

Supplementary information for

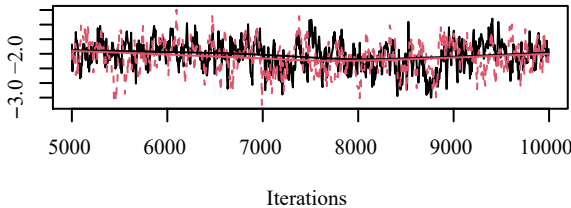
Identifying hotspots in the distribution of human infectious diseases using a Bayesian framework: A lead to drivers, prevention, and surveillance of disease emergence

This PDF contains:

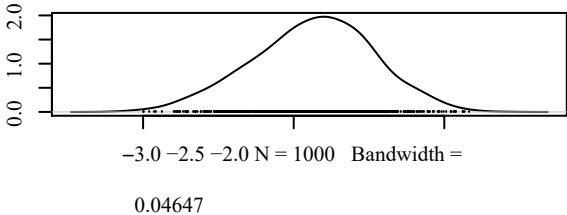
- MCMC traceplots: pages 2-46
- MCMC model summaries: pages 47- 63
- True Skill Statistic (TSS) plots: pages 64-66
- ZIB iCAR random effects: pages 67-69
- Significant hotspots based on TSS: pages 70-72
- Table1: Reservoirs of diseases analyzed: pages 73 - 75
- Analysis of Coroviridae outbreak distribution with SARS CoV 2 origins: pages 76 - 84

Figure S1: MCMC traceplots

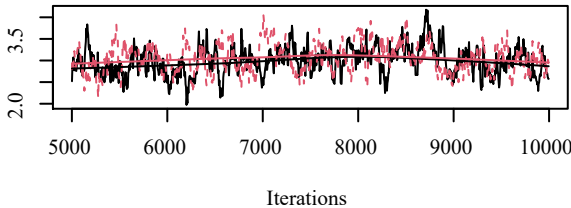
Trace of beta.(Intercept)



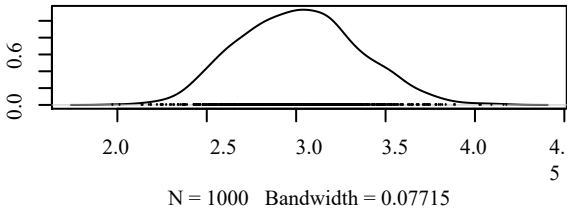
Density of beta.(Intercept)



