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Bayesian Hidden Markov Modelling of Blood Type Distribution for Covid-19 Cases Using Poisson Distribution

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Abstract

This paper proposes a model to describe the blood types distribution of new Coronavirus (COVID-19) cases using the Bayesian Poisson - Hidden Markov Model (BP-HMM). With the help of the Gibbs sampler algorithm, using OpenBugs, the study first identifies the number of hidden states fitting European (EU) and African (AF) data sets of COVID-19 cases by blood type frequency. The study then compares the state-dependent mean of infection within and across the two geographical areas. The study findings show that the number of hidden states and infection rate within and across the two geographical areas differ according to blood type.

Keywords: Bayesian Poisson Hidden Markov Model (BP-HMM), COVID-19, Blood Types, Gibbs sampler

1. Introduction

The whole world is experiencing the new infectious coronavirus infection, which began spreading in the year 2019 hence the name COVID-19 since then. The outbreak seems to have spread to every country, making the infection a global pandemic. There are ongoing studies to understand the dynamics of infection transmission, and this is very important in discovering the diffusion potential that may be sustainable going forward. In this vein, models and simulations might be a key and powerful tool that can be used to monitor the infection's dynamics in question. In doing so, there is a need to build an adequate statistical model that would be able to describe the actual situation.

Several studies associate blood groups A, B, and O (ABO blood group) and their Rhesus factors with the COVID-19 infection. For instance, the study by such as El-Shitany et al. (2021); Zhao et al.(2020); Fan et al. (2020); Zietz et al.(2020a); Muniz-Diaz et al. (2020); Wu et al. (2020); Ad'hiah et al. (2020); Obayes AL-Khikani (2020) and Göker et al. (2020) concluded that there is an association between ABO blood types and COVID-19 infection. Meanwhile, other studies also indicate that certain factors generate the spread of infections. Moon (2014) examined the relationship between ABO blood group and lifespan in a Hospitalized population in the Southeastern United States and said the individual ABO blood group remains the same irrespective of the environment. However, because the environment keeps changing, it is possible that a gene that impeded survival and reproduction in the past might be factor in survival and reproduction today. Moon (2014). The study continues that natural selection and adaptation work to adjust the prevalence of traits suited for a particular environment. In other words, changes brought by humans, creating an environment never known, could influence these tendencies. Therefore, it is always prudent to examine the distribution of ABO blood groups and causes for any prevalence of blood groups considering the population, environment, and other factors, Moon (2014). In the study of Tewara et al., (2018) the findings show that factors such as urban-rural location and rainfall do generate the spread of malaria. The study concluded that malaria cases were associated with population density and environmental covariates such as rainfall.

Although, as some studies suggest, ABO blood groups might contribute to the susceptibility of COVID-19 infection incidence, there might be other factors that might also be a cause for the spread of the infection, environmental conditions (Humidity), one's location- urban or rural, weather condition, governmental policies, and others. In their study, Hedell et al., (2018) explained that a potentially sensitive way to detect infection outbreaks is syndromic surveillance, monitoring the number of syndromes reported in the population of interest and comparing it to the baseline

rate, then finally concluding the outbreak using statistical methods. They further asserted that in assessing the probability of an outbreak, information such as the total count of syndromes, clustering of syndromes in space and time, seasonality of the infection, and others needed to be considered. In a recent study by Miotto et al.,(2021) on "does, blood type affect the COVID-19 infection pattern? The study concluded that overall, the hypothesis of blood type affects COVID-19 and further stated that even though blood types are associated with COVID-19, there are possibilities that other population-dependent antigen distribution may contribute to the spreading of infection because of the geographical heterogeneity. These are a clear indication that before concluding on the susceptibility of the ABO blood group to COVID-19 infection, then there might be other latent variables that might contribute to the spread of the infection; hence the need to consider the spread of the COVID-19 infection when considering its susceptibility to blood types.

Watkins et al., (2009) explained that Hidden Markov Model (HMM) is noted in disease surveillance applications, especially where data is scarce. In their study, they proposed Bayesian temporal HMM for infection surveillance, and as part of their recommendation, further research is required to evaluate the generalized HMMs for infection surveillance. Since the study of Watkins et al., (2009) there have been several studies on hidden Markov modeling (HMM), for instance, Marfak et al., (2020) on Hidden Markov chain modeling of COVID-19 spreading using a Moroccan dataset. The study used a generalized logistic growth model, exponential model, segmented Poisson model Susceptible-Infected -Recovered derivative models, and ARIMA to predict the evolution of COVID-19. Prabhu & Subramanyam, (2020) on Surveillance of COVID-19 Pandemic using Hidden Markov Model aimed at applying Hidden Markov model to assess the extent of the spread of COVID-19 pandemic; Hedell et al., (2018) used Bayesian temporal HMM to determine the probability of occurrence of neurological syndromes in horses in France. Again, Ozonoff et al.,(2018) also compared the performance of HMM to a cyclic regression model using pneumonia and influenza mortality data, while Williams et al.,(2018) studied on Bayesian Approach to Multi-State Hidden Markov models on Dementia Progression.

Moreover, Yen and Chen, (2018) again used the Bayesian measurement – error-driven hidden Markov regression model for androgenetic alopecia. Liu and Song, (2018) used Bayesian Analysis of Mixture Structural Equation Models on risk factors of osteoporotic fractures in older people. Zhang et al., (2016) also used the hidden Markov model to identify infection states associated with coagulopathy in trauma. Finally, Morimoto, (2016) studied Hidden Markov models to estimate the lagged effect of weather on stroke and ischemic heart infection.

The Hidden Markov model describes the relationship between an experimental process and an underlying and unobserved or latent process. The hidden process is assumed to follow a Markov chain whose realization governs the distribution of the number of disease cases when considering blood type frequencies. In the study of Prabhu & Subramanyam, (2020) on the surveillance of the COVID-19 pandemic using the Hidden Markov Model, the study defined some significant situations they assumed as the hidden states governing the number of observed counts of infection (COVID-19) at the hospitals, are:" Healthy," "Infected," "Symptomatic," "Detected," "Catastrophe-1" and "Castastrphpe-2" the study assumed the first four as the hidden central states. Again, the study listed some of the variables that hospitals use to define the number of reported cases of COVID-19, which include: "Active," "Recovered," Dead," and "Inactive" most countries use the cumulative count of these cases as confirmed cases of COVID-19. In this study, we analyze the COVID-19 incidence data for European (EU) and African (AF) countries regarding their blood type frequencies by adopting the Bayesian Poisson – Hidden Markov Model (BP-HMM). The study aims to ascertain the number of hidden states that best fit COVID-19 incidence data with its blood distribution and compare the state-dependent mean s of infection that occur within the two geographical areas. This study is a follow-up of Miotto et al., (2021) who recommended further studies as to whether other population-dependent antigen distribution may play a role in the geographically heterogeneous infection spreading of COVID-19 infection with blood frequency. This study is categorized into four sections, following this section is Methodology, Data analysis, and finally, Discussion and Conclusion.

2. Methodology

Suppose $N_c^{O^+} = (\mathrm{n}_1^{\mathrm{O}^+}, \mathrm{n}_2^{\mathrm{O}^+}, \ldots, \mathrm{n}_{\mathrm{m}}^{\mathrm{O}^+})$, $N_c^{A^+} = (\mathrm{n}_1^{\mathrm{A}^+}, \mathrm{n}_2^{\mathrm{A}^+}, \ldots, \mathrm{n}_{\mathrm{m}}^{\mathrm{A}^+})$, . . ., $N_c^{AB^-} = (, \mathrm{n}_2^{\mathrm{AB}^-}, \ldots, \mathrm{n}_{\mathrm{m}}^{\mathrm{AB}^-})$ are counts of number of cases of COVID-19 for blood types, O^+, $\mathrm{A}^+, \ldots, \mathrm{AB}^-$ while $\mathrm{c} = 1, 2, \ldots, \mathrm{m}$ specify a particular country with COVID-19 infection cases. This can be simplified in contingency table form as

Table 1. Description of COVID -19 cases per blood type are distributed

Country (c)	O^+	A^+	B^+	AB^+	O^-	A^-	B^-	AB^-	Total
1	$n_1^{O^+}$	$n_1^{A^+}$	.	.	.	.	.	$n_1^{AB^-}$	N_1
2	$n_2^{O^+}$	$n_2^{A^+}$	.	.	.	.	.	$n_2^{AB^-}$	N_2
.	.	.	.	.	.	.	.	.	.
.	.	.	.	.	.	.	.	.	.
.	.	.	.	.	.	.	.	.	.
m	$n_m^{O^+}$	$n_m^{A^+}$	.	.	.	.	.	$n_m^{AB^-}$	N_c
Total	$N_{mc}^{O^+}$	$N_{mc}^{A^+}$	.	.	.	.	.	$N_{mc}^{AB^-}$	N

Assuming the number of cases for each blood type $N_c^{O^+}, N_c^{A^+}, \ldots, N_c^{AB^-}$ is governed by an unobserved (latent) process , $Y_c^{O^+} = \{y_1^{O^+}, y_2^{O^+}, \ldots, y_m^{O^+}\}, Y_c^{A^+} = \{y_1^{A^+}, y_2^{A^+}, \ldots, y_m^{A^+}\}, \ldots, Y_c^{AB^-} = \{y_1^{AB^-}, y_2^{AB^-}, \ldots, y_m^{AB^-}\}$ respectively. If we further assume the number of cases is independent. Then the model for each of the number of cases $\{N_c^{O^+}, N_c^{A^+}, \ldots, N_c^{AB^-}\}$ is assumed Poisson distribution with mean $\theta_E^{O^+} = \{\theta_1^{O^+}, \theta_2^{O^+}, \ldots, \theta_K^{O^+}\}$, $\theta_E^{A^+} = \{\theta_1^{A^+}, \theta_2^{A^+}, \ldots, \theta_K^{A^+}\}, \ldots \theta_E^{AB^-} = \{\theta_1^{AB^-}, \theta_2^{AB^-}, \ldots, \theta_K^{AB^-}\}$ on a finite state space $E = (1, \ldots, K)\}$ i.e.,

$$\omega(N_c^{O^+} | Y_c^{O^+}) = E \sim \text{Poisson}(\theta_K^{O^+}), \quad (1)$$

$$\omega(N_c^{A^+} | Y_c^{A^+}) = E \sim \text{Poisson}(\theta_K^{A^+}), \quad (2)$$

$$\omega(N_c^{AB^-} | Y_c^{AB^-}) = E \sim \text{Poisson}(\theta_K^{AB^-}) \quad (3)$$

$$\omega(P_i^{O^+}) \propto \prod_{j=1}^{K} P_{ij}^{(O+)\mu_{ij-1}} \quad (4)$$

$$\omega(P_i^{A^+}) \propto \prod_{j=1}^{K} P_{ij}^{(A+)\mu_{ij-1}} \quad (5)$$

$$\omega(P_i^{AB^-}) \propto \prod_{j=1}^{K} P_{ij}^{(AB-)\mu_{ij-1}} \quad (6)$$

Where μ_{ij} is the parameter vector and $i, j = 1, \ldots, K$. This implies $P_i's$ are here independent of each other. Where $\mu_{ij} \geq 0$ and $P_{ij} \geq 0$ and $\sum P_{ij} = 1$

Assuming Gamma prior for each of the state – dependent means $\{\theta_i^{O^+}, \theta_i^{A^+}, \ldots, \theta_i^{AB^-}\}$ for a given state $i = 1, \ldots, K$. i.e.,

$$\theta_i^{O^+} \sim \gamma(\alpha_i^{O^+}, \beta_i^{O^+}) \quad (7)$$

$$\theta_i^{A^+} \sim \gamma(\alpha_i^{A^+}, \beta_i^{A^+}) \quad (8)$$

$$\theta_i^{AB^-} \sim \gamma\ (\alpha_i^{AB^-}, \beta_i^{AB^-}) \quad (9)$$

Here, $\theta_i^{O^+}, \theta_i^{A^+}, \ldots, \theta_i^{AB^-}$ are independent of each other. The independence of prior distribution is a result of no association of information between states.

Therefore, given number of COVID-19 cases by each country according to their blood type distributions as: $N_c^{O^+} = \{n_1^{O^+}, n_2^{O^+}, \ldots, n_m^{O^+}\}$, $N_c^{A^+} = \{n_1^{A^+}, n_2^{A^+}, \ldots, n_m^{A^+}\}$, . . ., $N_c^{AB^-} = \{n_1^{AB^-}, n_2^{AB^-}, \ldots, n_m^{AB^-}\}$, we are interested in the joint posterior distribution of unknown parameters of each blood type $\pi^{O^+} = (\theta_i^{O^+}, P_i^{O^+}), \ldots$, $\pi^{AB^-} = (\theta_i^{AB^-}, P_i^{AB^-})$ With the help of Gibbs sampler, we can draw samples from the joint posterior distribution since evaluating the joint posterior distribution of π computationally is not possible in close form.

