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Maastricht University

Faculty of Sciences
School for Information Technology
Master of Statistics and Data Science

Master's thesis

Spatio-temporal evolution of COVID-19 incidence and hospitalization in Belgium in 2020 -2022

Nkem Gloria Ibeh

Thesis presented in fulfillment of the requirements for the degree of Master of Statistics and Data Science, specialization Quantitative Epidemiology

SUPERVISOR :
Prof. dr. Geert MOLENBERGHS
Mevrouw Yessika Adelwin NATALIA

2024
2025

Transnational University Limburg is a unique collaboration of two universities in two countries: the University of Hasselt and Maastricht University.

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Abstract of the thesis presented to the Senate of Hasselt University in fulfillment of the requirement for the Masters degree in Statistics and Data Science

SAPTIO-TEMPORAL EVOLUTION OF COVID-19 IN BELGIUM FROM 2020-2022

By

IBEH NKEM GLORIA - 2158877

June 2025

Background.

Since the outbreak of coronavirus disease 2019 (COVID-19) in 2019, over 4 million people in Belgium have been the disease. The primary mode of transmission of this disease is through breathing in the respiratory droplets of an infected person, or the droplets can land on the eyes or in the month. During the pandemic, various studies were conducted to support policy makers with insights to make relevant decision on implementation of intervention strategies. However, it is imperative to evaluate the impact of some of these intervention; vaccination, stringency on even after the pandemic. We evaluated the effect of vaccination and the stringency index, a proxy for non-pharmaceutical intervention, against COVID-19 infection and hospitalization in Belgium from 2020 to 2022.

Methods.

Data on COVID-19 confirmed cases, hospitalizations, and vaccination coverage in Belgium were made publicly available by Sciensano, the Belgian institute for public health. A Bayesian spatiotemporal dynamic model was used assess the impact of vaccination and stringency on incidence of COVID-19 infections and hospitalizations putting into consideration the space and time variability.

Our findings revealed that the interaction of vaccination and stringency decreased incidence of COVID-19 cases and hospitalizations.

Modeling incidence of COVID-19 cases and hospitalization on split data for the periods; no vaccination period in 2020, primary dose period in 2021, and booster dose period in

2022 showed significant effect of the interaction between stringency and vaccination in reducing the risk of infection and hospitalization during the year 2021 and 2022. However, these effects decline from 0.02% reduction in infection risk in 2021 to 0.01% reduction in 2022. Likewise, a decline from 0.09% reduction in hospitalization risk in 2021 to 0.04% reduction in 2022 was observed. The risk of hospitalization increases by 128% in 2020, 63% in 2021 and 82% in 2022 with one unit increase in the logarithm of incidence of COVID-19.

Conclusion.

Our findings highlights combined effect of vaccination and stringency as an effective control measure to contain the spread of COVID-19.

Keywords: Bayesian Hierarchical model, COVID-19, Hospitalization, Random Effect, Temporal effect.
Sustainable Development Goal (SDG): Goal 3 Good Health and Well-being

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Finally, my profound gratitude to God Almighty whose love and mercy sustained me through this journey. All I can say is "God did it!".

Declaration by the Graduate Student
I hereby confirm that:

- this thesis is my original work;
- quotations, illustrations and citations have been duly referenced;
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LIST OF ABBREVIATIONS

BYM Besag–York–Molli‘e

COVID-19 coronavirus disease 2019

CPO Conditional Predictive Ordinate

DIC Deviance Information Criterion

FPS Federal Public Service

INLA Integrated nested Laplace approximations algorithm

RW2 random walk of order two

SARS-CoV-2 severe acute respiratory syndrome coronavirus

SDG Sustainable Development Goal

THFCSE The Health Food Chain Safety and Environment

CHAPTER 1

INTRODUCTION

1.1 Background

1. Background

In late 2019, the viral pneumonia outbreak was first reported in Wuhan City, the capital of Hubei Province in China (Cheng et al., 2020), and the pneumonia was identified to be caused by a pathogen i.e severe acute respiratory syndrome coronavirus (SARS-CoV-2). The World Bank Organization named it the new COVID-19. On 30 January 2020, the WHO declared the COVID-19 epidemic a public health emergency of international concern. This virus, considered to be spreading rapidly, causes infection across the globe. As at 13 January 2023, more than 270 million cases of COVID-19 cases have been reported in Europe, with Belgium accounting for over 4 million of these cases (Statista, 2025). According to the World Health Organization, as at 22 June, 2025, over 778 million cases of COVID-19 have been confirmed globally. At a time, beyond the health crisis, the pandemic disrupted economic and social activities, limiting productivity that left some countries to struggle post pandemic. This is a reflection of limited preparation in emergency situations.

The disease is characterized by dry cough, fatigue, fever, dyspnea, myalgia among others (Chilamakuri and Agarwal, 2021). A clinical diagnosis is required to detect and confirm the presence of the virus in the human system. Infected individuals can show symptoms or remain asymptomatic. The asymptomatic state of the disease does not reveal the actual burden of the disease, but is a much more significant public health concern, being a hidden source of new infection. Previous study in Belgium showed that the proportion of SARS-CoV-2 infections that were asymptomatic ranged from 20% to 88% (Hoxha et al., 2021). The disease is highly contagious and can be transmitted from person-to-person

(Chan et al., 2020).

Rapid spread and high infectious nature of the disease did not only burden health facilities but had a cascade impact on socioeconomic development due to limited interaction between people. A lockdown measure, which began on 18 March 2020, was applied in Belgium (Wagener et al., 2022) along side other protective behaviors, e.g face masking, social distance, were enforced. In late December 2020, the Belgian government began the roll-out of the vaccination campaign, with several vaccine campaigns targeting different groups and other population in Belgium at successive phases. It reached a primary vaccination (first dose) coverage of more than 80% of its adult population aged 18 years and older by October 2021 (Braeye et al., 2023). A primary vaccination coverage of 96% was attained by January 1 2023, for those 65 year and older. While 93% and 75% of the same age group received at least one or two booster doses respectively(Stouten et al., 2025).

Belgium administered two viral vector vaccines, AstraZeneca and Janssen brands, and two mRNA vaccines Pfizer and Moderna brands. Clinical trials of mRNA COVID-19 vaccines demonstrated their efficacy in reducing both incidence and hospitalization in real-world settings among individuals who received at least one dose of either vaccine; BNT162b2 (Pfizer/BioNTech) and mRNA-1273 (Moderna) (Pawlowski et al., 2021). However, study by (Braeye et al., 2023) also stated that the emergence of the Delta variant of the disease and the subsequent Omicron variant resulted in an increase in the intensive care unit and hospitalization occupancy. Period of predominance circulation of Alpha variant is from 26 January 2021 to 30 June 2021, Delta from 1 July 2021 to 2 January 2022 and Omicron from 3 January 2022 to 31 January 2023 (including all subvariants) (Stouten et al., 2025).

Vaccine protection against COVID-19 wanes over time. Data from six European countries showed that for residents of the community aged 65-79 years and 80 years and older, the effectiveness of vaccination against hospitalization declined over 6 months after primary

vaccination with a decrease from 66.9% (95% CI: 60.1; 72.6) to 36.1% (95% CI: 27.3; 67.9). The efficacy of the first booster vaccine against hospitalization decreased from 95.6% (95% CI: 88.0; 98.4) to 67.7% (95% CI: 45.9; 80.8). However, for the second booster, an increase in effectiveness from 39.3% (95% CI: 3.9; 64.5) to 80.6% (95% CI: 67.2; 88.5) for those aged 65-79 years and a slight increase from 82.0% (95% CI: 75.9; 87.0) to 83.9% (95% CI: 77.7; 88.4) for those 80 years and older were observed within the study period (Kislaya et al., 2023). According to study by Braeye T. et al, that evaluated the variant-specific effects of vaccination and prior infection against COVID-19 incidence and hospitalization showed that while primary vaccine reduced incidence and hospitalization, this effect fades away and becomes less effective. While the booster vaccine increased protection against COVID-19 incidence and hospitalization over the study period (Braeye et al., 2023).

The incidence and hospitalization of COVID-19 has fluctuated over time and space in Belgium and was influenced by different factors and regional disparities. Studies have integrated spatial and temporal components into the analysis of various drivers of change in COVID-19 incidence and hospitalization. The effects of mobility on the evolution of the pandemic have been investigated at the level of all 581 Belgian municipalities and it revealed that the reduction of mobility significantly affected the reduction of new infection and this impact is greater in most populated area (Ensoy-Musoro et al., 2023). Less stringent travel policies showed that a greater cases during this period were imported from other areas (Nguyen et al., 2023).

Understanding how vaccination and the composite measure of strictness of government policies impact temporal evolution and spatial heterogeneity in spread of COVID-19 cases and hospitalization across Belgian province is relevant in assessing the effectiveness of the country's response and optimize findings for future response. The results will guide authorities in making decisions about emerging airborne infectious diseases.

In this research, we explore factors associated with spatial and temporal heterogeneity

of COVID-19 incidence and hospitalization in Belgian provinces, with the aim to assess the changes in their effectiveness during different phases of the study. The neighborhood structure was used to describe dependency and spatial similarities among provinces.

Research Questions

1. What is the effect of vaccination and non pharmaceutical intervention on incidence of COVID-19 infections and hospitalizations?

2. What is the association between incidence of COVID-19 infections and hospitalizations?

3. What are the spatial disparities in COVID-19 cases and hospitalization?

CHAPTER 2

MATERIALS AND METHODS

This section focuses on the description of the data source, preparation and exploration, and statistical method and analysis.

2.1 Description of the dataset and pre-processing

COVID-19 cases data

The daily confirmed number of cases of COVID-19 across all 581 municipalities in Belgium was obtained from publicly available data on the Sciencano website, the Belgian Institute for Public Health, from 4 March 2020 to 3 September 2023. Cases of COVID-19 less than 5 were replaced by 2.5 in the data. Data were aggregated in a weekly time frame.

Hospitalization data

The total number of daily COVID-19 hospitalization for each of the 10 provinces of Belgium and the capital region of Brussels was also obtained from Sciensano. Weekly aggregate of the data was carried out.

Population data

The population size of each municipality in Belgium in 2021 was retrieved from STATBEL, the Belgian Statistical Office. The total population size of Belgium was about 11.5 million on 1 January 2020, this value was assumed to remain constant for the period of 2020 to 2022 in this analysis.

Vaccination data

The vaccination data containing cumulative counts of doses administered in Belgium classified by dose type (A, B, C, E, E2, E3), age group, and week in each municipality were retrieved from Sciensano. Dose types A and B are the initial dose (first dose) and the follow-up dose (second dose) for the primary vaccine schedule that requires two doses,

respectively. However, dose-type C is a single-dose vaccine required to complete the primary vaccine schedule. Dose types E, E2, and E3 are first, second, and third booster doses, respectively, given after completing the primary vaccine schedule. Typically, an individual can only receive dose E2 after receiving dose E and can receive dose E3 after receiving dose E2. Cumulative vaccination values less than 10 were replaced by the number 5 in the data.

Stringency data

Stringency index data are publicly available from Our World in Data. The stringency index is a measure of the severity of government policies, not necessarily the effectiveness of a country's response. It is a summary measure of non pharmaceutical intervention: school closure, workplace closure, travel bans, cancellation of public events, restriction of public gathering, closure of public transport, stay-at-home requirement, public information campaigns and restriction on internal movement, with values ranging from 0 to 100 (Roser, 2021). When stringency is equal to 0, there are no restrictions in the society, but when equal to 100 the highest restriction is obtainable. The data set contains daily stringency index records for 255 locations in the following geographical regions: Asia, Europe, Africa, Oceania, and North America and South America from the period of "01-01-2020" to "10-10-2023".

Table 2.1: Overview of the datasets used in the analysis, including details on their temporal resolution, spatial scale, and time frame.

Dataset	Resolution	Spatial Level	Time Frame
Cases	Daily	Municipalities	04 March 2020-03 Sept., 2023
Hospitalization	Daily	Provinces	06 March 2020-27 June 2023
Vaccination	Weekly	Municipalities	Week 53, 2020-Week 43, 2022
Population	Year	Individual	2021
Stringency Index	Daily	National	03 Jan, 2020–04 Oct., 2023

A summary of the data sets used in our study can be found in Table 2.1.

2.2 Data processing

The process of data cleaning and processing involves identifying relevant parts(variables), modifying them as required, and discarding irrelevant parts. The five data sets retrieved and described above were transformed and merged into suitable structure for our analysis. From the stringency data set, a subset of Belgium stringency index data was obtained. The ISO 8601 week numbering system of the international standard was used to create a time variable in year-week. The aggregate of the average weekly stringency index was calculated. In Belgium, a weekly period from January 2020 to December 2022, the stringency index ranged from 0 to 81.5 approximately. The data set of cases of COVID-19 was transformed into a weekly aggregate by province (to increase the opportunity for events and pool together larger populations) to obtain the sum of infection in a given week per province. Information on all 581 unique municipality-to-province mapping was obtained and joined to the vaccination data set, this way, we were able to obtain the weekly aggregate by province of the cumulative number of people that received the vaccine. The number of new lab-confirmed COVID-19 hospitalized patients in the last 24 hours (incidence) was aggregated into weekly counts per province. This number excludes patients who were admitted to the hospital for other reasons but tested positive for COVID-19 in a screening context. The population data was then assessed to ensure that the names of the provinces were spelled in the same language across all other data sets. The trimming of white space and the removal of characters within the variables were performed.

The five data sets were then merged using the time point in year-week and province identifiers to ensure accurate linkage at the provincial level. The data frame now contains weekly records of the observed number of infections, hospitalizations, cumulative vaccinations, stringency index, the province id's, dose, and population size per province. Additional key variables such as hospitalization rate and infection rate, were calculated using existing raw data following standardized definition. A new variable dose type was

created. This variable (dose-type) splits the data into three time periods as follows: No vaccination period -2020, primary series vaccination - 2021 (those who received dose B or dose C; full initial vaccination) and booster (those who received at least one dose of the booster vaccine). Again, the cumulative vaccination rate was calculated. Finally, the expected cases of hospitalization and expected cases of infections were calculated.

The rate of incidence of COVID-19 infection (confirmed infections, also called confirmed cases) was defined as the number of cases per 100,000 over a week per province. The rate of incidence of hospitalizations was calculated as the number of hospitalizations per 100,000, over a week per province. The cumulative vaccination rate was calculated as the weekly proportion of cumulative vaccination per 100 individuals per province-dose type. The expected value of COVID-19 incidence was derived by multiplying the weekly global risk of infection for Belgium by the population at risk in each province. Likewise, the expected value of COVID-19 incidence of hospitalization was derived using the same formula.

The data set was then filtered based on dose type, while we ensured a real final coverage for each of the three vaccination periods was captured, and analysis of infections and hospitalizations was conducted on the three data sets separately.

2.3 Description of data set

Table 2.2: Data dictionary of study variables

Variable	Variable Description	Data Type
n-case-r	Weekly rate of cases per 100,000 per province	Continuous
n-hosp-r	Weekly rate of hospitalization per 100,000 per province	Continuous
CASES	Weekly counts of infection per province	Discrete
Incidence	Weekly counts of hospitalization per province	discrete
CUMUL	Cumulative number of COVID-19 vaccine administered	discrete
stringency-index	Measure of restriction policy in Belgium	Numeric

2.3.1 Primary outcome

The weekly number of confirmed incidence of COVID-19 infection is the primary outcome of this study.

2.3.2 Secondary outcome

The secondary outcome is the weekly number of new lab-confirmed COVID-19 patients. This number excludes patients who were admitted to the hospital for other reasons but tested positive for COVID-19 in a screening context.

2.4 Exploratory data analysis

Exploratory data analysis was performed to visualize the characteristics of the study data. This involved plotting the time plot of the rate of infection and hospitalization over time and across provinces. The time plot of the stringency index variable was visualized. We also plotted time plot of the rate of vaccination by province and dose types. The minimum and maximum values of the variables by province and time are reported in the Appendix. Data were presented in tables and figures as appropriate.

2.5 Statistical model

2.5.1 Bayesian hierarchical models

This study used Bayesian hierarchical models extended to account for time dependency, spatial similarities, and space-time interaction to investigate the effect of factors associated with infections and hospitalizations and the extent to which infections and hospitalizations change at the provincial and temporal levels over time. The model incorporates information from the spatial neighbors structure to estimate relative risk with reduced variance of estimates and smooth implausible values. It explicitly models the auto-correlation too. This approach was chosen because the idea is that some sources of variation between regions are spatially dependent while some are not, thus Besag-Yorke-Mollie-2 (Besag–York–Molli‘e (BYM)2) prior was used as a spatial prior. The temporal structured and unstructured effect was modeled. Inference from models was made using the Integrated Nested Laplace Approximation Integrated nested Laplace approximations algorithm (INLA) as it is a more efficient strategy for approximating the posterior.

