Modeling multivariate, overdispersed binomial data with additive and multiplicative random effects

Supplementary material

DEL FAVA, Emanuele; SHKEDY, Ziv; AREGAY, Mehreteab & MOLENBERGHS, Geert (2014) Modeling multivariate, overdispersed binomial data with additive and multiplicative random effects. In: Statistical modelling, 14 (2), p. 99-133.

DOI: 10.1177/1471082X13503450
Handle: http://hdl.handle.net/1942/16620

Supplementary Material to Modeling Multivariate, Overdispersed Binomial Data with Additive and Multiplicative Random Effects

Emanuele Del Fava[1,2], Ziv Shkedy[1], Mehreteab Aregay[3], and Geert Molenberghs[1,3]

[1]I-BioStat, Hasselt University, Diepenbeek, Belgium.

[2]DONDENA Centre for Research on Social Dynamics, Bocconi University, Milan, Italy.

[3]I-BioStat, Catholic University of Leuven, Leuven, Belgium.

This appendix provides supplementary material for the analyses presented in Del Fava *et al.* (2013), giving more details about the output of the presented models. Section 1 gives details about the convergence assessment of the variance components for the models discussed in Section 3 in Del Fava *et al.* (2013). Section 2 presents individual prevalence and marginal prevalence profiles, estimated by the models discarded by the selection criteria. In Section 3 we discuss the implementation of the models in the JAGS software and in Section 4 the raw data are presented. An Excel file with the data is available upon request from the first authour at the following e-mail address: emanuele.delfava@unibocconi.it.

1 Convergence Assessment for the Variance Components

Tables 1–3 present the posterior means, with their respective 95% credible intervals (CI), of the variance components of each of the models, as well as the convergence diagnostic statistics that were used for convergence assessment, namely, the potential scale reduction factor $\hat{R}$ (Gelman and Rubin, 1992) and the Geweke's Z-diagnostic (Geweke, 1992). For Gelman and Rubin's

statistic, approximate convergence is diagnosed when the factor approaches one. As a practical rule of thumb, we consider a 0.975 quantile for $\hat{R} \leq 1.2$ to be sufficient to claim convergence (Smith, 2007). Geweke's diagnostic tool compares the mean and variance of the monitored parameter at various points in the chain and whose Z-score has an asymptotic standard normal distribution in case of convergence.

Table 1: Posterior mean, C.I., and convergence measures for the variance parameters of the basic model.

Model	Par.	Post. Mean (C.I.)	Upper C.I. $\hat{R}$	Geweke's Z
(3.2)	σ_{γ_1}	0.57 (0.42–0.80)	1.01	0.68
	σ_{γ_2}	0.84 (0.60–1.20)	1.01	−0.37
	ρ_γ	0.70 (0.42–0.88)	1	−0.58

Table 2: Posterior mean, C.I., and convergence measures for the variance parameters of the additive overdispersion models.