Given the Markov chain, $(Y_j^{O^+}, Y_j^{A^+}, \ldots, Y_j^{AB^-})$ where , $j = 1, \ldots, K$, we estimate the full conditional distribution of the elements of $(P_j^{O^+}, P_j^{A^+}, \ldots, P_j^{AB^-})$which is proportional to the prior probability distribution in equations (4-6) and its likelihood functions which is the multinomial distribution function as:

$$\omega(P_j^{O^+}, P_j^{A^+}, \ldots, P_j^{AB^-} | Y_j^{O^+}, Y_{i,j}^{A^+}, \ldots, Y_{i,j}^{AB^-})$$

$$\propto \omega(P_j^{O^+}, P_j^{A^+}, \ldots, P_j^{AB^-}) \omega(Y_j^{O^+}, Y_j^{A^+}, \ldots, Y_j^{AB^-} | P_j^{O^+}, P_j^{A^+}, \ldots, P_j^{AB^-}) \quad (10)$$

$$\omega\left(P_j^{O^+}\right)\omega\left(Y_j^{O^+}\middle|P_j^{O^+}\right) = \omega(P_j^{O^+}|\mu_{i,1}^{O^+},\ldots,\mu_{i,j}^{O^+})\prod_j^k \omega(Y_j^{O^+}|P_j^{O^+})$$

$$= \left(\frac{\prod_j^k \Gamma\mu_k}{\Gamma\left(\sum_j^k \mu_k\right)}\prod_{j=1}^{k}(P_j^{O^+})^{\mu_{ij-1}}\right)\left(\frac{\mathrm{m!}}{y_1^{O^+}!\ldots y_j^{O^+}!}(P_1^{O^+})^{\mathrm{y_1^{O^+}}},\ldots,(P_j^{O^+})^{\mathrm{y_j^{O^+}}}\right)$$

$$\propto \prod_{j=1}^{k}(P_j^{O^+})^{\mu_{ij-1}}\prod_{j}^{k}(P_j^{O^+})^{\mathbf{1}\{\mathrm{y_{c=j}^{O^+}}\}}$$

$$\omega(P_j^{O^+}|Y_j^{O^+}) \propto \prod_{j=1}^{k}\left(P_j^{O^+}\right)^{\mu_{ij-1}+\sum \mathbf{1}\{\mathrm{y_{c=j}^{O^+}}\}} \tag{11}$$

Therefore, with the GIBSS sampler while given $(Y_j^{O^+}, Y_j^{A^+},\ldots,Y_j^{AB^-})$ the full conditional distribution of each of $P_j^{O^+}, P_j^{A^+},\ldots,P_j^{AB^-}$ is derived as

$$\omega(\mathrm{P_j^{O^+}}|Y_j^{O^+}) \sim \mathrm{Dirichlet}\left(\mu_{\mathrm{i,j}}^{\mathrm{O^+}} + \sum \mathbf{1}\left\{\mathrm{Y_c^{O^+}} = \mathrm{j}\right\}\right) \tag{12}$$

$$\omega(\mathrm{P_j^{A^+}}|\mathrm{Y_j^{A^+}}) \sim \mathrm{Dirichlet}\left(\mu_{\mathrm{i,j}}^{\mathrm{A^+}} + \sum \mathbf{1}\left\{\mathrm{Y_c^{A^+}} = \mathrm{j}\right\}\right) \tag{13}$$

$$\omega(\mathrm{P_j^{AB^-}}|\mathrm{Y_j^{AB^-}}) \sim \mathrm{Dirichlet}\left(\mu_{\mathrm{i,j}}^{\mathrm{AB^-}} + \sum \mathbf{1}\{\mathrm{Y_c^{AB^-}} = \mathrm{j}\}; \mathrm{i,j} = (1,2,\ldots,\mathrm{K})\right) \tag{14}$$

Where each of $\sum \mathbf{1}\{\mathrm{Y_c'} = \mathrm{j}\}$ is an indicator function that represents the counts of instances $\mathrm{Y_c'} = \mathrm{j}$ in the simulated sample path of the Markov chain. Here, the $\mathrm{P_j'}$s are also obtained as independent Dirichlet vectors.

Next is the derivation of the posterior distribution $(\theta_j^{O^+}, \theta_j^{A^+},\ldots,\theta_j^{AB^-})$ which has Gamma prior with Poisson distribution function as its likelihood. Given the State- dependent means $(\theta_i^{O^+}, \theta_i^{A^+},\ldots,\theta_i^{AB^-})$ and the Transition Probability $(P_i^{O^+}, P_i^{A^+},\ldots,P_i^{AB^-})$ the joint likelihood function for the observations and the Markov – Chain is given as:

$$\omega\left(N_c^{O^+}, Y_j^{O^+}\middle|\theta_{\mathrm{i}}^{O^+}, P_i^{O^+}\right) = \omega(\mathrm{n_1^{O^+}}|\ \mathrm{y_1^{O^+}}\theta_1^{\mathrm{O^+}},),\ldots\ \omega(\mathrm{n_m^{O^+}}|\ \mathrm{y_m^{O^+}},\ \theta_{\mathrm{K}}^{\mathrm{O^+}})\times\ \omega\left(\mathrm{y_1^{O^+}}\middle|P_1^{O^+},\ldots,\mathrm{y_m^{O^+}}\middle|P_k^{O^+}\right) \tag{15}$$

$$\omega(N_c^{O^+}|Y_i^{O^+},\theta_{\mathrm{i}}^{O^+},P_i^{O^+}) = \prod_{i=1}^{K}\left\{\prod_{c=1}^{m}P_{y_{c,}y_{c+1}}^{O^+}\frac{\left(\theta_{\mathrm{i}}^{O^+}\right)^{n_c^{O^+}}}{n_c^{O^+}!}\mathrm{e}^{-\theta_{\mathrm{i}}^{O^+}}\right\}$$

$$= \left(\prod_{\mathrm{c=1}}^{\mathrm{m}}\frac{1}{n_c^{O^+}!}P_{y_{c,}y_{c+1}}^{O^+}\right).\prod_{\mathrm{i=1}}^{\mathrm{k}}\left\{\left[\theta_{\mathrm{i}}^{O^+}\right]^{\sum_{\mathrm{c}}^{\mathrm{m}}\mathbf{1}(Y_c^{O^+}=\boldsymbol{i})\mathrm{n_{ic}^{O^+}}}\mathrm{e}^{-\theta_{\mathrm{i}}^{O^+}.\sum_c^m\mathbf{1}(\boldsymbol{Y}_c^{O^+}=\boldsymbol{i})}\right\}$$

$$\omega(N_c^{O^+}|Y_i^{O^+},\theta_{\mathrm{i}}^{O^+},P_i^{O^+}) \propto \prod_{\mathrm{i=1}}^{\mathrm{k}}\left\{\left[\theta_{\mathrm{i}}^{O^+}\right]^{\sum_{\mathrm{c}}^{\mathrm{m}}\mathbf{1}(Y_c^{O^+}=\boldsymbol{i})\mathrm{n}_c^{O^+}}\mathrm{e}^{-\theta_{\mathrm{i}}^{O^+}.\sum_c^m\mathbf{1}(\boldsymbol{Y}_c^{O^+}=\boldsymbol{i})}\right\} \tag{16}$$

Next, we derive the posterior distribution $\theta_{\mathrm{j}}^{O^+}$ which has Gamma prior from equation (7) with its likelihood function in equation (16) as

$$\omega\left(\theta_j^{O^+}\middle|N_c^{O^+},Y_j^{O^+},\theta_{\mathrm{j}}^{O^+}\right) = \theta_{\mathrm{j}}^{O^+}\sim\gamma\left(\alpha_{\mathrm{j}}^{O^+},\beta_{\mathrm{j}}^{O^+}\right)\times\omega(N_c^{O^+}|Y_j^{O^+},\theta_{\mathrm{j}}^{O^+},P_j^{O^+}) \tag{17}$$

$$\omega\left(\theta_j^{O^+}\middle|N_c^{O^+},Y_j^{O^+},\theta_{\mathrm{j}}^{O^+}\right) \propto \prod_j^k[\theta_{\mathrm{j}}^{O^+}]^{\alpha_j^{O^+}-1}e^{-\beta_{\mathrm{j}}^{O^+}\theta_j^{O^+}}\times\prod_{\mathrm{j=1}}^{\mathrm{k}}\left\{\left[\theta_{\mathrm{j}}^{O^+}\right]^{\sum_{\mathrm{c}}^{\mathrm{m}}\mathbf{1}(Y_c^{O^+}=\boldsymbol{j})\mathrm{n_{jc}^{O^+}}}\mathrm{e}^{-\theta_{\mathrm{j}}^{O^+}.\sum_c^m\mathbf{1}(\boldsymbol{Y}_c^{O^+}=\boldsymbol{j})}\right\} \tag{18}$$

$$\omega\left(\theta_j^{O^+}\middle|N_c^{O^+},Y_j^{O^+},\theta_j^{O^+}\right)\propto\prod_{j=1}^{k}\left\{\left[\theta_j^{O^+}\right]^{\alpha_j^{O^+}-1+\left(\sum_c^m \mathbf{1}(Y_c^{O^+}=j)n_{jc}^{O^+}\right)}e^{-\beta_j^{O^+}\theta_j^{O^+}+\left(-\theta_j^{O^+}.\sum_c^m \mathbf{1}(Y_c^{O^+}=j)\right)}\right\} \quad (19)$$

$$\omega\left(\theta_j^{O^+}\middle|N_c^{O^+},Y_j^{O^+},\theta_j^{O^+}\right)\propto\prod_{j=1}^{k}\left\{\left[\theta_j^{O^+}\right]^{\alpha_j^{O^+}-1+\sum_c^m \mathbf{1}(Y_c^{O^+}=j)n_{jc}^{O^+}}e^{-\theta_j^{O^+}\left(\beta_j^{O^+}+\sum_c^m \mathbf{1}(Y_c^{O^+}=j)\right)}\right\} \quad (20)$$

The full conditional posterior distribution of the mean of each blood type, $\theta_j^{O^+},\ \theta_j^{A^+},\ldots,\ \theta_j^{AB^-}$ is obtained as

$$\theta_j^{O^+}\,|N_c^{O^+},\ Y_c^{O^+}\ \sim\ \gamma\ \left(\alpha_j^{O^+}+\sum_{c=1}^{m}\mathbf{1}(\mathbf{Y_c^{O^+}}=j)N_{jc}^{O^+},\beta_j^{O^+}+\mathbf{1}\sum_{\mathbf{c=1}}^{\mathbf{m}}(\mathbf{Y_c^{O^+}}=j)\right) \quad (21)$$

$$\theta_j^{A^+}\,|N_c^{A^+},\ Y_c^{A^+}\sim\ \gamma\left(\alpha_j^{A^+}+\sum_{c}^{m}\mathbf{1}(\mathbf{Y_c^{A^+}}=j)N_{jc}^{A^+},\beta_j^{A^+}+\mathbf{1}\sum_{\mathbf{t=1}}^{\mathbf{m}}(\mathbf{Y_c^{A^+}}=j)\right) \quad (22)$$

$$\theta_j^{AB^-}\,|N_c^{AB^-},Y_c^{AB^-}\sim$$

$$\gamma\left(\alpha_j^{AB^-}+\sum_{c=1}^{m}\mathbf{1}(\mathbf{Y_c^{AB^-}}=j)N_{jc}^{AB^-},\beta_j^{AB^-}+\mathbf{1}\sum_{\mathbf{c=1}}^{\mathbf{m}}(\mathbf{Y_t^{AB^-}}=j);\ j=(1,2,\ldots,K)\right) \quad (23)$$

Where,

$\{\alpha_j^{O^+},\ \alpha_j^{A^+},\ldots.,\ \alpha_j^{AB^-}\}$ and $\{\beta_j^{O^+},\ \beta_j^{A^+},\ldots,\ \beta_j^{AB^-}\}$ are the prior shape and rate parameters for each blood type respectively

$\{\mathbf{1}(\mathbf{Y_c'}=j)$ is an indicator function representing each counts of instances $\{\mathbf{Y_c'}=j\}$in the simulated sample path of the Markov chain.

$\{\sum_{c=1}^{n}\mathbf{1}(\mathbf{Y_c'}=j)N_{jc}'\}$ the contribution of regime j to each of the observed values of $\{N_c^{O^+},N_c^{A^+},\ldots,N_c^{AB^-}\}$.

In Gibbs Sampler, the model will generate first sample path of the Markov chain (MC). The model then uses this sample path to decompose the observed counts into (simulated) regime contributions. Finally, with the availability of the Markov chain sample path, and the regime contributions, the developed model can now update $P_i^{O^+},\ P_i^{A^+},\ldots,\ P_i^{AB^-}$ and $\theta_i^{O^+},\ \theta_i^{A^+},\ldots\ \theta_i^{AB^-}$.

If the steps above are repeated several times, the resulting samples of values of $\widehat{P}_j^{O^+},\widehat{P}_j^{A^+},\ldots,\widehat{P}_j^{AB^-}$ and $\hat{\theta}_j^{O^+},\ \hat{\theta}_j^{A^+},\ldots,\hat{\theta}_j^{AB}$ provide the required estimates of their posterior distributions. In the posterior, the hidden states are ranked according to the state – dependent mean of infection occurrence respecting each blood type. i.e. $\hat{\theta}_j^{O^+}=\{\hat{\theta}_1^{O^+},\hat{\theta}_2^{O^+},\ldots\hat{\theta}_K^{O^+}\},\ \hat{\theta}_j^{A^+}=\{\hat{\theta}_1^{A^+},\hat{\theta}_2^{A},\ldots\hat{\theta}_K^{A^+}\},\ldots,\hat{\theta}_j^{AB^-}=\{\hat{\theta}_1^{AB^-},\hat{\theta}_2^{AB^-},\ldots\hat{\theta}_K^{AB^-}\}$ for a given state $j=1,\ldots,K$. Given this, a smaller rate of infection occurring in a state is an indication of a lesser probability of getting that infection of that blood type.

The deviance information criterion (DIC) is used as a measure of model comparison and adequacy. Mathematically, it is given as DIC $(K)=D\left(\hat{\theta}_K^B,K\right)+2\tau$, where $D\left(\hat{\theta}_K^B,K\right)$ is the deviance measure equal to minus twice the log-likelihood, , $\hat{\theta}_K^{A^+}$ is the posterior mean of the model K for blood type, and τ are the numbers of effective parameters for model K. Smaller DIC values indicates a better fitting model.

In this study, the Monte Carlo (MC) error, trace plot, and autocorrelations were monitored to check the convergence of the analyses. Monte Carlo errors measure the variation of the mean of the parameter of interest due to simulation. Therefore, a lower MC error compared with the corresponding estimated posterior standard deviation indicates that the posterior mean was estimated with high precision. The trace plot shows the generated values versus each iteration number. When there is an indication of no patterns or irregularities, we assumed convergence of the algorithm. The autocorrelation plots the chain of each parameter of interest. In this study, the plot was done using lag from 1 to 50 to monitor the autocorrelations. When a lower autocorrelation is observed for all parameters at a certain lag, then that would imply that an independent sample can be obtained by re-running the algorithm with **a thin-set** equal to that lag as an update.

In selecting starting values for this study, quantiles of observation were used, which implies that when considering two states' independent mean, i.e., $K=2$, the lower and upper quantiles of the sample mean were used. However, when considering $K=3$, the lower quantile, the median, and the upper quantile were used as starting values. Again, for transition probabilities, a common starting value of 0.05 was assigned to all off-diagonal transition probabilities

Zucchini et al., (2018).

3. Result and Discussion

This section first considers the analysis of the data and then follows the discussion of the findings.

3.1 Result

The Bayesian Poisson – Hidden Markov Model (BP-HMM) developed above is applied to a series of COVID-19 incidence counts of blood types distributions for European (EU) and African (AF) countries. In the study of Miotto et al., [8] the percentage distribution of COVID-19 incidences per blood type for Seventy-Eight (78) countries were provided. With this information, the current study extracted the data for European (EU) and African (AF) countries using the World Health Organization dashboard on COVID-19 as of 1st September 2021. These data sets were used for this study for two reasons, first, to assess whether the model will select the same hidden states for each blood type distribution across these two continents, and second, to compare the state-dependent mean of infection occurrence within and across each continent regarding blood type distribution. This comparison is feasible because the study uses the Markov Chain Monte Carlo (MCMC) sampling procedure by employing Gibbs sampling with 98,000 iterations with 2000 burn-in.