Spatial neighbors are defined using the spatial weight matrix that quantifies the distance between neighbors. The graph that assigns the sets of neighbors to each province was produced from a Belgian shape file using information on area boundaries. We first define the adjacency matrix. In this case, we are adopting a contiguous (shared either boundary edges or boundary corners) neighbor definition. We accept contiguous polygons that share at least one vertex. For any unit with no shared borders (no neighbors), we get the nearest unit and list it as a neighbor. The nb2INLA functions of the spdep package in R was used to make the adjacency matrix into a graph format that can be used in R-INLA.

This model assumes that each spatial unit (province in this case) is spatially dependent on every other spatial unit and that infections are likely to show some degree of temporal correlation.

Model selection

To identify the most appropriate spatiotemporal model for both outcomes, several models with different combinations of structured and unstructured components for temporal and spatial random effects were estimated. The spatial trend was modeled using BYM2 with default priors. likewise, the space-time interaction, temporal trends, and regression parameters for fixed effects were set to the default.

Their fits were compared using Deviance Information Criterion (DIC) while the sum of the log of the Conditional Predictive Ordinate (CPO) values was used to check the model prediction. The DIC criterion accounts for the complexity of the model. Smaller DIC indicates better model.

$$D(\theta) = 2\log(p(y \mid \theta)) \tag{2.1}$$

$$p_D = \mathbb{E}_{\theta|y}[D(\theta)] - D(\mathbb{E}_{\theta|y}[\theta]) \tag{2.2}$$

$$\text{DIC} = D + p_D \tag{2.3}$$

2.5.2 Model formulation

Infection: spatio-temporal model formulation

The spatiotemporal model assumes that the number of incidence of infection in Belgium provinces ($i = 1, \ldots, 11$) and week (t = 1,. . . ,105) follows a Poisson distribution as:

$$z_{it} \sim \text{Poisson}(\lambda_{it}) \tag{2.4}$$

$$\lambda_{it} = E_{it}\rho_{it} \tag{2.5}$$

$$\log(\rho_{it}) = \eta_{it} \tag{2.6}$$

$$\eta_{it} = \beta_0 + \beta_1 x_{1,it} + \beta_2 x_{2,it} + \beta_3 x_{1,it} x_{2,it} + b_i + \gamma_t + \phi_t + \delta_{it} \tag{2.7}$$

where:

- E_{it} is the expected number of cases of COVID-19 in the i-th province.

- ρ_{it} is the relative risk of infection for each province i and week t, this is essentially the relative deviation of this province at week t from expected.
- η_{it} is the linear predictor,
- β_0 is the intercept (average rate of infection in the entire study region),
- β_1 is the parameter estimate for rate of vaccination,
- β_2 is the parameter estimate for the stringency index,
- β_3 is the parameter estimate for the interaction between vaccine and stringency index,
- b_i is a spatial random component modeled using BYM-2,
- ϕ_t is an unstructured temporal effect,
- γ_t is a temporally structured effect modeled,
- δ_{it} is the space-time interaction term.

The BYM2 model uses a scaled spatially structured component and an unstructured component: $b = \frac{1}{\sqrt{\tau_b}} \left(\sqrt{1-\psi}\, v^* + \sqrt{\psi}\, u^* \right)$
The random walk in time of first order is as follows:

$$\gamma_t \mid \gamma_{t-1} \sim \text{Normal}(\gamma_{t-1}, \sigma^2)$$

$\tau = 1/\sigma^2$ is the precision while the unstructured temporal effect is modeled with an independent and identically distributed normal(Gaussian exchangeable) as follows

$$\phi_j \sim \mathcal{N}(0, \sigma_\phi^2)$$

The interaction between space and time (no spatial or temporal structure) follows a Gaussian distribution as:

$$\delta_{ij} \sim \mathcal{N}(0, \sigma_\delta^2)$$

Hospitalization: spatiotemporal model formulation

To assess the effect of incidence of COVID-19 infection, vaccination, and stringency index on the incidence of hospitalization, we fitted the Bayesian hierarchical model extended to account for time dependency, spatial similarities, and space-time interaction.

The number of hospitalizations in each Belgian province ($i = 1, \ldots, 11$) and week (t = 1,...,105) follows a Poisson distribution as follows:

$$y_{it} \sim \text{Poisson}(\lambda_{it}) \tag{2.8}$$

$$\lambda_{it} = E_{it}\rho_{it} \tag{2.9}$$

$$\log(\rho_{it}) = \eta_{it} \tag{2.10}$$

$$\eta_{it} = \beta_0 + \beta_1 x_{1,it} + \beta_2 x_{2,it} + +\beta_3 x_{3,it} + \beta_4 x_{1,it} x_{2,it} + b_i + \gamma_t + \phi_t + \delta_{it} \tag{2.11}$$

where:

- E_{it} is the expected number of hospitalization,
- ρ_{it} is the relative risk of hospitalization for each province i and week t,
- β_0 is the intercept (average rate of hospitalization in the entire study region),
- β_1 is parameter estimate for rate of vaccination,
- β_2 is the parameter estimate for the stringency index,
- β_3 is the parameter estimate for COVID-19 infection,
- β_4 is the parameter estimate for the interaction between vaccine and stringency index.

and the remaining parameters are defined as earlier.

CHAPTER 3

THE RESULTS

3.1 Exploratory data analysis

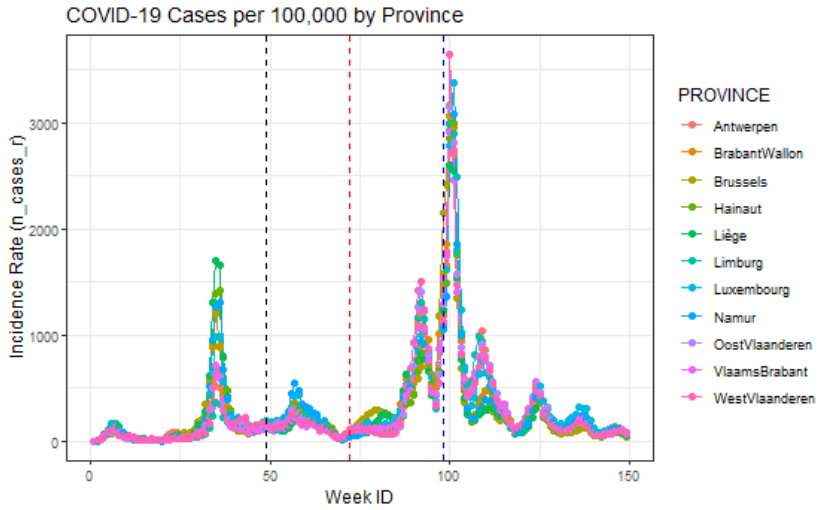

Figure 3.1: Rate of incidence of COVID-19 infections in Belgium provinces from 20W09 to 22W52

The time series plot in Figure 3.1 shows the evolution of the confirmed incidence of COVID-19 infection rate in Belgium provinces from week 09 of 2020 (i.e week_id 01 on the rescaled axis) to the last week 52 of 2022 (i.e week_id 150 on the rescaled axis). We see a peak between week_id 49 and 73 (January-June 2021) that is associated with the Alpha variant of concern (VOC) (Phylogenetic Assignment of Named Global Outbreak (Pango) (Stouten et al., 2025). A gradual increase is noticed from week_id 73 to week_id 97 (July 021 to January 2022) with a peak at week_id 95. This period was attributed to the Delta variant of the virus (Stouten et al., 2025). We see a sharp deep around week_id 98 possibly due to the end of year holiday period, which was followed by a sharp rise with peak at week_id 100 corresponding to increase cases of COVID-19 due to the Omicron variant spread which began in January 2022.

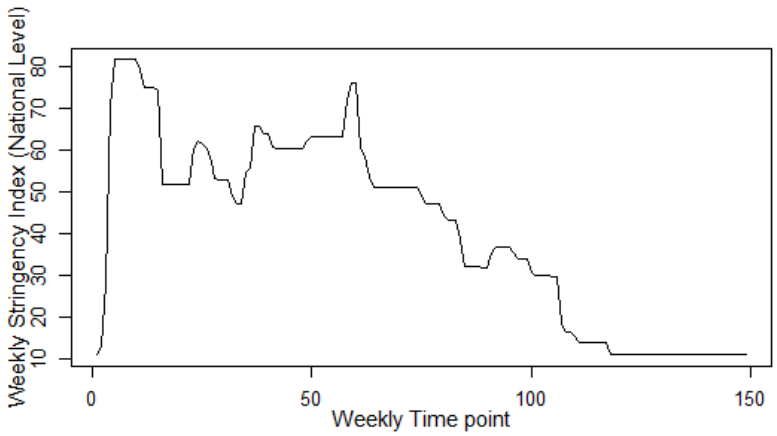

Figure 3.2: Weekly Stringency Index (National Level) from 20W09 to 22W52

Across all provinces, per week, we observe consistency in stringency indicating uniformity in the national policy rather than provincial policy. Figure 3.2 shows how stringency increased in the early weeks of 09 2020, with the highest value of 80 indicating intense public health restrictions in the early period of this study. We observe a gradual relaxation of public health restrictions in Belgium that fluctuated over the years.

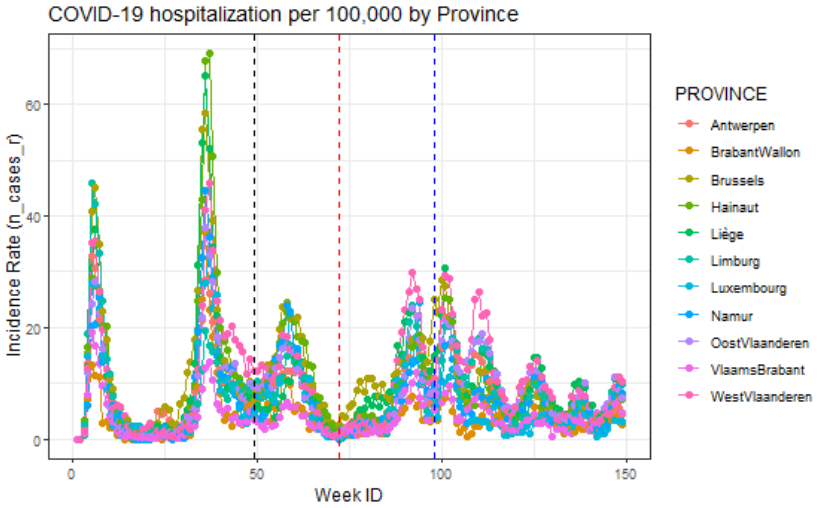

Figure 3.3: Rate of hospitalizations per province in Belgium from 20W09 to 22W52

Figure 3.3 shows the evolution of COVID-19 hospitalizations in Belgium provinces. It can be seen in Figure 3.3 that there is a random fluctuation of the rate of hospitalizations across all provinces, but more specifically, we see the highest peak towards the end of the year 2020. A peak in hospitalizations was also observed during the period of the Alpha variant and a gradual increase during the Delta variant was also observed.

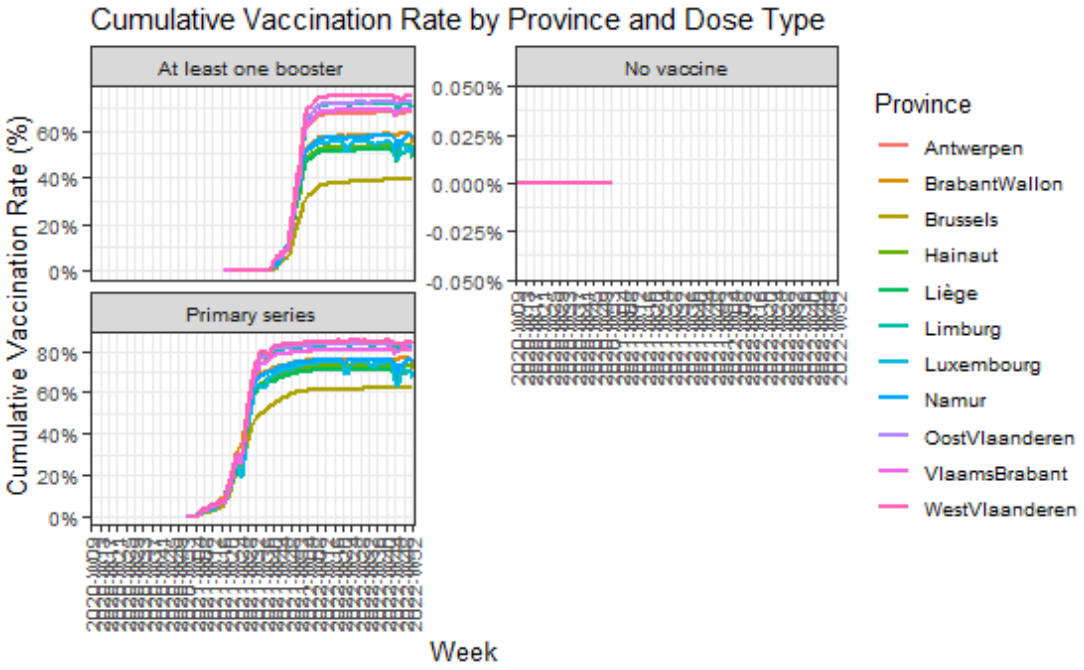

Figure 3.4: Rate of vaccination per province and dose type in Belgium from 20W53 to 22W52

Figure 3.4 shows vaccination campaign began in Belgium during the end of year 2020. The cumulative vaccination coverage rate for population who completed the primary vaccination increased gradually starting from week 53 year 2020. By week 33 year 2021, all province attained 60% coverage and above but Brussels that did not exceed 60%. The population percentage that received at least one dose of booster vaccination started week 16 year 2021. All provinces reached 40% and above except for Brussels. WestVlaanderen had the highest primary and booster dose coverage of 82% and 75%, respectively, at the end of year 2022.

Summary statistics and visuals

The ranges of key variables by province-year-week for the three periods can be found in the Appendix.

3.2 Results for spatio-temporal data analysis

3.2.1 Result: Model selection for models fitted to infections data during the three periods separately

No vaccination period

Table 3.1: Model fitted to infections for population percentage with no vaccination

Model	Structure	Log CPO Sum	DIC
Model 1	BYM2, RW2	-2987.89	4774.461
Model 2	BYM2, RW 1	-2992.188	4774.315

Table 3.2: Modle 4: Log transformed estimates of model fitted to infection (Using 2020 data)

Parameter	**Estimate**	**Std. Error**	**LCI**	**UCI**
Intercept	0.9043	0.0723	0.7715	1.0561
Stringency_index	1.0012	0.0012	0.9988	1.0036

All models in Table 3.1 have the stringency index as the only predictor. From Table3.1 we selected model 4 with the smallest DIC value of -28712.39 as the best model among the models. The component of the model included spatial and temporal random effects and the interaction between unstructured spatial and structured temporal random effects.

Table 3.2 shows the parameter estimate for model fitted to infection during the period when the percentage of the population did not receive vaccination in 2020. After accounting for spatial and temporal components, changes in the stringency index are not associated with a significant increase or decrease in infections. The effect is practically zero and non-significant, meaning that policy stringency did not measurably influence the infections in year 2020.

Primary vaccination

From table 3.3 model 7 shows smallest DIC value of 6256.349 among the models high-

Table 3.3: Model fitted to infections for initial(primary) dose completion-2021

Model	Structure	Log CPO Sum	DIC
Model 7	BYM2, RW2	-3690.252	6256.349
Model 8	BYM2, RW2	-3691.698	6256.752
Model 9	BYM2, RW1	-3692.128	6257.394
Model 10	BYM2, RW1	-3694.123	6257.299

Table 3.4: Model 8: Log transformed estimates of model fitted to infection (Using 2021 data)

Parameter	**Estimate**	**Std. Error**	**LCI**	**UCI**
Intercept	1.3760	0.2289	0.9865	1.8855
CUMUL_vacc_rate	0.9941	0.0026	0.9888	0.9991
Stringency_index	1.0004	0.0029	0.9946	1.0061

lighting the effect of vaccination, stringency index and the interaction between stringency and vaccination on the incidence of confirmed COVID-19 cases. The removal of interaction between vaccination and stringency achieved a DIC value of 6256.752 with a very small negligible difference. For these models, the spatial trend was modeled using BYM2, the structured temporal trend modeled using the random walk of order two (RW2), unstructured temporal trend with exchangeability and interaction between unstructured spatial and unstructured temporal effect.

Table 3.4 shows parameter estimates for model-8 fitted to infection when the population percentage received complete primary vaccination (period dominated by primary dose B or C). A one-unit increase in vaccination is associated with a decrease of 0.53% in the risk of infections in the population that completed primary vaccination. During this period, policy restriction had negligible impact on the risk of infection. In Table 3.5 of the parameter estimates from Model 7, model with interaction, shows that the effect of interaction between the stringency index and vaccination significantly decreased the risk of infection by 0.02%.

Booster vaccination

Table3.6 shows that model 12 had the smallest DIC value of 6562.722 among the models.