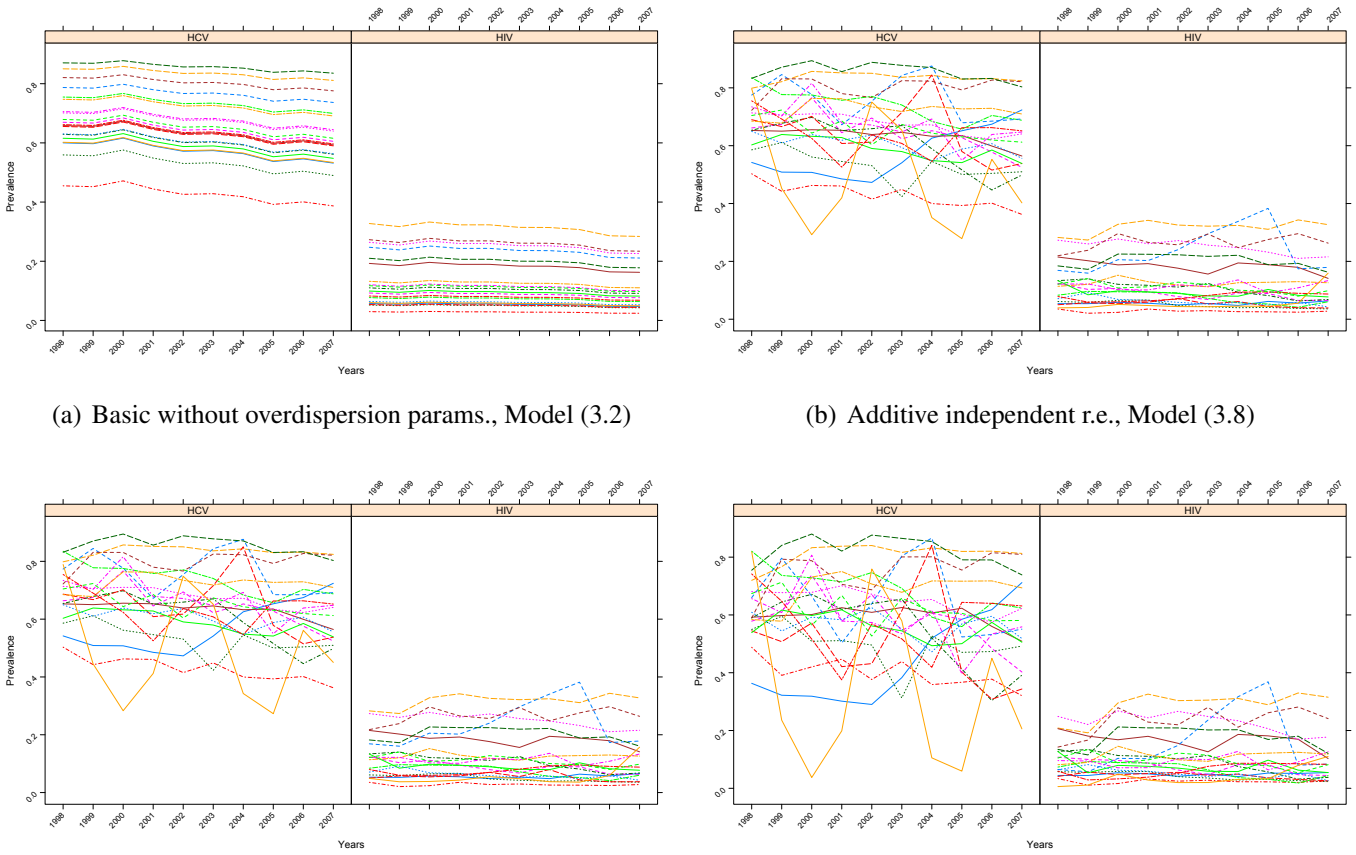
Model	Par.	Post. Mean (C.I.)	Upper C.I. $\hat{R}$	Geweke's Z
(3.7)	σ_{γ_1}	0.58 (0.42–0.80)	1.01	−0.85
	σ_{γ_2}	0.83 (0.60–1.18)	1.02	−2.00
	ρ_γ	0.70 (0.41–0.87)	1.01	−1.71
	σ_θ	0.30 (0.27–0.34)	1	−0.46
	δ	0.64 (0.58–0.69)	1	0.98
(3.8)	σ_{γ_1}	0.58 (0.43–0.82)	1	0.33
	σ_{γ_2}	0.84 (0.61–1.21)	1.01	−0.23
	ρ_γ	0.70 (0.41–0.88)	1	0.98
	σ_{θ_1}	0.31 (0.27–0.35)	1.01	−1.33
	σ_{θ_2}	0.25 (0.21–0.29)	1	0.87
(3.10)	σ_{γ_1}	0.58 (0.43–0.80)	1	0.23
	σ_{γ_2}	0.83 (0.60–1.18)	1.01	0.40
	ρ_γ	0.70 (0.43–0.88)	1.03	0.40
	σ_{θ_1}	0.32 (0.28–0.36)	1.01	1.20
	σ_{θ_2}	0.27 (0.23–0.30)	1.01	0.34
	ρ_θ	0.36 (0.18–0.53)	1	0.72
(3.11)	σ_{γ_1}	0.58 (0.42–0.82)	1.01	0.20
	σ_{γ_2}	0.85 (0.61–1.18)	1	−0.66
	ρ_γ	0.72 (0.45–0.89)	1	−0.99
	$\rho_{\theta_{1998}}$	−0.09 (−0.61–0.45)	1	−0.30
	$\rho_{\theta_{1999}}$	−0.04 (−0.50–0.43)	1.03	−1.72
	$\rho_{\theta_{2000}}$	0.08 (−0.45–0.59)	1.03	1.43
	$\rho_{\theta_{2001}}$	0.17 (−0.30–0.59)	1.03	0.29
	$\rho_{\theta_{2002}}$	−0.12 (−0.61–0.44)	1	−0.65
	$\rho_{\theta_{2003}}$	0.17 (−0.34–0.61)	1	−0.84
	$\rho_{\theta_{2004}}$	0.44 (−0.05–0.78)	1	−0.68
	$\rho_{\theta_{2005}}$	0.19 (−0.32–0.63)	1	2.71
	$\rho_{\theta_{2006}}$	0.47 (0.05–0.77)	1	0.24
	$\rho_{\theta_{2007}}$	0.14 (−0.36–0.60)	1	0.30

Table 3: Posterior mean, C.I., and convergence measures for the variance parameters of the multiplicative overdispersion models.