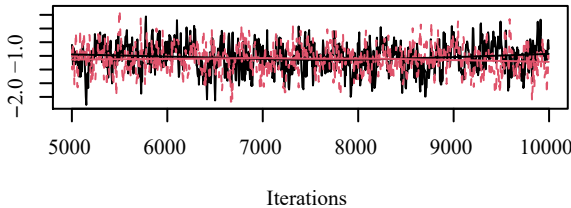
Trace of beta.layer.1



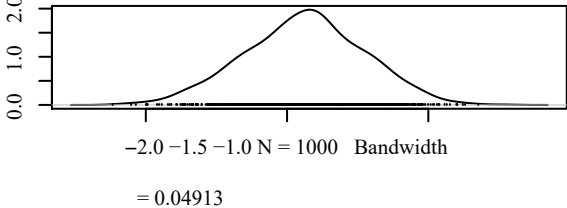
Density of beta.layer.1



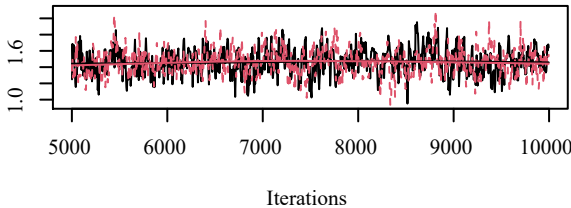
Trace of beta.layer.2



Density of beta.layer.2



Trace of beta.layer



Density of beta.layer

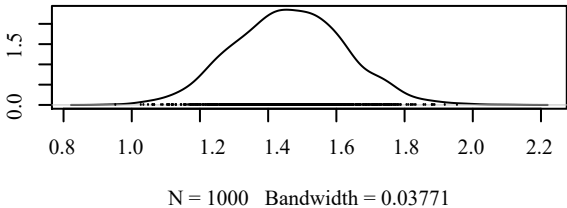
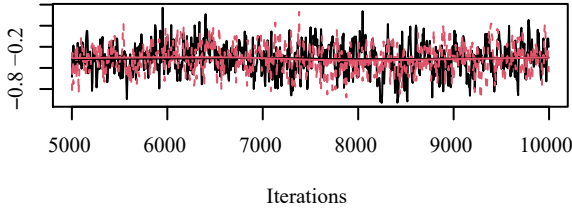
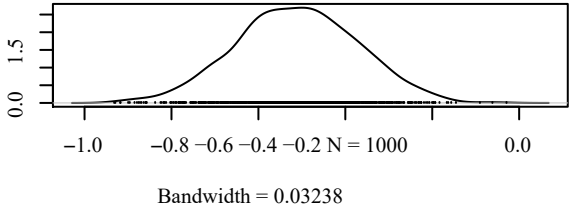