Table 2 is the prior probability estimation for EU and AF based on data from WHO as of 1st September 2021 for COVID-19 cases per blood type. The result in table 2 shows that the probability rate within and across each geographical area per blood type differs as individuals with blood type A+ in the EU have a higher infection rate while individuals with blood type O+ have a higher infection rate in AF. In addition, the summary statistic shows that the sample variance in each blood type is greater than the sample mean, which is a clear indication of overdispersion (See Appendix).

Table 2. Probability of COVID-19 cases per blood type for European (EU) and Africa (AF) countries

	Europe (EU)	Africa (AF)	EU and AF
Blood Type	Probability of Blood Type	Probability of Blood Type	The proportion of COVID-19 cases per Blood Type (EU and AF)
O^+	0.334	0.418	0.376
A^+	0.346	0.298	0.322
B^+	0.116	0.141	0.129
AB^+	0.045	0.034	0.039
O^-	0.062	0.049	0.055
A^-	0.068	0.037	0.053
B^-	0.020	0.016	0.018
AB^-	0.009	0.007	0.008

Figure1 to figure6 are the plots of the Deviance Information Criterion (DIC) against the number of states of the BP-HMM. The figures show that the lower DIC with the corresponding states selected for each blood type distribution within the number of states. Table 3 presents the relevant model comparison for model selection. The table τ represents the number of parameters while K the model number of hidden states. For BP-HMM $= K^2$. Here the model considered the lower DIC selects the most suitable one. The Figures and Table 3 show that blood types O^+, A^+, AB^+, O^-, A^-, B^-, $AB^-$for both EU and AF select five [5] states to fit the COVID-19 data. Meanwhile, blood type B^+ selects Six [6] states for EU countries and four [4] states for AF countries.

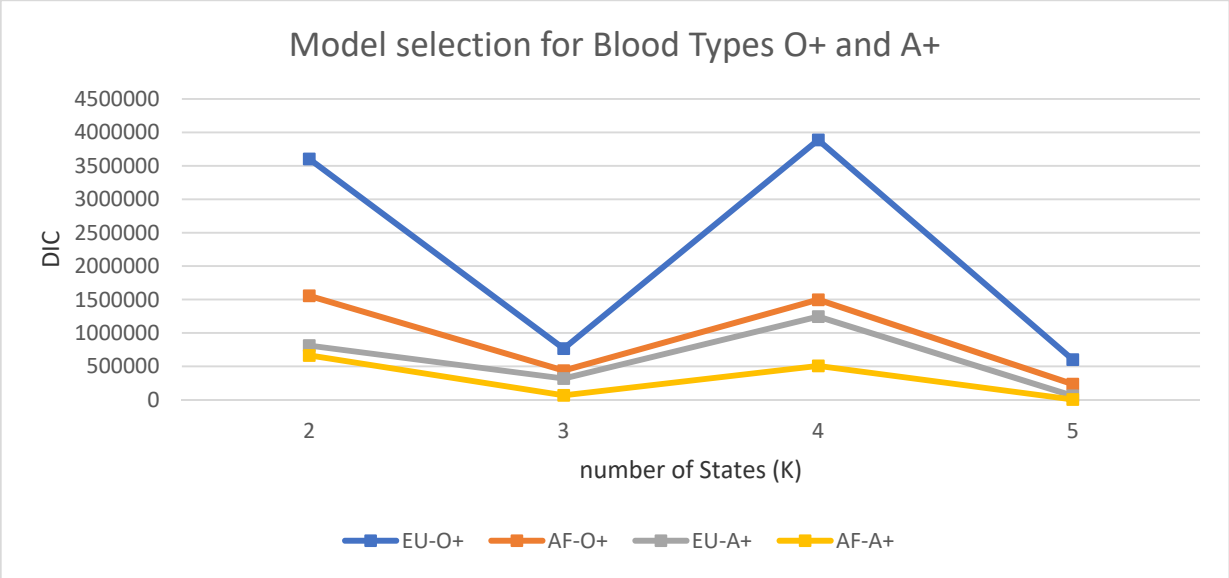

Figure 1. Deviance Information Criterion model selection for blood types O+ and A+

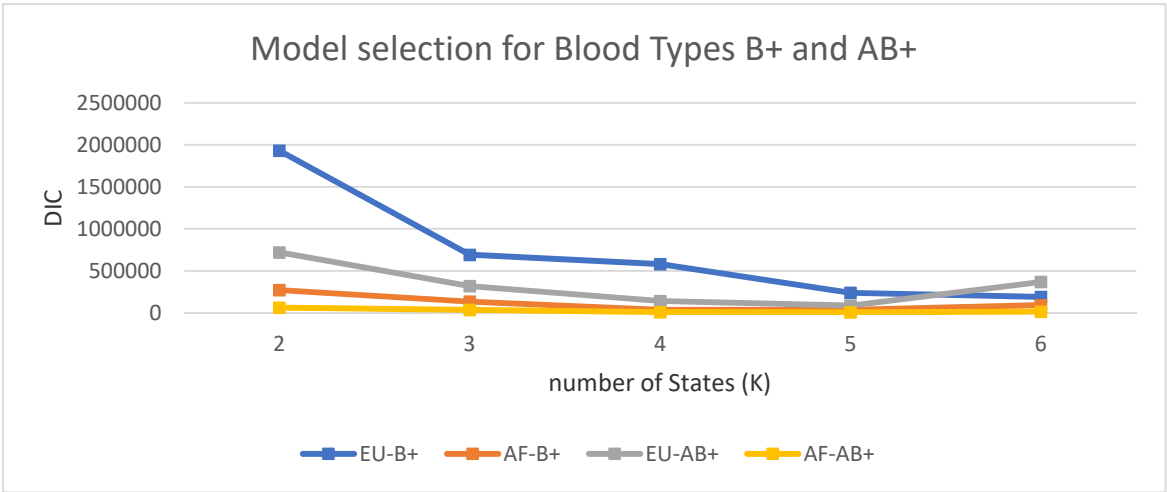

Figure 2. Deviance Information Criterion model selection for blood types B+ and AB+

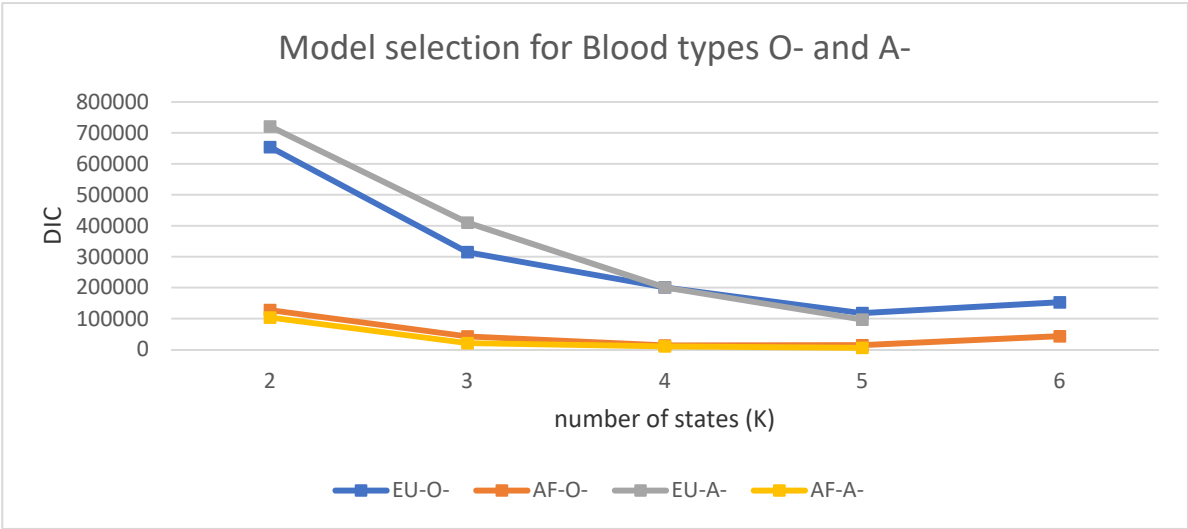

Figure 3. Deviance Information Criterion model selection for blood types O- and A-

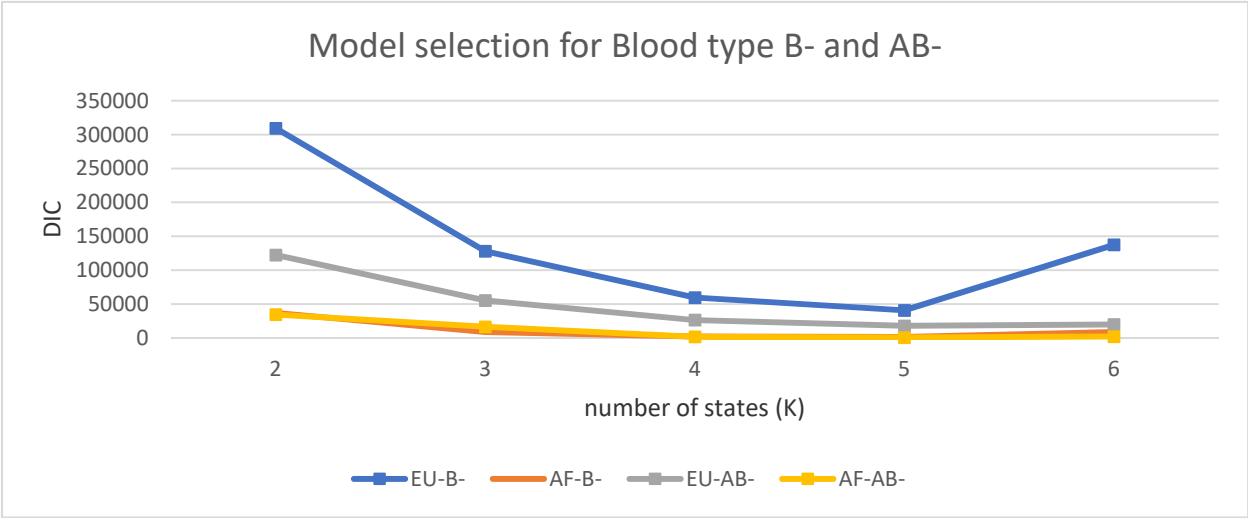

Figure 4. Deviance Information Criterion model selection for blood types B- and AB-

Table 3. Summary results of model selection for COVID-19 cases of blood type

Blood Type	(BP-HMM) Selected State (K)	τ	Deviance (EU)	Deviance (AF)	DIC (EU)	DIC (AF)
O^+	5	25	665099.30	67315.38	665149.30	67365.80
A^+	5	25	507933.30	50848.14	507983.30	5134.14
B^+	6(4)	36(16)	190439.30	35537.60	190511.30	35569.60
AB^+	5	25	86162.27	7104.46	86212.27	7154.46
O^-	5	25	117735.00	12938.36	117785.00	12970.36
A^-	5	25	96798.14	5515.95	96848.14	5565.95
B^-	5	25	40621.00	1320.46	40671.00	1370.46
AB^-	5	25	17771.03	535.10	17821.03	585.10

The posterior summary statistics for each mean parameter are presented in Table 4 to Table 11. Each table provides the estimated posterior mean for each blood type, standard deviation (SD), Monte Carlo (MC) error, the percentage distribution of MC error compared with the SD, quantiles including median, and the total number of iterations (generated sample size) and the number of iterations that the generated sample started which is the burin period. In all, the estimated posterior mean was estimated with high precision as the MC error in comparison with each corresponding estimated posterior standard deviation (MC error %) is low in all cases. Therefore, for a sample of 98000 iterations after discarding 2000 iterations as a burin, each MC error is lower than the corresponding standard deviation given a lower MC error% of 0.4239% on the average for all posterior mean estimates for each blood type distribution of COVID-19 cases. The Monte Carlo variability of the transition probabilities of the posterior summaries is all low in comparison with their corresponding standard deviations (see Appendix), making the estimated transition probability with high precision.

Table 4. Posterior summary of the estimated mean for blood type O+

$\hat{\theta}_j^{O+}$	Mean	SD	MC error	MC error%	Val2.5%	Median	Val97.5%	start	sample
				EU O+					
[1]	87750.0	104.4	0.4567	0.4374	87550.0	87750.0	87960.0	2001	98000
[2]	322700.0	171.1	0.6086	0.3556	322400.0	322700	323100.0	2001	98000
[3]	830600.0	644.9	3.755	0.5822	8294400	830600.0	831900.0	2001	98000
[4]	1615000	731.1	3.278	0.4483	1614000	1615000	1616000	2001	98000
[5]	2066000	992.9	3.214	0.3236	2064000	2066000	2068000	2001	98000
				AF O+					
[1]	20260.0	63.80	0.2503	0.3923	20140.0	20260.0	20380.0	2001	98000
[2]	107800.0	147.6	0.4878	0.3304	107500	107800.0	108100.0	2001	98000
[3]	362100.0	600.4	2.4900	0.4147	360900.0	362100.0	363300.0	2001	98000
[4]	737600.0	6187.0	26.059	0.4212	577500.0	736400.0	949300.0	2001	98000
[5]	1000000.0	964.1	2.9560	0.3066	993600.0	1000000.0	1002000.0	2001	98000

Table 5. Posterior summary of the estimated mean for blood type A+

$\hat{\theta}_j^{A+}$	Mean	SD	MC error	MC error%	Val2.5%	Median	Val97.5%	start	sample
				EU A+					
[1]	92070.0	107.6	0.462	0.4293	91860.0	92070.0	92290.0	2001	98000
[2]	321800.0	189.9	0.7642	0.4024	321400.0	321800.0	322100.0	2001	98000
[3]	746200.0	431.9	1.9880	0.4602	745300.0	746200.0	747000.0	2001	98000
[4]	1612000.0	730.8	3.0850	0.4221	1611000.0	1612000.0	1614000.0	2001	98000
[5]	2164000.0	1020.0	2.9790	0.2920	2162000.0	2164000.0	2166000.0	2001	98000
				AF A+					
[1]	10410.0	35.7.0	0.2125	0.5956	8012.0	10580.0	10670.0	2001	98000
[2]	56220.0	362.1	2.2482	0.6209	32020.0	57930.0	58150.0	2001	98000
[3]	223300.0	2910.2	18.770	0.6450	71410.0	254600.0	256000.0	2001	98000
[4]	302500.0	3037.4	15.879	0.5228	254300.0	282700.0	433000.0	2001	98000
[5]	820900.0	874.7	2.8700	0.3281	819200.0	820900.0	822600.0	2001	98000