Model	Par.	Post. Mean (C.I.)	Upper C.I. $\hat{R}$	Geweke's Z
(3.13)	σ_{γ_1}	0.68 (0.43–1.08)	1	−0.37
	σ_{γ_2}	0.84 (0.61–1.16)	1.02	−1.19
	ρ_γ	0.62 (0.17–0.88)	1	−0.15
(3.14)	σ_{γ_1}	0.68 (0.49–0.94)	1	−1.08
	σ_{γ_2}	0.85 (0.62–1.21)	1.01	0.17
	ρ_γ	0.52 (0.12–0.80)	1.01	1.03
	σ_θ	0.02 (0.02–0.03)	1	0.81

2 Graphs for the Discarded Models

In this section, we present the plots of the individual profiles and of the marginal prevalence esrimates by the following models: the additive independent model (3.8), the additive correlated model (3.10), and the multiplicative Be(a,b) model (3.14). Comparing the plots in Figures 1–2 with the respective plots in the manuscript, we notice that there are almost no differences, those being quite small, as also indicated by the MSEs for the in-sample and the out-sample predictions, exhibited in Table 2 of the manuscript.



(a) Basic without overdispersion params., Model (3.2)

(b) Additive independent r.e., Model (3.8)

(c) Additive correlated r.e., Model (3.10)

(d) Multiplicative Be(a,b), Model (3.14)

Figure 1: Individual fitted prevalence profiles of HCV and HIV infections for the 20 Italian regions between 1998 and 2007, resulting from the basic model not accounting for overdispersion (panel a) and from the models discarded by the various selection criteria.

3 JAGS Codes for the Fitted Models

In this section, we present the JAGS codes used to fit all the Bayesian hierarchical models presented in the main manuscript. JAGS is a program for the analysis of Bayesian hierarchical models using MCMC simulation and is quite similar to BUGS. Differently from the BUGS programs (WinBUGS and OpenBUGS), JAGS is not only available for Windows and Linux platforms, but also for Apple platforms. All models discussed here can be easily adapted to work also in WinBUGS, after minimal changes in the syntax. We refer to the manual of JAGS (Plummer, 2011) for the main differences between JAGS and BUGS syntax. Similarly to the BUGS programs, JAGS is licensed under the GNU General Public License.

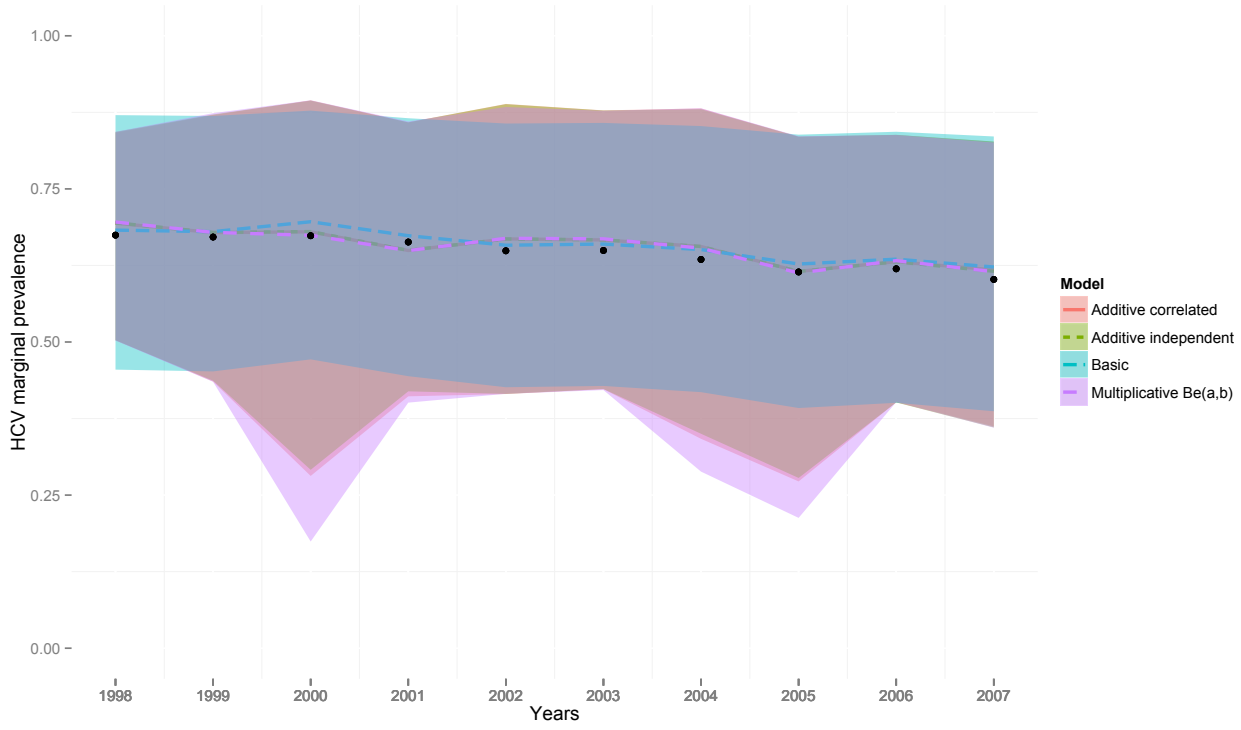
3.1 Basic Model Without Overdispersion Parameters