Figure S1: MCMC
traceplots

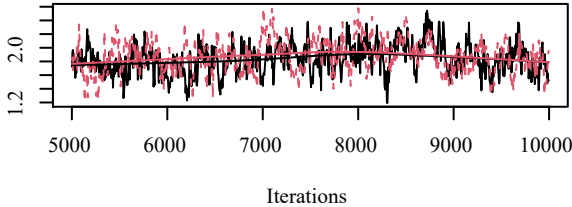
Trace of beta.lc



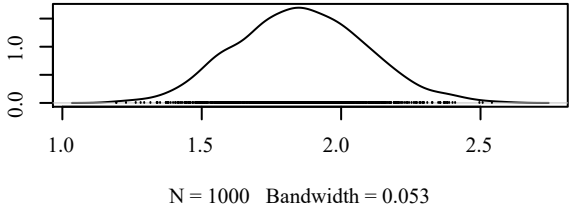
Density of beta.lc



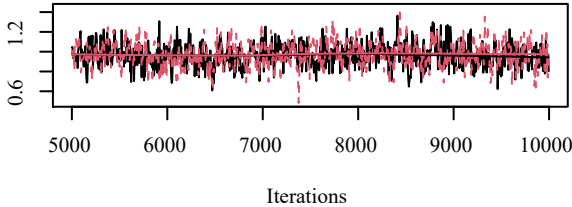
Trace of beta.alt



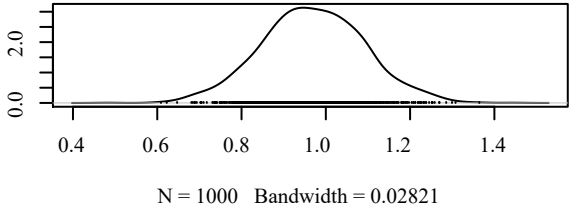
Density of beta.alt



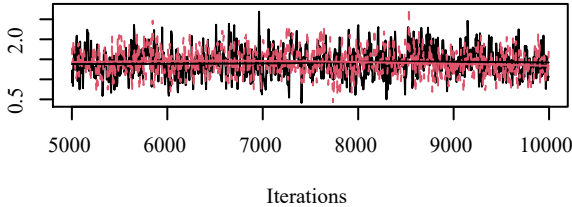
Trace of beta.lc_modi



Density of beta.lc_modi



Trace of beta.pop_den



Density of beta.pop_den

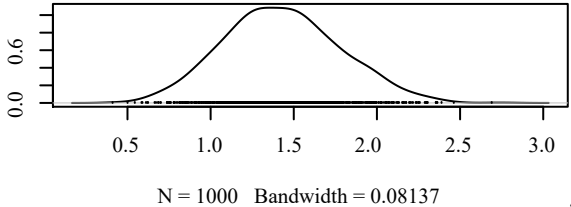
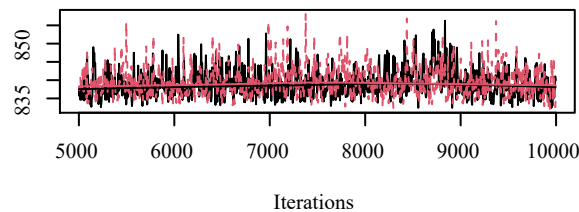
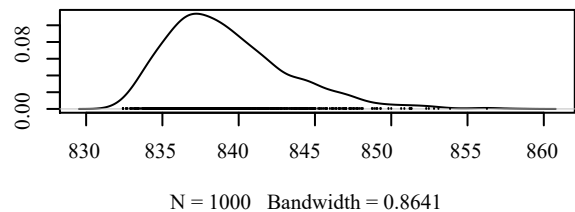


Figure S1: MCMC
traceplots

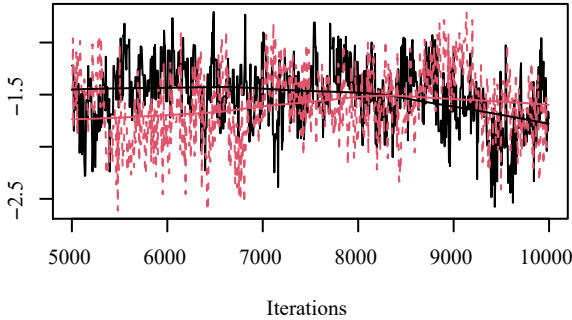
Trace of Deviance



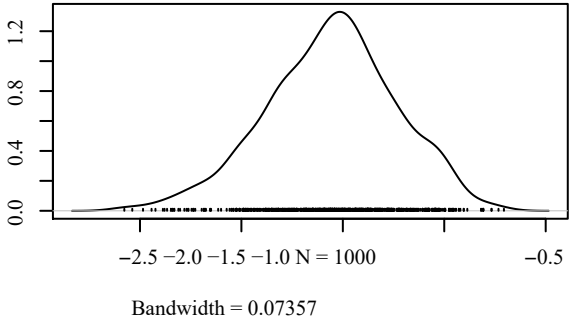
Density of Deviance



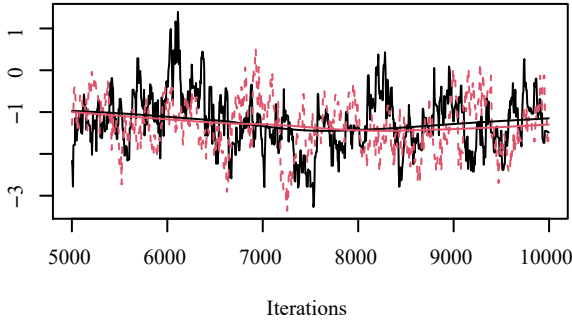
Trace of beta.(Intercept)



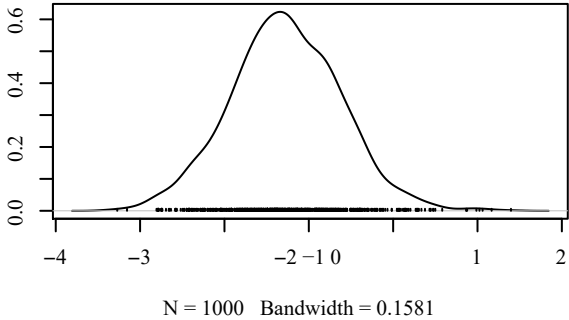
Density of beta.(Intercept)



