

# SUPPLEMENTARY MATERIAL TO “A BAYESIAN MIXTURE MODEL ACCOUNTING FOR INDIVIDUAL HETEROGENEITY IN RESPONSE TO PATHOGENIC INFECTION”

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## A. Additional details regarding bivariate skew-normal distribution

The left skewed behavior observed in the log-transformed antibody levels in individuals whom experienced PVB19 infection in the past (see Figure 1 in the main text of Section 2), possibly owing to decaying antibody titer concentrations (Parker, Erdman and Anderson, 1990) prompt us to consider a mixture of bivariate skew-normal distribution (Azzalini, 1985, 1986):

$$\begin{cases} f_{11}(\mathbf{y}_i|\psi_{11}) = 2\phi_2(\mathbf{y}_i - \boldsymbol{\mu}_{11}; \boldsymbol{\Omega})\Phi(\boldsymbol{\alpha}_{11}^T \boldsymbol{\omega}^{-1}(\mathbf{y}_i - \boldsymbol{\mu}_{11})) \\ \boldsymbol{\Omega}_{11} = \boldsymbol{\omega}_{11}\bar{\boldsymbol{\Omega}}_{11}\boldsymbol{\omega}_{11}, \quad \boldsymbol{\alpha}_{11} = \frac{\bar{\boldsymbol{\Omega}}_{11}^{-1}\boldsymbol{\delta}_{11}}{\sqrt{1 - \boldsymbol{\delta}_{11}^T \boldsymbol{\delta}_{11}}}, \end{cases} \quad (\text{A.1})$$

where  $\psi_{11} = (\boldsymbol{\mu}_{11}, \boldsymbol{\Omega}_{11}, \boldsymbol{\omega}_{11}, \boldsymbol{\alpha}_{11})^T$ ,  $\phi_2(\mathbf{y}_i - \boldsymbol{\mu}_{11}, \boldsymbol{\Omega}_{11})$  is the p.d.f of the bivariate normal distribution with zero mean vector and variance-covariance matrix  $\boldsymbol{\Omega}_{11}$ ,  $\Phi(\cdot)$  is the cumulative density function (c.d.f) of the standard univariate normal distribution, and  $\boldsymbol{\alpha}_{11}^T$  is the vector of skewness parameters. Frühwirth-Schnatter and Pyne (2010) argued that estimation of model parameters directly from (A.1)

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results in a complex computational problem. However, a stochastic representation of the model (A.1) is quite simple to implement using Bayesian Markov Chain Monte Carlo (MCMC) method

$$\begin{cases} \mathbf{y}_i^o | (\mathbf{y}_i^m = 1) = \boldsymbol{\mu}_{11} + \boldsymbol{\Delta}_{11} \boldsymbol{\xi}_i + \boldsymbol{\epsilon}_i, & \boldsymbol{\xi}_i \sim \text{TN}_{[0, \infty)}(0, 1), \quad \boldsymbol{\epsilon}_i \sim \mathcal{N}_2(\mathbf{0}, \boldsymbol{\Sigma}_{11}) \\ \boldsymbol{\Omega}_{11} = \boldsymbol{\Sigma}_{11} + \boldsymbol{\Delta}_{11} \boldsymbol{\Delta}_{11}^T, \quad \boldsymbol{\alpha}_{11} = \frac{\boldsymbol{\omega}_{11} \boldsymbol{\Omega}_{11}^{-1} \boldsymbol{\Delta}_{11}}{\sqrt{1 - \boldsymbol{\Delta}_{11}^T \boldsymbol{\Omega}_{11}^{-1} \boldsymbol{\Delta}_{11}}}, \end{cases} \quad (\text{A.2})$$

with  $\boldsymbol{\xi}_i$  being a random effect with truncated normal distribution  $\text{TN}_{[0, \infty)}(0, 1)$  and mutually independent with measurement error  $\boldsymbol{\epsilon}_i$ . Essentially, model (A.1) is represented in terms of finite mixtures of random-effects models with truncated normal random effects (Frühwirth-Schnatter and Pyne, 2010).

## B. Additional results

### B.1 Model selection results

In order to investigate the parametric shape to be used in the mixture probabilities, we compared different baseline hazard functions such as derived from Exponential, Weibull, Gompertz, log-logistic and log-normal distributions and more flexible ones such as the piece-wise exponential baseline hazard function. Table B.2 to Table B.4 display the WAIC and deviance for the bivariate normal mixture models and bivariate skew-normal mixture models in which (1) we assume equal variance-covariance matrices for the component-specific variance covariance matrices and (2) where the component-specific variance-covariance matrices are assumed to be different. Here the mean IgG antibodies is assumed to be (a) age-invariant (see Table B.1 and Table B.3), and (b) age-dependent mean IgG antibodies (see Table B.2 and Table B.4). Furthermore, Table B.5 shows the model comparison results for the bivariate normal and skew-normal mixture models with age-independent and -dependent mean IgG antibodies. Here the mixing proportions are based on the bivariate generalized linear mixed models with different link functions. The models are fitted to serological data on VZV( $j = 1$ ) and PVB19( $j = 2$ ) from Belgium-anno 2001-2003 assuming age-dependent mean IgG antibodies. Based on WAIC and deviance, the bivariate skew-normal mixture models with different variance-covariance matrices and mixing proportions based on the bivariate logit random effects model are preferred, outperforming all other models with equal variance-covariance matrices irrespective of the choices for the baseline hazard function.

**Table B.1.** Model comparison results: WAIC and deviance for the bivariate normal mixture model with age-independent mean IgG antibodies, assuming constant and different variance-covariance matrices. The mixing proportions are based on different correlated gamma frailty distribution and different baseline hazards functions for the FOI. The models are fitted to serological data on VZV ( $j = 1$ ) and PVB19 ( $j = 2$ ) from Belgium-anno 2001-2003.