Table 3.5: Model 7: Log transformed estimates of Model fitted to infection (Using 2021 data) with interaction

Parameter	**Estimate**	**Std. Error**	**LCI**	**UCI**
Intercept	1.1415	0.2321	0.7568	1.6667
CUMUL_vacc_rate	1.0014	0.0050	0.9915	1.0112
Stringency_index	1.0039	0.0036	0.9968	1.0110
CUMUL_vacc_rate:Stringency_index	0.9998	0.0001	0.9996	1.0000

Table 3.6: Booster: Fitted to infection-2022

Model	structure	Log CPO Sum	DIC
Model 11	BYM2, RW2	-3763.619	6562.827
Model 12	BTM2, RW2	-3763.266	6562.722
Model 13	BYM1, RW1	-3763.739	6562.957
Model 14	BYM1, RW1	-3763.553	6562.862

Model 12 shows the effect of vaccination and the stringency index on the incidence of confirmed COVID-19 cases. An extension of this model to include the interaction between vaccination and stringency index achieved a DIC value of 6562.827 that did not change much compared to Model 12.

Table 3.7 shows the parameter estimates for model 12 fitted to infections when percentage of the population received at least one booster vaccine dose (E). It indicates that one-unit increase in vaccination and stringency index is associated, respectively with 0.5% significant increase and 0.8% non significant increase in the risk of infection. The parameter estimates of the extended model that included interaction between stringency and vaccination, Table3.8 shows that each unit increase in both vaccination and stringency is jointly associated with a 0.01% decrease in the risk of infection, though not significant.

From 2020 to 2022, the relationship between vaccination, policy stringency, and COVID-19 infection risk evolved considerably in different vaccination phases during the pandemic. Policy restriction when a percentage of the population has not received a vaccine did not necessarily contain spread of infection. In addition to government restriction as a mitigation measure, receiving a complete primary dose of the vaccine corresponds to a reduction in infection risk by 0.02%. For the percentage population of those who

Table 3.7: Model 12: Log transformed estimates of model fitted to infection (Using 2022 data)

Parameter	**Estimate**	**Std. Error**	**LCI**	**UCI**
Intercept	0.615	0.079	0.476	0.786
CUMUL_vacc_rate	1.005	0.002	1.000	1.009
Stringency_index	1.008	0.006	0.996	1.020

Table 3.8: Model 11: Log transformed estimates of Model fitted to infection (Using 2022 data) with interaction

Parameter	**Estimate**	**Std. Error**	**LCI**	**UCI**
Intercept	0.579	0.107	0.406	0.827
CUMUL_vacc_rate	1.006	0.003	0.999	1.012
Stringency_index	1.011	0.008	0.994	1.028
CUMUL_vacc_rate × Stringency_index	0.9999	0.00005	0.9998	1.000

received at least one dose of the booster vaccine, the synergistic effect of vaccination and stringency corresponds to a decrease by 0.01% in infection risk. The risk of infection weakened from 0.02% in 2021 to 0.01% in 2022. This could be as a result of the waning immunity from primary doses and the emergence of more transmissible variants that made it harder for relatively relaxed restrictions to control spread.

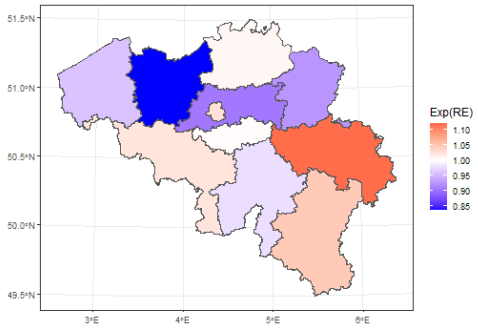

Figure 3.5: Spatial trend of model fitted on infection: No vaccination(2020)

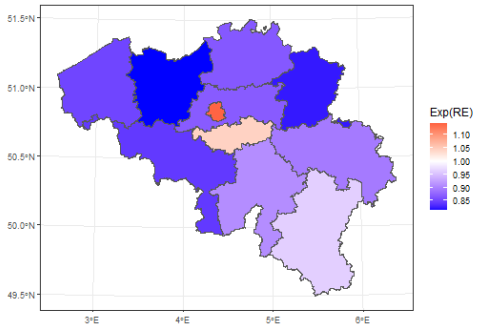

Figure 3.6: Spatial trend of model fitted on infection: primary vaccination(2021)

Before widespread of vaccination in 2020, a spatially heterogeneous burden of COVID-19 was observed, see Figure 3.5. Brussels which is an urban center, Liege, Luxemburg

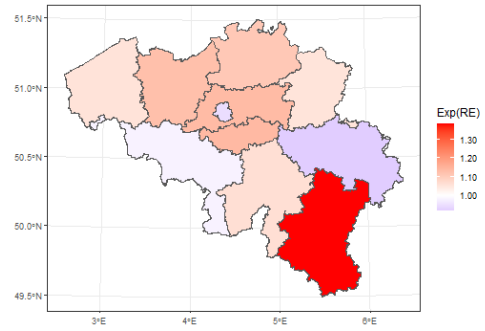

Figure 3.7: Spatial trend of model fitted on infection: Booster vaccination(2022)

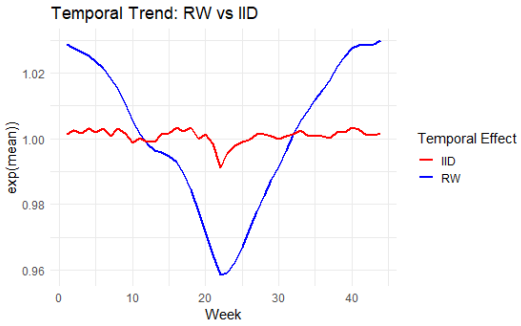

Figure 3.8: Temporal trend of model fitted on infection: No vaccination(2020)

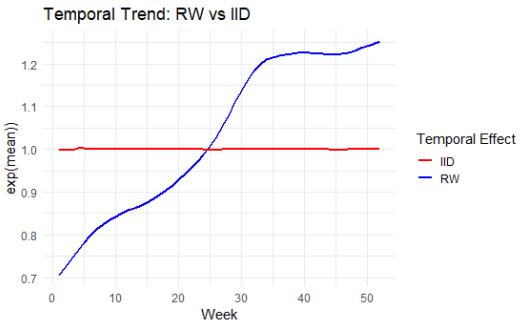

Figure 3.9: Temporal trend of model fitted on infection: - primary vaccination(2021)

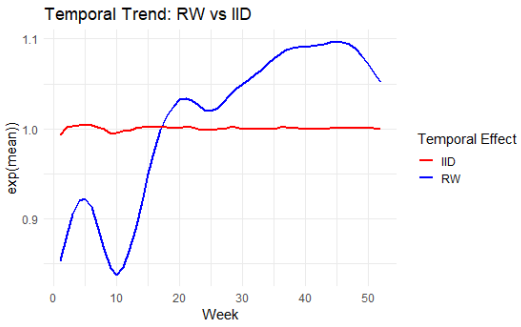

Figure 3.10: Temporal trend of model fitted on infection: booster(2022)

and Hainaut experienced an elevated infection risk characterised by a spatial relative risk above 1, compared to the entire Belgium after stringency index has been taken into account, which could be attributed to a higher population density and mobility. Other provinces showed reduced residual risk possibly due to lower exposure. Moving to the period characterized with the percentage of population who completed primary vaccination (B or C) in 2021, Brussels maintained a high infection risk, Waloon Brabant now showed a higher infection risk compared to the entire Belgium. This could reflect a lag in vaccine uptake, population mobility or socioeconomic disparities in Walloon Brabant.

Regardless of the booster roll out, a spatial surge was seen across provinces in Belgium, with Luxembourg with the highest residual risk. The possible driver could be the

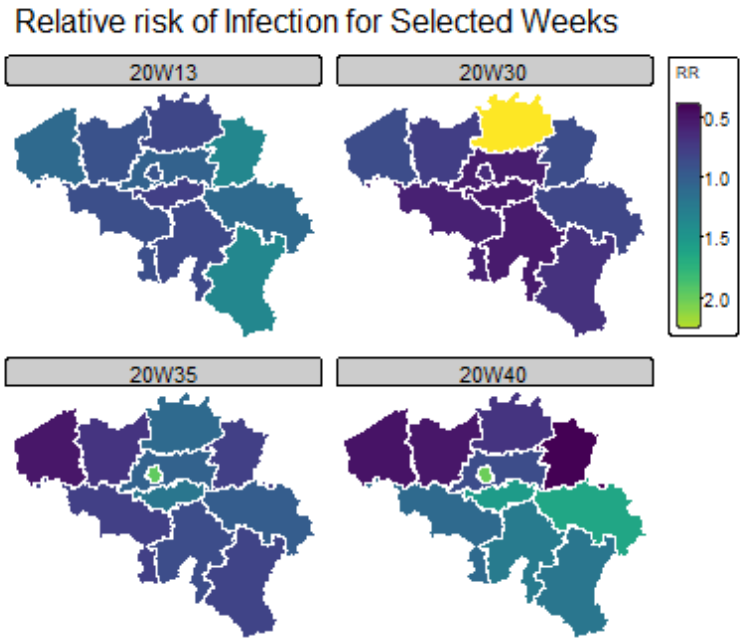

Figure 3.11: Relative risk of COVID-19 infection in Belgium-2020

emergence of more transmissible variants (e.g Omicron) of the disease, reduced policy stringency, behavioral fatigue or waning of primary vaccine immunity. However, the risk in Brussels and Liege remained low.

In 2020 Figure 3.8, we see a decrease and later an increase in temporal infection risk, peaking around week 27 year 2020 (week_id 33 on the rescaled x-axis), reflecting the second wave of infection in Belgium. This is followed with a steep decline in the risk towards the end of 2020. A steady rise in infection risk from early 2021, though low from week 1 to week 25, and rise above the threshold of 1 from week 25, mirroring the Delta variants wave and waning of immunity, see Figure 3.9. In 2022, the risk of infection was low early in the year, see Figure 3.10 indicating the positive effect of the booster interventions against the emergence of Omicron variant of the disease. However,this was followed by a gradual rise in risk later in the year from week 17. Thus, infection risk was time-dependent.

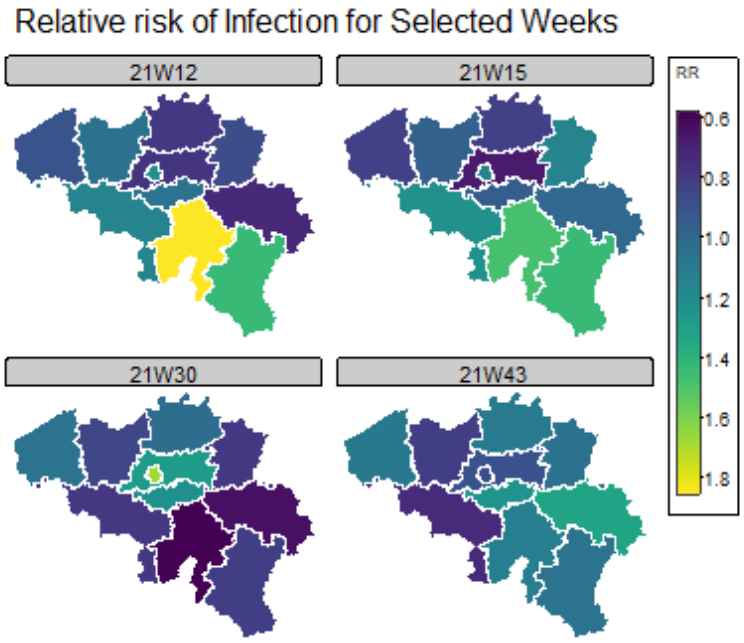

Figure 3.12: Relative risk of COVID-19 infection in Belgium-2021

From figure 3.11 to figure 3.13 shows the relative risk of COVID-19 infection in Belgium-nfew selected weeks in 2020, 2021 and 2022.

3.2.2 Result: Model selection for model fitted to hospitalizations data during the three periods separately

No vaccination period

Table 3.9: Model fitted to hospitalization during no vaccination period

Model	Structure	DIC
Model 15	BYM2, RW2	3309.257
Model 16	BYM2, RW2	3309.646
Model 17	BYM2, RW1	3341.120
Model 18	BYM2, RW1	3313.741

Table 3.9 compares models that estimate the relative risk of hospitalizations for the percentage population that did not receive vaccination. From 3.9 Model 15 with the smallest DIC value of 3309.257 to be the best among the models, the model highlighted

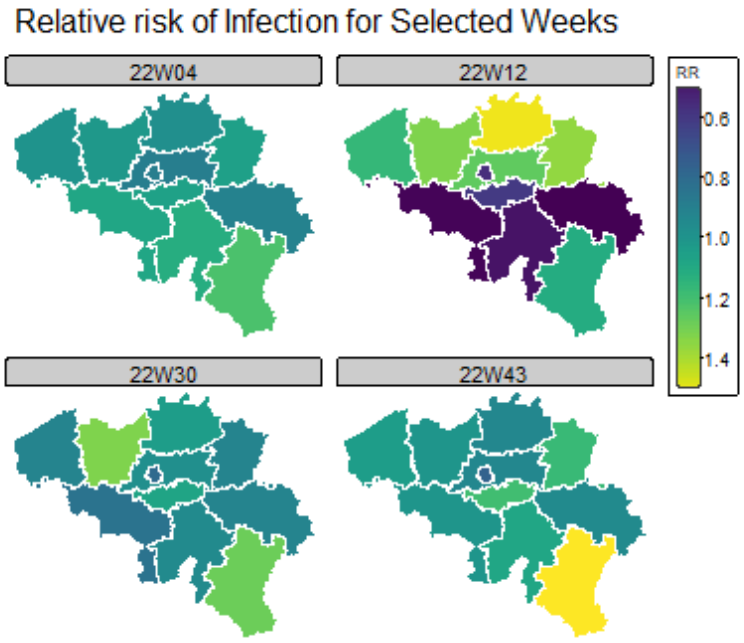

Figure 3.13: Relative risk of COVID-19 infection in Belgium-2022

Table 3.10: Model 16: log transform estimates of model fitted to hospitalization (Using 2020 data)

Parameter	**Mean**	**Std. Error**	**LCI**	**UCI**
Intercept	0.1225	0.0492	0.0515	0.2425
Stringency_index	0.9938	0.0052	0.9836	1.0042
logCASES	2.2868	0.0888	2.1164	2.4656

the effect of stringency index, confirmed cases of COVID-19 and interaction between vaccination and cases of COVID-19 on the incidence of hospitalizations. The interaction effect is non significant. The removal of the interaction between cases and stringency index in the model achieved a DIC value of 3309.646 (Model 15) with little change in value. So Model 16 was chosen. We modeled the spatial structure effect using BYM2 and the structured and unstructured temporal effect using 2 and exchangeability respectively. Table 3.10 shows the parameter estimates for model 16 fitted to hospitalizations when the percentage of the population did not receive any vaccination (no vaccination period).

Table 3.11: Model 15: log transformed estimates of model fitted to hospitalization (Using 2020 data) with interaction

Parameter	Mean	Std. Error	LCI	UCI
Intercept	0.0539	0.0433	0.0098	0.1705
Stringency_index	1.0109	0.0115	0.9885	1.0338
logCASES	2.7447	0.3126	2.1831	3.4100
Stringency_index:logCASES	0.9970	0.0018	0.9935	1.0005

After accounting for the spatial and temporal component, a one-unit increase in log confirmed cases is associated with a significant increase 128% in the risk of hospitalization in the population that did not receive vaccination. The policy restriction reduced the risk of hospitalization but the reduction is non significant.

Primary vaccination period

Table 3.12: Model fitted to hospitalization for primary dose-2021 population.

Model	structure	Sum log CPO	DIC
Model 19	BYM2, RW2	-2343.14	4130.364
Model 20	BYM2, RW2	-2359.114	4130.879
Model 21	BYM2, RW1	-2363.69	4135.450
Model 22	BYM2, RW1	-2380.347	4136.996

Table 3.13: Model 20: Log transformed estimates of model fitted to hospitalization (Using 2021 data)

Parameter	Estimate	Std. Error	LCI	UCI
Intercept	0.6290	0.3366	0.1941	1.4865
CUMUL_vacc_rate	0.9802	0.0028	0.9747	0.9857
Stringency_index	1.0035	0.0078	0.9882	1.0191
logCASES	1.6521	0.0657	1.5255	1.7837

Table 3.12 compares models that estimates the relative risk of hospitalizations for the percentage population that completed primary vaccination. From 3.12 we selected model 19 with the smallest DIC value of 4130.364 to be the best model among the models, the model highlighted the effect of stringency index, vaccination, confirmed cases and the interaction of vaccination and stringency on the incidence of hospitalizations. We modeled the spatial structure effect using BYM2 and the structured and unstructured

Table 3.14: Model 19:Log transformed estimates of model fitted to hospitalization (Using 2021 data) with interaction

Parameter	Mean	SD	LCI	UCI
Intercept	0.3593	0.1985	0.1071	0.8681
CUMUL_vacc_rate	1.0145	0.0092	0.9966	1.0328
Stringency_index	1.0190	0.0089	1.0018	1.0368
logCASES	1.6326	0.0612	1.5153	1.7556
CUMUL_vacc_rate:Stringency_index	0.9991	0.0002	0.9986	0.9995

temporal effect using 2 and exchangeability respectively.