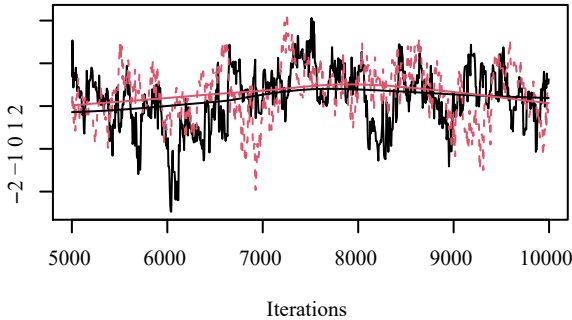
Trace of beta.layer.1



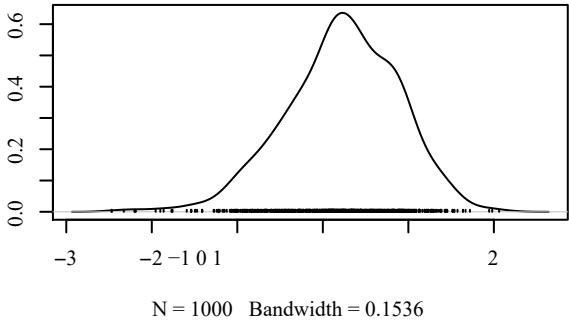
Density of beta.layer.1



Trace of beta.layer.2



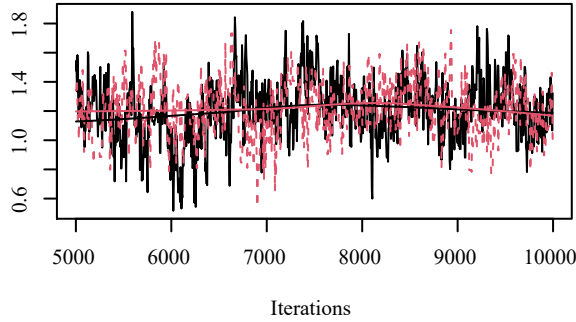
Density of beta.layer.2



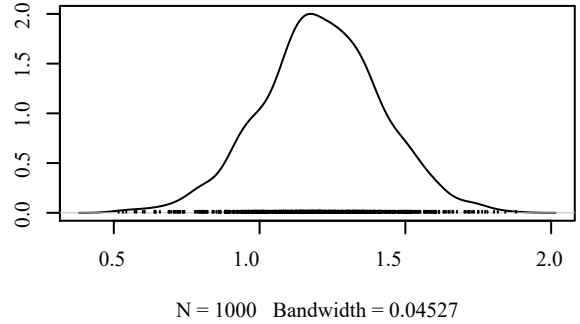
Filoviridae ZIB mcmc traceplot

Figure S1: MCMC
traceplots

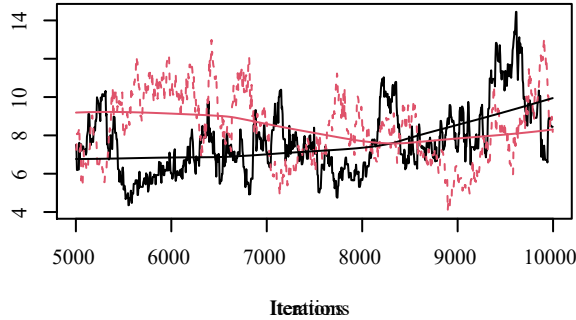