Table 6. Posterior summary of the estimated mean for blood type B+

$\hat{\theta}_j^{B+}$	Mean	SD	MC error	MC error%	Val2.5%	Median	Val97.5%	start	sample
				EU B+					
[1]	17,600.0	44.7	0.2866	0.6412	17450.0	17650.0	17700.0	2001	98000
[2]	82,500.0	332.0	2.1354	0.6432	82300.0	82500.0	825500.0	2001	98000
[3]	110,820.0	472.0	3.0387	0.6438	109620.0	110820.0	120000.0	2001	98000
[4]	339,400.0	79.0	0.5008	0.6340	332300.0	347300.0	354000.0	2001	98000
[5]	729,400.0	897.0	5.7712	0.6434	721400.0	738400.0	740000.0	2001	98000
[6]	1,211,000.0	2265.0	14.5821	0.6438	1209600.0	1221000.0	131,100.0	2001	98000
				AF B+					
[1]	9762.0	40.24	0.1392	0.3459	9683.0	9762.0	9841.0	2001	98000
[2]	47480.0	109.4	0.3800	0.3473	47270.0	47480.0	47700.0	2001	98000
[3]	122400.0	352.4	1.5890	0.4509	121700.0	122400.0	123100.0	2001	98000
[4]	307800.0	534.3	1.8090	0.3385	306800.0	307800.0	308900.0	2001	98000

Table 7. Posterior summary of the estimated mean for blood type AB+ 965384

$\hat{\theta}_j^{AB^+}$	Mean	SD	MC error	MC error%	Val2.5%	Median	Val97.5%	start	sample
EU AB+									
[1]	11400.0	37.69	0.1617	0.4290	11330.0	11400.0	11480.0	2001	98000
[2]	45160.0	67.15	0.2773	0.4129	45030.0	45160.0	45290.0	2001	98000
[3]	116600.0	171.0	0.7765	0.4540	116300.0	116600.0	116600.0	2001	98000
[4]	185500.0	247.6	0.9321	0.3764	185100.0	185500.0	186000.0	2001	98000
[5]	448500.0	642.4	2.093	0.3258	447200.0	448500.0	449700.0	2001	98000
AF AB+									
[1]	1858.0	17.52	0.0627	0.3578	1823.0	1857.0	1892.0	2001	98000
[2]	8607.0	53.3	0.2090	0.3921	8502.0	8607.0	8712.0	2001	98000
[3]	15340.0	123.5	0.5501	0.4454	15100.0	15340.0	15580.0	2001	98000
[4]	35100.0	187.0	0.8670	0.4636	34730.0	35100.0	35470.0	2001	98000
[5]	76960.0	265.6	0.8774	0.3303	76440.0	76960.0	77480.0	2001	98000

Table 8. Posterior summary of the estimated mean for blood type O-

$\hat{\theta}_j^{O^-}$	Mean	SD	MC error	MC error%	Val2.5%	Median	Val97.5%	start	sample
EU O-									
[1]	15230.0	43.8	0.1938	0.4424	15140.0	15230.0	15310	2001	98000
[2]	56730.0	75.6	0.2893	0.3826	56590.0	56740.0	56880.0	2001	98000
[3]	144300.0	219.3	1.0670	0.4865	143900.0	144300.0	144800.0	2001	98000
[4]	277000.0	371.0	2.101	0.5663	276300.0	277000.0	277700.0	2001	98000
[5]	379500.0	352.7	1.094	0.3101	378800.0	379500.0	380100.0	2001	98000
AF O-									
[1]	2118.0	16.3	0.0537	0.3294	2086.0	2118.0	2150.0	2001	98000
[2]	11810.0	77.2	0.2906	0.3764	11660	11810.0	11960.0	2001	98000
[3]	38520.0	196.4	0.7197	0.3664	38140.0	38520.0	38910.0	2001	98000
[4]	102000.0	1287.0	3.9961	0.3105	59040.0	100100.0	151500.0	2001	98000
[5]	153900.0	376.8	1.1470	0.3044	153200.0	153900.0	154700.0	2001	98000

Table 9. Posterior summary of the estimated mean for blood type A-

$\hat{\theta}_j^{A^-}$	Mean	SD	MC error	MC error%	Val2.5%	Median	Val97.5%	start	sample
EU A-									
[1]	17470.0	46.9	0.1948	0.4153	17380.0	17470.0	17560.0	2001	98000
[2]	62670.0	88.85	0.3603	0.4055	62490.0	62670.0	62840.0	2001	98000
[3]	136700.0	184.8	0.8754	0.4737	136400.0	136700.0	137100.0	2001	98000
[4]	250000.0	289.0	1.494	0.5169	249400.0	250000.0	250600.0	2001	98000
[5]	389500.0	355.8	1.173	0.3296	388800.0	389500.0	390200.0	2001	98000
AF A-									
[1]	985.1	11.1	0.0356	0.3207	963.3	985.1	1007.0	2001	98000
[2]	5950.0	54.7	0.1973	0.3606	5843.0	5950.0	6057.0	2001	98000
[3]	25600.0	165.8	0.9346	0.5637	14340.0	26510.0	26850.0	2001	98000
[4]	53590.0	1326.0	6.8129	0.5138	26400.0	46510.0	103500.0	2001	98000
[5]	128300.0	344.8	1.0970	0.3181	127600.0	128300.0	128900.0	2001	98000

Table 10. Posterior summary of the estimated mean for blood type B-

$\hat{\theta}_j^{B^-}$	Mean	SD	MC error	MC error%	Val2.5%	Median	Val97.5%	start	sample
EU B-									
[1]	6840.0	24.9	0.1008	0.4048	6792.0	6840.0	6889.0	2001	98000
[2]	21150.0	54.8	0.2330	0.4251	21040.0	21150.0	21260.0	2001	98000
[3]	57490.0	106.8	0.4332	0.4056	57280.0	57490.0	57700.0	2001	98000
[4]	87900.0	209.6	0.8567	0.4087	87490.0	87490.0	88310.0	2001	98000
[5]	205000.0	434.7	1.398	0.3216	204200.0	205000.0	205900.0	2001	98000
AF B-									
[1]	301.8	7.809	0.0292	0.3739	286.7	301.7	317.2	2001	98000
[2]	1659.0	15.40	0.0508	0.3301	1595.0	1636.0	1932.0	2001	98000
[3]	3882.0	150.80	0.5446	0.3612	2964.0	3075.0	12890.0	2001	98000
[4]	14240.0	312.90	1.1011	0.3519	1262.0	12850.0	34720.0	2001	98000
[5]	51310.0	218.1	0.6934	0.3179	50880.0	51310.0	51740.0	2001	98000

Table 11. Posterior summary of the estimated mean for blood type AB-

$\hat{\theta}_j^{AB^-}$	Mean	SD	MC error	MC error%	Val2.5%	Median	Val97.5%	start	sample
EU AB-									
[1]	2544.0	17.83	0.0813	0.4559	17380.0	17470.0	17560.0	2001	98000
[2]	8336.0	28.88	0.1048	0.3628	62490.0	62670.0	62840.0	2001	98000
[3]	23090.0	68.00	0.2627	0.3863	136400.0	136700.0	137100.0	2001	98000
[4]	38430.0	195.90	1.062	0.5421	249400.0	250000.0	250600.0	2001	98000
[5]	68120.0	181.0	0.5455	0.3013	388800.0	389500.0	390200.0	2001	98000
AF AB-									
[1]	83.0	3.463	0.0123	0.3551	76.35	82.96	89.89	2001	98000
[2]	466.1	15.32	0.0539	0.3518	436.6	495.9	496.8	2001	98000
[3]	3089.0	78.05	0.189	0.2421	2964.0	3078.0	3278.0	2001	98000
[4]	4967.0	4581.0	25.50	0.5566	3314.0	3434.0	21420.0	2001	98000
[5]	25660.0	155.2	0.4638	0.2988	25350.0	25660.0	25960.0	2001	98000

The algorithm is assumed convergence as there is no indication of patterns or irregularities in samples of the trace plot. Moreover, the autocorrelation observed is very low (at lag below 50) for both the estimated posterior mean and the transition probabilities.

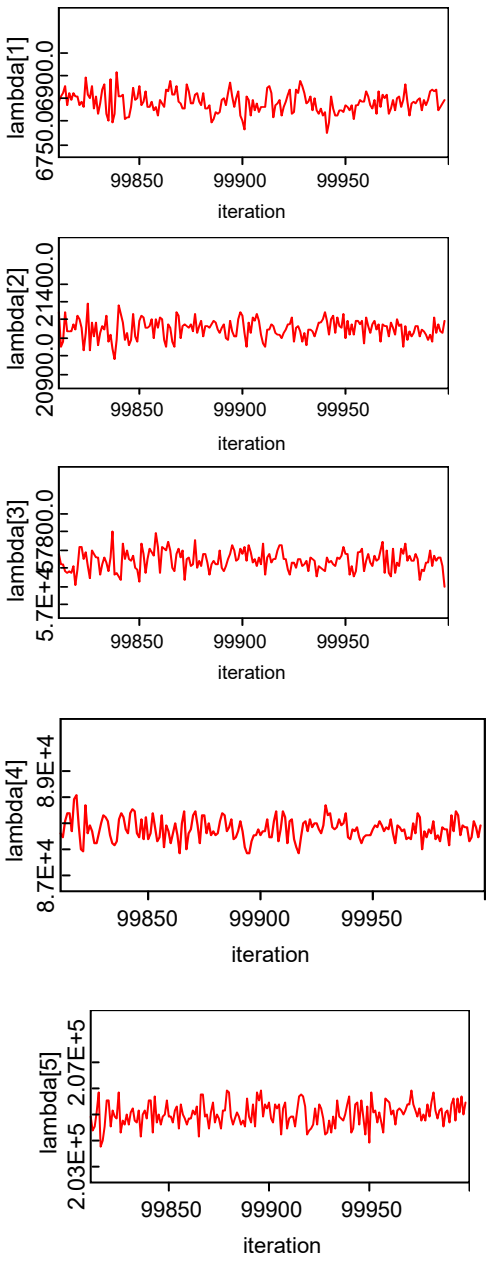

Figure 5. Trace plots for estimated posterior mean for the state [1] to state [5]

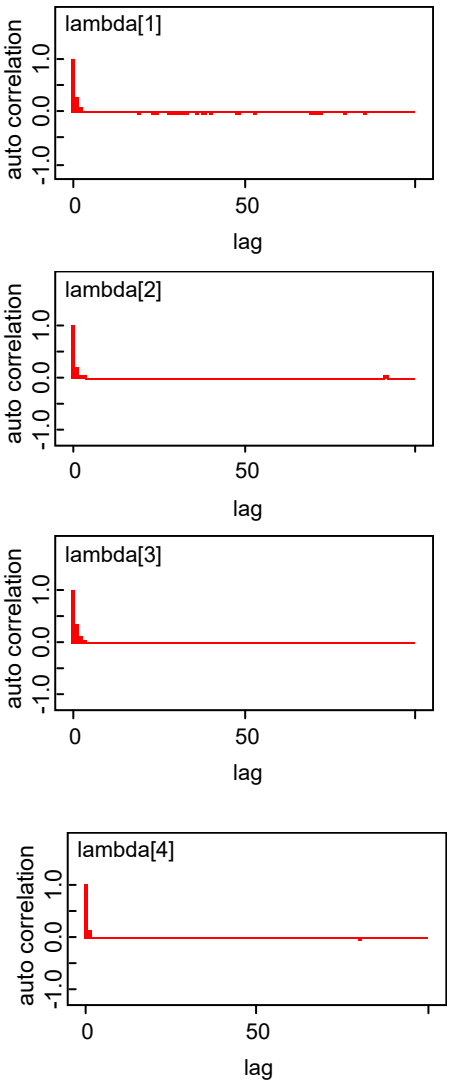

Figure 6. Autocorrelation for estimated posterior mean for the state [1] to state [5]

Table 12 and Table 13 give the parameters for the estimated posterior mean and infection rate within the selected states for both EU and AF. Both tables indicate a higher value for all EU data sets compared to AF. The Table results clearly distinguish between the two continents regarding blood type distribution for COVID-19 cases. The total rate of COVID-19 infection occurrence is higher in the EU compared to AF.

Table 12. Summary statistics of blood types by states for European (EU) countries

Blood Type	State (1)	State (2)	State (3)	State (4)	State (5)	State (6)	**Total**
$\hat{\theta}_i^{EU-O^+}$	87,750.00	322,700.00	830,600.0	1,615,000.00	2,066,000.00	-	4,922,050.00
$\hat{\theta}_i^{EU-O^-}$	15,230.00	56,730.00	144,300.00	277,000.00	379,500.00	-	872,760.00
Total	102,980.00	379,430.00	974,900.00	1,892,000.00	2,445,500.00		5,794,810.00
$\hat{\theta}_i^{EU-A^+}$	92,070.00	321,800.00	746,200.00	1,612,000.00	2,164,000.00	-	4,936,070.00
$\hat{\theta}_i^{EU-A^-}$	17,470.00	62,670.00	136,700.00	250,000	389,500.00	-	856,340.00
Total	109,540.00	384,470.00	882,900.00	1,862,000.00	2,553,500.00		5,792,410.00
$\hat{\theta}_i^{EU-B^+}$	17,600.00	82,500.00	110,820.00	339,400.00	729,400.00	1,211,000.00	2,490,720.00
$\hat{\theta}_i^{EU-B^-}$	6,840.00	21,150.00	57,490.00	87,900.00	205,000.00	-	378,380.00
Total	24,440.00	103,650.00	168,310.00	427,300.00	934,400.00	1,211,000.00	2,869,100.00
$\hat{\theta}_i^{EU-AB^+}$	11,400.00	45,160.00	116,600.00	185,500.00	448,500.00	-	807,160.00
$\hat{\theta}_i^{EU-AB^-}$	2,544.0	8,336.00	23,009.00	38,430.00	68,120.00	-	140,439.00
Total	13,944.00	53,496.00	139,609.00	223,930.00	516,620.00	-	947,599.00

Table 13. Summary statistics of blood types by state of African (AF) countries

Blood Type	State (1)	State (2)	State (3)	State (4)	State (5)	**Total**
$\hat{\theta}_i^{AF-O^+}$	20,260.00	107,780.00	362,100.00	737,000.00	1,000,000.00	2,227,140.00
$\hat{\theta}_i^{AF-O^-}$	2118.00	11810.00	38520.00	102000.00	153900.00	308,348.00
Total	22,378.00	119,590.00	400,620.00	839,000.00	1,153,900.00	2,535,488.00
$\hat{\theta}_i^{AF-A^+}$	10,410.00	56,220.00	223300.00	302,500.00	820,900.00	1,413,330.00
$\hat{\theta}_i^{AF-A^-}$	985.10	5,950.00	25600.00	53590.00	128,300.00	214,425.10
Total	11,395.10	62,170.00	248,900.00	356,090.00	949,200.00	1,627,755.10
$\hat{\theta}_i^{AF-B^+}$	9,762.00	47,480.00	122,400.00	307,800.00	-	487,442.00
$\hat{\theta}_i^{AF-B^-}$	301.80	1,639.00	3,882.00	14240.00	51,310.00	71,372.80
Total	10,063.80	49,119.00	126,282.00	322,040.00	51,310.00	558,814.80
$\hat{\theta}_i^{AF-AB^+}$	1,858.00	8,607.00	15,340.00	35,100.00	76,960.00	137,865.00
$\hat{\theta}_i^{AF-AB^-}$	83.00	466.10	3089.00	4967.00	25660.00	34,265.10
Total	1,941.00	9,073.10	18,429.00	40,067.00	102,620.00	172,130.10

Table 14 shows the percentage distribution of infection rates within each state. The Table shows that, on average, the blood types from the EU exhibit a higher percentage from state (1) to state (4) as compared to AF, with a significant difference in the state (5). In addition, the estimated posterior transition probabilities show that the most significant transition occurs in states (1) for both EU and AF blood type distribution of COVID -19; this implies that the probability of a patient remaining in state (1) when in the state (1) is high otherwise, most patients are transited to state (2) or state (3), and comparing the transition probabilities across blood types there is no significant difference between the two geographical areas (See Appendix).