	Constant Variance		Different Variances	
	WAIC	Deviance	WAIC	Deviance
Baseline hazard model			Van den Berg	
Exponential	9936.27	9688.78	9749.24	9183.83
Weibull	9937.44	9684.72	9721.17	9157.16
Gompertz	9936.60	9687.65	9714.82	9152.22
Log-logistic	9908.99	9676.50	9698.15	9115.25
Log-normal	9919.45	9679.89	9703.09	9124.08
			Loáiciga-Leipnik	
Exponential	9919.01	9679.1	9744.18	9186.99
Weibull	9927.52	9680.80	9717.65	9153.14
Gompertz	9922.93	9679.84	9716.27	9150.51
Log-logistic	9902.73	9673.07	9681.50	9104.72
Log-normal	9916.89	9677.77	9668.14	9098.67
			Yashin	
Exponential	9932.38	9688.29	9753.04	9206.16
Weibull	9934.03	9683.59	9752.13	9181.72
Gompertz	9930.70	9688.35	9821.63	9507.97
Log-logistic	9902.38	9673.74	9696.51	9116.98
Log-normal	9917.12	9678.01	9974.65	9206.18
			Kibble-Wicksell	
Exponential	9937.97	9690.28	9700.54	9140.22
Weibull	9925.26	9680.79	9718.78	9154.76
Gompertz	9932.32	9686.54	9711.82	9149.24
Log-logistic	9902.44	9673.16	9654.54	9086.57
Log-normal	9917.96	9678.86	9692.27	9119.58

**Table B.2.** Model comparison results: WAIC and deviance for the bivariate normal mixture model with age-dependent mean IgG antibodies, assuming constant and different variance-covariance matrices. The mixing proportions are based on different correlated gamma frailty distribution and different baseline hazards functions for the FOI. The correlated gamma frailty models are fitted to serological data on VZV ( $j = 1$ ) and PVB19 ( $j = 2$ ) from Belgium.

	Constant Variance		Different Variances	
	WAIC	Deviance	WAIC	Deviance
Baseline hazard model			Van den Berg	
Exponential	9884.71	9630.89	9696.11	9158.89
Weibull	9892.91	9628.83	9698.01	9168.83
Gompertz	9885.48	9629.48	9696.36	9159.39
Log-logistic	9844.34	9613.62	9644.07	9076.02
Log-normal	9869.13	9624.34	9668.28	9108.26
			Loaiciga-Leipnik	
Exponential	9867.38	9620.79	9694.95	9158.26
Weibull	9878.56	9625.51	9739.32	9191.08
Gompertz	9888.47	9628.99	9661.16	9106.56
Log-logistic	9844.61	9614.73	9673.32	9107.95
Log-normal	9865.23	9622.34	9662.46	9097.01
			Yashin	
Exponential	9883.62	9630.79	9757.68	9261.02
Weibull	9913.64	9640.59	9719.78	9198.99
Gompertz	9922.57	9634.74	9789.36	9251.62
Log-logistic	9848.31	9614.42	9658.75	9094.09
Log-normal	9871.11	9626.42	9666.87	9110.30
			Kibble-Wicksell	
Exponential	9863.79	9623.05	9652.55	9105.22
Weibull	9875.96	9624.63	9667.21	9112.08
Gompertz	9894.00	9630.60	9804.57	9253.81
Log-logistic	9839.04	9614.87	9642.94	9081.38
Log-normal	9864.53	9621.44	9634.32	9068.24

**Table B.3.** Model comparison results: WAIC and deviance for the bivariate skew-normal mixture model with age-independent mean IgG antibodies, assuming constant and different variance-covariance matrices. The mixing proportions are based on different correlated gamma frailty distribution and different baseline hazards functions for the FOI. The correlated gamma frailty models are fitted to serological data on VZV ( $j = 1$ ) and PVB19 ( $j = 2$ ) from Belgium.

	Constant Variance		Different Variances	
	WAIC	Deviance	WAIC	Deviance
Baseline hazard model	Van den Berg			
Exponential	9920.81	9478.73	6428.61	4623.26
Weibull	8569.84	6946.58	8126.72	5484.38
Gompertz	9912.30	9434.30	6615.74	4757.22
Log-logistic	9893.57	9462.01	6417.27	4636.51
Log-normal	8506.61	6917.50	6698.15	4821.80
	Loaiciga-Leipnik			
Exponential	9896.51	9412.72	6297.05	4486.45
Weibull	9907.59	9446.15	6424.21	4601.40
Gompertz	9904.88	9442.78	6599.26	4744.22
Log-logistic	8413.48	6804.02	6660.98	4792.87
Log-normal	8517.29	6898.40	6753.66	4930.89
	Yashin			
Exponential	9910.65	9464.14	6385.06	4551.17
Weibull	9921.40	9422.80	7762.21	5395.41
Gompertz	9919.31	9463.55	6391.54	4539.98
Log-logistic	8402.37	6809.64	6657.01	4855.52
Log-normal	8615.32	6998.4	6577.77	4746.68
	Kibble-Wicksell			
Exponential	8504.19	6925.62	6672.90	4887.44
Weibull	8530.57	6934.91	6510.35	4729.72
Gompertz	8559.70	6934.83	6308.82	4473.98
Log-logistic	9879.48	9417.86	6290.99	4440.55
Log-normal	8515.29	6894.40	6711.16	4913.37

**Table B.4.** Model comparison results: WAIC and deviance for the bivariate skew-normal mixture model with age-dependent mean IgG antibodies, assuming constant and different variance-covariance matrices. The mixing proportions are based on different correlated gamma frailty distribution and different baseline hazards functions for the FOI. The correlated gamma frailty models are fitted to serological data on VZV ( $j = 1$ ) and PVB19 ( $j = 2$ ) from Belgium.