Trace of beta.layer



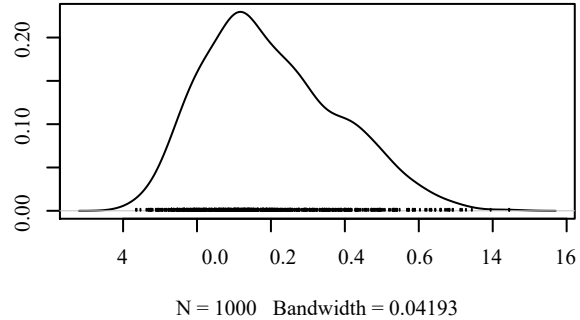
Density of beta.layer



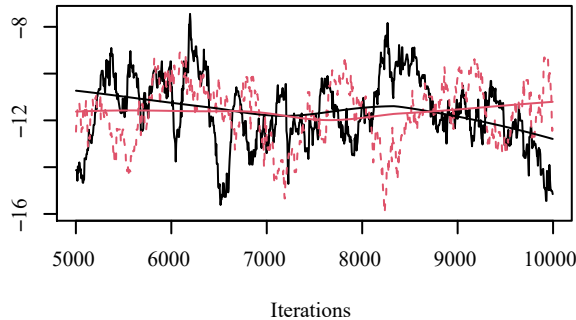
Trace of beta.lc



Density of beta.lc



Trace of beta.alt



Density of beta.alt

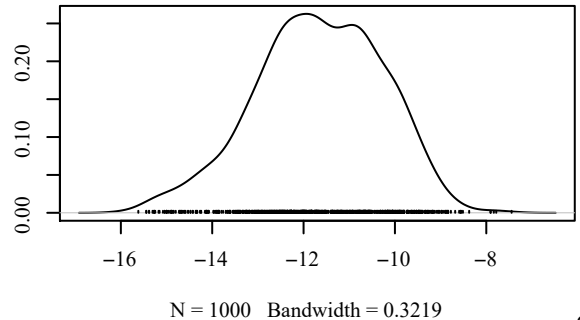
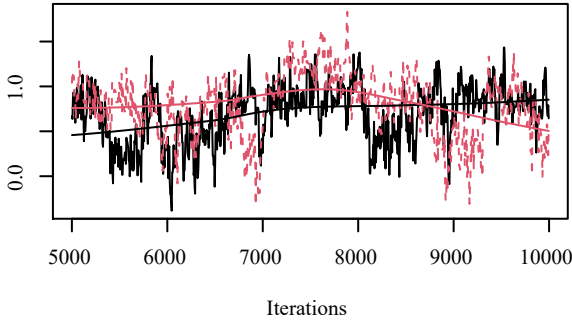
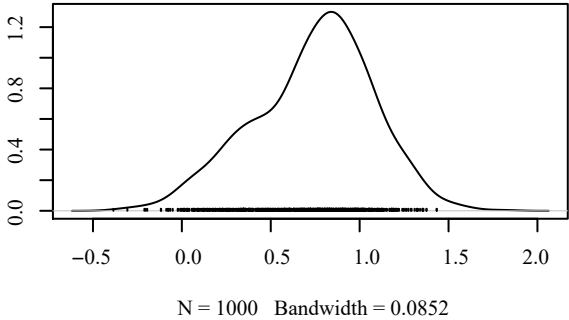