Table 14. Estimated percentage rate of infection per state of blood types and Rhesus for EU and AF countries for COVID-19

Blood Type	State (1)	State (2)	State (3)	State (4)	State (5)	State (6)
O+	1.78(0.91)	6.55(4.84)	16.83(16.26)	32.64(33.09)	42.20(44.90)	
O-	1.74(0.69)	6.51(3.83)	16.53(12.49)	31.74(33.08)	43.48(49.91)	
A+	1.87(0.74)	6.52(3.98)	15.11(15.80)	32.66(21.40)	43.84(58.08)	
A-	2.04(0.46)	7.33(2.77)	15.96(11.94)	29.19(24.99)	45.48(59.84)	
B+	0.71(2.00)	3.31(9.74)	4.45(25.11)	13.63(63.14)	29.28(0.00)	48.62(0.00)
B-	1.81(0.42)	5.59(2.29)	15.19(5.45)	23.23(19.95)	54.18(71.89)	
AB+	1.41(1.35)	5.59(6.24)	14.45(11.13)	22.98(25.46)	55.56(55.82)	
AB-	1.81(0.24)	5.94(1.36)	16.38(9.01)	27.36(14.50)	48.51(74.89)	

Table 15 is the estimated percentage rate of infection per state of ABO blood type and their rhesus factors for EU and AF. The order is EU(AF), meaning the first number is the percentage rate of infection for Europe, and the second is that of Africa. Assessing each blood type distribution across states shows an increasing order as the states increase for all blood types within EU and AF. However, assessing each state across blood type distribution shows there is not much difference across blood types for both EU and AF. Meanwhile, the percentage distribution of blood type for COVID-19 is higher in the EU than in AF. Again, the table shows that at the lowest state [1], blood types A- and A+ are the first and second highest estimated percentage rate of infection, respectively, in the EU, while blood types B+ and O+ are the first and the second highest estimated percentage rate of infection respectively in AF. However, at the highest state [5] (excluding blood type B+), the blood type with the first and second highest percentage rate of infections is AB+ and B- respectively for EU, while AB- and B- is the estimated percentage rate of infection in the first and second order for AF. In state [5], the blood type with the first and second lowest infection rate is O+ and O- respectively for both EU and AF (exclude blood type B+ because there is nothing to compare).

Table 15. Estimated percentage rate of infection per state of blood types and Rhesus for EU and AF countries for COVID-19

Blood Type	State [1]	State [2]	State [3]	State [4]	State [5]	State [6]
O+	1.78(0.91)	6.55(4.84)	16.83(16.26)	32.64(33.09)	42.20(44.90)	
O-	1.74(0.69)	6.51(3.83)	16.53(12.49)	31.74(33.08)	43.48(49.91)	
A+	1.87(0.74)	6.52(3.98)	15.11(15.80)	32.66(21.40)	43.84(58.08)	
A-	2.04(0.46)	7.33(2.77)	15.96(11.94)	29.19(24.99)	45.48(59.84)	
B+	0.71(2.00)	3.31(9.74)	4.45(25.11)	13.63(63.14)	29.28(0.00)	48.62(0.00)
B-	1.81(0.42)	5.59(2.29)	15.19(5.45)	23.23(19.95)	54.18(71.89)	
AB+	1.41(1.35)	5.59(6.24)	14.45(11.13)	22.98(25.46)	55.56(55.82)	
AB-	1.81(0.24)	5.94(1.36)	16.38(9.01)	27.36(14.50)	48.51(74.89)	

Table 16 is the estimated percentage rate of infection per state of ABO blood type (merging both rhesus factors). The table indicates that blood type A has the highest infection rate at the lowest state [1] when considering EU data sets, while blood type B has the highest infection rate for AF. Conversely, in the highest state [5], blood type AB has the highest infection rate for both EU and AF, and the lowest infection rate is blood type O (excluding blood type B).

The estimated posterior transition probabilities show that the most significant transition occurs in states [1] for both EU and AF blood type distribution of COVID -19. This finding implies that the probability of a patient remaining in the state [1] when in the state [1] is high; otherwise, most patients are transited to state [2] or state [3] and comparing the transition probabilities across blood types there is no significant difference between the two geographical areas (See Appendix).

Table 16. Estimated percentage rate of infection per state of blood types for EU and AF countries for COVID-19

Blood Type	State (1)	State (2)	State (3)	State (4)	State (5)	State (6)
O	1.76(0.80)	6.53(4.34)	16.68(14.38)	32.19(33.08)	42.84(47.41)	
A	1.96(0.60)	6.93(3.38)	15.54(13.87)	30.93(23.20)	44.66(58.96)	
B	1.26(1.21)	4.45(6.02)	9.82(15.28)	18.43(41.55)	41.73(35.95)	24.31(0.00)
AB	1.61(0.80)	5.77(3.80)	15.42(10.07)	25.17(19.98)	52.04(65.36)	

3.2 Discussion

The BP-HMM was applied to the blood type distribution of COVID-19 infection data sets of European (EU) and African (AF) countries, which is this study's third objective. The main reasons for applying BP-HMM to these data sets were to identify the number of hidden states in these geographical areas and assess the rate of infection based on the states selected by the models.

The estimated posterior mean was highly precise as the MC error compared with each corresponding estimated posterior standard deviation (MC error %) was low in all cases. Therefore, for a sample of 98000 iterations after discarding 2000 iterations as a burin, each MC error was lower than the corresponding standard deviation given a lower MC error% of an interval 0.2971% - 1.5236%. Furthermore, the algorithm assumed convergence as there was no indication of patterns or irregularities in samples of the trace plot. Therefore, the developed model performs better in estimating parameters of Poisson hidden Markov models.

The findings indicate that the EU data sets of blood type distribution for COVID-19 fitted into a minimum of five (5) and a maximum of six (6) hidden states. However, The AF data sets of COVID-19 fitted into a minimum of four (4) and a maximum of five (5) hidden states. Therefore, if we assume the defined hidden states by Prabhu & Subramanyam (2020), then we can infer that per the available data by WHO as of 1st Sept 2021, this study assumes that for individuals with blood type B+, having six(6) hidden states from EU the data set is being governed by "Castastrphpe-2"(state[1]), "Catastrophe-1"(state[2]), "Detected"(state[3]), "Symptomatic"(state [4]), "Infected" (state[5]), "Healthy"(state[6]). However, for individuals with blood types $O^+, O^-, A^+, A^-, AB^+, AB^-, B^-$ and having five (5) hidden states[5], the data sets is governed by “Catastrophe-1”(state[1]), “Detected”(state[2]), “Symptomatic”(state[3]), "Infected"(state[4]) and "Healthy"(state[5]) for both EU and AF. Again, the estimated posterior mean for each blood type indicates an increasing

order from "Catastrophe- 2" (state [1]) to" Healthy" (state [6]) and "Catastrophe-1(state [1]) to "Healthy" (state [5]) for EU and AF respectively. However, comparing the estimated posterior mean for each blood type across the two geographical areas show a higher rate for EU at "Catastrophe-2" (state [1]) to "Infected" (state [4]) while AF has a higher rate at "Healthy" (state [5]). The transition probabilities indicate that the probability of a patient in "Catastrophe-2" (state [1]) state and to remain that state is high; otherwise, most patients are transited to either "Catastrophe-1" (state 2) state or "Detected" (state 3) state for both EU and AF for most blood types (see appendix).

The study also estimated the percentage rate of infection of each blood type across states and discovered an increasing order as the state increased for all blood types within EU and AF. Meanwhile, assessing each state across blood type distribution shows there is not much difference across blood types for both EU and AF. In all, the percentage distribution of blood type for COVID-19 is higher in the EU than in AF. Further, the findings show that individuals with blood type A are at a higher risk of "Catastrophe-1" (state [1]) of COVID-19 in European countries, and individuals with blood type B are at a higher risk "Catastrophe-1" (state [1]) in African countries. However, individuals with blood type O are at the lowest risk of attracting COVID-19 and would be "Healthy" (state [5]) in both European and African counties. The current study support studies such as: El-Shitany et al. (2021); Zhao et al.(2020); Fan et al. (2020); Muniz-Diaz et al. (2020); Ad'hiah et al. (2020) and Obayes AL-Khikani (2020). Most of these studies were conducted in European countries and associated the relationship between ABO blood types and COVID-19 infections. Again, these studies concluded that individuals with blood type A were at higher risk of COVID-19 and individuals with blood type O were at a lower risk of COVID-19, as this current study has suggested for persons living in Europe or countries with similar environmental conditions like Europe.

As Miotto et al., (2021) suggested, population-dependent antigen distribution might play a role in the geographically heterogeneous spreading of COVID-19 infection with blood frequency. In addition, other latent variables might contribute to the spread of the infection since the findings across the two geographical areas give a different infection rate per blood type distribution. Therefore, as Hedell et al.,(2018) suggested, a potentially sensitive way to detect disease outbreaks is syndromic surveillance, which is monitoring the number of syndromes reported in the population of interest and comparing it to the baseline rate. Finally, concluding the outbreak using statistical methods Hedell et al., (2018).

4. Conclusion

In conclusion, as a follow-up from Miotto et al.,(2021) other population-dependent antigen distribution might play a role in the geographically heterogeneous infection spreading of COVID-19 infection with blood frequency. This study has indicated that geographical area might contribute to the spread and infection rate of the COVID-19 pandemic, therefore as we associate the spread of the infection with blood frequency, we need to consider other factors such as weather conditions, environmental conditions, lifestyle, population density, infection rate, etc. This current study is in line with the study of Hedell et al.,(2018)who concluded in their study that before assessing the probability of an outbreak, pieces of information such as the total count of syndromes, clustering of syndromes in space and time, seasonality of the infection and others needed to be considered. Therefore, the study findings suggest that using four variable names such as "Active," "Recovered," Dead," and "Inactive" to define several counted cases by policymakers of COVID-19 infection might not be adequate to classify the distinction of number cases in these two geographical areas. In addition, there might be other hidden states within EU and AF countries, and the number of hidden states might differ from one geographical area. Therefore, the study recommends further studies using additional geographical areas to affirm this current study.

This study is a follow-up of Miotto et al., (2021), who recommended further studies as to whether other population-dependent antigen distribution may play a role in the geographically heterogeneous infection spreading of COVID-19 infection with blood frequency.

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Data Availability

The data that support the findings of this study is openly available in

WHO: Coronavirus (COVID-19) Dashboard, https://covid19.who.int

Consent

No written consent has been obtained from the patients as there are no patient identifiable data included in this study.

Conflict of Interest

The authors declare no conflicts of interest

Appendix

Table A.1: Summary Statistics of COVID-19 per blood type for European (EU) Countries

Blood Type	Summary Statistics						
	Minimum	1st Quartile	Median	Mean	3rd Quartile	Maximum	Variance
O+	26,485	146,017	307,654	584,742	748,710	2,360,555	432,692,066,623
A+	27,998	142,946	347,506	613,670	752646	2,426,126	464,045,500,322
B+	6810	56820	98738	204542	318035	1383793	82,133,136,454
AB+	3026	19424	41300	78855	114077	484327	10233284013
O-	4540	24259	50677	109419	137633	436257	16274586663
A-	4540	29827	70709	120678	164285	458997	16372282945
B-	1513	8070	17991	34922	49214	221406	2149888111
AB-	756	3939	7930	15356	21202	76108	359935368

Table A. 2: Summary Statistics of COVID-19 per blood type for African (AF) Countries

Blood Type	Summary Statistics						
	Minimum	1st Quartile	Median	Mean	3rd Quartile	Maximum	Variance
O+	8085	23744	81012	173563	127203	1080524	91063173725
A+	2894	11910	37667	123691	73346	886583	62439079264
B+	2065	9188	28688	58616	53661	332469	8600666050
AB+	326	2109	4149	14210	12048	83117	565650025
O-	136	1152	3652	20442	10505	166234	2223241465
A-	41	647	1500	15404	5856	138529	1557269924
B-	27	326	1344	6614	2355	55412	248332655
AB-	14	71	151	2976	1199	27706	62092995