	Constant Variance		Different Variances	
	WAIC	Deviance	WAIC	Deviance
<b>Baseline hazard model</b>				
			<b>Van den Berg</b>	
Exponential	8572.67	6945.46	6308.9	4456.31
Weibull	9869.25	9404.19	6602.19	4761.32
Gompertz	9867.75	9404.86	6411.17	4591.43
Log-logistic	8487.09	6866.79	6251.99	4428.11
Log-normal	9839.19	9368.42	6450.99	4618.61
			<b>Loaiciga-Leipnik</b>	
Exponential	9858.06	9410.78	6168.12	4274.12
Weibull	8551.04	6961.83	6647.39	4863.87
Gompertz	8572.40	6947.45	6624.49	4758.09
Log-logistic	8489.36	6881.29	6768.88	4972.37
Log-normal	8498.12	6899.19	6476.74	4492.61
			<b>Yashin</b>	
Exponential	8570.74	6963.79	6130.41	4229.08
Weibull	9861.48	9403.32	6555.89	4671.28
Gompertz	9868.84	9407.38	6456.89	4561.28
Log-logistic	9826.73	9399.34	6604.51	4743.87
Log-normal	9839.19	9402.42	6564.01	4698.88
			<b>Kibble-Wicksell</b>	
Exponential	8542.54	6957.82	6661.83	4831.49
Weibull	8557.96	6967.40	6562.88	4738.49
Gompertz	8527.81	6913.77	6296.03	4429.16
Log-logistic	8468.74	6855.81	<b>6196.03</b>	<b>4329.16</b>
Log-normal	8481.11	6865.51	8294.74	5594.99

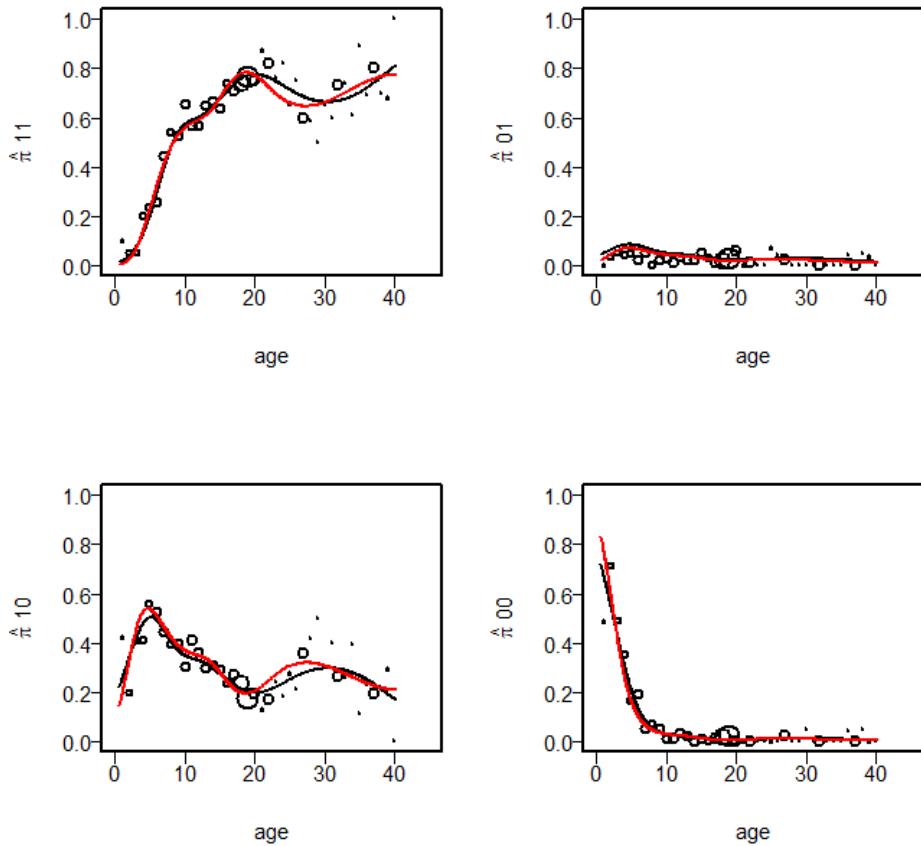
**Table B.5.** Model comparison results: WAIC for the bivariate normal and skew-normal mixture models with age-independent and -dependent mean IgG antibodies. The mixing proportions are based on the bivariate generalized linear mixed models with different link functions. The models are fitted to serological data on VZV ( $j = 1$ ) and PVB19 ( $j = 2$ ) from Belgium.

Link function	Age Independent Mean				Age Dependent Mean			
	Constant Variance		Different Variances		Constant Variance		Different Variances	
	WAIC	Deviance	WAIC	Deviance	WAIC	Deviance	WAIC	Deviance
Normal								Normal
Logit	9948.20	9754.96	9822.50	9626.70	9896.90	9703.15	9768.80	9571.41
Probit	9965.30	9764.46	9816.40	9630.24	9906.10	9710.45	9769.50	9576.20
Cloglog	9972.50	9765.66	9824.01	9633.34	9919.90	9713.72	9775.80	9581.98
Skew-Normal								Skew-Normal
Logit	8554.00	7454.25	6410.01	5125.59	8556.60	7476.04	<b>6097.31</b>	<b>4195.21</b>
Probit	8583.30	7482.19	6451.40	5164.90	8552.01	7492.19	6344.40	5017.77
Cloglog	9628.80	8173.75	6430.01	5124.86	9891.50	9574.86	6281.70	4940.91

**Table B.6.** Number of individuals in different age categories. 00 ≡ Negative for both infections, 10 ≡ Negative positive VZV and PVB19, 01 ≡ negative VZV and Positive PVB19, 11 ≡ Positive for both infections.