Figure S1: MCMC traceplots

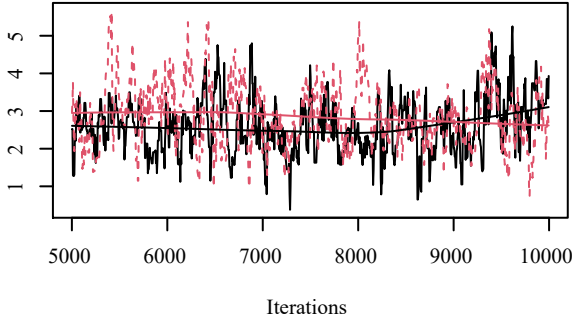
Trace of beta.lc_modi



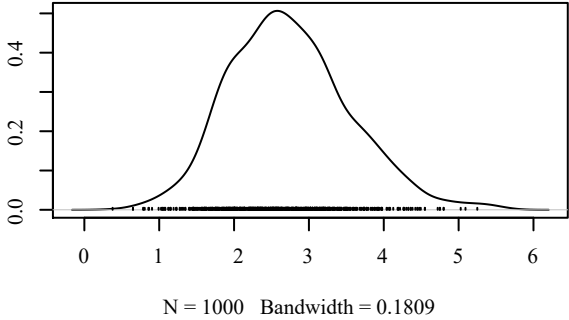
Density of beta.lc_modi



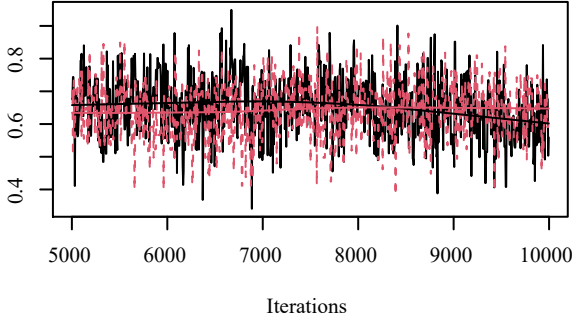
Trace of beta.pop



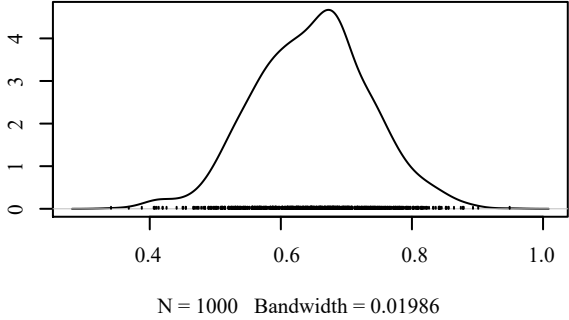
Density of beta.pop_den



Trace of gamma.(Intercept)



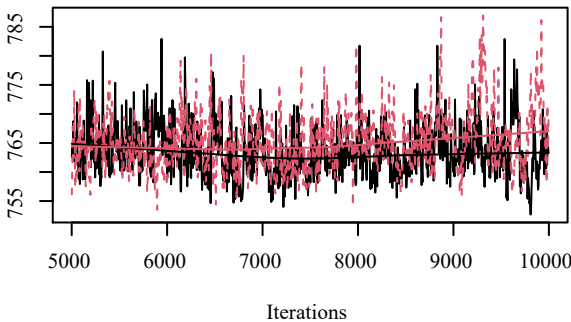
Density of gamma.(Intercept)