Table A.3: Posterior summary of the estimated transition probability for blood typeO^+, EU

	mean	sd	MC_error	val2.5pc	median	val97.5pc	start	sample
Gamma[1,1]	0.3015	0.1211	0.001072	0.09574	0.2914	0.5598	2001	98000
Gamma[1,2]	0.1632	0.1005	7.32E-4	0.02253	0.1454	0.4006	2001	98000
Gamma[1,3]	0.23	0.1126	8.836E-4	0.05414	0.216	0.4826	2001	98000
Gamma[1,4]	0.1526	0.09642	7.496E-4	0.01987	0.1346	0.3839	2001	98000
Gamma[1,5]	0.1527	0.09626	7.404E-4	0.02036	0.1343	0.3839	2001	98000
Gamma[2,1]	0.2575	0.1088	9.341E-4	0.07995	0.2467	0.4961	2001	98000
Gamma[2,2]	0.4189	0.1251	0.001202	0.1874	0.415	0.6679	2001	98000
Gamma[2,3]	0.0646	0.06074	4.337E-4	0.001791	0.04657	0.2261	2001	98000
Gamma[2,4]	0.1303	0.0834	6.941E-4	0.01754	0.1141	0.3335	2001	98000
Gamma[2,5]	0.1287	0.08362	6.856E-4	0.01697	0.112	0.3329	2001	98000
Gamma[3,1]	0.2796	0.1573	0.001233	0.04241	0.2572	0.6341	2001	98000
Gamma[3,2]	0.2984	0.1625	0.001243	0.04661	0.2786	0.6537	2001	98000
Gamma[3,3]	0.14	0.1207	9.871E-4	0.004147	0.1073	0.4482	2001	98000
Gamma[3,4]	0.1408	0.1222	9.068E-4	0.004186	0.1068	0.4507	2001	98000
Gamma[3,5]	0.1412	0.1224	9.547E-4	0.004115	0.1076	0.4557	2001	98000
Gamma[4,1]	0.2415	0.1409	9.748E-4	0.03523	0.2195	0.5637	2001	98000
Gamma[4,2]	0.3923	0.1624	0.001239	0.1071	0.3841	0.7234	2001	98000
Gamma[4,3]	0.1216	0.1077	7.7E-4	0.003528	0.09159	0.4	2001	98000
Gamma[4,4]	0.1231	0.1081	8.564E-4	0.003667	0.09305	0.4027	2001	98000
Gamma[4,5]	0.1215	0.1073	8.161E-4	0.003508	0.09172	0.3978	2001	98000
Gamma[5,1]	0.1379	0.1205	8.386E-4	0.004098	0.1044	0.4482	2001	98000
Gamma[5,2]	0.2972	0.1624	0.001212	0.04642	0.2768	0.6569	2001	98000
Gamma[5,3]	0.1412	0.1232	0.001006	0.004194	0.1074	0.457	2001	98000
Gamma[5,4]	0.283	0.1587	0.001261	0.04261	0.2615	0.6351	2001	98000
Gamma[5,5]	0.1408	0.1216	0.001002	0.00419	0.1076	0.4509	2001	98000

Table A.4: Posterior summary of the estimated transition probability for blood type A^+, EU

	Mean	sd	MC_error	val2.5pc	median	val97.5pc	start	sample
Gamma[1,1]	0.3017	0.1205	0.001018	0.09839	0.2917	0.5592	2001	98000
Gamma[1,2]	0.08323	0.07589	5.434E-4	0.002356	0.0615	0.2823	2001	98000
Gamma[1,3]	0.305	0.1231	9.008E-4	0.09772	0.2944	0.569	2001	98000
Gamma[1,4]	0.1552	0.0971	7.224E-4	0.02148	0.1368	0.3889	2001	98000
Gamma[1,5]	0.1548	0.09629	7.567E-4	0.02149	0.1373	0.3859	2001	98000
Gamma[2,1]	0.2053	0.1034	9.26E-4	0.04706	0.191	0.4411	2001	98000
Gamma[2,2]	0.3777	0.1282	0.00123	0.1493	0.371	0.6427	2001	98000
Gamma[2,3]	0.138	0.08792	7.113E-4	0.01855	0.1209	0.3511	2001	98000
Gamma[2,4]	0.1389	0.08869	6.988E-4	0.01822	0.122	0.3519	2001	98000
Gamma[2,5]	0.1401	0.0899	7.575E-4	0.01854	0.1227	0.3565	2001	98000
Gamma[3,1]	0.3615	0.1584	0.001288	0.09504	0.3488	0.6945	2001	98000
Gamma[3,2]	0.2702	0.1499	0.00125	0.0418	0.2505	0.6052	2001	98000
Gamma[3,3]	0.1212	0.107	8.765E-4	0.003457	0.09122	0.3961	2001	98000
Gamma[3,4]	0.1231	0.1091	8.647E-4	0.003597	0.09247	0.4054	2001	98000
Gamma[3,5]	0.1241	0.1102	8.875E-4	0.003508	0.09316	0.409	2001	98000
Gamma[4,1]	0.2397	0.141	0.001061	0.03489	0.2172	0.5645	2001	98000
Gamma[4,2]	0.3969	0.1635	0.0013	0.1098	0.3886	0.7291	2001	98000
Gamma[4,3]	0.1205	0.1067	7.65E-4	0.003519	0.09085	0.3965	2001	98000
Gamma[4,4]	0.1211	0.1076	8.955E-4	0.003465	0.0906	0.3967	2001	98000
Gamma[4,5]	0.1217	0.1077	8.284E-4	0.00352	0.09175	0.4012	2001	98000
Gamma[5,1]	0.1376	0.1203	8.713E-4	0.00414	0.1041	0.4463	2001	98000
Gamma[5,2]	0.3013	0.1629	0.001309	0.04782	0.283	0.6577	2001	98000
Gamma[5,3]	0.1378	0.1205	8.703E-4	0.004129	0.1044	0.446	2001	98000
Gamma[5,4]	0.2823	0.1594	0.001279	0.04216	0.2602	0.6401	2001	98000
Gamma[5,5]	0.1411	0.1213	0.001059	0.004047	0.1087	0.4503	2001	98000

Table A.5: Posterior summary of the estimated transition probability for blood type B^+, EU

	mean	sd	MC_error	val2.5pc	median	val97.5pc	start	sample
Gamma[1,1]	0.1643	0.102	9.346E-4	0.02266	0.1459	0.4068	2001	98000
Gamma[1,2]	0.226	0.1236	0.002843	0.03746	0.2101	0.5043	2001	98000
Gamma[1,3]	0.1169	0.09767	0.002797	0.003668	0.0921	0.361	2001	98000
Gamma[1,4]	0.200	0.1172	0.00265	0.02995	0.1808	0.4716	2001	98000
Gamma[1,5]	0.1645	0.1024	9.935E	0.022	0.1455	0.4068	2001	98000
Gamma[1,6]	0.1283	0.1001	0.002699	0.005381	0.1052	0.3756	2001	98000
Gamma[2,1]	0.1603	0.1105	0.004425	0.005132	0.149	0.4024	2001	98000
Gamma[2,2]	0.2769	0.1367	0.005363	0.03983	0.2761	0.5459	2001	98000
Gamma[2,3]	0.201	0.147	0.006982	0.01903	0.1619	0.5454	2001	98000
Gamma[2,4]	0.1994	0.1095	0.002867	0.04278	0.1804	0.4626	2001	98000
Gamma[2,5]	0.06563	0.06354	9.716E-4	0.001695	0.04632	0.2362	2001	98000
Gamma[2,6]	0.09676	0.07401	0.001045	0.004951	0.08028	0.2815	2001	98000
Gamma[3,1]	0.3034	0.1498	0.00198	0.0564	0.2901	0.6277	2001	98000
Gamma[3,2]	0.1615	0.1217	0.001413	0.007156	0.1361	0.4595	2001	98000
Gamma[3,3]	0.1177	0.1107	0.002129	0.003115	0.08352	0.4103	2001	98000
Gamma[3,4]	0.1516	0.1156	0.001244	0.006555	0.1268	0.4386	2001	98000
Gamma[3,5]	0.1164	0.1099	0.002141	0.003177	0.08249	0.4108	2001	98000
Gamma[3,6]	0.1494	0.1143	0.00132	0.007116	0.1241	0.4326	2001	98000
Gamma[4,1]	0.2382	0.1303	0.001893	0.04034	0.2196	0.5315	2001	98000
Gamma[4,2]	0.3243	0.1452	0.002346	0.08413	0.3119	0.6337	2001	98000
Gamma[4,3]	0.1365	0.1076	0.002421	0.005101	0.1116	0.4004	2001	98000
Gamma[4,4]	0.1001	0.09162	0.001059	0.002843	0.07303	0.3415	2001	98000
Gamma[4,5]	0.1015	0.09347	0.001113	0.002804	0.07388	0.3488	2001	98000
Gamma[4,6]	0.09945	0.09075	9.757E-4	0.002678	0.07341	0.3381	2001	98000
Gamma[5,1]	0.1394	0.1213	0.001082	0.004037	0.1062	0.4497	2001	98000
Gamma[5,2]	0.236	0.1646	0.004675	0.01076	0.2081	0.612	2001	98000
Gamma[5,3]	0.1406	0.1219	0.00107	0.004216	0.1069	0.4519	2001	98000
Gamma[5,4]	0.2039	0.1568	0.00466	0.007641	0.1694	0.5787	2001	98000
Gamma[5,5]	0.1407	0.1213	0.001192	0.004372	0.1072	0.4488	2001	98000
Gamma[5,6]	0.1394	0.1221	0.001121	0.00415	0.1055	0.4522	2001	98000
Gamma[6,1]	0.1318	0.1146	0.001107	0.00373	0.100	0.426	2001	98000
Gamma[6,2]	0.2155	0.1502	0.003637	0.01022	0.1898	0.5616	2001	98000
Gamma[6,3]	0.1891	0.1531	0.005187	0.00604	0.1515	0.5649	2001	98000
Gamma[6,4]	0.2026	0.1444	0.003523	0.009772	0.1756	0.542	2001	98000
Gamma[6,5]	0.1326	0.1163	0.001206	0.003639	0.1004	0.4327	2001	98000
Gamma[6,6]	0.1283	0.1135	0.00131	0.003657	0.09652	0.423	2001	98000

Table A.6: Posterior summary of the estimated transition probability for blood type AB^+, EU

	mean	sd	MC_error	val2.5pc	median	val97.5pc	start	sample
Gamma[1,1]	0.1518	0.09497	6.837E-4	0.0206	0.1337	0.3788	2001	98000
Gamma[1,2]	0.3225	0.1253	0.001013	0.1074	0.3135	0.5886	2001	98000
Gamma[1,3]	0.2248	0.1109	8.818E-4	0.05316	0.2101	0.4756	2001	98000
Gamma[1,4]	0.2256	0.1111	9.205E-4	0.0524	0.2115	0.4773	2001	98000
Gamma[1,5]	0.07538	0.07021	5.021E-4	0.002014	0.05501	0.2608	2001	98000
Gamma[2,1]	0.3276	0.1169	9.033E-4	0.1236	0.3200	0.5735	2001	98000
Gamma[2,2]	0.2805	0.1146	9.015E-4	0.08898	0.2702	0.528	2001	98000
Gamma[2,3]	0.1955	0.09797	7.053E-4	0.04614	0.1819	0.4204	2001	98000
Gamma[2,4]	0.0652	0.06126	4.635E-4	0.001767	0.04701	0.2275	2001	98000
Gamma[2,5]	0.1312	0.08382	6.912E-4	0.01757	0.1149	0.3347	2001	98000
Gamma[3,1]	0.3684	0.1609	0.001272	0.09551	0.3575	0.7038	2001	98000
Gamma[3,2]	0.2631	0.1483	0.001181	0.03897	0.2423	0.5968	2001	98000
Gamma[3,3]	0.1216	0.1086	8.935E-4	0.00348	0.09105	0.4049	2001	98000
Gamma[3,4]	0.1226	0.1087	8.545E-4	0.003555	0.09222	0.4058	2001	98000
Gamma[3,5]	0.1242	0.1099	8.791E-4	0.003677	0.09355	0.4086	2001	98000
Gamma[4,1	0.2476	0.143	0.001073	0.03656	0.2264	0.571	2001	98000
Gamma[4,2]	0.2615	0.1472	0.001211	0.03997	0.2409	0.5939	2001	98000
Gamma[4,3]	0.1234	0.1087	7.837E-4	0.00362	0.0931	0.4046	2001	98000
Gamma[4,4]	0.2435	0.1412	0.001409	0.03532	0.2223	0.5666	2001	98000
Gamma[4,5]	0.1239	0.1089	8.67E-4	0.003738	0.09355	0.4054	2001	98000
Gamma[5,1]	0.1643	0.1392	9.864E-4	0.004787	0.1272	0.5151	2001	98000
Gamma[5,2]	0.3469	0.18	0.001355	0.05756	0.3295	0.7265	2001	98000
Gamma[5,3]	0.1649	0.1408	0.001121	0.004842	0.1273	0.5192	2001	98000
Gamma[5,4]	0.1631	0.1386	0.001121	0.004847	0.1262	0.5146	2001	98000
Gamma[5,5]	0.1608	0.1347	0.001154	0.00497	0.1251	0.4962	2001	98000

Table A.7: Posterior summary of the estimated transition probability for blood typeO^-, EU

	mean	sd	MC_error	val2.5pc	median	val97.5pc	start	sample
Gamma[1,1]	0.3021	0.1211	0.001021	0.09735	0.2922	0.5604	2001	98000
Gamma[1,2]	0.1637	0.1001	7.784E-4	0.02258	0.1464	0.3996	2001	98000
Gamma[1,3]	0.2286	0.1117	8.267E-4	0.05419	0.215	0.4793	2001	98000
Gamma[1,4]	0.1534	0.09585	7.496E-4	0.02111	0.1359	0.3823	2001	98000
Gamma[1,5]	0.1523	0.09565	7.09E-4	0.0208	0.134	0.3833	2001	98000
Gamma[2,1]	0.2582	0.1084	8.784E-4	0.08015	0.2474	0.4964	2001	98000
Gamma[2,2]	0.3492	0.1216	0.001185	0.1355	0.3421	0.6022	2001	98000
Gamma[2,3]	0.1297	0.0831	6.138E-4	0.01712	0.114	0.33	2001	98000
Gamma[2,4]	0.06499	0.06075	4.687E-4	0.001726	0.04723	0.2263	2001	98000
Gamma[2,5]	0.1978	0.09906	7.842E-4	0.04531	0.1844	0.4235	2001	98000
Gamma[3,1]	0.2743	0.1559	0.00119	0.04086	0.2518	0.6249	2001	98000
Gamma[3,2]	0.3045	0.1646	0.001375	0.04826	0.2857	0.6629	2001	98000
Gamma[3,3]	0.1389	0.1202	9.391E-4	0.004222	0.1065	0.4452	2001	98000
Gamma[3,4]	0.1408	0.1224	9.266E-4	0.004261	0.1072	0.456	2001	98000
Gamma[3,5]	0.1414	0.1222	9.398E-4	0.004065	0.1082	0.451	2001	98000
Gamma[4,1]	0.2799	0.1587	0.001241	0.04177	0.2574	0.6371	2001	98000
Gamma[4,2]	0.298	0.1626	0.001281	0.0462	0.2781	0.6544	2001	98000
Gamma[4,3]	0.1395	0.1214	8.942E-4	0.004084	0.1064	0.4507	2001	98000
Gamma[4,4]	0.1426	0.1243	0.001132	0.004317	0.1085	0.4585	2001	98000
Gamma[4,5]	0.14	0.1221	9.618E-4	0.004073	0.1065	0.4527	2001	98000
Gamma[5,1]	0.1213	0.1076	7.699E-4	0.003359	0.09111	0.3987	2001	98000
Gamma[5,2]	0.3914	0.1619	0.001316	0.1096	0.3822	0.7234	2001	98000
Gamma[5,3]	0.1225	0.1092	7.875E-4	0.003445	0.09144	0.4063	2001	98000
Gamma[5,4]	0.2437	0.1427	0.001197	0.035	0.2213	0.5718	2001	98000
Gamma[5,5]	0.1212	0.1074	9.559E-4	0.003485	0.09066	0.3979	2001	98000
lambda[1]	15230.0	43.8	0.1938	15140.0	15230.0	15310.0	2001	98000