Table 3.14 shows the parameter estimates for model 19 fitted to hospitalizations when the population percentage completed primary vaccination dose. A one unit increase in log cases is associated with a 63% significant increase in hospitalization risk, reflecting that infections drive more hospitalizations. The interaction term between vaccination and stringency was significantly less than one, indicating that when both interventions increased jointly, they were associated with a small (0.09%) reduction in hospitalization risk, suggesting a potential synergistic effect in reducing the burden on health facilities.

Booster period

Table 3.15: Model fitted to hospitalization booster dose-2022 population.

Model	structures	**Log CPO sum**	**DIC**
Model 23	BYM2, RW2	-2335.437	4304.136
Model 24	BYM2, RW2	-2353.95	4303.522
Model 25	BYM2, RW1	-2353.722	4310.620
Model 26	BYM2, RW1	-2373.134	4309.958

Table 3.16: Model 24: Log transformed estimates of model fitted to hospitalization (Using 2022 data)

Parameter	**Estimate**	**Std. Error**	**LCI**	**UCI**
Intercept	0.1193	0.0563	0.0437	0.2609
CUMUL_vacc_rate	0.9975	0.0033	0.9914	1.0042
Stringency_index	1.0153	0.0136	0.9885	1.0422
logCASES	1.8046	0.0868	1.6381	1.9795

Table 3.17: Model 23: Log transformed estimates of model fitted to hospitalization (Using 2022 data) with interaction

Parameter	**Mean**	**SD**	**LCI**	**UCI**
Intercept	0.0684	0.0335	0.0240	0.1530
CUMUL_vacc_rate	1.0075	0.0046	0.9990	1.0170
Stringency_index	1.0370	0.0150	1.0076	1.0667
logCASES	1.8207	0.0850	1.6577	1.9920
CUMUL_vacc_rate:Stringency_index	0.9996	0.0001	0.9994	0.9998

Table 3.15 compares models that estimate the relative risk of hospitalizations for the percentage population that received at least one booster vaccination. From Table3.15 we selected model 24 with the smallest DIC value of 4303.522 to be the best among the models, the model highlighted the effect of stringency, vaccination, confirmed cases on the incidence of hospitalizations. Extending the model to include interaction between vaccination and stringency resulted to Model 23 with DIC value of 4304.136. We modeled the spatial structure effect using BYM2 and the structured and unstructured temporal effect using RW2 and exchangeability respectively.

Table 3.16 shows parameter estimates for Model 24 fitted to hospitaization for population percentage that received at least one booster vaccine. Vaccination reduced the risk of hospitalization by 0.25% but the reduction is not significant. A one unit increase in log cases increased the risk of hospitalization by 80%. Further more, Table 3.17 shows parameter estimates for the extended model with interaction. A one-unit increase in log cases is associated with a 82% increase in the risk of hospitalization. Each unit increase in vaccination and stringency is jointly associated with 0.04% decrease in hospitalization risk.

In 2020, strict government policy reduced the risk of hospitalizations by 0.5%, though this reduction is not significant. A significant increase in the risk of hospitalization 128% during this period was shown. The synergistic effect of vaccination and stringency index on reducing COVID-19 hospitalization risk was weakened from 0.09% in 2021 to 0.04% in 2022. Furthermore, the effect of COVID-19 cases on the increase in hospitalization

risk was reduced from 128% in 2020 to 63% in 2021, then increased to 82% in 2022.

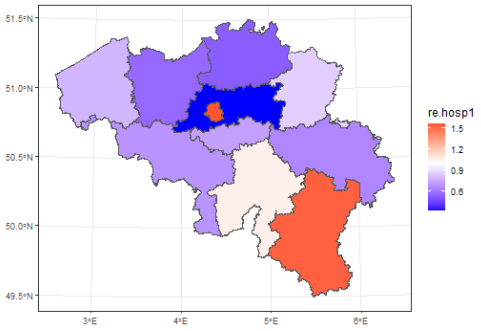

Figure 3.14: Spatial trend of model fitted on hospitalization: No vaccination(2020)

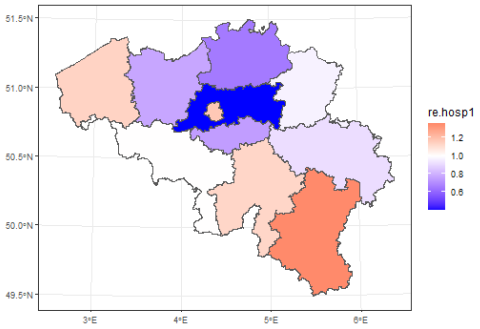

Figure 3.15: Spatial trend of model fitted on hospitalization: primary vaccination(2021)

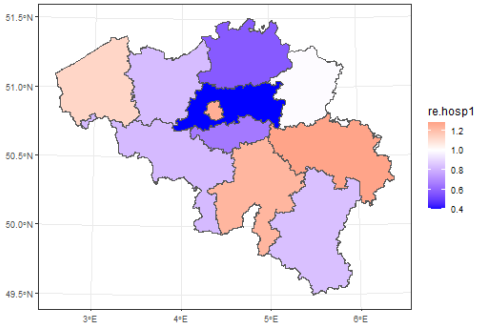

Figure 3.16: Spatial trend of model fitted on hospitalization: Booster vaccination(2022)

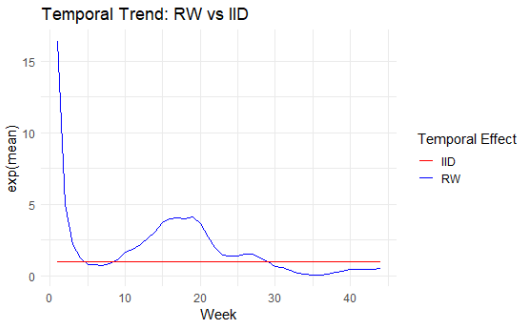

Figure 3.17: Temporal trend of model fitted on hospitalization: No vaccination(2020)

The risk of COVID-19 hospitalization in 2020, period when percentage of the population has not received vaccination, was elevated in Brussels and in Luxemburg, see Figure 3.14. During the widespread spread of primary vaccine doses in 2021, Figure 3.15, the risk of hospitalization remained high in Brussels and Luxembourg and spread to Namur, West Flander. In 2022, Figure 3.16, their was an elevated risk in Brussels, West Flander, Namur and Liege.

In 2020, hospitalization risk started high early in the year, with a sharp decline, then slight fluctuation in the year, then followed by a sharp rise towards the end of the year,

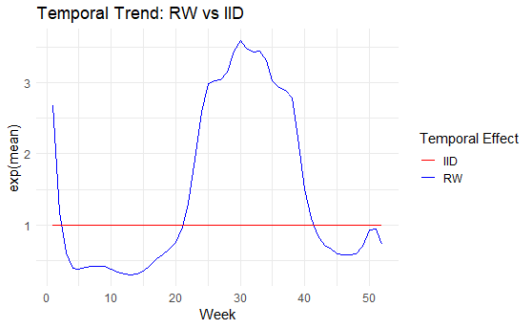

Figure 3.18: Temporal trend of model fitted on hospitalization: primary vaccination(2021)

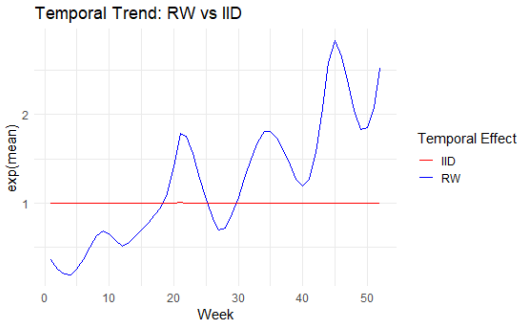

Figure 3.19: Temporal trend of model fitted on hospitalization: booster(2022)

see Figure 3.17. The year 2021 began with a high risk of hospitalization, aligned with the emergence of the Alpha variant of the disease, the risk dropped rapidly going below 1 then began to rise in week 21 and peaked at about week 30 which aligns with the emergence of Delta variant period. The risk began to drop gradually again around week 36 and went below 1 after week 41 and began to rise towards the end of the year, finally showed a drop, see Figure3.18. In 2022, there was an indication of a gradual increase in hospitalization risk with fluctuation across the year, see Figure 3.19.

From figure 3.20 to figure 3.22 shows the relative risk of COVID-19 hospitalization in Belgium from 2020 - 2022 for a few selected weeks.

In 2020, we can see an increased risk of infection in Liege, Namur and Hainaut, Figure 3.23, characterised by posterior probabilities above 0.8. The risk of hospitalization in this period was high at Luxembourg and Namur, see Figure 3.26. Most provinces in 2021 are unlikely to experience increased risk of infection see Figure 3.24 while we are uncertain if there is risk in Luxembourg, Walloon Brabant and Brussels. The risk of hospitalization in this period is high at Luxembourg, Namur and West Flanders, see Figure 3.27. Further, the risk of infection in 2022 Figure 3.25 was increased in Luxembourg, Namur, Walloon Brabant, Flemish Brabant, Antwerp and East Flander, the risk of hospitalization in this period was noticed at Namur and Liege, see Figure 3.28.

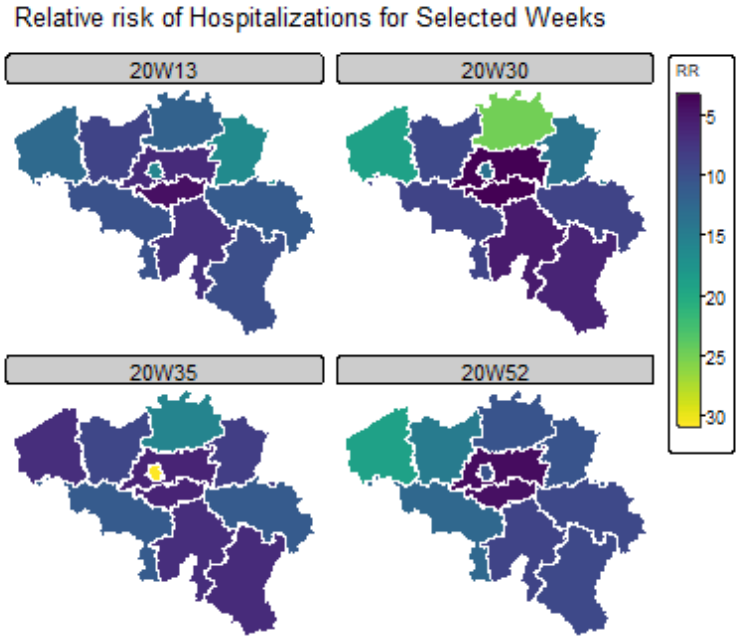

Figure 3.20: Relative risk of COVID-19 hospitalization in Belgium-2020

In Appendix Figure 1-12, we show the posterior probabilities of the risk of infection for the interactions between space and time. Different provinces show evidence of interaction larger than 1 that changes for different week-year.

Appendix Figure 13-24 shows the posterior probabilities of the risk of hospitalization for the interactions between space and time.

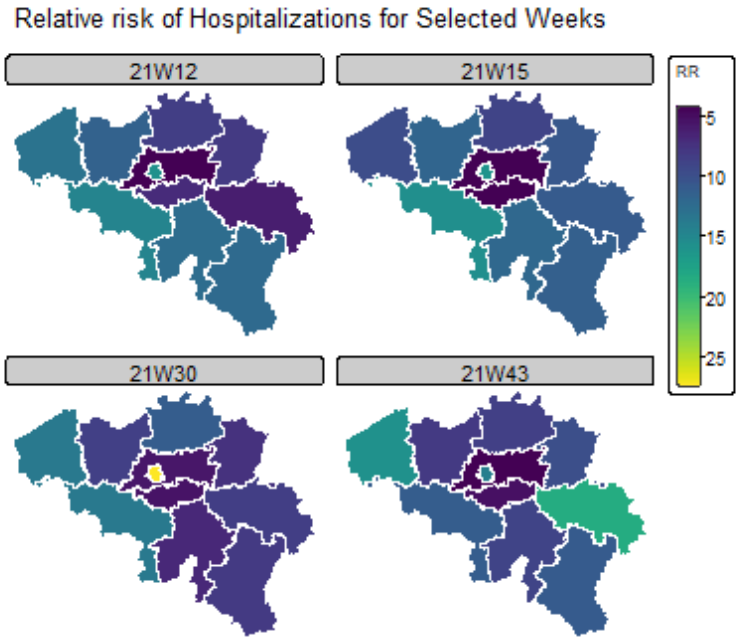

Figure 3.21: Relative risk of COVID-19 hospitalization in Belgium-2021

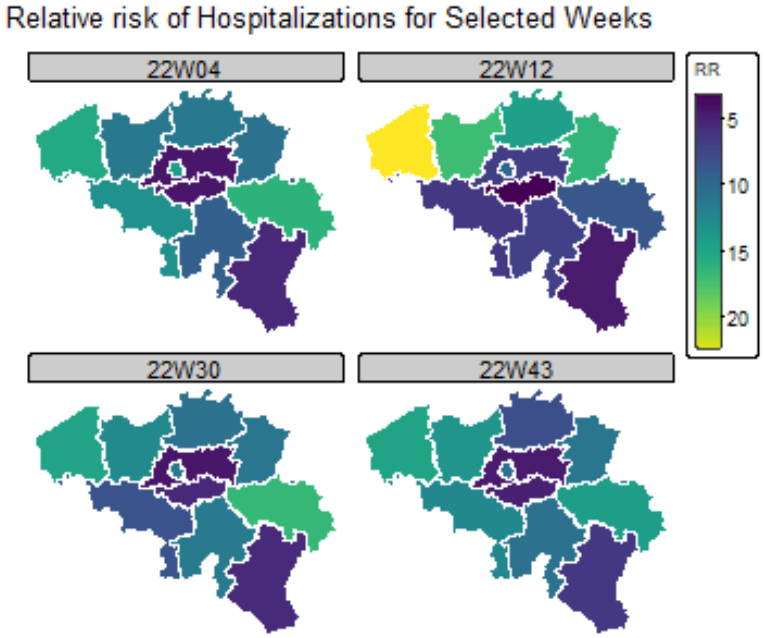

Figure 3.22: Relative risk of COVID-19 hospitalization in Belgium-2022

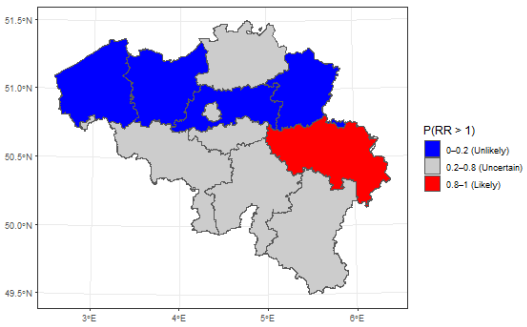

Figure 3.23: Posterior probability that the relative risks of infection exceed 1-No vaccination

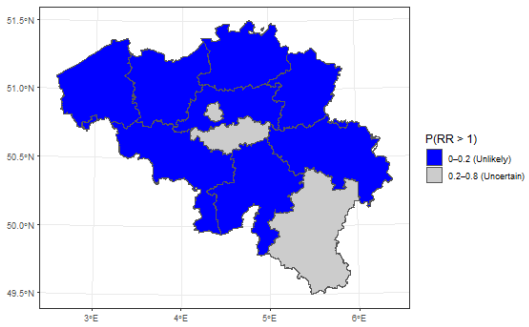

Figure 3.24: Posterior probability that the relative risks of infection exceed 1- primary vaccination

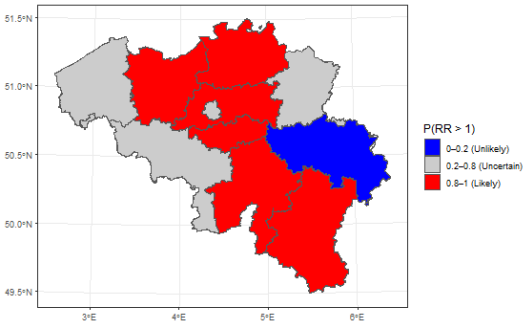

Figure 3.25: Posterior probability that the relative risks of infection exceed 1-boost vaccination

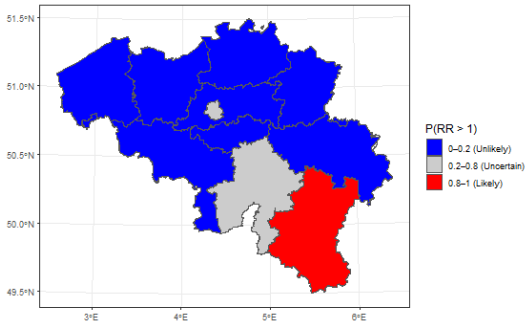

Figure 3.26: Posterior probability that the relative risks of hospitalization exceed 1-No vaccination

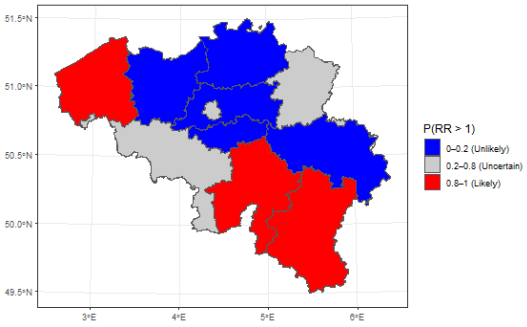

Figure 3.27: Posterior probability that the relative risks of hospitalization exceed 1-primary vaccination

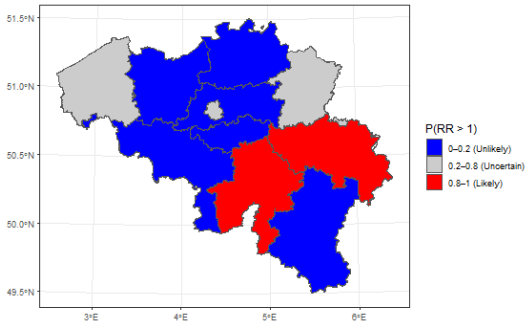

Figure 3.28: Posterior probability that the relative risks of hospitalization exceed 1-booster vaccination

CHAPTER 4

DISCUSSION

This study examined the influence of vaccination and government-imposed stringency measures on the risk of COVID-19 infection and the influence of these factors plus COVID-19 infection on the risk of hospitalization in Belgium's provinces from 2020 to 2022. The findings from year-specific models consistently showed reduction in the risk for infection and hospitalization, particularly through the interaction of vaccination and stringency levels. This finding closely aligned with the global study that used data from 216 countries across the continent in 2022, which found that maintaining a certain level of government stringency measures in addition to increasing vaccination coverage is a good strategy to control infection Yang et al., 2022. Our finding is comparable to results of the 2024 study conducted in the United State (USA) which examined the relative effectiveness of vaccination and non phermaceutical Intervention (NPIs) on COVID-19 infection, deaths, reproduction rate, and unemployment rate in the USA Khatiwada et al., 2024.