The basic code for fitting the Bayesian hierarchical models in the main manuscript is presented below. For the overdispersed models, discussed in the subsequent sections, we highlight what must be changed or added.

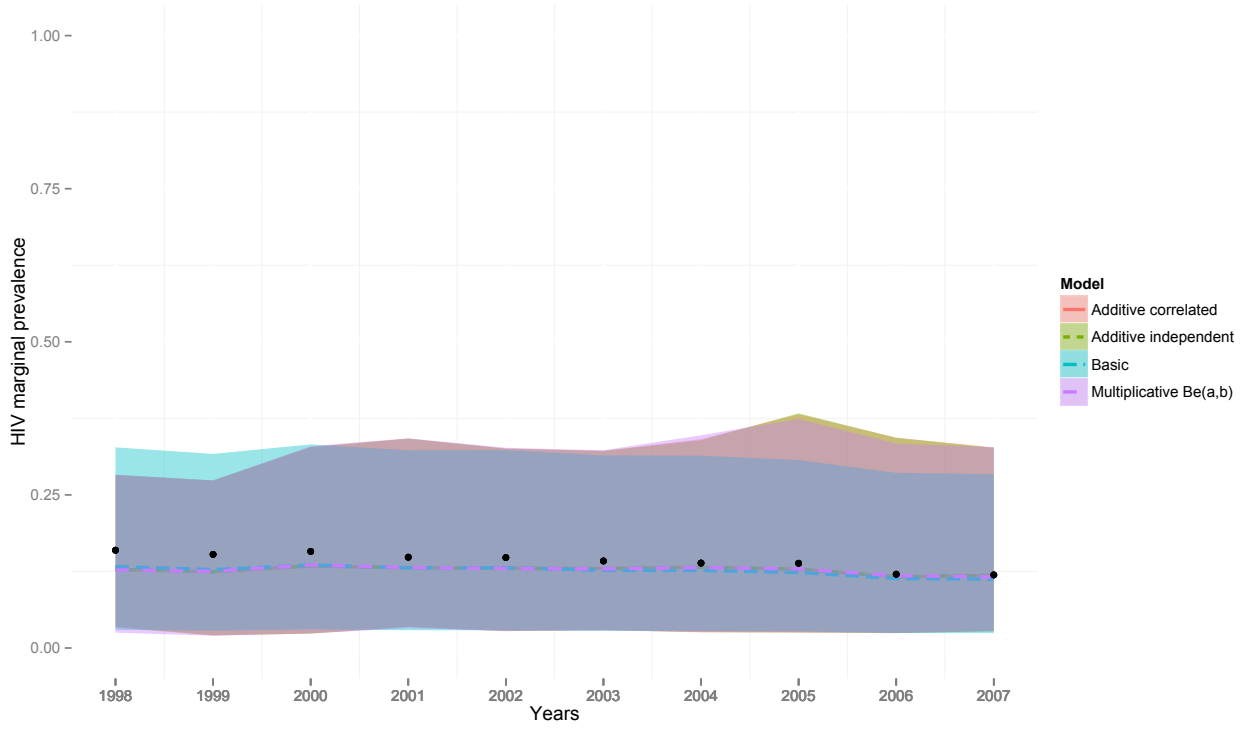
```
model{
for(i in 1:Nreg){
for(j in 1:Ntime){
for(k in 1:Ndis){
events[i,j,k] ~ dbin(p[i,j,k],trials[i,j,k])

#Posterior predictive distribution
y.rep[i,j,k]~dbin(p[i,j,k],trials[i,j,k])
    r2[i,j,k]<-pow(y.rep[i,j,k]-events[i,j,k],2)

#Discrepancy measures between observed and replicated data
r[i,j,k]<-events[i,j,k]-(trials[i,j,k]*p[i,j,k])
sr[i,j,k]<-r[i,j,k]*sqrt(trials[i,j,k]*p[i,j,k]*(1-p[i,j,k]))
r.rep[i,j,k]<-y.rep[i,j,k]-(trials[i,j,k]*p[i,j,k])
```