Table A.8. Posterior summary of the estimated transition probability for blood typeB^-, EU

	mean	sd	MC_error	val2.5pc	median	val97.5pc	start	sample
Gamma[1,1]	0.246	0.1032	8.066E-4	0.07749	0.2356	0.4726	2001	98000
Gamma[1,2]	0.2664	0.1076	8.99E-4	0.08578	0.2565	0.4986	2001	98000
Gamma[1,3]	0.3653	0.1158	9.622E-4	0.1576	0.3593	0.6065	2001	98000
Gamma[1,4]	0.0612	0.05764	4.367E-4	0.001648	0.04416	0.2142	2001	98000
Gamma[1,5]	0.06115	0.05749	4.567E-4	0.001659	0.04414	0.213	2001	98000
Gamma[2,1]	0.4107	0.137	0.001265	0.1623	0.4054	0.6881	2001	98000
Gamma[2,2]	0.1772	0.1089	8.542E-4	0.02453	0.1578	0.435	2001	98000
Gamma[2,3]	0.08181	0.0757	5.545E-4	0.002187	0.05987	0.281	2001	98000
Gamma[2,4]	0.1652	0.1024	7.941E-4	0.02254	0.1467	0.4081	2001	98000
Gamma[2,5]	0.1651	0.1029	8.385E-4	0.02252	0.1464	0.4101	2001	98000
Gamma[3,1]	0.4396	0.1562	0.001384	0.1552	0.435	0.7492	2001	98000
Gamma[3,2]	0.1196	0.1048	8.762E-4	0.003473	0.09092	0.3898	2001	98000
Gamma[3,3]	0.1088	0.09742	8.349E-4	0.003097	0.08099	0.3613	2001	98000
Gamma[3,4]	0.2227	0.1313	0.001073	0.03242	0.2017	0.5271	2001	98000
Gamma[3,5]	0.1093	0.09755	7.946E-4	0.00315	0.08183	0.362	2001	98000
Gamma[4,1]	0.2798	0.1581	0.001248	0.04121	0.2586	0.6334	2001	98000
Gamma[4,2]	0.3029	0.1635	0.001256	0.04786	0.2839	0.66	2001	98000
Gamma[4,3]	0.1387	0.1213	8.84E-4	0.004014	0.105	0.4511	2001	98000
Gamma[4,4]	0.1391	0.1204	0.001001	0.004239	0.1061	0.4473	2001	98000
Gamma[4,5]	0.1396	0.1211	9.421E-4	0.003942	0.1064	0.4511	2001	98000
Gamma[5,1]	0.1628	0.1389	0.001091	0.004876	0.1256	0.5144	2001	98000
Gamma[5,2]	0.3476	0.1804	0.00145	0.05681	0.3301	0.7282	2001	98000
Gamma[5,3]	0.1626	0.1387	0.001069	0.004834	0.1252	0.5127	2001	98000
Gamma[5,4]	0.1625	0.1383	0.001031	0.005032	0.1257	0.5149	2001	98000
Gamma[5,5]	0.1646	0.1398	0.001429	0.004895	0.1269	0.5179	2001	98000

Table A.9: Posterior summary of the estimated transition probability for blood type B^-, EU

	mean	sd	MC_error	val2.5pc	median	val97.5pc	start	sample
Gamma[1,1]	0.2999	0.12	9.569E-4	0.09596	0.29	0.556	2001	98000
Gamma[1,2]	0.1645	0.1009	7.704E-4	0.02268	0.1475	0.4024	2001	98000
Gamma[1,3]	0.3055	0.1224	9.342E-4	0.09813	0.296	0.5687	2001	98000
Gamma[1,4]	0.07754	0.07199	5.385E-4	0.002128	0.05648	0.2670	2001	98000
Gamma[1,5]	0.1525	0.09484	7.658E-4	0.02116	0.135	0.3794	2001	98000
Gamma[2,1]	0.2592	0.1087	7.926E-4	0.08042	0.248	0.4971	2001	98000
Gamma[2,2]	0.3503	0.1207	0.001022	0.1365	0.3437	0.6012	2001	98000
Gamma[2,3]	0.1951	0.09813	7.583E-4	0.04566	0.1815	0.419	2001	98000
Gamma[2,4]	0.06524	0.06106	4.384E-4	0.001762	0.04716	0.2255	2001	98000
Gamma[2,5]	0.1301	0.08319	6.895E-4	0.01706	0.1137	0.3314	2001	98000
Gamma[3,1]	0.3203	0.1462	0.001114	0.08066	0.3062	0.6354	2001	98000
Gamma[3,2]	0.3536	0.1516	0.001199	0.0951	0.3428	0.6686	2001	98000
Gamma[3,3]	0.1081	0.09664	7.066E-4	0.003065	0.08067	0.3602	2001	98000
Gamma[3,4]	0.1102	0.09835	8.089E-4	0.003202	0.08271	0.366	2001	98000
Gamma[3,5]	0.1078	0.09671	7.23E-4	0.003069	0.08022	0.3597	2001	98000
Gamma[4,1]	0.1619	0.1384	0.001027	0.004828	0.1241	0.5133	2001	98000
Gamma[4,2]	0.3472	0.1806	0.001469	0.05711	0.3297	0.7298	2001	98000
Gamma[4,3]	0.1623	0.1391	0.001043	0.004833	0.1242	0.5159	2001	98000
Gamma[4,4]	0.1636	0.1391	0.001282	0.004967	0.1268	0.5156	2001	98000
Gamma[4,5]	0.165	0.1398	0.001179	0.005024	0.128	0.518	2001	98000
Gamma[5,1]	0.138	0.1206	8.615E-4	0.004041	0.1048	0.4488	2001	98000
Gamma[5,2]	0.2992	0.1625	0.001228	0.04684	0.2796	0.6535	2001	98000
Gamma[5,3]	0.14	0.1213	8.491E-4	0.004244	0.1069	0.4515	2001	98000
Gamma[5,4]	0.2827	0.159	0.001232	0.04293	0.261	0.6373	2001	98000
Gamma[5,5]	0.1401	0.1217	0.001004	0.004192	0.1074	0.4505	2001	98000

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Table A.10: Posterior summary of the estimated transition probability for blood typeO^+, -AF

	mean	sd	MC_error	2.5pc	median	val97.5pc	start	sample
Gamma[1,1]	0.3606	0.1566	0.001858	0.09467	0.3494	0.6872	2001	98000
Gamma[1,2]	0.32	0.1474	0.001479	0.07841	0.3061	0.6379	2001	98000
Gamma[1,3]	0.1064	0.09651	8.939E-4	0.002969	0.07839	0.3597	2001	98000
Gamma[1,4]	0.1052	0.09629	9.568E-4	0.002944	0.07691	0.359	2001	98000
Gamma[1,5]	0.1078	0.09733	9.886E-4	0.003061	0.08019	0.364	2001	98000
Gamma[2,1]	0.219	0.1261	0.001191	0.03389	0.2003	0.507	2001	98000
Gamma[2,2]	0.2917	0.1337	0.001207	0.0732	0.278	0.5821	2001	98000
Gamma[2,3]	0.1938	0.1176	0.001034	0.02669	0.1736	0.4713	2001	98000
Gamma[2,4]	0.09732	0.0888	7.685E-4	0.002645	0.07154	0.3319	2001	98000
Gamma[2,5]	0.1982	0.1199	0.001145	0.02719	0.1783	0.4777	2001	98000
Gamma[3,1]	0.1831	0.1495	0.001292	0.005717	0.1463	0.5546	2001	98000
Gamma[3,2]	0.327	0.177	0.001481	0.05171	0.3068	0.712	2001	98000
Gamma[3,3]	0.162	0.1371	0.001318	0.004797	0.1258	0.5099	2001	98000
Gamma[3,4]	0.1612	0.1375	0.001232	0.004806	0.1245	0.5072	2001	98000
Gamma[3,5]	0.1667	0.1414	0.001307	0.004984	0.1287	0.5249	2001	98000
Gamma[4,1]	0.2198	0.1719	0.001598	0.007451	0.1804	0.6323	2001	98000
Gamma[4,2]	0.1984	0.1627	0.001381	0.006132	0.1574	0.6006	2001	98000
Gamma[4,3]	0.1936	0.1597	0.001352	0.006044	0.1529	0.5885	2001	98000
Gamma[4,4]	0.1906	0.1563	0.001646	0.005818	0.1514	0.5768	2001	98000
Gamma[4,5]	0.1976	0.162	0.001379	0.006149	0.157	0.5975	2001	98000
Gamma[5,1]	0.3594	0.1817	0.001774	0.06262	0.3438	0.7408	2001	98000
Gamma[5,2]	0.1623	0.1381	0.001259	0.00495	0.1256	0.5123	2001	98000
Gamma[5,3]	0.1576	0.1353	0.001117	0.004598	0.1209	0.5006	2001	98000
Gamma[5,4]	0.1623	0.1372	0.00117	0.005074	0.1257	0.5125	2001	98000
Gamma[5,5]	0.1584	0.1338	0.001363	0.004683	0.1231	0.495	2001	98000

Table A.11: Posterior summary of the estimated transition probability for blood type A^+, AF

	mean	sd	MC_error	val2.5pc	median	val97.5pc	start	sample
Gamma[1,1]	0.3168	0.1463	0.001911	0.07496	0.3036	0.6312	2001	98000
Gamma[1,2]	0.3433	0.1595	0.003472	0.0555	0.3353	0.669	2001	98000
Gamma[1,3]	0.1246	0.1219	0.003866	0.00319	0.08729	0.4613	2001	98000
Gamma[1,4]	0.1081	0.0971	9.638E-4	0.003071	0.0806	0.3598	2001	98000
Gamma[1,5]	0.1072	0.09686	9.462E-4	0.002915	0.07917	0.36	2001	98000
Gamma[2,1]	0.2996	0.1407	0.001743	0.07344	0.2846	0.6063	2001	98000
Gamma[2,2]	0.208	0.1285	0.001725	0.02391	0.1864	0.5059	2001	98000
Gamma[2,3]	0.1599	0.1197	0.002804	0.006867	0.1349	0.4491	2001	98000
Gamma[2,4]	0.1346	0.1123	0.002748	0.004377	0.1062	0.4163	2001	98000
Gamma[2,5]	0.1979	0.1209	0.001301	0.0278	0.1766	0.4825	2001	98000
Gamma[3,1]	0.1716	0.147	0.001665	0.004893	0.1323	0.5436	2001	98000
Gamma[3,2]	0.3019	0.1881	0.003974	0.01969	0.2792	0.7107	2001	98000
Gamma[3,3]	0.1769	0.147	0.00198	0.005585	0.1394	0.5441	2001	98000
Gamma[3,4]	0.1784	0.148	0.00193	0.005497	0.1411	0.5496	2001	98000
Gamma[3,5]	0.1711	0.1468	0.001841	0.005032	0.1315	0.5441	2001	98000
Gamma[4,1]	0.1846	0.1548	0.001682	0.005687	0.144	0.5725	2001	98000
Gamma[4,2]	0.2717	0.1872	0.004219	0.01182	0.2421	0.6903	2001	98000
Gamma[4,3]	0.1845	0.1544	0.001755	0.005637	0.1443	0.569	2001	98000
Gamma[4,4]	0.1802	0.1517	0.001892	0.005235	0.1404	0.5609	2001	98000
Gamma[4,5]	0.1791	0.1511	0.001566	0.005346	0.139	0.5596	2001	98000
Gamma[5,1]	0.3313	0.1773	0.001679	0.05263	0.312	0.7135	2001	98000
Gamma[5,2]	0.1783	0.1468	0.001378	0.00562	0.1416	0.5448	2001	98000
Gamma[5,3]	0.166	0.1405	0.001266	0.005158	0.1284	0.5221	2001	98000
Gamma[5,4]	0.1645	0.1392	0.001266	0.005135	0.1278	0.517	2001	98000
Gamma[5,5]	0.1599	0.134	0.001353	0.004943	0.1252	0.4965	2001	98000

Table A.12: Posterior summary of the estimated transition probability for blood type B^+, EU

	mean	sd	MC_error	val2.5pc	median	val97.5pc	start	sample
Gamma[1,1]	0.4792	0.162	0.002132	0.1734	0.4791	0.7869	2001	98000
Gamma[1,2]	0.3111	0.146	0.001522	0.07417	0.2959	0.6304	2001	98000
Gamma[1,3]	0.1037	0.09439	9.503E-4	0.002858	0.07644	0.3498	2001	98000
Gamma[1,4]	0.1061	0.09649	0.001037	0.00294	0.0781	0.3583	2001	98000
Gamma[2,1]	0.272	0.1497	0.001725	0.04226	0.2528	0.6064	2001	98000
Gamma[2,2]	0.2401	0.1392	0.001318	0.03448	0.2198	0.5561	2001	98000
Gamma[2,3]	0.2424	0.1412	0.001457	0.036	0.2203	0.5662	2001	98000
Gamma[2,4]	0.2455	0.1421	0.001473	0.03578	0.2234	0.5685	2001	98000
Gamma[3,1]	0.2171	0.1701	0.001768	0.007307	0.1782	0.627	2001	98000
Gamma[3,2]	0.3922	0.1988	0.002081	0.06668	0.3757	0.7994	2001	98000
Gamma[3,3]	0.1932	0.1582	0.001682	0.006034	0.1534	0.5846	2001	98000
Gamma[3,4]	0.1975	0.1619	0.001615	0.006486	0.1565	0.5947	2001	98000
Gamma[4,1]	0.4274	0.2008	0.002238	0.07924	0.4181	0.8233	2001	98000
Gamma[4,2]	0.1909	0.1574	0.001465	0.005811	0.1513	0.5839	2001	98000
Gamma[4,3]	0.191	0.1588	0.001535	0.005994	0.1497	0.5848	2001	98000
Gamma[4,4]	0.1907	0.1564	0.001836	0.006034	0.1511	0.5776	2001	98000