Insight from disaggregated data by year showed that during the period when vaccination was not administered in 2020, policy stringency did not measurably influence the risk of infection and hospitalization. The interaction of vaccination and stringency showed a decrease effect from 0.02% reduction in infection risk in 2021 to 0.01% reduction in 2022. The decrease effect in 2022 when the booster dose dominated may not only be a reflection of vaccine fatigue but also waning vaccine protection; however, there was still a significant reduction in risk. Hence, timely booster campaigns and adaptive public health strategies are important. By conducting analysis on disaggregated data, we were able to see how the temporal dynamics of vaccine effectiveness, particularly waning immunity, can influence the infection pattern at the population level.

Similarly, analysis on split data sets shows a synergistic effect of cumulative vaccination and stringency to decrease hospitalization risk. A decrease of 0.09% and 0.04% was observed from analysis of the split data 2021 and 2022, respectively. Again, the effect declined in 2022. Despite the cases of COVID-19 that consistently increase hospitalization risk in 2020, 2021 and 2022, there is a decline in this risk from 128% increase in 2020, 63% increase in 2021 and 82% increase in 2022.

In all analysis, over 90% of the variability in infection and COVID-19 hospitalization is explained by spatial differences. Our findings have implications for public health intervention planning. For example, in terms of resource allocation, since COVID-19 incidence and hospitalization risk are highly spatially structured, we need a targeted intervention by province, rather than uniform strategies, to achieve more effective results in the control of the pandemic. These findings will also support future outbreak response.

4.1 Strength and limitations

A key strength is the validity of the data used in this study. Obtaining data from a trusted source enhanced the reliability and validity of our results in this study. Methodologically, our study employed robust statistical approach, Bayesian hierarchical spatio-temporal models, accounting for time dependency and spatial similarities between provinces. That is, statistical strength is borrowed from spatio-temporal neighbors, which is an efficient way to improve the reliability and precision of small area disease risk estimates. The method explicitly modeled spatial auto-correlation which is important to allow estimation under assumption of conditional independence. The models allowed for quantification of the influence of covariates. Despite the strength, our study has some limitation, as such, strength of these conclusions is limited. A notable constraint is that the study used information only on detected cases, and not all COVID-19 infections in Belgium were confirmed especially among asymptomatic individuals. Likewise, the number of hospitalization included number of new laboratory-confirmed COVID-19 and excludes patients who were admitted to the hospital for other reasons, but tested positive for

COVID-19. This under- reporting could bias the effect estimates. Although different variants of the virus were in circulation during different periods, the study did not account for the dominant variants of COVID-19 which varied across years with likely influence on infection and hospitalization risk. The implication is that the temporal association between interventions and incidence and hospitalization could be distorted and the model might wrongly attribute the variation in incidence and hospitalization to other covariates. Incorporating variant data will disentangle the impact of evolving virus characteristics from public health interventions or vaccination effects.

Another limitation is that the study did not model the incidence and hospitalization data for the different age groups, which definitely experienced different severity in terms of infection and hospitalization. More so, there is a lag between vaccination and change in infection and between infection and change in hospitalization, we did not set this lag.

4.2 Ethical thinking

Data were collected from Open Data sources which permits free use in as much as it's use is in a correct manner without misinterpretations. All data sets retrieved for this study were aggregated at the municipal or provincial level, so privacy and confidentiality are not a concern, since there is no individual identifier. Hence, the issue of consent or ethical approval is not a concern. It is not the intent of this study to stigmatize any province; therefore a careful analysis was carried out.

4.3 Societal relevance

According to Statista 2025, as at January 2023, Belgium accounts for 1% (4 million) of the 270 millions of COVID-19 cases reported in Europe. This means 36% of Belgium population were infected by the virus, which is a huge number. Therefore, the results of this study will help identify or provide a clear understanding of provincial disparities in terms of the burden of the disease and the response to intervention (vaccination and stringency). This insight will guide future pandemic preparation.

The high variability explained by spatial difference stresses the importance of targeted

intervention by province, thus enhancing effective implementation of equitable public health strategies. This could include strengthening primary health care facilities for wider vaccination coverage in regions that showed lower vaccination coverage.

This study is a contribution to the global effort to understand the impact of pharmaceutical and non-pharmaceutical interventions in the control of COVID-19 in space and time.

4.4 Stakeholder awareness

Some of the relevant stakeholders for this study include the public health authorities like The Health Food Chain Safety and Environment (THFCSE) - Federal Public Service (FPS) and Regional Health Authorities in Belgium, the National Institute for Health and Disability Insurance, hospitals, research institution like Sciensano and the general public.

The insights from this study will be relevant for THFCSE - FPS to understand the provincial and temporal impact of strategies and measures (vaccination and stringency) deployed to contain the pandemic and it will also equip them to prepare for a future health emergency. Healthcare providers will be able to anticipate spatial surge in service demand in the event of an infectious disease outbreak, thus working with guided strategies to provide relevant and timely support. Researchers could build upon methodologies used in this study. communities will have a clear picture of the impact of the pandemic and how containment measures worked.

CHAPTER 5

CONCLUSION AND FUTURE RESEARCH

This study emphasizes the synergistic effectiveness of vaccination and government stringency policy as a control measure of COVID-19 infection and hospitalization. The effectiveness was better in 2021, a period dominated by the primary vaccine dose B, C. In addition, the incidence of COVID-19 significantly increased the rate of hospitalization, but more research is required to confirm this.

The high variability observed in infection and hospitalization for COVID-19 explained by spatial differences points to the spatial driver of the pandemic. Our findings from this study highlight the need for a targeted provincial-level intervention in Belgium that addresses vaccination uptake and adherence to stringency policy during future outbreaks. For future studies, explicitly accounting for the emergence of variants of SARS-CoV-2 is important because of it's likely influence on infection risk and vaccination effectiveness. This will prevent the possibility of obtaining a wrong estimate of the effect size for other variables. Future studies could also explore incorporating different age group.

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APPENDICES

.1 Appendix A: Figures

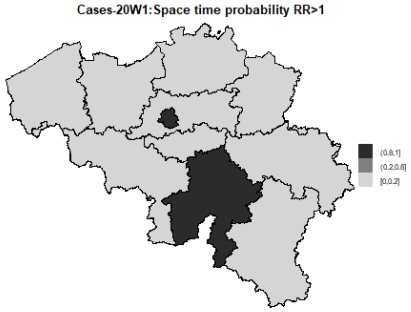


Figure 1: Posterior probability for spatio-temporal interaction -20W01

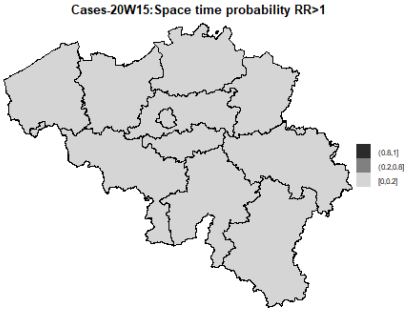


Figure 2: Posterior probability for spatio-temporal interaction -20W15

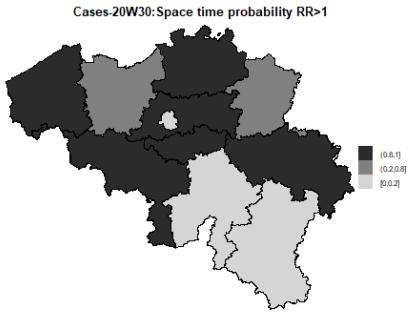


Figure 3: Posterior probability for spatio-temporal interaction -20W30

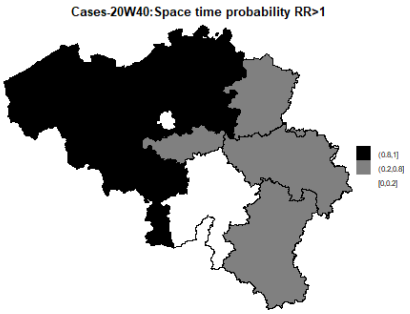
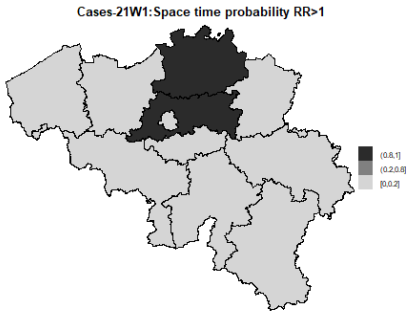


Figure 4: Posterior probability for spatio-temporal interaction -20W40



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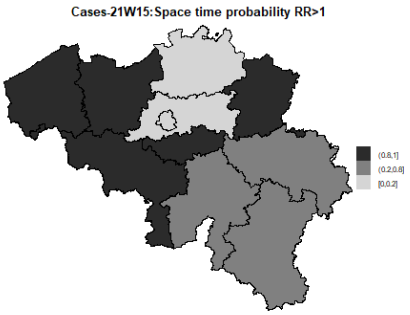

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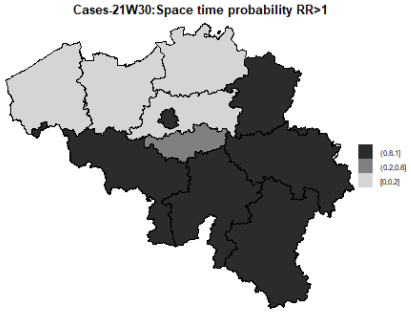

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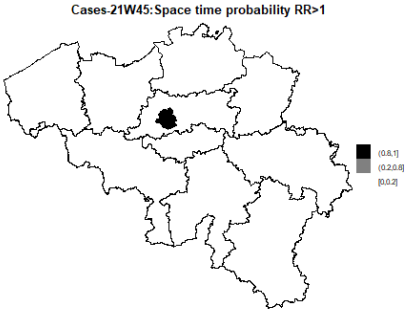


Figure 8: Posterior probability for spatio-temporal interaction -21W45

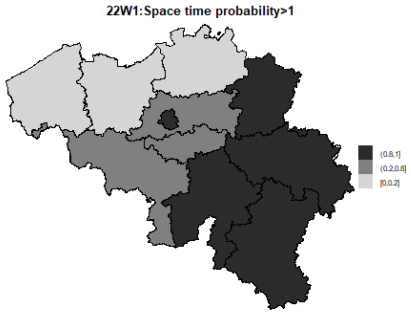


Figure 9: Posterior probability for spatio-temporal interaction -22W01

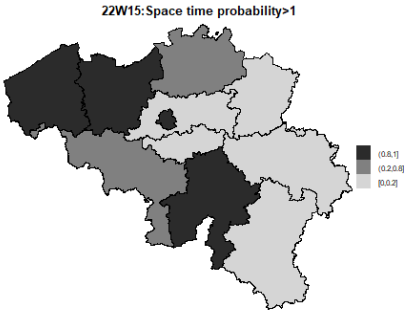


Figure 10: Posterior probability for spatio-temporal interaction -22W15

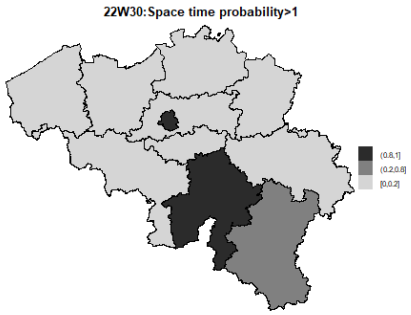
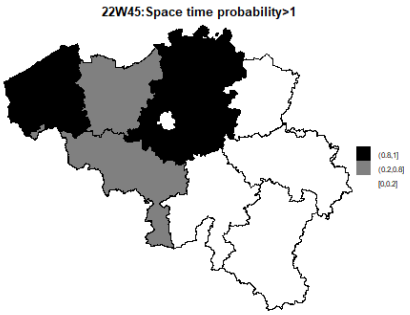


Figure 11: Posterior probability for spatio-temporal interaction -22W30



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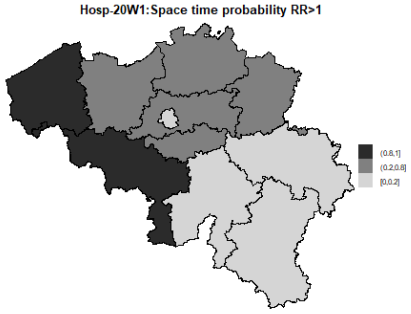

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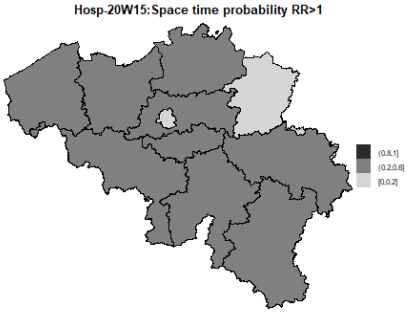

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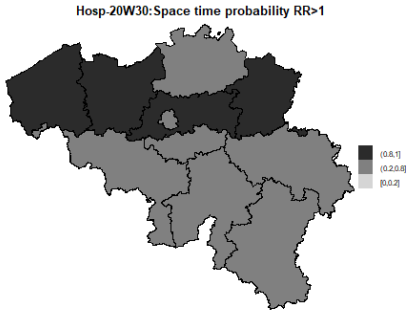

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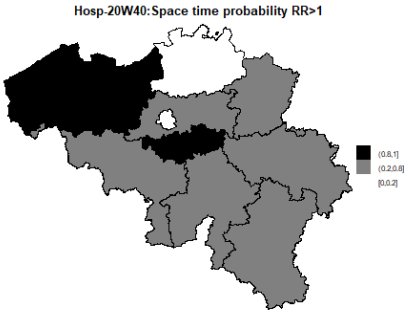
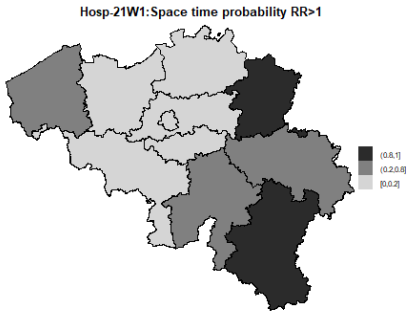


Figure 16: Posterior probability for spatio-temporal interaction -20W40



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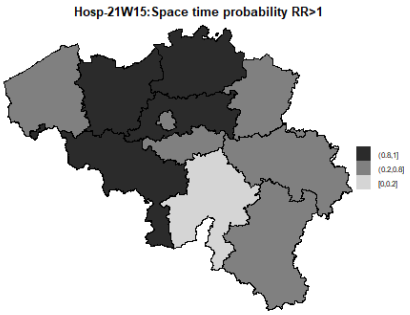

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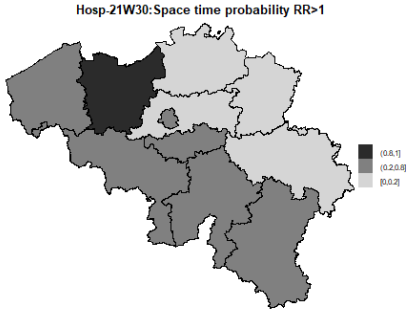

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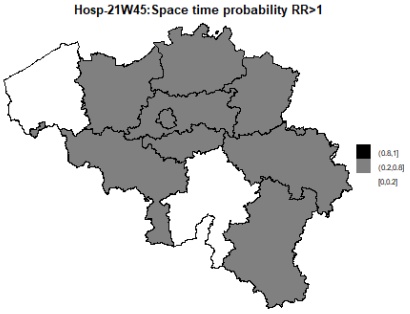