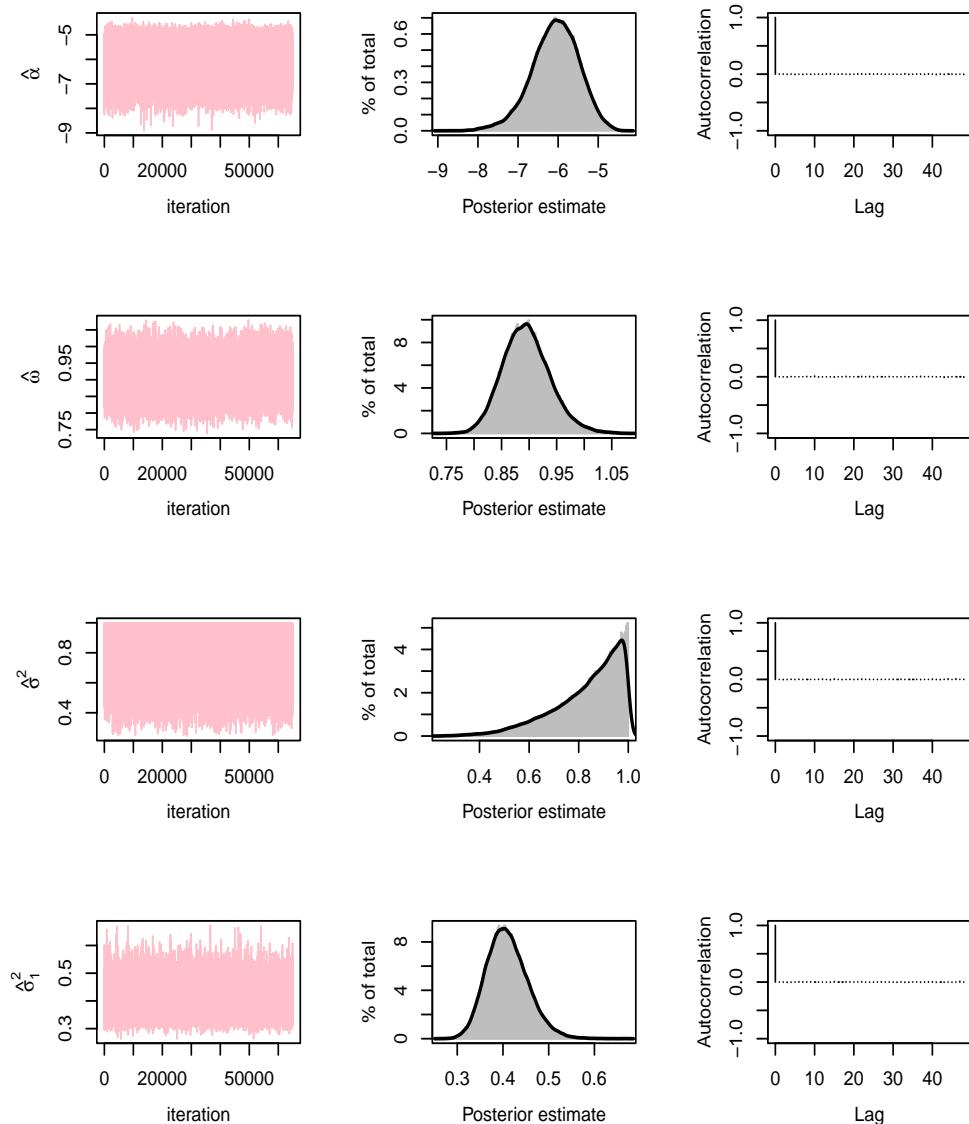
Age group	00	10	01	11	Age group	00	10	01	11
0.6 – 10	152	260	20	200	0.6 – 10	152	260	20	200
10 – 20	15	262	27	668	10 – 20	15	262	27	668
20 – 40	5	201	10	556	20 – 30	2	103	7	271
					30 – 40	3	98	3	285
0.6 – 10	152	260	20	200	0.6 – 10	152	260	20	200
10 – 20	15	262	27	668	10 – 20	15	262	27	668
20 – 25	0	36	2	155	20 – 35	2	103	7	404
25 – 30	2	67	5	116	35 – 40	3	98	3	152
30 – 40	3	98	3	285					
					0.6 – 10	152	260	20	200
					10 – 15	7	140	11	239
					15 – 20	8	122	16	429
					20 – 24	0	31	2	137
					24 – 30	2	72	5	134
					30 – 35	1	57	0	133
					35 – 40	2	41	3	152

