistically. This EVD epidemic provides a unique opportunity to evaluate this inference framework in a real-world scenario, explore its performance, compare it with traditional methods, learn about its limitations, and consider its potential use in future epidemics.

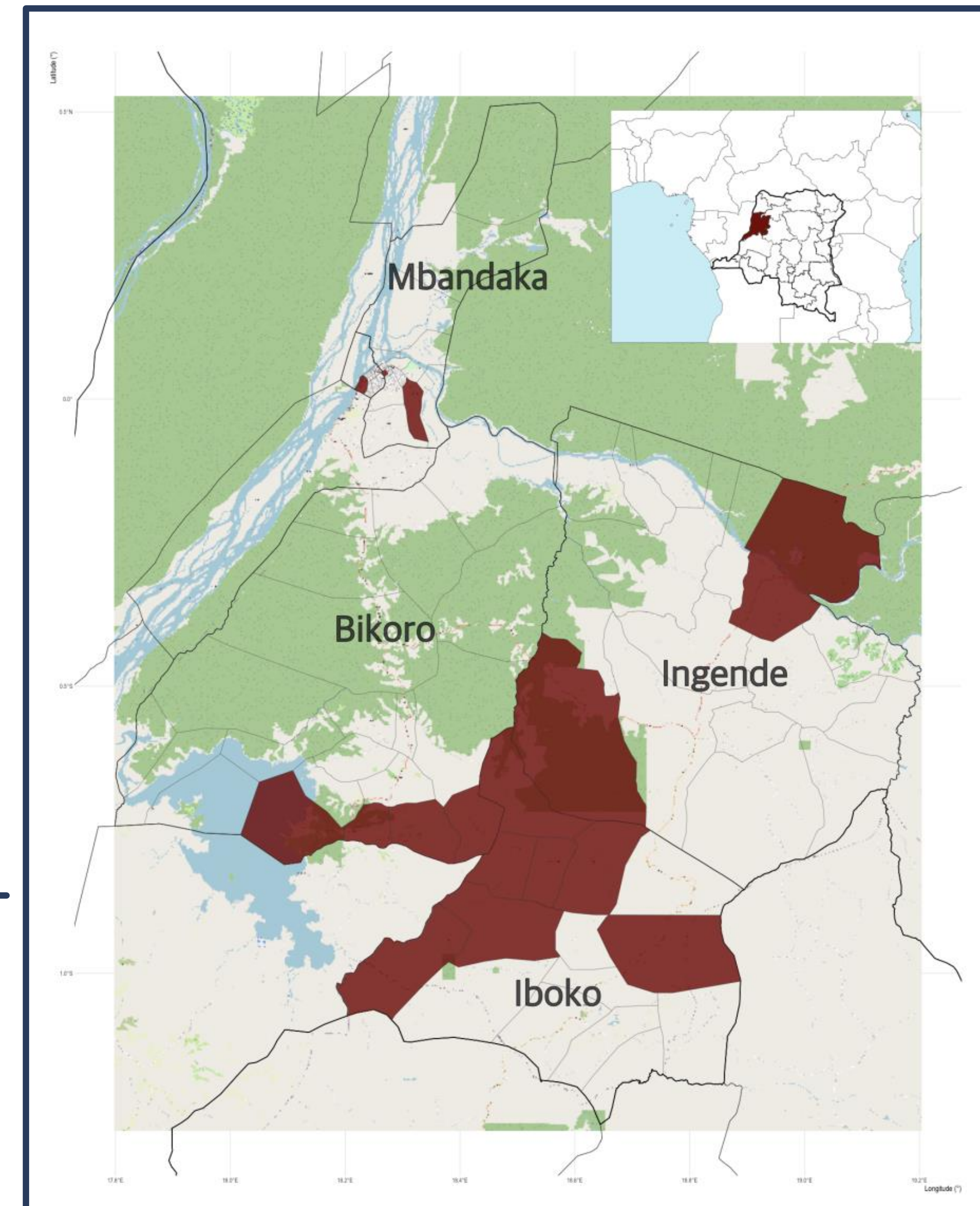## Aims & Objectives

I. Outbreak Description

- Clean and compile different data sources (WHO, MSF, CDC)
- Time, Place, Person
- Phylogeny: situate the genetic sequences in the global EBOV genetic landscape
- Compare the transmission chains of the two separate epidemiological field teams to identify key differences.
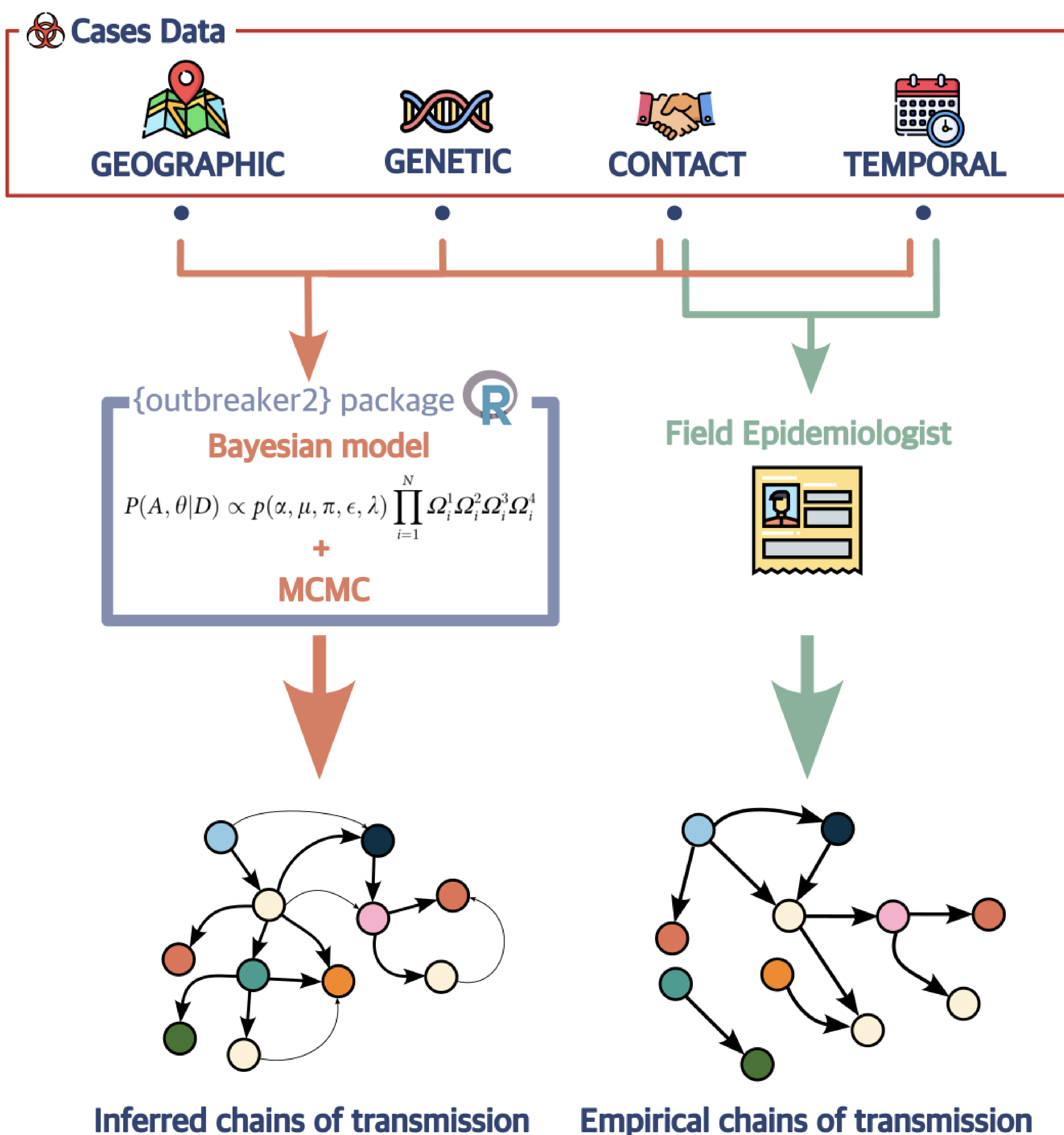
II. Infer transmission chains

- Improve the algorithm to account for geographic information
- Infer transmission chains using geographical, contact, temporal and genetic data
- Compare and assess the differences to manually reconstructed transmission chains
- Assess the limitations of the statistical framework

III. Knowledge sharing

- Joint publication with all partners to describe the 9th EVD outbreak and the use of Bayesian model
- Workshop at IPD on Bayesian modelling for outbreak reconstruction using R

Methods

Cases Data

GEOGRAPHIC   GENETIC   CONTACT   TEMPORAL

{outbreaker2} package R

Bayesian model

$$P(A, \theta|D) \propto p(\alpha, \mu, \pi, \epsilon, \lambda) \prod_{i=1}^{N} \Omega_i^1 \Omega_i^2 \Omega_i^3 \Omega_i^4$$

+

MCMC

Field Epidemiologist

Inferred chains of transmission   Empirical chains of transmission

Research Questions

How does inference performs compare to manual methods ?
- Do we get similar results to empirical chains of transmissions ?
- Can we resolve conflicting who infected whom ?
- Does it suggest missing transmission links ?

What are the added values of the different data ?
- Inference on contact and temporal data only vs empirical chains
- Addition of genetic data ?
- Addition of geographic data ?
- Challenges of partial sampling of genetic sequences ?
- Are there any inconsistencies between the data?

Is Bayesian inference of transmission chains useful for operations during outbreaks?
- Feasibility of real-time outbreak reconstructions ?
- What are the limits in terms of reliability and operationalisation ?

Why bother ?

This modelling approach assigns **probabilities** to given ancestries

Why infer *Who infected Whom ?*

- Understand the mechanisms of transmissions (reproduction number)
- Understand the drivers of transmission (type of contact)
- Identify heterogeneity between cases (superspreaders)
- Evaluate effectiveness of interventions (ring vaccination)

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Map showing Mbandaka, Bikoro, Ingende, Iboko regions in DRC.