Table A.13: Posterior summary of the estimated transition probability for blood type AB^{+}, EU

	mean	sd	MC_error	val2.5pc	median	val97.5pc	start	sample
Gamma[1,1]	0.4264	0.1511	0.001943	0.1509	0.4219	0.728	2001	98000
Gamma[1,2]	0.2843	0.1344	0.00136	0.06897	0.2696	0.5782	2001	98000
Gamma[1,3]	0.09724	0.08833	7.711E-4	0.002785	0.07212	0.329	2001	98000
Gamma[1,4]	0.09445	0.08603	7.934E-4	0.002608	0.06991	0.3199	2001	98000
Gamma[1,5]	0.09768	0.08836	8.986E-4	0.002698	0.07255	0.3279	2001	98000
Gamma[2,1]	0.1363	0.1174	0.001098	0.004096	0.1042	0.4335	2001	98000
Gamma[2,2]	0.1206	0.1077	0.001008	0.003326	0.08989	0.3999	2001	98000
Gamma[2,3]	0.2483	0.1439	0.001354	0.03666	0.2265	0.5783	2001	98000
Gamma[2,4]	0.2452	0.1435	0.001285	0.03532	0.2233	0.5739	2001	98000
Gamma[2,5]	0.2497	0.1439	0.001391	0.03711	0.2281	0.5763	2001	98000
Gamma[3,1]	0.3547	0.1822	0.001801	0.05921	0.3377	0.7374	2001	98000
Gamma[3,2]	0.1607	0.1373	0.00122	0.005026	0.1234	0.5089	2001	98000
Gamma[3,3]	0.1618	0.1373	0.001363	0.004655	0.1252	0.51	2001	98000
Gamma[3,4]	0.1594	0.136	0.001258	0.004669	0.1228	0.5054	2001	98000
Gamma[3,5]	0.1635	0.1401	0.001226	0.004906	0.1251	0.5199	2001	98000
Gamma[4,1]	0.1804	0.1476	0.001295	0.005643	0.1436	0.5454	2001	98000
Gamma[4,2]	0.3278	0.1766	0.001578	0.05127	0.3076	0.7083	2001	98000
Gamma[4,3]	0.1667	0.1394	0.001136	0.005191	0.1307	0.5162	2001	98000
Gamma[4,4]	0.1604	0.1366	0.001305	0.005041	0.1239	0.506	2001	98000
Gamma[4,5]	0.1648	0.1395	0.001201	0.00512	0.1279	0.5164	2001	98000
Gamma[5,1]	0.3578	0.1802	0.001594	0.06308	0.343	0.7366	2001	98000
Gamma[5,2]	0.1592	0.1361	0.001172	0.004785	0.1227	0.5061	2001	98000
Gamma[5,3]	0.1625	0.1381	0.001163	0.004958	0.1254	0.5115	2001	98000
Gamma[5,4]	0.1591	0.136	0.001227	0.00469	0.1222	0.5056	2001	98000
Gamma[5,5]	0.1613	0.1356	0.001278	0.004787	0.1259	0.5031	2001	98000

Table A.14: Posterior summary of the estimated transition probability for blood typeO^{-} , AF

	Mean	sd	MC_error	val2.5pc	median	val97.5pc	start	sample
Gamma[1,1]	0.4393	0.1399	0.001751	0.1807	0.4361	0.7148	2001	98000
Gamma[1,2]	0.1599	0.1002	9.951E-4	0.02177	0.1412	0.3996	2001	98000
Gamma[1,3]	0.1603	0.1009	0.00101	0.02171	0.1413	0.4026	2001	98000
Gamma[1,4]	0.08038	0.07487	6.961E-	0.002205	0.05842	0.27912001	98000	
Gamma[1,5]	0.1603	0.1003	9.801E-4	0.02197	0.1413	0.402	2001	98000
Gamma[2,1]	0.3027	0.163	0.001502	0.04836	0.2843	0.6593	2001	98000
Gamma[2,2]	0.2807	0.1572	0.0017	0.0428	0.2591	0.6327	2001	98000
Gamma[2,3]	0.1386	0.12	0.001038	0.0041	0.106	0.445	2001	98000
Gamma[2,4]	0.137	0.1197	0.001062	0.00406	0.1041	0.4452	2001	98000
Gamma[2,5]	0.141	0.1226	9.996E-4	0.004021	0.1071	0.4541	2001	98000
Gamma[3,1]	0.3496	0.1804	0.001601	0.05735	0.3335	0.7317	2001	98000
Gamma[3,2]	0.1652	0.141	0.001233	0.00485	0.1271	0.521	2001	98000
Gamma[3,3]	0.1619	0.1379	0.001335	0.004862	0.1248	0.5123	2001	98000
Gamma[3,4]	0.1608	0.138	0.001279	0.004852	0.1232	0.5092	2001	98000
Gamma[3,5]	0.1626	0.1387	0.001227	0.004884	0.1251	0.5137	2001	98000
Gamma[4,1]	0.2118	0.1679	0.001478	0.006976	0.1721	0.6177	2001	98000
Gamma[4,2]	0.1957	0.1611	0.001403	0.006046	0.1544	0.5916	2001	98000
Gamma[4,3]	0.199	0.163	0.001337	0.005973	0.1587	0.6034	2001	98000
Gamma[4,4]	0.1951	0.1602	0.00174	0.006262	0.1542	0.5902	2001	98000
Gamma[4,5]	0.1984	0.1617	0.001416	0.006489	0.1585	0.5987	2001	98000
Gamma[5,1]	0.3511	0.1804	0.001763	0.05792	0.3352	0.7304	2001	98000
Gamma[5,2]	0.1635	0.1394	0.001257	0.004778	0.1262	0.5173	2001	98000
Gamma[5,3]	0.1614	0.1373	0.001196	0.004747	0.125	0.5107	2001	98000
Gamma[5,4]	0.1614	0.1379	0.001252	0.004622	0.1238	0.5109	2001	98000
Gamma[5,5]	0.1626	0.1378	0.001754	0.005084	0.1264	0.5067	2001	98000

Table A.15. Posterior summary of the estimated transition probability for blood type A^-, AF

	Mean	sd	MC_error	val2.5pc	median	val97.5pc	start	sample
Gamma[1,1]	0.4405	0.1407	0.001612	0.1802	0.437	0.7199	2001	98000
Gamma[1,2]	0.1604	0.1008	9.404E-4	0.02143	0.142	0.4016	2001	98000
Gamma[1,3]	0.149 0	0.1008	0.001747	0.01194	0.1305	0.3915	2001	98000
Gamma[1,4]	0.08893	0.08226	0.001601	0.002448	0.06457	0.3088	2001	98000
Gamma[1,5]	0.1608	0.101	0.001023	0.02161	0.1417	0.4029	2001	98000
Gamma[2,1]	0.3034	0.1635	0.001408	0.04853	0.2835	0.6605	2001	98000
Gamma[2,2]	0.2774	0.1554	0.001566	0.04236	0.2564	0.6258	2001	98000
Gamma[2,3]	0.1406	0.1227	0.001046	0.004086	0.1068	0.454	2001	98000
Gamma[2,4]	0.1393	0.1215	0.001085	0.004016	0.1051	0.4546	2001	98000
Gamma[2,5]	0.1393	0.1211	0.00102	0.004252	0.1065	0.4523	2001	98000
Gamma[3,1]	0.3359	0.1862	0.00299	0.03741	0.318	0.7297	2001	98000
Gamma[3,2]	0.1665	0.1425	0.001375	0.005024	0.1274	0.5286	2001	98000
Gamma[3,3]	0.1636	0.1398	0.001535	0.004716	0.1268	0.5206	2001	98000
Gamma[3,4]	0.1668	0.1421	0.001384	0.004961	0.1287	0.5256	2001	98000
Gamma[3,5]	0.1671	0.1422	0.001426	0.004822	0.1297	0.5298	2001	98000
Gamma[4,1]	0.2299	0.176	0.002907	0.00807	0.1915	0.6445	2001	98000
Gamma[4,2]	0.1925	0.1593	0.001508	0.005781	0.1516	0.5874	2001	98000
Gamma[4,3]	0.1939	0.1595	0.001522	0.006031	0.1534	0.5891	2001	98000
Gamma[4,4]	0.1918	0.1589	0.001849	0.006222	0.1507	0.5874	2001	98000
Gamma[4,5]	0.1919	0.1585	0.001528	0.005888	0.152	0.5867	2001	98000
Gamma[5,1]	0.3536	0.1806	0.001677	0.06005	0.3379	0.7355	2001	98000
Gamma[5,2]	0.1635	0.1389	0.001247	0.004902	0.1271	0.5158	2001	98000
Gamma[5,3]	0.1623	0.138	0.00119	0.00479	0.1255	0.5117	2001	98000
Gamma[5,4]	0.1622	0.1388	0.001279	0.004879	0.1242	0.5135	2001	98000
Gamma[5,5]	0.1584	0.1336	0.001234	0.004883	0.123	0.4938	2001	98000

Table A.16. Posterior summary of the estimated transition probability for blood type B^- AF

	Mean	sd	MC_error	val2.5pc	median	val97.5pc	start	sample
Gamma[1,1]	0.3605	0.1562	0.001812	0.0955	0.3493	0.6862	2001	98000
Gamma[1,2]	0.3228	0.1483	0.001428	0.07999	0.3082	0.6421	2001	98000
Gamma[1,3]	0.1051	0.09532	8.871E-4	0.002904	0.07755	0.3542	2001	98000
Gamma[1,4]	0.1037	0.09471	8.353E-4	0.002835	0.07653	0.3546	2001	98000
Gamma[1,5]	0.1079	0.09718	9.695E-4	0.003002	0.08023	0.3612	2001	98000
Gamma[2,1]	0.2407	0.137	0.00151	0.03642	0.2214	0.5503	2001	98000
Gamma[2,2]	0.1246	0.1134	0.003046	0.003422	0.09156	0.4229	2001	98000
Gamma[2,3]	0.2126	0.1282	0.001272	0.02915	0.1916	0.5107	2001	98000
Gamma[2,4]	0.2052	0.13	0.002134	0.02056	0.1833	0.5094	2001	98000
Gamma[2,5]	0.2169	0.1293	0.001228	0.03057	0.196	0.5179	2001	98000
Gamma[3,1]	0.1805	0.1481	0.001446	0.005885	0.1434	0.5494	2001	98000
Gamma[3,2]	0.3263	0.1762	0.001683	0.04955	0.3061	0.7087	2001	98000
Gamma[3,3]	0.1645	0.1392	0.001379	0.0051	0.1273	0.5153	2001	98000
Gamma[3,4]	0.1638	0.1384	0.001205	0.005028	0.127	0.515	2001	98000
Gamma[3,5]	0.1649	0.1403	0.001282	0.004967	0.1275	0.5208	2001	98000
Gamma[4,1]	0.1846	0.1502	0.001421	0.005939	0.1488	0.5591	2001	98000
Gamma[4,2]	0.32	0.1793	0.002464	0.03979	0.2997	0.7084	2001	98000
Gamma[4,3]	0.1656	0.1412	0.001347	0.004901	0.1278	0.5238	2001	98000
Gamma[4,4]	0.1624	0.1372	0.001349	0.004883	0.1264	0.5077	2001	98000
Gamma[4,5]	0.1674	0.1421	0.001329	0.004888	0.1298	0.5267	2001	98000
Gamma[5,1]	0.3572	0.1823	0.001779	0.0598	0.3412	0.7399	2001	98000
Gamma[5,2]	0.1596	0.1367	0.001076	0.004709	0.1224	0.5069	2001	98000
Gamma[5,3]	0.161	0.1379	0.001233	0.004726	0.1237	0.5116	2001	98000
Gamma[5,4]	0.1589	0.1366	0.001129	0.004724	0.1222	0.5064	2001	98000
Gamma[5,5]	0.1632	0.1389	0.001408	0.00476	0.1262	0.5159	2001	98000

Table A.17. Posterior summary of the estimated transition probability for blood type AB^- ,AF

	mean	sd	MC_error	val2.5pc	median	val97.5pc		start	sample
Gamma[1,1]	0.3888	0.1445	0.001722	0.1319	0.3817	0.6831	2001	98000
Gamma[1,2]	0.1749	0.1086	9.489E-4	0.02345	0.1554	0.4329	2001	98000
Gamma[1,3]	0.09664	0.08829	0.001857	0.002608	0.07119	0.3295	2001	98000
Gamma[1,4]	0.1648	0.1089	0.00183	0.01481	0.1447	0.4255	2001	98000
Gamma[1,5]	0.175	0.1084	0.001033	0.024	0.1556	0.4337	2001	98000
Gamma[2,1]	0.3073	0.1652	0.001556	0.0491	0.2883	0.6681	2001	98000
Gamma[2,2]	0.1376	0.1188	0.001072	0.004082	0.105	0.4396	2001	98000
Gamma[2,3]	0.2746	0.1561	0.001386	0.04059	0.2523	0.6256	2001	98000
Gamma[2,4]	0.1388	0.122	0.001056	0.004073	0.1049	0.4527	2001	98000
Gamma[2,5]	0.1416	0.1229	0.001156	0.004266	0.1078	0.456	2001	98000
Gamma[3,1]	0.1927	0.1545	0.002729	0.006224	0.1556	0.5689	2001	98000
Gamma[3,2]	0.3237	0.1761	0.00197	0.04942	0.303	0.7072	2001	98000
Gamma[3,3]	0.1558	0.1319	0.001202	0.004499	0.1207	0.4891	2001	98000
Gamma[3,4]	0.1643	0.1398	0.001268	0.004893	0.127	0.5196	2001	98000
Gamma[3,5]	0.1634	0.1394	0.001349	0.004828	0.1259	0.5162	2001	98000
Gamma[4,1]	0.3354	0.1853	0.00297	0.03862	0.3173	0.728	2001	98000
Gamma[4,2]	0.1684	0.1423	0.00124	0.005105	0.1314	0.5276	2001	98000
Gamma[4,3]	0.1633	0.1396	0.001379	0.004822	0.1257	0.5166	2001	98000
Gamma[4,4]	0.1645	0.1384	0.001526	0.005048	0.128	0.5126	2001	98000
Gamma[4,5]	0.1684	0.1425	0.001392	0.005068	0.1308	0.5289	2001	98000
Gamma[5,1]	0.3528	0.1815	0.00184	0.05766	0.3366	0.7327	2001	98000
Gamma[5,2]	0.1631	0.1394	0.001266	0.00492	0.1253	0.518	2001	98000
Gamma[5,3]	0.1602	0.1375	0.001284	0.004853	0.1231	0.5109	2001	98000
Gamma[5,4]	0.1623	0.1383	0.001185	0.004713	0.1254	0.5129	2001	98000
Gamma[5,5]	0.1616	0.1381	0.00151	0.004859	0.1246	0.5101	2001	98000