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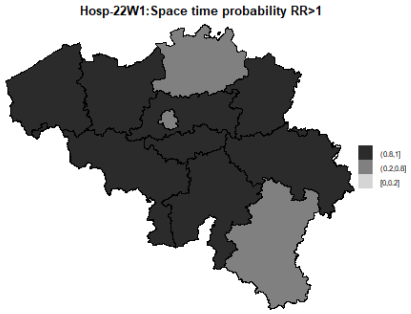
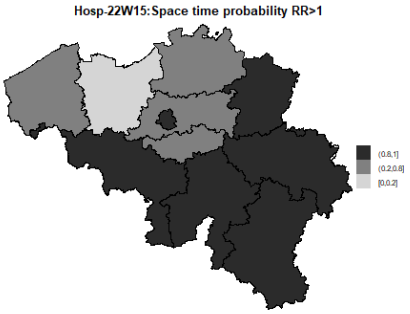


Figure 21: Posterior probability for spatio-temporal interaction -22W01



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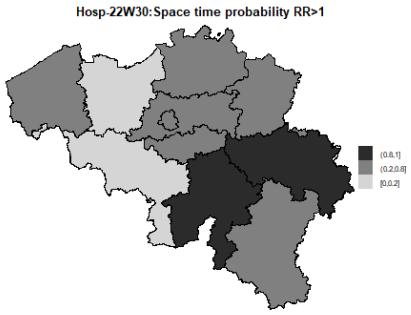

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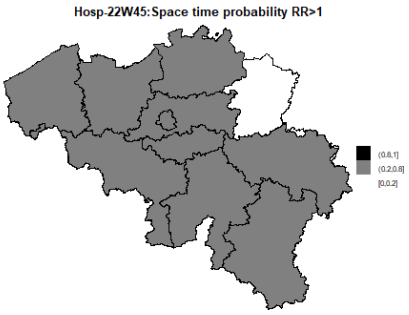

Figure 24: Posterior probability for spatio-temporal interaction -22W45

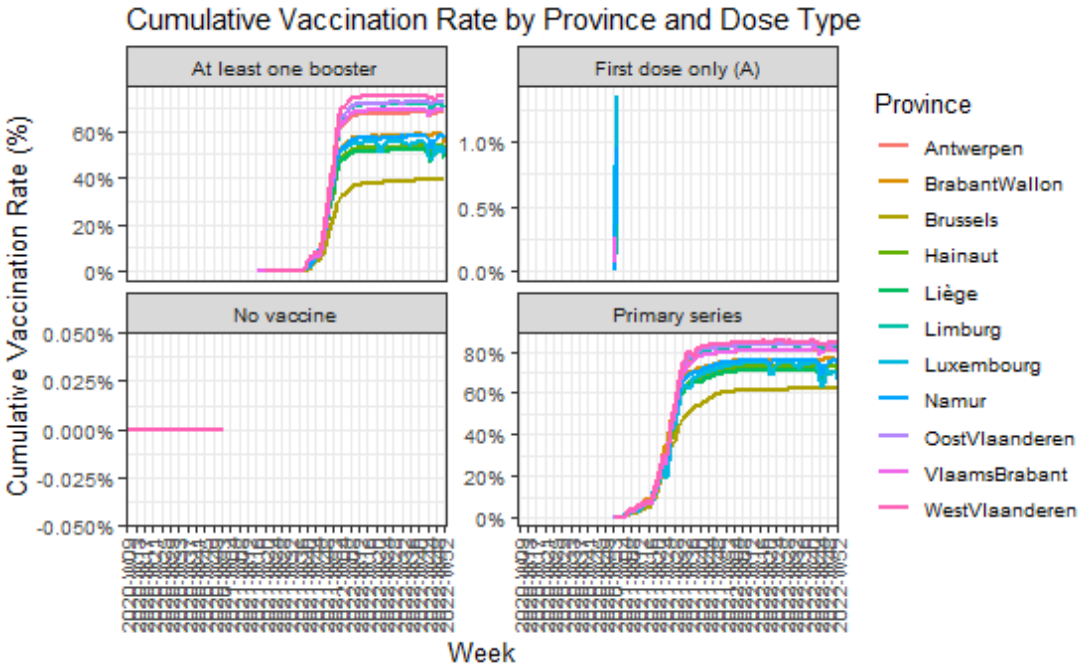

Figure 25: Rate of vaccination per province and dose type in Belgium from 20W53 to 22W52

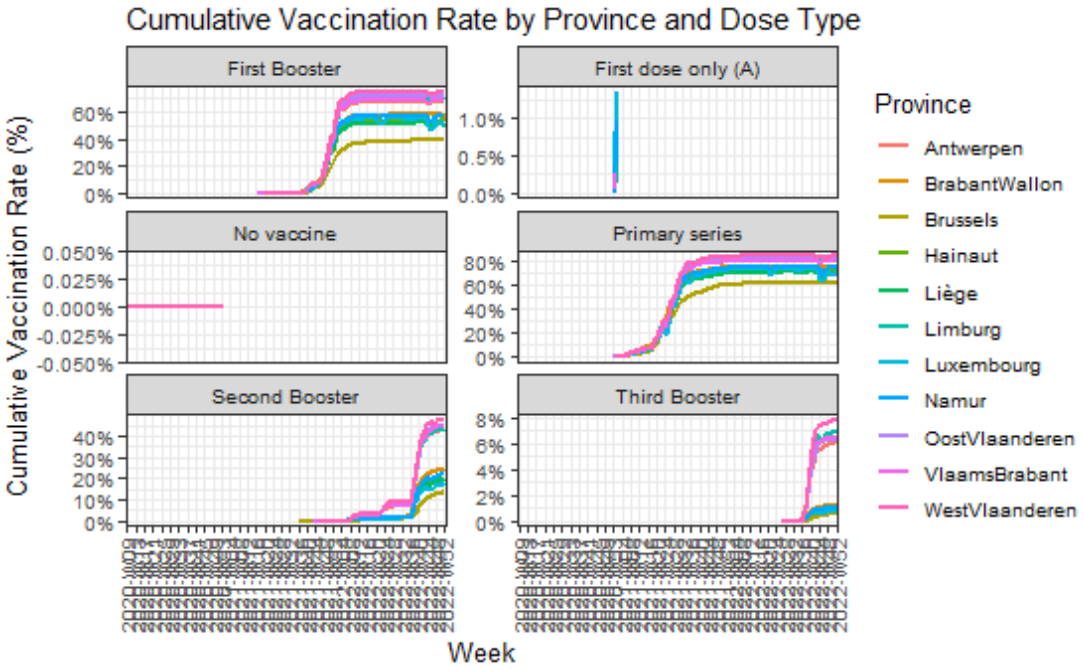

Figure 26: Rate of vaccination per province and dose type in Belgium from 20W53 to 22W52

Variable	Stat	Province	Year-Week	Value
cum_rate_vacc	Min	Antwerpen	20W09	0.000000e+00
cum_rate_vacc	Max	Antwerpen	20W09	0.000000e+00
Incidence	Min	Hainaut	20W10	0.000000e+00
Incidence	Max	Hainaut	20W45	9.310000e+02
stringency_index	Min	Antwerpen	20W09	1.111000e+01
stringency_index	Max	Antwerpen	20W13	8.148000e+01
CASES	Min	Hainaut	20W44	2.500000e+00
CASES	Max	Hainaut	20W44	1.906050e+04
CUMUL	Min	Antwerpen	20W09	0.000000e+00
CUMUL	Max	Antwerpen	20W09	1.339201e+01
n_cases_r	Min	Liège	20W43	1.693676e+03
n_cases_r	Max	Hainaut	20W45	6.917063e+01
n_hosp_r	Min	Antwerpen	20W10	0.000000e+00
n_hosp_r	Max	Hainaut	20W45	6.917063e+01
expected_cases	Min	Limburg	20W09	3.961272e+01
expected_cases	Max	Antwerpen	20W43	1.701228e+04
expected_hosp	Min	Antwerpen	20W09	0.000000e+00
expected_hosp	Max	Antwerpen	20W44	7.175817e+01

Table 1: Summary statistics for dataset 1

Variable	Stat	Province	Year_Week	Value
cum_rate_vacc	Min	WestVlaanderen	21W01	4.155198e-04
cum_rate_vacc	Max	WestVlaanderen	21W52	8.449009e-01
Incidence	Min	Namur	21W27	0.000000e+00
Incidence	Max	OostVlaanderen	21W47	3.580000e+02
stringency_index	Min	Antwerpen	21W45	3.191348e+01
stringency_index	Max	Antwerpen	21W14	7.590000e+01
CASES	Min	OostVlaanderen	21W01	1.850000e+01
CASES	Max	Antwerpen	21W47	2.220695e+04
CUMUL	Min	OostVlaanderen	20W53	5.000000e+00
CUMUL	Max	Antwerpen	21W52	1.493044e+06
n_cases_r	Min	OostVlaanderen	21W01	1.207737e+00
n_cases_r	Max	WestVlaanderen	21W47	1.500625e+03
n_hosp_r	Min	Namur	21W27	0.000000e+00
n_hosp_r	Max	WestVlaanderen	21W47	2.975122e+02
expected_cases	Min	OostVlaanderen	20W53	2.050000e+01
expected_cases	Max	Antwerpen	21W47	2.032316e+03
expected_hosp	Min	Luxembourg	21W26	2.264368e+01
expected_hosp	Max	Antwerpen	21W47	3.206538e+01

Table 2: Summary statistics for selected COVID-19 variables by province and week for data 2-primary dose series.

Variable	Stat	Province	Year_Week	Value
cum_rate_vacc	Min	Brussels	22W02	2.884333e+01
cum_rate_vacc	Max	Antwerpen	22W01	9.942091e+01
Incidence	Min	Luxembourg	22W45	1.000000e+00
Incidence	Max	Antwerpen	22W05	4.170000e+02
stringency_index	Min	Antwerpen	22W21	1.111000e+01
stringency_index	Max	Antwerpen	22W01	3.387714e+01
CASES	Min	Luxembourg	22W45	2.175000e+02
CASES	Max	Antwerpen	22W03	5.593550e+04
CUMUL	Min	Luxembourg	22W01	1.284170e+05
CUMUL	Max	Antwerpen	22W43	1.277938e+06
n_cases_r	Min	Brussels	22W52	3.750092e+01
n_cases_r	Max	WestVlaanderen	22W03	3.643860e+03
n_hosp_r	Min	Luxembourg	22W45	3.463539e-01
n_hosp_r	Max	Liège	22W04	3.074656e+01
expected_cases	Min	Luxembourg	22W45	1.422530e+02
expected_cases	Max	Antwerpen	22W03	5.683725e+04
expected_hosp	Min	Luxembourg	22W46	7.306092e-01
expected_hosp	Max	Antwerpen	22W04	3.561208e+01

Table 3: Summary statistics for selected COVID-19 variables by province and week for data 3- Boost dose series.