(a) HCV



(b) HIV

Figure 2: Marginal prevalence π_{jk} for HCV (panel a) and HIV (panel b) with 95% CI, obtained by averaging out all over the regions the prevalence per year j and infection k, from the basic model (blue dashed line), the additive independent model (green dotted line), the additive correlated model (red solid line), and the multiplicative Be(a,b) model (purple dash-and-dot line). The black dots stand for the national observed prevalence, obtained pooling together all the regional prevalences per each year.

```
sr.rep[i,j,k]<-r.rep[i,j,k]*sqrt(trials[i,j,k]*p[i,j,k]*(1-p[i,j,k]))
m3[i,j,k]<-pow(sr[i,j,k],3)
m3.rep[i,j,k]<-pow(sr.rep[i,j,k],3)
}
}
#Model with logit link function
logit(p[i,1,1]) <- gamma[i,1] #HCV
logit(p[i,1,2]) <- gamma[i,2] #HIV
for(j in 2:Ntime){
logit(p[i,j,1]) <- gamma[i,1] + alpha[j-1] #HCV
logit(p[i,j,2]) <- gamma[i,2] + beta[j-1] #HIV
}
}

#Mean squared error of in-sample predictions
mse.y_in<-sum(r2[,,])/(Nreg*Ntime*Ndis)

#Mean squared error of out-sample predictions
#The following line requires that we set all the observed events
#for the last two time points equal to 'NA'
mse.y_out<-sum(r2[,9:10,])/(Nreg*2*Ndis)

#Fixed effects
for(j in 1:(Ntime-1)){
alpha[j] ~ dnorm(0,tau.beta) #unstructured coefficients for HCV
beta[j] ~ dnorm(0,tau.beta) #unstructured coefficients for HIV
}
sigma.beta ~ dunif(0,100)
tau.beta<-pow(sigma.beta,-2)
```

```
#Standard inverse-Wishart for the covariance matrix of random effects
for(i in 1:Nreg){
gamma[i,1:Ndis] ~ dmnorm(beta0[],Omega.gamma[,])
}
for(k in 1:Ndis){
beta0[k] ~ dnorm(0,tau.beta)
}
Omega.gamma[1:Ndis,1:Ndis] ~ dwish(W[,],df)
df<-Ndis
Sigma.gamma[1:Ndis,1:Ndis]<-inverse(Omega.gamma[,])
for(k in 1:Ndis){
for(k.prime in 1:Ndis){
rho.gamma[k,k.prime]<-Sigma.gamma[k,k.prime]/
    sqrt(Sigma.gamma[k,k]*Sigma.gamma[k.prime,k.prime])
}
sigma.gamma[k]<-sqrt(Sigma.gamma[k,k])
}

#Summarizing diagnostics
skew<-mean(m3[,,])
skew.rep<-mean(m3.rep[,,])
p.skew<-step(skew.rep-skew)
cv<-sd(events[,,])/mean(events[,,])
cv.rep<-sd(y.rep[,,])/mean(y.rep[,,])
p.cv<-step(cv.rep-cv)
}
```

3.2 Additive Model with Shared Random Effects

In order to include shared overdispersed parameters in model (3.7), discussed in Section 3.2.1 in the manuscript, we add the following line for the distribution of the θ_{ijk} parameters:

```
theta[i,j] ~ dnorm(0,tau.theta)}
```