## B.2 Additional output of mixing proportions

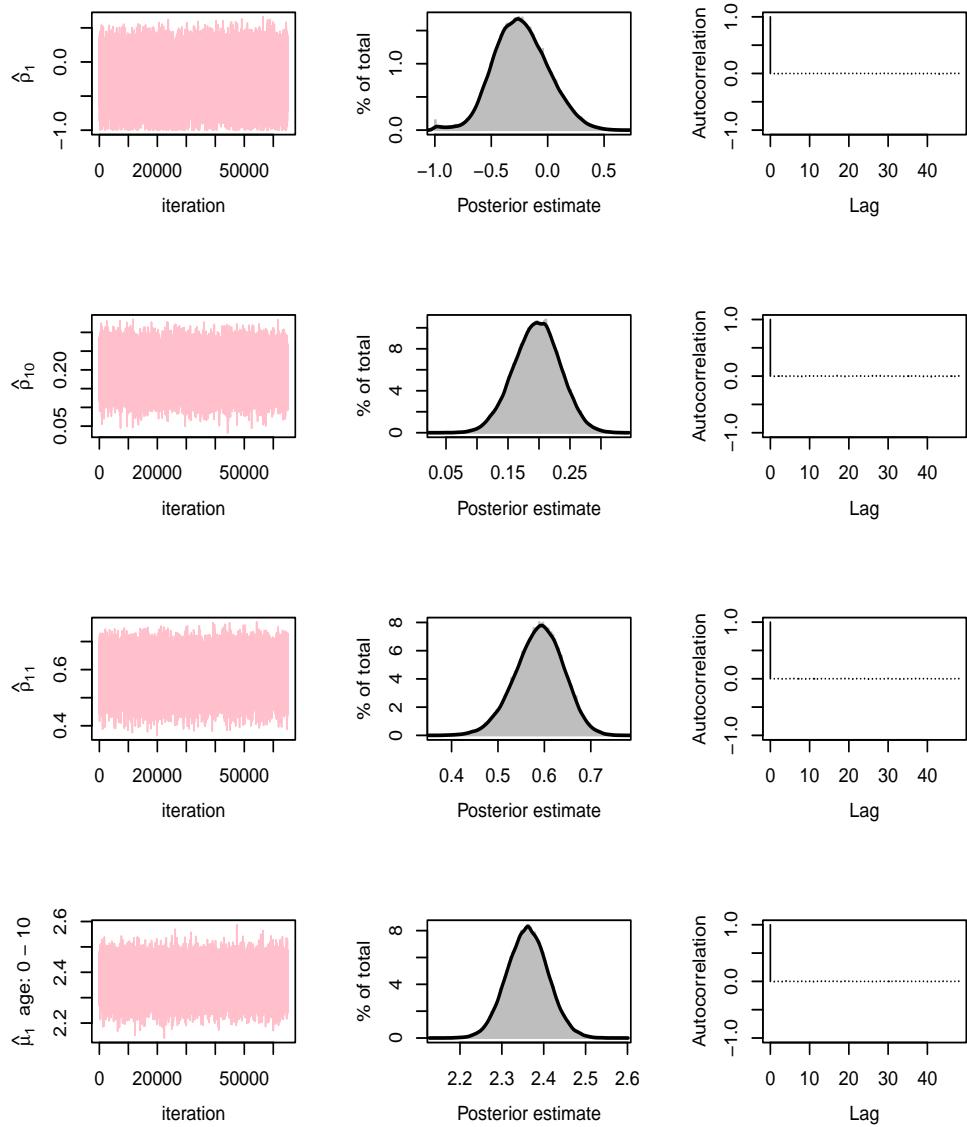


**Figure B.1.** Observed proportions that tested positive for PVB19 and VZV (left upper panel), that tested positive for PVB19 but not for VZV (right upper panel), that tested positive for VZV but not for PVB19 (left lower panel) and that tested negative for both infections (right lower panel) based on a cross-sectional survey in Belgium anno 2001–2003 with dots proportional to the size, and estimated joint proportions: (1) Bayesian mixture skew-normal model with age-dependent mean IgG antibodies assuming different variance-covariance matrices, and mixing proportions base on the bivariate logit random effects model (black solid line), (2) Bivariate logit random effects model based on binary data-threshold approach (red solid line).