.2 R-CODE

```
1
2  #R-CODE for spatio-temporal modeling.
3  #stringency data
4  OWID_stringency_index <- read_excel("C:/Users/Nkem/Desktop/Stat Data Sc/
       Masters thesis/OWID_stringency index.xlsx")
5  string_data <- OWID_stringency_index
6  sub_string_data <- subset(string_data, string_data$continent=="Europe")
7  bel_sub_string_data <- subset(sub_string_data, sub_string_data$location
       == "Belgium")
8  bel_sub_string_data$date <- as.Date(bel_sub_string_data$date)
9  bel_sub_string_data.ml <- bel_sub_string_data %>%
10   mutate(YEAR = isoyear(date),
11         WEEK = isoweek(date),
12          YEAR_WEEK = paste0(substr(isoyear(date), 3, 4), "W", sprintf("
               %02d", isoweek(date)))) %>%
13   group_by(YEAR_WEEK, YEAR,WEEK) %>%
14   summarize(stringency_index=mean(stringency_index, na.rm = TRUE), .
         groups = "keep")  # Applies only to numeric columns
15 #View(bel_sub_string_data.ml)
16 colSums(is.na(bel_sub_string_data.ml))
17 #Population data
18 TF_SOC_POP_STRUCT_2021 <- read_excel("C:/Users/Nkem/Desktop/Stat Data Sc
       /Masters thesis/TF_SOC_POP_STRUCT_2021.xlsx")
19
20 population_data<-TF_SOC_POP_STRUCT_2021
21 demographics<-population_data %>% mutate(
22                               CD_REFNIS = as.integer(CD_REFNIS),
23                               CD_AGE = as.character(CD_AGE))
24 # Prepare population_data
25 demographics_data <- demographics%>%
26   dplyr::select(CD_REFNIS, TX_DESCR_NL, CD_DSTR_REFNIS, TX_ADM_DSTR_
         DESCR_NL, CD_PROV_REFNIS,
```

```
27                  TX_PROV_DESCR_NL, CD_RGN_REFNIS, TX_RGN_DESCR_NL, CD_SEX
                        , CD_NATLTY,
28                  TX_NATLTY_NL, CD_CIV_STS, TX_CIV_STS_NL, CD_AGE, MS_
                        POPULATION) %>%
29    mutate(AGEGROUP = case_when(
30      CD_AGE < 18 ~ "0-17",
31      CD_AGE >= 18 & CD_AGE <= 24 ~ "18-24",
32      CD_AGE >= 25 & CD_AGE <= 34 ~ "25-34",
33      CD_AGE >= 35 & CD_AGE <= 44 ~ "35-44",
34      CD_AGE >= 45 & CD_AGE <= 54 ~ "45-54",
35      CD_AGE >= 55 & CD_AGE <= 64 ~ "55-64",
36      CD_AGE >= 65 & CD_AGE <= 74 ~ "65-74",
37      CD_AGE >= 75 & CD_AGE <= 84 ~ "75-84",
38      CD_AGE >= 85 ~ "85+",
39      TRUE ~ NA_character_
40    ))
41  unique(demographics_data$CD_RGN_REFNIS)
42
43
44  clean_province_names <- function(df, colname) {
45    df %>%
46      mutate(
47        !!colname := str_replace_all(!!sym(colname), "Provincie\\s*", ""),
                # remove "Provincie"
48        !!colname := str_replace_all(!!sym(colname), "-", ""),
                          # remove hyphens
49        !!colname := str_trim(!!sym(colname))
                                              # trim any extra whitespace
50      )
51  }
52
53  demographics_data <- clean_province_names(demographics_data, "TX_PROV_
      DESCR_NL")
```

```
54
55 demographics_data<- demographics_data %>%
56                                  mutate(TX_PROV_DESCR_NL = recode(TX_
                                        PROV_DESCR_NL,
57                                          "WaalsBrabant" ="BrabantWallon",
58                                            "Henegouwen"    = "Hainaut",
59                                            "Luik"          = "Li ge",
60                                            "Namen"         = "Namur",
61                                          "Luxemburg" = "Luxembourg" ))
62
63 demographics_data <- demographics_data %>%
64   mutate(TX_PROV_DESCR_NL = case_when(
65     is.na(TX_PROV_DESCR_NL) & TX_RGN_DESCR_NL == "Brussels␣
           Hoofdstedelijk␣Gewest" ~ "Brussels",
66     TRUE ~ TX_PROV_DESCR_NL
67   ))
68
69 demographics_data_grouped.prov <-demographics_data%>%
70   group_by( TX_PROV_DESCR_NL,CD_PROV_REFNIS) %>%
71   summarise(
72     MS_POPULATION = sum(MS_POPULATION, na.rm = TRUE) ,.groups = 'keep')
73 #colSums(is.na(demographics_data_grouped.prov))
74 #View(demographics_data_grouped.prov)
75 #CD_REFNIS, TX_DESCR_NL,
76
77 #Vaccination data
78 COVID19BE_VACC_MUNI_CUM <- read.csv("C:/Users/Nkem/Desktop/Stat␣Data␣Sc/
       Masters␣thesis/COVID19BE_VACC_MUNI_CUM.csv")
79 vaccin_data<- COVID19BE_VACC_MUNI_CUM
80 vaccine_data.ml <- vaccin_data %>%
81   mutate(
82     CUMUL = as.numeric(ifelse(grepl("<", CUMUL), 5, CUMUL)),
83    )
```

```
84 View(vaccine_data.ml)
85  vaccine_data.ml%>% arrange(YEAR_WEEK, NIS5, AGEGROUP, DOSE)
86 #E for extra/booster dose of vaccine administered since Week 36 of 2021
       (started on September 6, 2021)
87 #E2 for second booster administered since week 4 of 2022 (Monday,
       January 24, 2022)
88 # E3 for third booster
89
90 vacc.NIS <- vaccine_data.ml%>% group_by(YEAR_WEEK, NIS5,DOSE)%>%
91                                    summarise(CUMUL = sum(CUMUL, na.rm =
                                           TRUE),.groups = "drop")
92
93
94 colSums(is.na(vacc.NIS))
95
96 #colSums(is.na(vaccin_data))
97 View(vacc.NIS)
98
99 #View(COVID19BE_CASES_MUNI)
100
101 COVID19BE_CASES_MUNI <- read.csv("C:/Users/Nkem/Desktop/Stat␣Data␣Sc/
       Masters␣thesis/COVID19BE_CASES_MUNI.csv")
102 cases_data<- COVID19BE_CASES_MUNI
103 View(cases_data)
104 cases_data.base <- cases_data %>%
105   dplyr::select(NIS5, DATE, TX_DESCR_NL, TX_ADM_DSTR_DESCR_NL, PROVINCE,
          REGION, CASES) %>%
106   mutate(
107     CASES = as.numeric(ifelse(grepl("<", CASES), 2.5, CASES)),  #
          Convert "<" cases to 2.5
108     DATE = as.Date(DATE, format = "%Y-%m-%d"),  # Convert DATE to Date
          format
109     YEAR = isoyear(DATE),
```

```
110      WEEK = isoweek(DATE),
111     YEAR_WEEK = paste0(substr(isoyear(DATE), 3, 4), "W", sprintf("%02d",
            isoweek(DATE)))%>%
112    group_by(YEAR_WEEK, YEAR, WEEK,NIS5, PROVINCE) %>%
113   summarise(
114     CASES = sum(CASES, na.rm = TRUE),
115      .groups = "keep"
116   )
117 View(cases_data.base)
118  View(vacc.NIS)
119 dim(cases_data.base)
120
121 cases_data.base%>% arrange(NIS5)
122 cases_data.base <- cases_data.base %>%
123   filter(!is.na(PROVINCE))
124  unique(cases_data.base$PROVINCE)
125 View(cases_data.base)
126
127 vacc_cases <- full_join(cases_data.base, vacc.NIS,
128                         by = c("NIS5" = "NIS5", "YEAR_WEEK"="YEAR_WEEK")
                                )
129 View(vacc_cases)
130
131 vacc_cases_by_province <- vacc_cases%>%group_by(YEAR_WEEK,YEAR,WEEK,
    PROVINCE,DOSE) %>%
132  summarise(CUMUL = sum(CUMUL, na.rm = TRUE),
133            CASES = sum(CASES, na.rm = TRUE),
134                    .groups = "drop")
135 unique(vacc_cases_by_province$PROVINCE)
136 vacc_cases_by_province <- vacc_cases_by_province %>%
137   filter(!is.na(PROVINCE))
138 View(vacc_cases_by_province)
139 colSums(is.na(vacc_cases_by_province))
```

```
140
141 #Hospitalization data
142 COVID19BE_HOSP <- read.csv("C:/Users/Nkem/Desktop/Stat␣Data␣Sc/Masters␣
        thesis/COVID19BE_HOSP.csv")
143 #View(COVID19BE_HOSP)
144 hosp_data.sp<- COVID19BE_HOSP
145 hosp_data.base <- hosp_data.sp %>%
146   mutate(DATE = as.Date(DATE, format = "%Y-%m-%d"),  # Convert DATE to
          Date format
147     YEAR = isoyear(DATE),
148     WEEK = isoweek(DATE),
149     YEAR_WEEK = paste0(substr(isoyear(DATE), 3, 4), "W", sprintf("%02d",
            isoweek(DATE))))%>%
150   group_by(YEAR_WEEK, YEAR, WEEK,PROVINCE) %>%
151   summarise(
152         Incidence = sum(NEW_IN, na.rm = TRUE),
153     .groups = "keep"
154   )
155 unique(hosp_data.base$PROVINCE)
156 #merge vaccine/cases and hosp data
157 vacc_cases_hosp_by.prov<- vacc_cases_by_province%>%
158   full_join(hosp_data.base, by = c("YEAR_WEEK" = "YEAR_WEEK","YEAR" = "
        YEAR","WEEK" = "WEEK", "PROVINCE" = "PROVINCE" ))
159 colSums(is.na(vacc_cases_hosp_by.prov))
160 unique(vacc_cases_hosp_by.prov$PROVINCE)
161 #merge vaccine/cases/hosp and string data
162 vacc_cases_hosp_bel_by.prov<- vacc_cases_hosp_by.prov%>%
163   full_join(bel_sub_string_data.ml, by = c("YEAR_WEEK" = "YEAR_WEEK", "
        YEAR"="YEAR", "WEEK"="WEEK" ))
164 #View(vacc_cases_hosp_bel_by.prov)
165 colSums(is.na(vacc_cases_hosp_bel_by.prov))
166 vacc_cases_hosp_bel_by.prov <- vacc_cases_hosp_bel_by.prov %>%
167   filter(!is.na(PROVINCE))
```

```
168 unique(vacc_cases_hosp_bel_by.prov$PROVINCE)
169 vacc_cases_hosp_bel_pop_by.prov<-vacc_cases_hosp_bel_by.prov%>%
170   full_join(demographics_data_grouped.prov, by = c("PROVINCE"="TX_PROV_
        DESCR_NL"))
171 #View(demographics_data_grouped.prov)
172 #View(vacc_cases_hosp_bel_by.prov)
173 unique(vacc_cases_hosp_bel_pop_by.prov$PROVINCE)
174  vacc_cases_hosp_bel_pop_by.prov <-  vacc_cases_hosp_bel_pop_by.prov
       %>%
175   mutate(n_cases_r = (CASES/ MS_POPULATION) * 100000,
176          cum_rate_vacc =(CUMUL/ MS_POPULATION) * 100,
177          n_hosp_r  = (Incidence / MS_POPULATION) * 100000)
178  #filter from 2020 -2022
179 vacc_cases_hosp_bel_pop_by.prov <- vacc_cases_hosp_bel_pop_by.prov%>%
180   filter(YEAR_WEEK >= "20W01" & YEAR_WEEK <= "22W52")
181 colSums(is.na(vacc_cases_hosp_bel_pop_by.prov))
182 View(vacc_cases_hosp_bel_pop_by.prov)
183 # Create a unique numeric ID for each province
184 vacc_cases_hosp_bel_pop_by.prov <- vacc_cases_hosp_bel_pop_by.prov %>%
185   mutate(provID = as.numeric(as.factor(CD_PROV_REFNIS)))
186 vacc_cases_hosp_bel_pop_by.prov.1<- vacc_cases_hosp_bel_pop_by.prov %>%
187 mutate(row_id = as.numeric(interaction(PROVINCE, YEAR_WEEK, drop = TRUE)
       ))
188
189 vacc_cases_hosp_bel_pop_by.prov.imprv <- vacc_cases_hosp_bel_pop_by.prov
       .1%>%
190   mutate(
191     ISO_week = paste0(YEAR, "-W", sprintf("%02d", WEEK)),
192     DATE = ISOweek2date(paste0(ISO_week, "-1"))  # "-1" is Monday
193   ) %>%
194   dplyr::select(-ISO_week)  # Optional: remove helper column
195
```

```
196 vacc_cases_hosp_bel_pop_by.prov.imprv<-vacc_cases_hosp_bel_pop_by.prov.
        imprv[order(
197 vacc_cases_hosp_bel_pop_by.prov.imprv$PROVINCE,
198 vacc_cases_hosp_bel_pop_by.prov.imprv$provID,
199 vacc_cases_hosp_bel_pop_by.prov.imprv$YEAR_WEEK,
200 vacc_cases_hosp_bel_pop_by.prov.imprv$YEAR,
201 vacc_cases_hosp_bel_pop_by.prov.imprv$WEEK
202  ), ]
203
204   )
205
206 View( vacc_cases_hosp_bel_pop_by.prov.imprv )
207 df <- vacc_cases_hosp_bel_pop_by.prov.imprv %>%
208   dplyr::select(YEAR_WEEK, YEAR, WEEK, PROVINCE, DOSE, CUMUL, MS_
          POPULATION, cum_rate_vacc,row_id, CASES, Incidence, stringency_
          index, CD_PROV_REFNIS,n_cases_r, n_hosp_r,provID,logCASES) %>%
209   mutate(week_id_v = paste0(YEAR, "-W", sprintf("%02d", WEEK)))
210 #& YEAR == 2020
211 no_vacc <- df %>%
212   filter(is.na(DOSE) ) %>%
213   mutate(VACC_TYPE = "No␣vaccine")
214 View(no_vacc)
215
216 # Filter for Dose A only
217 #first <- df %>%
218  # filter(DOSE == "A") %>%
219   # Exclude those who also received B
220   #anti_join(df %>% filter(DOSE == "B") %>% #dplyr::select(row_id), by =
          "row_id") %>%
221   #mutate(VACC_TYPE = "First dose only (A)")
222 #View(first)
223 # Combine B and C as 'Primary series'
224 primary <- df %>%
```

```
  filter(DOSE %in% c("B", "C")) %>%
  group_by(PROVINCE, YEAR, WEEK, YEAR_WEEK, week_id_v,row_id, CD_PROV_
      REFNIS,provID) %>%
  summarise(
    cum_rate_vacc = sum(cum_rate_vacc, na.rm = TRUE),
   CUMUL =sum(CUMUL, na.rm = TRUE),
    MS_POPULATION =  mean(MS_POPULATION, na.rm = TRUE),
    CASES =  mean(CASES, na.rm = TRUE),
   Incidence=  mean(Incidence, na.rm = TRUE),
   stringency_index =  mean(stringency_index, na.rm = TRUE),
    n_cases_r =  mean(n_cases_r, na.rm = TRUE),
    n_hosp_r=  mean(n_hosp_r, na.rm = TRUE),
    logCASES =  mean(logCASES, na.rm = TRUE),
    .groups = "drop"
  ) %>%
  mutate(VACC_TYPE = "Primary␣series")
View(primary)

booster_any <- df %>%
  filter(DOSE == "E") %>%
  mutate(VACC_TYPE = "At␣least␣one␣booster")
View(booster_any)

library(scales)
# Combine all
df_combined <- bind_rows(no_vacc, primary, booster_any)

#Exploratory data analysis

ggplot(
  df_combined,
  aes(x = week_id_v, y = n_cases_r, color = PROVINCE, group = PROVINCE)
) +
```

```
  geom_line(size = 1) +
  facet_wrap(~ VACC_TYPE, ncol = 2, scales = "free_y") +
  scale_y_continuous(labels = percent_format(scale = 1)) +
  scale_x_discrete(
    breaks = unique(df_combined$week_id_v)[seq(1, length(unique(df_
        combined$week_id_v)), by = 4)]
  ) +
  labs(
    title = "Cumulative Vaccination Rate by Province and Dose Type",
    x = "Week",
    y = "Cumulative Vaccination Rate (%)",
    color = "Province"
  ) +
  theme_bw(base_size = 12) +
  theme(
    axis.text.x = element_text(angle = 90, vjust = 0.5, hjust = 1)
  )

# Aggregate to get the mean stringency per week
stringency_national <- df_combined %>%
  group_by(YEAR_WEEK) %>%
  summarise(stringency_index = mean(stringency_index, na.rm = TRUE))
 #Time plot for rate of hospitalization
  ggplot( df_combined , aes(x = YEAR_WEEK, y = n_hosp_r,         group =
      PROVINCE, color = PROVINCE)) +
  geom_line() +
  geom_point(size = 2) +
  theme_bw() +
  theme(axis.text.x = element_text(angle = 90, vjust = 0.5, hjust = 1))

ts_stringency_index  <- ts(stringency_national$stringency_index )
plot(ts_stringency_index , type="l", xlab="", ylab="")
```

```
287 title(xlab="Weekly␣Time␣point", ylab="Weekly␣Stringency␣Index␣(National␣
        Level)", line=2, cex.lab=1.2)
288  #filtering for "no-vaccination" data
289 first_vacc_week <- df_combined %>%
290   filter(VACC_TYPE != "No␣vaccine") %>%
291   summarise(first_week = min(YEAR_WEEK)) %>%
292   pull(first_week)
293 df_no_vacc <- df_combined %>%
294   filter(VACC_TYPE == "No␣vaccine" & YEAR_WEEK < first_vacc_week)
295 df_no_vacc <- df_no_vacc %>%
296   mutate(
297   year_week_strp = paste(YEAR, sprintf("%02d", WEEK), sep = "-")
298   ) %>% arrange(YEAR, WEEK) %>%
299    mutate(week_ID = as.numeric(factor(year_week_strp, levels = unique(
           year_week_strp))))
300 #View(df_no_vacc)
301 df_no_vacc<- df_no_vacc %>%
302   group_by(VACC_TYPE, YEAR_WEEK) %>%
303   mutate(
304     population = sum(MS_POPULATION, na.rm = TRUE),
305     weekly_case_rate = sum(CASES, na.rm = TRUE) / sum(MS_POPULATION, na.
            rm = TRUE),
306     weekly_hosp_rate = sum(n_hosp_r, na.rm = TRUE) / sum(MS_POPULATION,
            na.rm = TRUE),
307     # Expected counts per province-week
308     expected_cases = MS_POPULATION * weekly_case_rate,
309     expected_hosp  = MS_POPULATION * weekly_hosp_rate
310   ) %>%
311   ungroup()
312
313 View(df_no_vacc)
314
315 #filtering primary dose series
```

```
# Step 1: Filter to primary series
df_primary <- df_combined %>%
  filter(VACC_TYPE == "Primary series")


vacc_2022 <- df_primary %>%
  filter(YEAR_WEEK == "22W52") %>%
  group_by(PROVINCE) %>%
  summarise(CUMUL_2022 = sum(cum_rate_vacc, na.rm = TRUE), .groups = "drop")

# Step 3: Replace the 21W52 cumulative rate with 22W52's value
prim_updated <- df_primary %>%
  left_join(vacc_2022, by = "PROVINCE") %>%
  mutate(cum_rate_vacc = ifelse(YEAR_WEEK == "21W52",
                                coalesce(CUMUL_2022, cum_rate_vacc),
                                cum_rate_vacc)) %>%
  dplyr::select(-CUMUL_2022) # Step 4: Remove all 2022 rows (since 21W52 now holds final coverage)

vacc_2020<- prim_updated%>%
 filter(YEAR_WEEK == "20W53" ) %>%
group_by(PROVINCE) %>%
summarise(CUMUL_2020 = sum(cum_rate_vacc, na.rm = TRUE), .groups = "drop")
View(vacc_2020)

pri.final <-prim_updated %>%
  # Join 2020 cumulative totals by NIS5
  left_join(vacc_2020, by = "PROVINCE") %>%
  # If YEAR_WEEK is 21W01, add CUMUL_2020 to CUMUL
  mutate(cum_rate_vacc = ifelse(YEAR_WEEK == "21W01", cum_rate_vacc+coalesce(CUMUL_2020, 0), cum_rate_vacc)) %>%
```

```
345   # Remove the helper column
346   dplyr::select(-CUMUL_2020)
347 View(pri.final)
348 pri.final <- pri.final %>%
349   filter(!str_detect(YEAR_WEEK, "^20W" ))
350
351 pri.final <- pri.final%>%
352   filter(!str_detect(YEAR_WEEK, "^22W")) %>%
353   mutate(
354     year_week_strp = paste(YEAR, sprintf("%02d", WEEK), sep = "-")
355   ) %>%
356   arrange(YEAR, WEEK) %>%
357   mutate(week_ID = as.numeric(factor(year_week_strp, levels = unique(
        year_week_strp))))
358
359 # Step 5: Calculate weekly expected cases & hospitalizations
360 pri.final <- pri.final %>%
361   group_by(VACC_TYPE, YEAR_WEEK) %>%
362   mutate(
363     population        = sum(MS_POPULATION, na.rm = TRUE),
364     weekly_case_rate  = sum(CASES, na.rm = TRUE) / sum(MS_POPULATION, na.
          rm = TRUE),
365     weekly_hosp_rate  = sum(n_hosp_r, na.rm = TRUE) / sum(MS_POPULATION,
          na.rm = TRUE),
366     expected_cases    = MS_POPULATION * weekly_case_rate,
367     expected_hosp     = MS_POPULATION * weekly_hosp_rate
368   ) %>%
369   ungroup()
370 View(pri.final)
371 #filtering for at lest one booster
372 df_booster <- df_combined1%>% filter(VACC_TYPE == "At␣least␣one␣booster"
      )
373 #View(df_booster)
```

```
# Step 1: Filter rows from 21W01 to 21W52
vacc_2021 <- df_booster %>%
  filter(YEAR_WEEK == "21W52" )%>%
   group_by(PROVINCE) %>%
  summarise(CUMUL_2021 = sum(cum_rate_vacc, na.rm = TRUE), .groups = "
      drop")
#View(vacc_2021)

# Step 2: Add this to 22W01 rows
booster_updated <- df_booster%>%
  # Join 2022 cumulative totals by NIS5
  left_join(vacc_2021, by = "PROVINCE") %>%
  # If YEAR_WEEK is 22W01, add CUMUL_2021 to CUMUL
  mutate(cum_rate_vacc = ifelse(YEAR_WEEK == "22W01", cum_rate_vacc +
      coalesce(CUMUL_2021, 0), cum_rate_vacc)) %>%
  # Remove the helper column
  dplyr::select(-CUMUL_2021)
#View(booster_updated)
# Step 3: Remove all 21 W 0 1 21W52  rows since their values are now
    merged into 22W01
booster.final <- booster_updated %>%
  filter(!str_detect(YEAR_WEEK, "^21W"))
# View the result
#View(booster.final)
booster.final <- booster.final %>%
  mutate(
  year_week_strp = paste(YEAR, sprintf("%02d", WEEK), sep = "-")
  ) %>% arrange(YEAR, WEEK) %>%
   mutate(week_ID = as.numeric(factor(year_week_strp, levels = unique(
       year_week_strp))))
booster.final<- booster.final%>%
  group_by(VACC_TYPE, YEAR_WEEK) %>%
  mutate(
```

```
403     population = sum(MS_POPULATION, na.rm = TRUE),
404     weekly_case_rate = sum(CASES, na.rm = TRUE) / sum(MS_POPULATION, na.
            rm = TRUE),
405     weekly_hosp_rate = sum(n_hosp_r, na.rm = TRUE) / sum(MS_POPULATION,
            na.rm = TRUE),
406     # Expected counts per province-week
407     expected_cases = MS_POPULATION * weekly_case_rate,
408     expected_hosp  = MS_POPULATION * weekly_hosp_rate
409   ) %>%
410   ungroup()
411 View(booster.final)
412
413 #obtaining rangses of key variables
414 # List of variables you want to check
415 vars_to_check <- c("cum_rate_vacc", "Incidence", "stringency_index", "
        CASES", "CUMUL",
416                    "n_cases_r", "n_hosp_r", "expected_cases", "expected_
                        hosp")
417
418 # Function to get min and max with province and time for one variable
419 get_min_max_info <- function(data, var) {
420   var_sym <- sym(var)
421
422   min_row <- data %>%
423     filter(!!var_sym == min(!!var_sym, na.rm = TRUE)) %>%
424     slice(1) %>%
425     mutate(Stat = "Min", Variable = var)
426
427   max_row <- data %>%
428     filter(!!var_sym == max(!!var_sym, na.rm = TRUE)) %>%
429     slice(1) %>%
430     mutate(Stat = "Max", Variable = var)
431
```

```
  bind_rows(min_row, max_row) %>%
    dplyr::select(Variable, Stat, PROVINCE, YEAR_WEEK, Value = !!var_sym
        )
}

# Apply to all variables and combine
range_results <- bind_rows(lapply(vars_to_check, get_min_max_info, data
    = pri.final))
range_results

#Creating neighborhood matrix and graph
BE_581.shp<- st_read("BE_581.shp")
# Group by province ID and dissolve polygons
BE_581.shp<- BE_581.shp[order(BE_581.shp$C_PROVI),]
BE_581.shp_prov <- BE_581.shp %>%
  group_by(C_PROVI) %>%
  summarise(geometry = st_union(geometry)) %>%
  ungroup()

#Creating neighborhood matrix and graph
add_nb <- function(x){
  queen_nb <- poly2nb(x, queen = TRUE)
  count = card(queen_nb)
  if(!any(count==0)){
    return(queen_nb)
  }
  ## get nearest neighbour index, use centroids:
  nnbs = knearneigh(st_coordinates(st_centroid(x)))$nn
  no_edges_from = which(count==0)
  for(i in no_edges_from){
    queen_nb[[i]] = nnbs[i]
    queen_nb[[nnbs[i]]] = c(queen_nb[[nnbs[i]]],i)
  }
```

```
463   return(queen_nb)
464 }
465 nb.new <- add_nb(BE_581.shp_prov)
466 adj.mat_prov.1  <- nb2mat(nb.new, style="B", zero.policy=TRUE)
467 adj.mat_prov.2 <- nb2INLA("adj.mat_prov.1", nb.new)
468 grp<-inla.read.graph(filename="adj.mat_prov.1")
469 # Convert to listw object
470 lw <- nb2listw(nb.new, style = "W")
471 lw
472 adj.mat_prov.1
473 grp
474
475 #Repeat merge for the different data set
476 # join data to shape file to No-vaccine data
477 map <- full_join(BE_581.shp_prov,df_no_vacc, by = c("C_PROVI" = "CD_PROV
      _REFNIS"))
478 #View(map)
479 #str(vacc_cases_hosp_bel_pop_by.prov.imprv)
480 data.set<- data.frame(YEAR_WEEK=map$YEAR_WEEK, PROVINCE=map$PROVINCE,
      CASES= as.integer(map$CASES), n_cases_r= map$n_cases_r, n_hosp_r=
      map$n_hosp_r, CUMUL_vacc_rate= map$cum_rate_vacc, C_PROVI=map$C_
      PROVI, provID=map$provID, CUMUL=as.numeric(map$CUMUL), stringency_
      index=map$stringency_index, week_ID = as.numeric(map$week_ID),
      Incidence=as.integer(map$Incidence), MS_POPULATION=map$MS_POPULATION
      , expected_cases =map$expected_cases, expected_hosp=map$expected_
      hosp, logCASES=map$logCASES)
481 #creating spatial and temporal identifiers for fitting spatio-temporal
      model
482 data.set$provID <- as.numeric(data.set$provID)
483 data.set$provID1 <- data.set$provID
484 data.set$week_id.1 <- data.set$week_ID
485 data.set$ID.prov.week <- interaction(data.set$PROVINCE, data.set$week_ID
      , drop = TRUE)
```

```
ID.prov.int <- data.set$provID
ID.week.int <- data.set$week.ID
data.set$ID.prov.week = seq(1,length(data.set$ID.prov.week))
 #creating linear combination for each week
lcs = inla.make.lincombs(week_ID = diag(52),  week_id.1 = diag(52))
#creating linear combination for each week for no_vaccination-2020 data
    set
lcs <- inla.make.lincombs(week_ID = diag(44), week_id.1 = diag(44))
#creating linear combination for each week for 2022 data set
lcs <- inla.make.lincombs(week_id = diag(52), week_id.1 = diag(52))
## default pc-priors
hyper <- list(prec = list(prior = "pc.prec", param = c(0.5, 0.01)))
# modeling infection in 2020
formula.cases.rw1.2C <- CASES ~ stringency_index +
f(provID, model="bym2",graph=grp,scale.model=TRUE) +
f(week_ID,model="rw1") +
f(week_id.1,model="iid") +
f(ID.prov.int,model="iid", group=ID.week.int, control.group=list(model="
    rw1"))
covid.case.rw1.2C <- inla(formula.cases.rw1.2C ,family="poisson",
        data=data.set,E=expected_cases,
        control.predictor=list(link=1, compute=TRUE), #enable prediction
        control.compute=list(dic=TRUE, cpo=TRUE),
        lincomb=lcs)
#Modeling infection in 2021
formula.cases.rw2.1A <- CASES ~ CUMUL_vacc_rate *stringency_index +
f(provID, model="bym2",graph=grp,scale.model=TRUE) +
f(week_ID,model="rw2") +
f(week_id.1,model="iid") +
f(ID.prov.week,model="iid")
covid.case.rw2.1A <- inla(formula.cases.rw2.1A,family="poisson",
        data=data.set,E=expected_cases,
        control.predictor=list(compute=TRUE), #enable prediction
```

```
517         control.compute=list(dic=TRUE, cpo=TRUE),  lincomb=lcs)
518 #Modeling infection in 2022
519 formula.cases.rw2.no.inter.1B <- CASES ~ CUMUL_vacc_rate +stringency_
        index +
520 f(provID, model="bym2",graph=grp,hyper = hyper,scale.model=TRUE) +
521 f(week_ID,model="rw2",hyper = hyper) +
522 f(week_id.1,model="iid",hyper = hyper) +
523 f(ID.prov.week,model="iid",hyper = hyper)
524 covid.case.rw2.no.inter.1B <- inla(formula.cases.rw2.no.inter.1B,family=
        "poisson",
525         data=data.set,E=expected_cases,
526         control.predictor=list(compute=TRUE), #enable prediction
527         control.compute=list(dic=TRUE, cpo=TRUE))
528 #Modeling hospitalization in 2020
529 formula.hosp.rw2.no.inter.1B <- Incidence ~ 1 +stringency_index*logCASES
         +
530 f(provID, model="bym2",graph=grp,scale.model=TRUE) +
531 f(week_ID,model="rw2") +
532 f(week_id.1,model="iid") +
533 f(ID.prov.week,model="iid")
534 covid.hosp.rw2.no.inter.1B <- inla(formula.hosp.rw2.no.inter.1B,family="
        poisson",
535         data=data.set,E= expected_hosp,
536         control.predictor=list(compute=TRUE), #enable prediction
537         control.compute=list(dic=TRUE, cpo=TRUE),
538         lincomb=lcs)
539 #modeling hospitalization in 2021
540 formula.hosp.rw2.1A <- Incidence ~ 1 + CUMUL_vacc_rate*stringency_index+
         logCASES +
541 f(provID, model="bym2",graph=grp,scale.model=TRUE) +
542 f(week_ID,model="rw2") +
543 f(week_id.1,model="iid") +
544 f(ID.prov.week,model="iid")
```

```
covid.hosp.rw2.1A <- inla(formula.hosp.rw2.1A,family="poisson",
        data=data.set,E= expected_hosp,
        control.predictor=list(compute=TRUE), #enable prediction
        control.compute=list(dic=TRUE, cpo=TRUE),
        lincomb=lcs)
#modeling hospitalization in 2022
formula.hosp.rw2.1A <- Incidence ~ 1 + CUMUL_vacc_rate*stringency_index+
    logCASES +
f(provID, model="bym2",graph=grp,hyper = hyper, scale.model=TRUE) +
f(week_ID,model="rw2",hyper = hyper) +
f(week_id.1,model="iid",hyper = hyper) +
f(ID.prov.week,model="iid",hyper = hyper)
covid.hosp.rw2.1A <- inla(formula.hosp.rw2.1A,family="poisson",
        data=data.set,E= expected_hosp,
        control.predictor=list(compute=TRUE, link=1), #enable prediction
        control.compute=list(config = TRUE, dic=TRUE, cpo=TRUE),
        lincomb=lcs)
#Code for extraction parameter estimates
lapply(covid.hosp.rw2.1A$marginals.fixed, function(marg) {
  inla.zmarginal(inla.tmarginal(exp, marg))
})
#Code for ploting posterior mean of residual random effects
BE_581.shp_prov$re.hosp1 <- sapply(covid.hosp.rw2.1A$marginals.random$
    provID[1:11],
                                   function(x) inla.emarginal(exp, x))
  ggplot(BE_581.shp_prov)+geom_sf(aes(fill=re.hosp1))+
 scale_fill_gradient2(
 midpoint=1,low="blue",mid="white",high="red"
 )+
 theme_bw()

 # Posterior temporal trend