Therefore, the initial part of the code can be written (in brief) in the following way:

```
for(i in 1:Nreg){
for(j in 1:Ntime){
for(k in 1:Ndis){
events[i,j,k] ~ dbin(p[i,j,k],trials[i,j,k])
}
theta[i,j] ~ dnorm(0,tau.theta) #distribution of theta
}
logit(p[i,1,1]) <- gamma[i,1] + theta[i,1] #HCV
logit(p[i,1,2]) <- gamma[i,2] + delta*theta[i,1] #HIV
for(j in 2:Ntime){
logit(p[i,j,1]) <- gamma[i,1] + alpha[j-1] + theta[i,j] #HCV
logit(p[i,j,2]) <- gamma[i,2] + beta[j-1] + delta*theta[i,j] #HIV
}
}
```

At the end of the code, outside of any `for` cycle, we need to specify prior distributions for the variance components of θ_{ijk}:

```
#Variance components for overdispersion parameters
sigma.theta ~ dunif(0,100)
tau.theta<-pow(sigma.theta,-2)
```

3.3 Additive Model with Independent Random Effects

The initial part of the code should be changed in the following way:

```
for(i in 1:Nreg){
for(j in 1:Ntime){
for(k in 1:Ndis){
events[i,j,k] ~ dbin(p[i,j,k],trials[i,j,k])
}
theta[i,j,1] ~ dnorm(0,tau.theta[1])
theta[i,j,2] ~ dnorm(0,tau.theta[2])
}
logit(p[i,1,1]) <- gamma[i,1] + theta[i,1,1] #HCV
          logit(p[i,1,2]) <- gamma[i,2] + theta[i,1,2] #HIV
for(j in 2:Ntime){
         logit(p[i,j,1]) <- gamma[i,1] + alpha[j-1] + theta[i,j,1] #HCV
         logit(p[i,j,2]) <- gamma[i,2] + beta[j-1] + theta[i,j,2] #HIV
}
}
```

For the distribution of the variance components of the overdispersion parameters, we add the following code outside of any `for` cycle:

```
#Prior distributions for the variance components of the overdispersion parameters
  for(k in 1:Ndis){
sigma.theta[k] ~ dunif(0,100)
tau.theta[k]<-pow(sigma.theta[k],-2)
}
```

3.4 Additive Model with Correlated Random Effects

The initial part of the code turns into the following one, where the distribution of θ_{ijk} is left out of the `for` cycle and reported below:

```
for(i in 1:Nreg){
for(j in 1:Ntime){
```

```
for(k in 1:Ndis){
events[i,j,k] ~ dbin(p[i,j,k],trials[i,j,k])
}
}
logit(p[i,1,1]) <- gamma[i,1] + theta[i,1,1] #HCV
    logit(p[i,1,2]) <- gamma[i,2] + theta[i,1,2] #HIV
for(j in 2:Ntime){
         logit(p[i,j,1]) <- gamma[i,1] + alpha[j-1] + theta[i,j,1] #HCV
         logit(p[i,j,2]) <- gamma[i,2] + beta[j-1] + theta[i,j,2] #HIV
}
}
```

For the distribution of the variance components of the overdispersion parameters, we add the following lines outside of any `for` cycle:

```
#Standard inverse-Wishart for the covariance matrix of overdispersion parameters
for(i in 1:Nreg){
    for(j in 1:Ntime){
    theta[i,j,1:Ndis] ~ dmnorm(beta0[],Omega.theta[,])
    }
}
Omega.theta[1:Ndis,1:Ndis] ~ dwish(W[,],df)
Sigma.theta[1:Ndis,1:Ndis]<-inverse(Omega.theta[,])
for(k in 1:Ndis){
for(k.prime in 1:Ndis){
rho.theta[k,k.prime]<-Sigma.theta[k,k.prime]/
    sqrt(Sigma.theta[k,k]*Sigma.theta[k.prime,k.prime])
}
sigma.theta[k]<-sqrt(Sigma.theta[k,k])
}
```

The matrix `W[,]` is a two-by-two identity matrix, included as data in the model.

3.5 Additive Model with Time-specific Correlated Random Effects

Compared to the simple additive correlated overdispersion model, here we just need to change the distribution of the time-specific variance components of the distribution of θ_{ijk}:

```
#Standard inverse-Wishart for the covariance matrix of overdispersion parameters
#The correlation of theta is dependent on the years
for(i in 1:Nreg){
for(j in 1:Ntime){
    theta[i,j,1:Ndis] ~ dmnorm(beta0[],Omega.theta[,,j])
}
}
for(j in 1:Ntime){
Omega.theta[1:Ndis,1:Ndis,j] ~ dwish(Q[,,j],df)
Sigma.theta[1:Ndis,1:Ndis,j]<-inverse(Omega.theta[,,j])
for(k in 1:Ndis){
for(k.prime in 1:Ndis){
rho.theta[k,k.prime,j]<-Sigma.theta[k,k.prime,j]/
    sqrt(Sigma.theta[k,k,j]*Sigma.theta[k.prime,k.prime,j])
}
sigma.theta[j,k]<-sqrt(Sigma.theta[k,k,j])
}
}
```

