

# Data visualization for SORMAS

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## Software

SORMAS is an infectious-disease surveillance and response tool for recording:

- **cases** (persons infected)
- their **contacts**
- **events** and their **participants**

open source

deployed in France, Germany, Ghana, Nigeria, Switzerland

HZI + partners: development, training, support

current development focus on **COVID-19**

<https://www.sormas.org/>

<https://www.sormas-oegd.de/>

<https://github.com/hzi-braunschweig/SORMAS-Project>

# Data

High dimensional:

- person (address, phone number, sex, age, occupation, ...)
- disease course (symptoms, laboratory tests, ...)
- context (setting of event, ...)
- workflow of public-health workers (contact in quarantine, ...)

... and much more!

N.B. strong data privacy

In progress: generation of a **credible synthetic data set** for

- software testing
- training
- **analyses, visualizations, collaborations**

# Visualizations

## The usual

- distributions
- time series
- choropleth maps
- ...

## Indicators

- reproduction number  $R_e$
- dispersion factor  $K$
- anomaly detection
- ...

## Networks

the most interesting... and challenging!

Idea/requirement:

- graphs of **infections, contacts** and **event participation**
- both **abstract** and in geographical **space**
- highlight necessary collaboration between administrative units

Difficulty:

- quickly difficult to read, e.g. ~ 13,000 persons and events in COVID-19 test data for only 3 counties
- high-dimensionality of relevant information

⇒ need to hierarchize and navigate information!

# Networks: first idea

In progress, rough sketch... still messy!

## ❶ Build graph:

- nodes = persons and events
- edges = infection, contact and participation

## ❷ Filter nodes:

- by time, e.g. of reporting
- by **components** (connected subgraphs) ~ clusters

N.B. COVID19 component sizes skewed: most cases infect no one, a few larger clusters

## ❸ Aggregation at regional level:

- highlight *trans-regional* components

## ❹ Visualization:

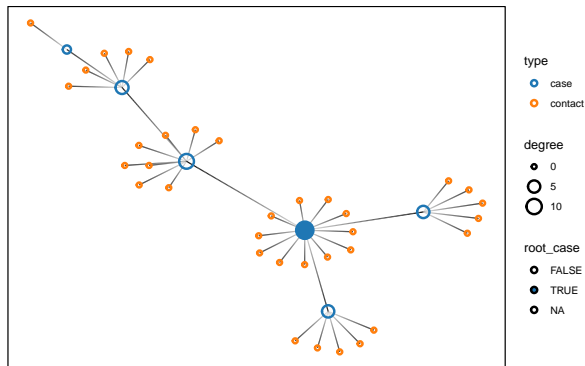
- node color = type of person or event
- node size = degree or betweenness (aggregated: number of persons)
- edge type = type relation (aggregated: number of relations)
- **interactive**

## Example 1: component with infection chain

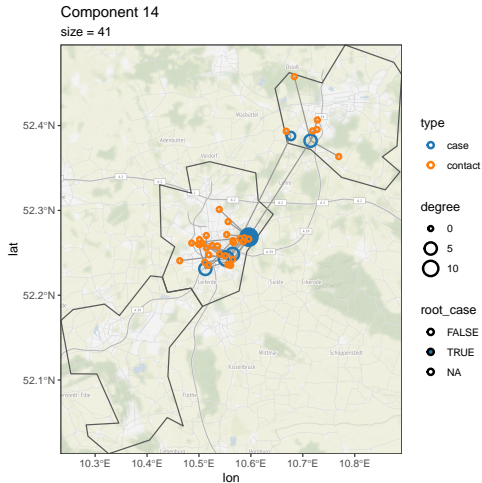
abstract visualization

Component 14

size = 41

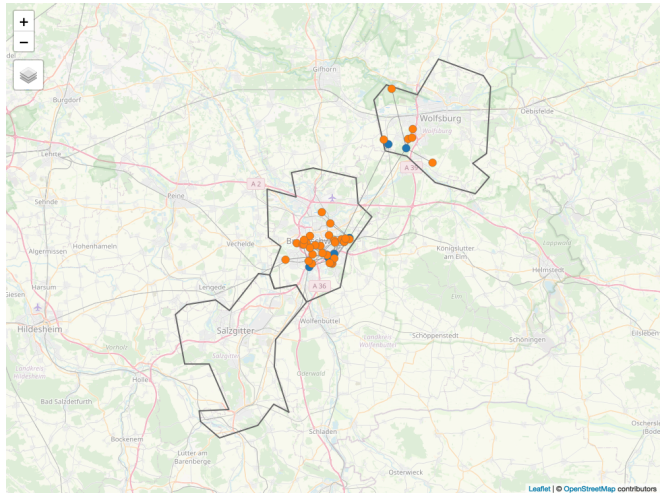


Component  
size = 41





## interactive visualization in space

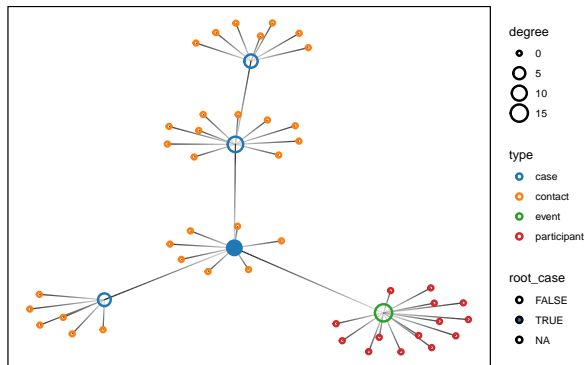


## Example 2: component with event

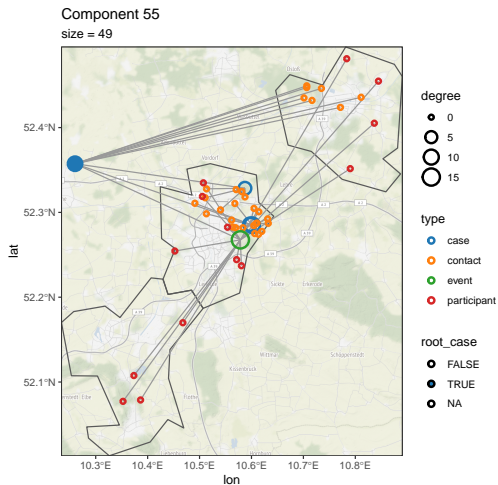
abstract visualization

Component 55

size = 49



## static visualization in space



## interactive visualization in space