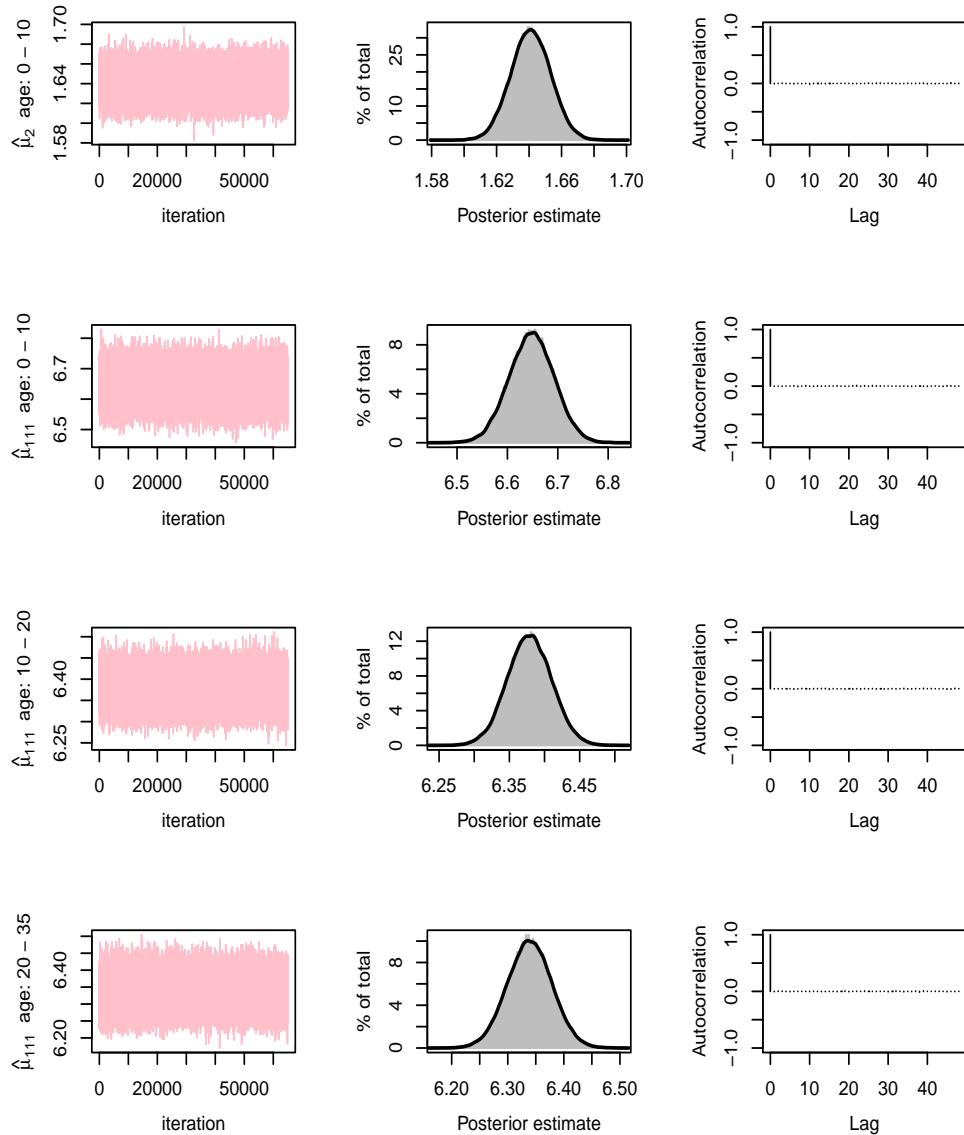
### C. Model convergence diagnostic



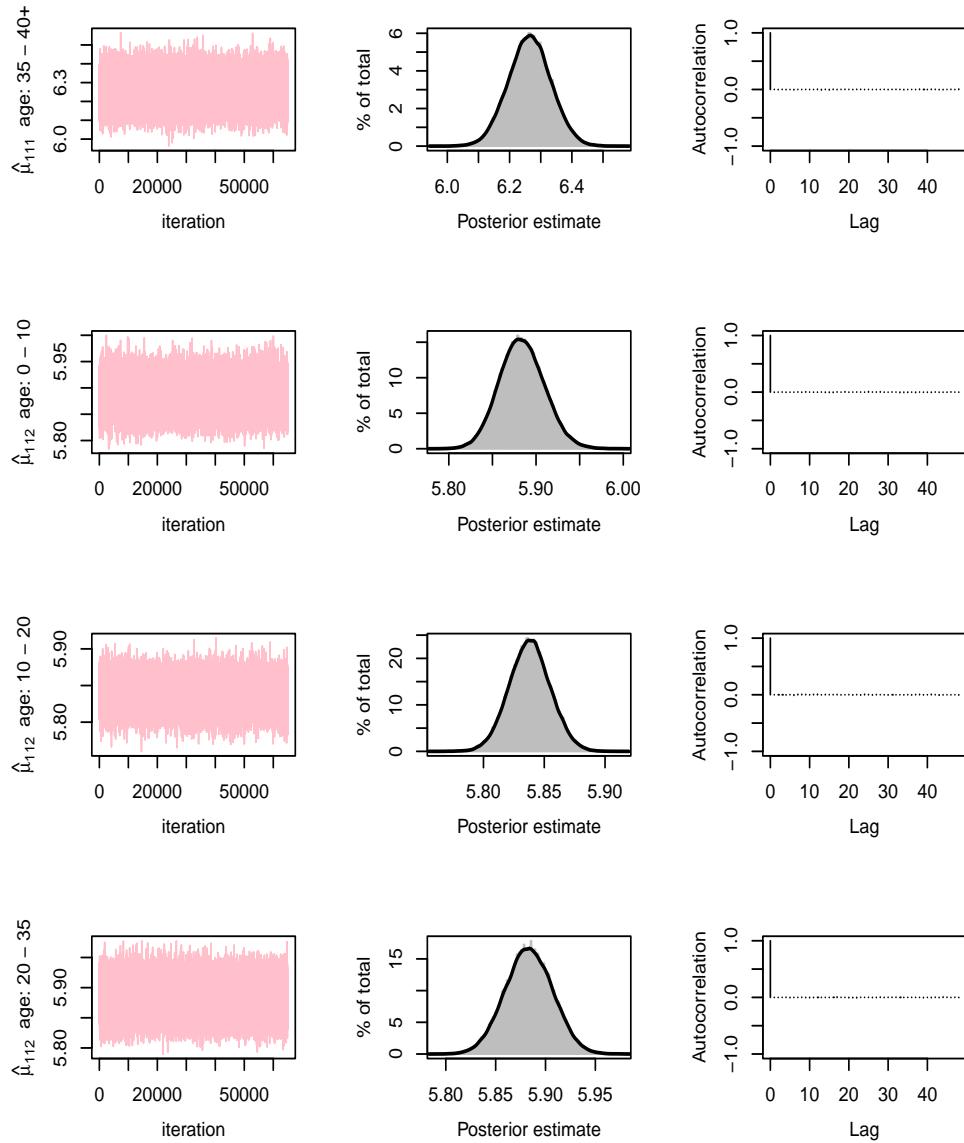
**Figure C.1.** Model convergence diagnostics: Trace plots (left panel), posterior distribution (middle panel) and auto-correlation plots (right panel). The MCMC algorithm was run for 100,000 iterations to ensure convergence excluding the initial 35,000 iterations so that the remaining 65,000 samples (single chain) was used to estimate the posterior distributions of the model parameters.