3.6 Multiplicative Models

The Bayesian hierarchical models with multiplicative overdispersion parameters (i.e., models (3.13) and (3.14), presented in Section 3.3 in the manuscript) are slightly different from the models with additive parameters, as it is shown below in the initial part of the code:

```
for(i in 1:Nreg){
for(j in 1:Ntime){
```

```
for(k in 1:Ndis){
events[i,j,k] ~ dbin(p[i,j,k],trials[i,j,k])
p[i,j,k]<-theta[i,j,k]*kappa[i,j,k]
}
theta[i,j,1] ~ dbeta(1,1)
theta[i,j,2] ~ dbeta(1,1)
}
logit(kappa[i,1,1]) <- gamma[i,1] #HCV
      logit(kappa[i,1,2]) <- gamma[i,2] #HIV
for(j in 2:Ntime){
         logit(kappa[i,j,1]) <- gamma[i,1] + alpha[j-1] #HCV
         logit(kappa[i,j,2]) <- gamma[i,2] + beta[j-1] #HIV
}
}
```

For the model with $\theta_{ijk} \sim Be(a,b)$, we have to replace the prior distribution `Beta(1,1)` in lines 7 and 8 with `Beta(a,b)`, and then add, outside of any `for` cycle, the following lines for the distribution of the hyperparameters a and b:

```
#Specification of the variance components of the overdispersion parameters
a ~ dunif(0,100)
b ~ dunif(0,100)
sigma.theta<-(a*b)/(pow(a+b,2)*(a+b+1))
```

4 Data

Table 4: HCV infection data by region and years: number of drug users tested (n) and number of drug users infected (y).

HCV	1998		1999		2000		2001		2002		2003		2004		2005		2006		2007	
REGION	n	y	n	y	n	y	n	y	n	y	n	y	n	y	n	y	n	y	n	y
Abruzzo	1669	902	1329	672	1662	839	2328	1126	2335	1100	1995	1078	1970	1235	1086	713	1894	1283	1983	1444
Basilicata	456	301	488	329	424	329	541	349	607	424	684	425	489	319	559	352	488	280	502	260
Calabria	2401	1407	1821	1115	1724	967	2117	1156	2235	1186	2152	905	2117	1156	2253	1128	2447	1234	1985	1013
Campania	7017	3530	8327	3685	8354	3864	9421	4341	9052	3757	9707	4356	10660	4261	9176	3607	9878	3965	10633	3852
Emilia R.	4968	3964	5333	4378	5159	4421	5261	4482	5476	4657	5611	4692	5649	4764	5480	4551	4949	4118	5244	4323
Friuli V.G.	1233	1035	1295	1007	1403	1088	1474	1117	1308	1009	1595	1181	1996	1362	2245	1474	2228	1569	886	609
Lazio	4187	2732	4250	2763	4054	2655	4000	2614	4253	2715	4540	2933	4171	2638	4603	2925	3714	2225	5467	3084
Liguria	1586	1228	1664	1412	1696	1317	3422	2295	3082	2322	3339	2819	2327	2045	717	484	990	675	1456	1006
Lombardia	15064	10747	15401	10875	14965	10625	15331	10872	14396	9882	14788	9921	14241	9573	14117	8951	13995	8718	12284	7871
Marche	1821	1191	1871	1269	2197	1536	1508	985	2211	1458	1897	1272	2306	1357	2369	1221	2206	979	2521	1255
Molise	295	204	319	212	266	188	207	124	260	157	343	248	116	109	371	214	480	243	410	218
Piemonte	7309	5003	7050	4775	6949	5305	7865	5998	7721	5670	7677	5512	7162	5269	7411	5391	7793	5684	7981	5664
Puglia	7939	4784	6494	4148	7202	4555	6741	4237	5505	3249	5539	3211	6211	3404	6257	3387	6259	3663	7656	4123
Sardegna	2539	1828	2349	1954	2608	2167	2543	1983	2434	1863	2362	1949	2723	2242	2662	2111	2813	2329	2724	2240
Sicilia	3557	2312	3821	2327	4601	2939	5086	3148	4826	3075	5748	3411	6148	3357	5431	3197	5842	3547	6402	3561
Toscana	4600	3379	4802	3376	5544	4531	4507	3059	5190	3485	5733	3709	4876	3376	3723	2042	4865	3106	4500	2914
Trentino A.A.	742	615	782	682	1005	901	677	580	1053	938	953	838	971	846	1006	836	1044	869	1058	848
Umbria	1354	1027	744	516	975	608	1030	537	1416	902	1284	778	1651	896	1014	674	1147	762	1259	823
Valle d'Aosta	176	153	142	61	68	9	60	22	264	209	248	168	74	19	83	15	108	63	98	37
Veneto	5023	3539	5355	3875	3915	2517	4465	3062	6138	3701	4405	2967	5275	3392	4791	3022	5072	3143	5044	3089