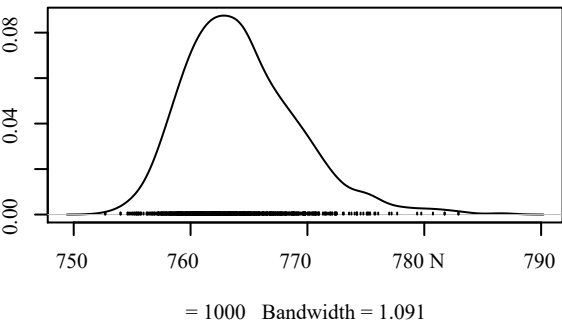
Filoviridae ZIB mcmc traceplot

Figure S1: MCMC
traceplots

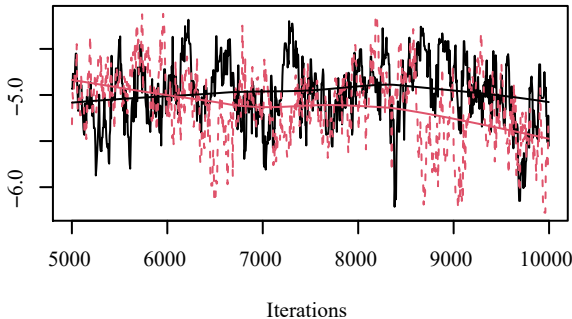
Trace of Deviance



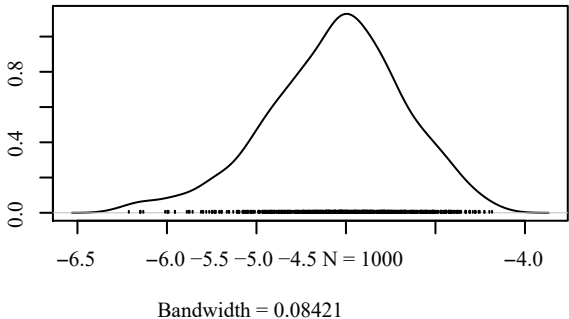
Density of Deviance



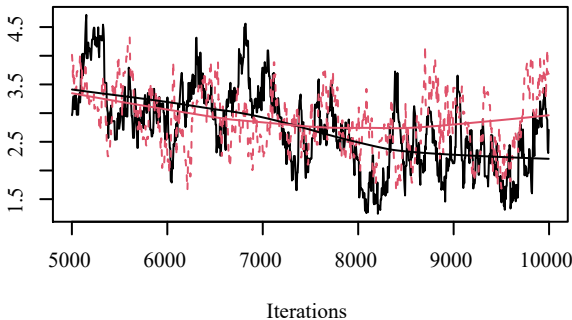
Trace of beta.(Intercept)



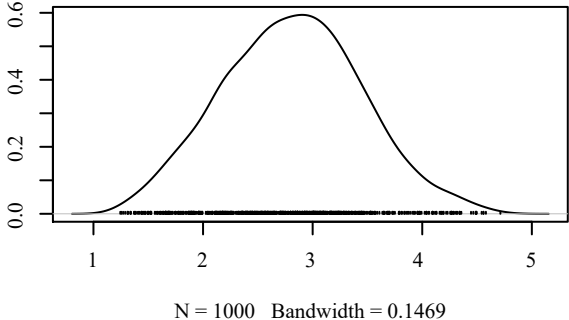
Density of beta.(Intercept)



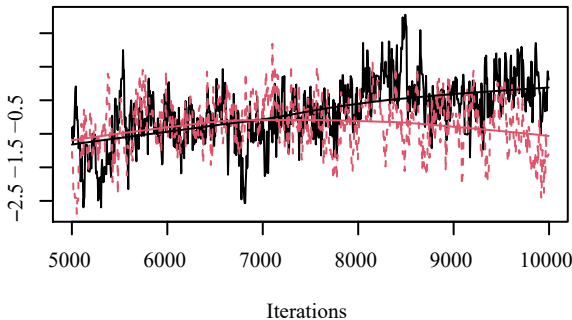
Trace of beta.layer.1



Density of beta.layer.1



Trace of beta.layer.2



Density of beta.layer.2

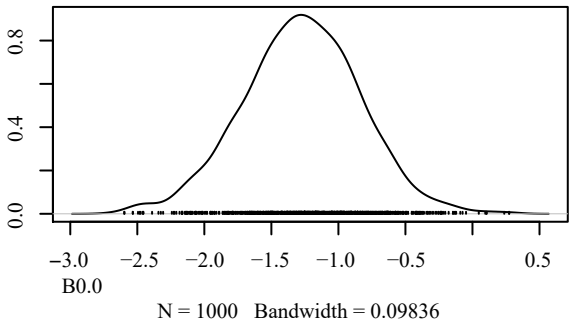
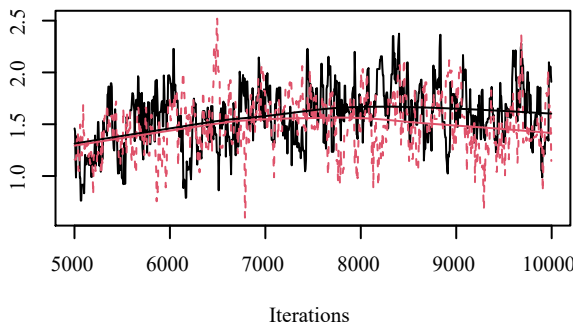
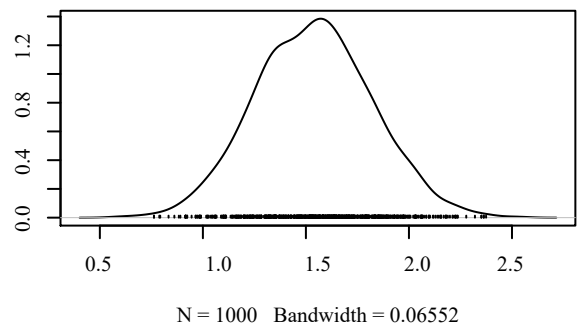