```

```r
temporal.RW <- lapply(covid.hosp.rw2.1A$marginals.random$week_ID,
 function(X){marg <- inla.tmarginal(function(x) exp(x), X)
 inla.emarginal(mean, marg)})
temporal.IID <- lapply(covid.hosp.rw2.1A$marginals.random$week_id.1,
 function(X){marg <- inla.tmarginal(function(x) exp(x), X)
 inla.emarginal(mean, marg)})
# Convert to numeric vectors
temporal.RW.vals <- unlist(temporal.RW)
temporal.IID.vals <- unlist(temporal.IID)

# Create week index
week_index <- seq_along(temporal.RW.vals)

# Combine into a data.frame
temporal_df <- data.frame(
  week = week_index,
  RW = temporal.RW.vals,
  IID = temporal.IID.vals
)

# Plot both CAR and IID on the same plot
ggplot(temporal_df, aes(x = week)) +
  geom_line(aes(y = RW, color = "RW")) +
  geom_line(aes(y = IID, color = "IID")) +
  scale_color_manual(values = c("RW" = "blue", "IID" = "red")) +
  labs(
    title = "Temporal Trend: RW vs IID",
    x = "Week",
    y = "exp(mean)",
    color = "Temporal Effect"
  ) +
  theme_minimal(base_size = 14)

```

```
 Posterior exceedance probability
csi.case <-covid.case.rw2.2A$marginals.random$provID[1:11]
a <- 0
# Ensure the column is a numeric vector (not a list)
BE_581.shp_prov$prob.csi.case <- unlist(
  lapply(csi.case, function(x) {1 - inla.pmarginal(a, x)})
)
# Create categorical variable
BE_581.shp_prov <- BE_581.shp_prov %>%
  mutate(prob_cat = cut(prob.csi.case,
                        breaks = c(0, 0.2, 0.8, 1),
                        labels = c("0  0  .2␣(Unlikely)",
                                   "0.2  0  .8␣(Uncertain)",
                                   "0.8  1  ␣(Likely)"),
                        include.lowest = TRUE))

# Plot with discrete fill
ggplot(BE_581.shp_prov) +
  geom_sf(aes(fill = prob_cat)) +
  scale_fill_manual(
    values = c("0  0  .2␣(Unlikely)" = "blue",
               "0.2  0  .8␣(Uncertain)" = "grey80",
               "0.8  1  ␣(Likely)" = "red"),
    name = "P(RR␣>␣1)"
  ) +
  theme_bw()
#Code for extracting the space-time interaction probability
BE_581.shp<- st_read("BE_581.shp")
# Group by province ID and dissolve polygons
BE_581.shp<- BE_581.shp[order(BE_581.shp$C_PROVI),]
BE_581.shp_prov <- BE_581.shp %>%
  group_by(C_PROVI) %>%
  summarise(geometry = st_union(geometry)) %>%
```

```
642   ungroup()
643 #Space-Time Interaction
644 delta <- data.frame(delta=covid.hosp.rw2.1A$summary.random$ID.prov.week
        [,2],week_ID=data.set$week_ID,provID=data.set$provID)
645 delta.matrix <- matrix(delta[,1], nrow(BE_581.shp_prov),52,byrow=FALSE)
646 rownames(delta.matrix)<- delta[seq_len(nrow(BE_581.shp_prov)),3]
647 #Space time probability>1
648 a=0
649 inlaprob.delta<-lapply(covid.hosp.rw2.1A$marginals.random[[4]], function
        (X){
650   1-inla.pmarginal(a, X)
651 })
652 pp.delta<-unlist(inlaprob.delta)
653
654 pp.cutoff.interaction <- c(0,0.2,0.8,1)
655 pp.delta.matrix <- matrix(pp.delta, nrow(BE_581.shp_prov),52,byrow=FALSE
        )
656 pp.delta.factor <- data.frame(C_PROVI=BE_581.shp_prov$C_PROVI)
657 for(i in 1:52){
658   pp.delta.factor.temp <- cut(pp.delta.matrix[,i],breaks=pp.cutoff.
          interaction,include.lowest=TRUE)
659   pp.delta.factor <- cbind(pp.delta.factor,pp.delta.factor.temp)
660 }
661 colnames(pp.delta.factor)<- c("C_PROVI",seq(1,52))
662
663 View(pp.delta.factor)
664 #Maps
665 BE_581.shp_prov<- cbind(BE_581.shp_prov, pp.delta.factor)
666 BE_581.shp_prov_sp <- sf::as_Spatial(BE_581.shp_prov)
667
668 trellis.par.set(axis.line=list(col=NA))
669 spplot(obj=BE_581.shp_prov_sp, zcol="X1", col.regions=gray(2.5:0.5/3),
        main="Hosp-21W1:Space␣time␣probability␣RR>1",par.settings=list(
```

```
    fontsize=list(text=10)))
trellis.par.set(axis.line=list(col=NA))
spplot(obj=BE_581.shp_prov_sp, zcol="X15", col.regions=gray(2.5:0.5/3),
    main="Hosp-21W15:Space time probability RR>1",par.settings=list(
    fontsize=list(text=10)))
trellis.par.set(axis.line=list(col=NA))
spplot(obj=BE_581.shp_prov_sp, zcol="X30", col.regions=gray(2.5:0.5/3),
    main="Hosp-21W30:Space time probability RR>1",par.settings=list(
    fontsize=list(text=10)))
trellis.par.set(axis.line=list(col=NA))
spplot(obj=BE_581.shp_prov_sp, zcol="X45", col.regions=gray(2:0/2),main=
    "Hosp-21W45:Space time probability RR>1",par.settings=list(fontsize=
    list(text=10)))
```

Table 4: Estimates of model fitted to infection - 2020 data

Parameter	**Mean**	**Std. Error**	**UCI**	**LCI**
(Intercept)	1.212	0.222	0.833	1.706
CUMUL_vacc_rate	2.36×10^{-39}	5.76×10^{-36}	-1.34×10^{-7}	-2.27×10^{-12}
Stringency_Index	0.998	0.0030	0.992	1.004
CUMUL_vacc_rate:Stringency_Index	1.158	0.659	0.350	2.867

Table 5: Estimates of model fitted to infection - 2020 data

Parameter	**Mean**	**SD**	**UCI**	**LCI**
(Intercept)	1.2071	0.2211	0.8304	1.6996
CUMUL Vaccination	23.6926	606.2359	-2.63×10^{27}	-4.44×10^{22}
Stringency_Index	0.9978	0.0030	0.9919	1.0038

Table 6: Log transform estimates of model fitted to infection (Using 2020 data)

Parameter	**Mean**	**Std. Error**	**2.5% CrI**	**97.5% CrI**
(Intercept)	1.043	0.0092	1.025	1.062
CUMUL_vacc_rate	26.918	679.567	-2.76×10^{27}	-4.65×10^{22}

BIODATA OF STUDENT