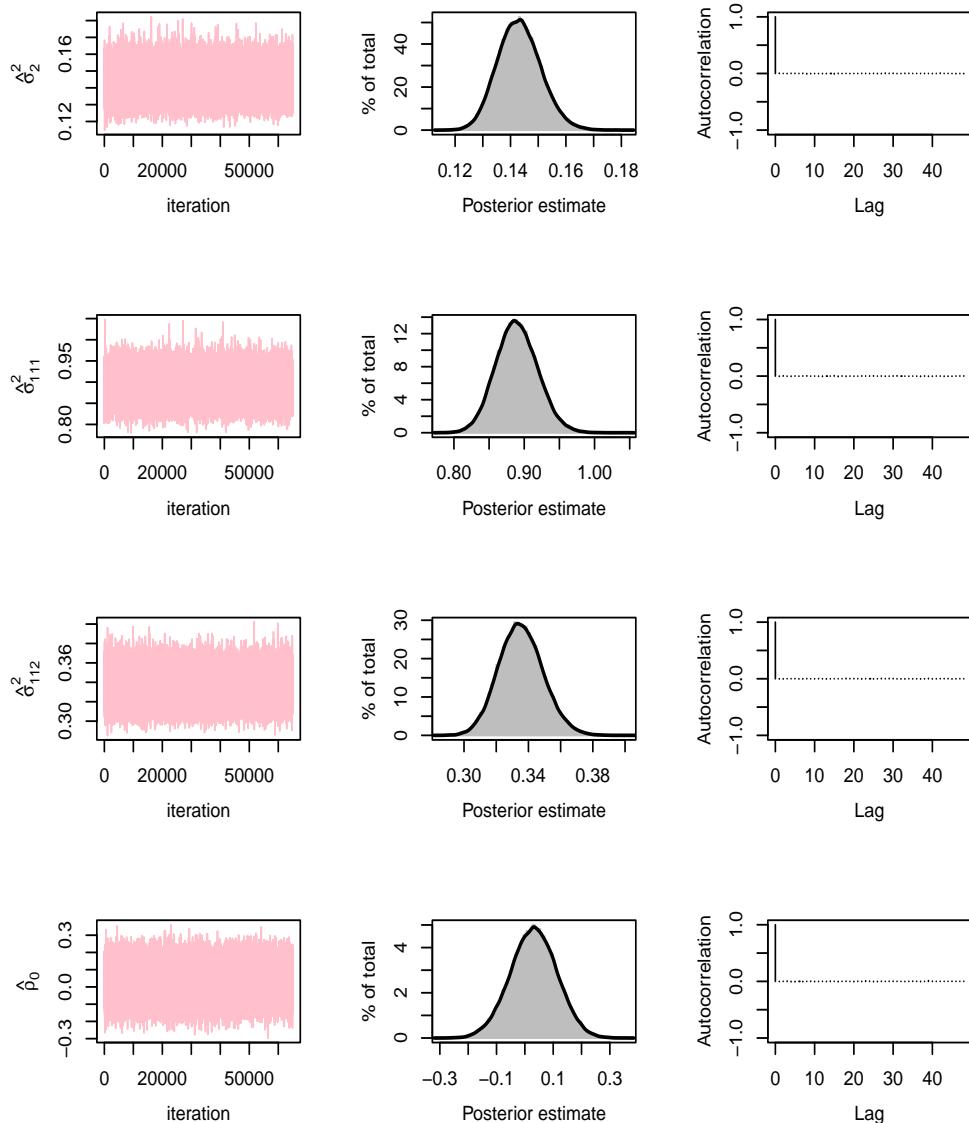
**Figure C.2.** Model convergence diagnostics: Trace plots (left panel), posterior distribution (middle panel) and auto-correlation plots (right panel). The MCMC algorithm was run for 100,000 iterations to ensure convergence excluding the initial 35,000 iterations so that the remaining 65,000 samples (single chain) was used to estimate the posterior distributions of the model parameters.



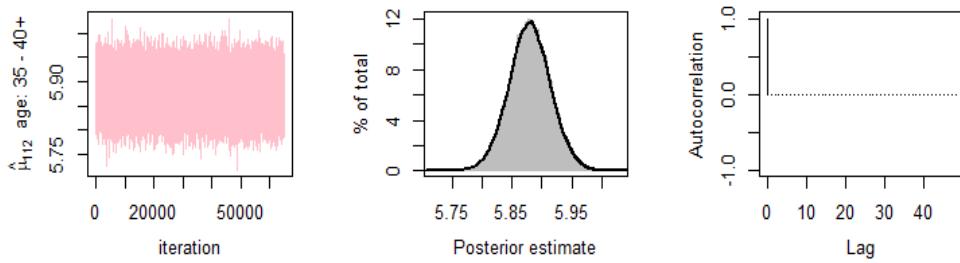
**Figure C.3.** Model convergence diagnostics: Trace plots (left panel), posterior distribution (middle panel) and auto-correlation plots (right panel). The MCMC algorithm was run for 100,000 iterations to ensure convergence excluding the initial 35,000 iterations so that the remaining 65,000 samples (single chain) was used to estimate the posterior distributions of the model parameters.



**Figure C.4.** Model convergence diagnostics: Trace plots (left panel), posterior distribution (middle panel) and auto-correlation plots (right panel). The MCMC algorithm was run for 100,000 iterations to ensure convergence excluding the initial 35,000 iterations so that the remaining 65,000 samples (single chain) was used to estimate the posterior distributions of the model parameters.



**Figure C.5.** Model convergence diagnostics: Trace plots (left panel), posterior distribution (middle panel) and auto-correlation plots (right panel). The MCMC algorithm was run for 100,000 iterations to ensure convergence excluding the initial 35,000 iterations so that the remaining 65,000 samples (single chain) was used to estimate the posterior distributions of the model parameters.



**Figure C.6.** Model convergence diagnostics: Trace plots (left panel), posterior distribution (middle panel) and auto-correlation plots (right panel). The MCMC algorithm was run for 100,000 iterations to ensure convergence excluding the initial 35,000 iterations so that the remaining 65,000 samples (single chain) was used to estimate the posterior distributions of the model parameters.