Table 5: HIV infection data by region and years: number of drug users tested (n) and number of drug users infected (y).

HIV	1998		1999		2000		2001		2002		2003		2004		2005		2006		2007	
REGION	n	y	n	y	n	y	n	y	n	y	n	y	n	y	n	y	n	y	n	y
Abruzzo	1682	89	1370	73	1716	100	2312	127	2216	107	1166	63	1673	77	840	54	1183	68	1068	71
Basilicata	417	57	475	52	295	34	415	40	468	34	559	34	388	36	432	39	460	27	472	27
Calabria	2201	137	1578	95	1461	99	1899	131	2215	103	2025	86	2091	79	1998	79	2197	80	1981	67
Campania	7006	251	8141	163	7293	170	9161	327	8636	240	9804	292	9485	246	7708	196	9837	240	9936	278
Emilia R.	4485	1265	4155	1134	3564	1169	3343	1143	3441	1121	3423	1101	3308	1074	3003	934	2461	849	2634	864
Friuli V.G.	1539	129	1548	154	1573	153	1701	163	1560	155	1645	118	1932	105	2058	103	2167	82	1726	102
Lazio	4541	979	4514	915	4328	813	4251	817	4376	771	4731	736	4052	790	4694	886	3534	636	5299	744
Liguria	1682	277	1653	256	1326	270	2579	520	2413	581	2191	654	1360	469	1475	578	942	161	1439	254
Lombardia	15922	4352	15624	4066	14702	4080	14670	3830	14039	3820	14300	3664	13067	3236	13075	3030	13299	2797	11594	2499
Marche	1852	251	1775	254	1727	210	1220	145	1979	221	1628	205	1811	167	2086	167	1880	112	2252	148
Molise	202	8	222	14	184	9	138	9	155	16	211	11	60	6	326	12	394	13	305	8
Piemonte	7935	901	6641	800	6110	932	6969	903	6951	819	6782	758	5549	700	6158	788	6163	803	6237	788
Puglia	6893	924	5285	445	6136	602	5505	520	4839	431	4590	367	5298	419	5975	618	5826	480	6292	484
Sardegna	2732	594	1982	470	1912	568	1889	501	1528	392	1364	404	1702	420	1542	426	1381	414	1565	413
Sicilia	3636	259	3659	343	4405	302	4516	296	4376	254	5406	282	5158	292	4635	222	4953	290	5573	233
Toscana	3999	486	3855	471	5027	511	4170	419	4237	503	3972	452	3193	437	3464	314	4292	467	3359	453
Trentino A.A.	667	120	599	100	593	135	374	85	558	126	485	107	503	113	625	117	625	122	722	114
Umbria	1336	104	758	40	870	47	1397	84	1180	80	1196	99	1181	114	953	94	939	89	1040	94
Valle d'Aosta	175	1	180	3	66	2	97	2	100	1	101	1	79	1	92	2	110	9	98	37
Veneto	4749	575	5135	725	4437	478	5163	579	4742	610	4902	589	5439	545	4709	451	4657	369	4184	411

References

Gelman, A. and Rubin, D.B. (1992) Inference from iterative simulation using multiple sequences. *Statistical Science*, **7**, 457–511.

Geweke, J. (1992) Evaluating the accuracy of sampling-based approaches to calculating posterior moments. In *Bayesian Statistics 4* (ed. Bernado, J.M., Berger, J.O., Dawid, A.P., and Smith, A.F.M.). Oxford, UK: Clarendon Press.

Plummer, M. (2011) JAGS Version 3.3. 0 user manual. International Agency for Research on Cancer.

Smith, B.J. (2007) Boa: An R package for MCMC output convergence assessment and posterior inference. *Journal of Statistical Software*, **21**, 1–37.