## D. R implementation of the Bayesian bivariate mixture model

The Bayesian bivariate skew-normal mixture models applied to the serological data taken from the results of a survey of IgG antibodies to parvovirus PVB19 and VZV in the main text of Section 4 are implemented in the statistical software package R version 4.3.0 (R Development Core Team 2023). We provide the R program to fit the proposed models. In order to run the R-code provided here, one requires (1) a vector  $a$  of individual's ages; (2) vectors of the log-transformed IgG antibodies  $y_1$  and  $y_2$  for VZV and PVB19, respectively.

```

writeLines("
model{
for(i in 1:Nsub){
Z[i,1:Nvar] ~ dmnorm(zMu[i,1:Nvar],zInvCovMat[Y[i],1:Nvar,1:Nvar])
Y[i] ~ dcat(P[agegroup[i],])
b[i] ~ dnorm(0,1)T(0,)
zMu[i,1] <- mu1[agegroup1[i],Y[i]] # Mean IgG antibodies VZV
zMu[i,2] <- mu2[agegroup1[i],Y[i]] + w[Y[i]]*b[i] # Mean IgG antibodies B19
logLike[i] <- logdensity.mnorm(Z[i,1:Nvar], zMu[i,1:Nvar],zInvCovMat[Y[i],
1:Nvar,1:Nvar])
}
#-----
# Mixing proportions
#-----
for(t in 1:Nage){
m1[t] <- inprod(beta1[], X[t,]) + inprod(b1[], Z1[t,])
m2[t] <- inprod(beta2[], X[t,]) + inprod(b1[], Z1[t,])
#-----
EP1[t] <- 1/(1+exp(-(m1[t]/(sqrt(1+sigmau1*pow((16*sqrt(3))/(15*3.14153),
2))))))
EP2[t] <- 1/(1+exp(-(m2[t]/(sqrt(1+sigmau2*pow((16*sqrt(3))/(15*3.14153),
2))))))
P[t,1] <- (1 - EP1[t])*(1 - EP2[t]) # P00=(B19=0 and VZV=0)
P[t,2] <- (1 - EP1[t])*EP2[t] # P01=(B19=1 and VZV=0)
P[t,3] <- EP1[t]*(1-EP2[t]) # P10=(B19=0 and VZV=1)
P[t,4] <- EP1[t]*EP2[t] # P11=(B19=1 and VZV=1)
S1[t] <- P[t,2] + P[t,1]
S2[t] <- P[t,3] + P[t,1]
}
for(j in 1:Nknots){b1[j] ~ dnorm(0, taub)}
#-----
for(q in 1:Km){
mu1[q,2] <- mu1[q,1] # Negative VZV
mu2[q,2] ~ dnorm(0,0.001)T(mu2[q,1],) # Positive B19
mu1[q,3] ~ dnorm(0,0.001)T(mu1[q,1],) # Positive VZV
}
}
```

```

mu2[q,3] <- mu2[q,1] # Negative B19
mu1[q,4] <- mu1[q,3] # Positive VZV
mu2[q,4] <- mu2[q,2] # Positive B19
}
#-----
mu1[1,1] ~ dnorm(0,0.001) # Negative VZV
mu2[1,1] ~ dnorm(0,0.001) # Negative B19
mu1[2,1] <- mu1[1,1]
mu2[2,1] <- mu2[1,1]
mu1[3,1] <- mu1[1,1]
mu2[3,1] <- mu2[1,1]
mu1[4,1] <- mu1[1,1]
mu2[4,1] <- mu2[1,1]
#-----
mu_Neg_vzv <- mu1[1,1]
mu_Neg_b19 <- mu2[1,1]
mu_Pos_vzv[1:4] <- mu1[1:4,4]
mu_Pos_b19[1:4] <- mu2[1:4,4]
#-----
# variance-covariance matrices-density components
rho00 ~ dunif(-1,1)
sig11 ~ dgamma(0.01,0.01) # standard deviation 1
sig12 ~ dgamma(0.01,0.01) # standard deviation 2
zCovMat[1,1,1] <- sig11*sig11
zCovMat[1,2,2] <- sig12*sig12
zCovMat[1,1,2] <- rho00*sqrt(zCovMat[1,1,1]*zCovMat[1,2,2])
zCovMat[1,2,1] <- zCovMat[1,1,2]
#-----
rho01 ~ dunif(-1,1)
zCovMat[2,1,1] <- zCovMat[1,1,1]
zCovMat[2,2,2] <- zCovMat[4,2,2]
zCovMat[2,1,2] <- rho01*sqrt(zCovMat[2,1,1]*zCovMat[2,2,2])
zCovMat[2,2,1] <- zCovMat[2,1,2]
#-----
rho10 ~ dunif(-1,1)
zCovMat[3,1,1] <- zCovMat[4,1,1]
zCovMat[3,2,2] <- zCovMat[1,2,2]
zCovMat[3,1,2] <- rho10*sqrt(zCovMat[3,1,1]*zCovMat[3,2,2])
zCovMat[3,2,1] <- zCovMat[3,1,2]
#-----
rho11 ~ dunif(-1,1)
sig41 ~ dgamma(0.01,0.01) # standard deviation 1
sig42 ~ dgamma(0.01,0.01) # standard deviation 2

```

```

zCovMat[4,1,1] <- sig41*sig41
zCovMat[4,2,2] <- sig42*sig42
zCovMat[4,1,2] <- rho11*sqrt(zCovMat[4,1,1]*zCovMat[4,2,2])
zCovMat[4,2,1] <- zCovMat[4,1,2]
#-----
# Convert invCovMat to sd and correlation:
zInvCovMat[1,1:2,1:2] <- inverse(zCovMat[1,1:2,1:2])
zInvCovMat[2,1:2,1:2] <- inverse(zCovMat[2,1:2,1:2])
zInvCovMat[3,1:2,1:2] <- inverse(zCovMat[3,1:2,1:2])
zInvCovMat[4,1:2,1:2] <- inverse(zCovMat[4,1:2,1:2])
#-----
sigma2001 <- zCovMat[1,1,1]
sigma2002 <- zCovMat[1,2,2]
sigma2111 <- zCovMat[4,1,1]
sigma2112 <- zCovMat[4,2,2]
#-----
w[1] <- 0          # Negative B19
w[2] ~ dnorm(0,0.01) # Positive B19
w[3] <- w[1]        # Negative B19
w[4] <- w[2]        # Positive B19
alpha <- w[2]/sqrt(sigma2112)
Omega <- sigma2112+pow(w[2],2)
#-----Prior Distributions-----
taub <- 1/sigmab
sigmab ~ dunif(0.01, 100)
sigmau1 ~ dunif(0.01, 100)
sigmau2 ~ dunif(0.01, 100)
for(l in 1:2){
  beta1[l] ~ dnorm(0,1.0E-6)
  beta2[l] ~ dnorm(0,1.0E-6)
}
#-----
}
", con="FinalModel.txt")
ModelFile <- 'FinalModel.txt'

```

## References

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