Figure S1: MCMC
traceplots

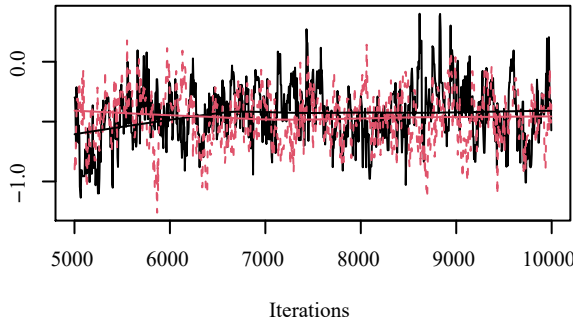
Trace of beta.layer



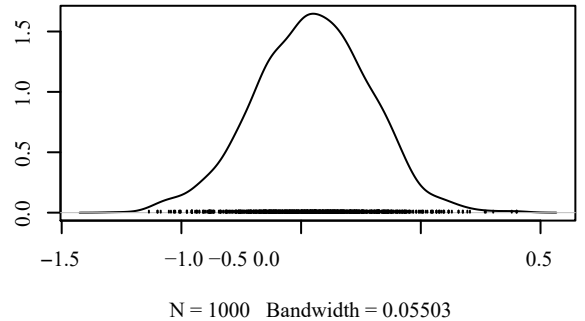
Density of beta.layer



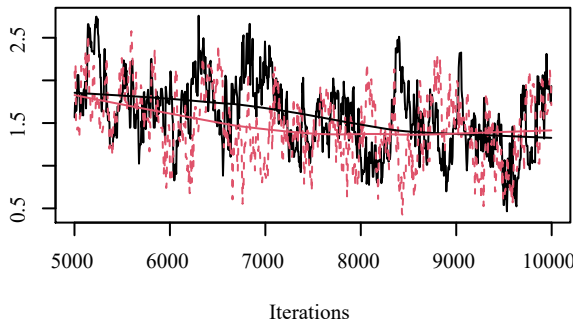
Trace of beta.lc



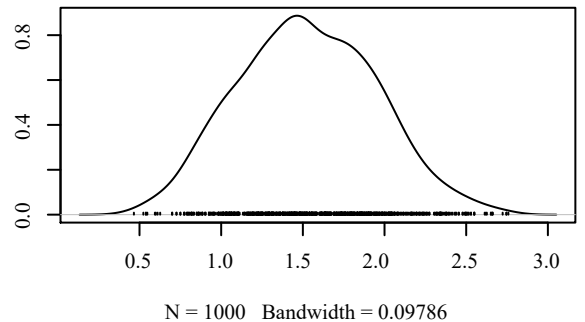
Density of beta.lc



Trace of beta.alt

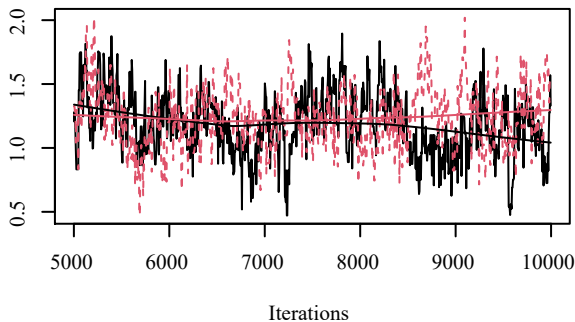


Density of beta.alt

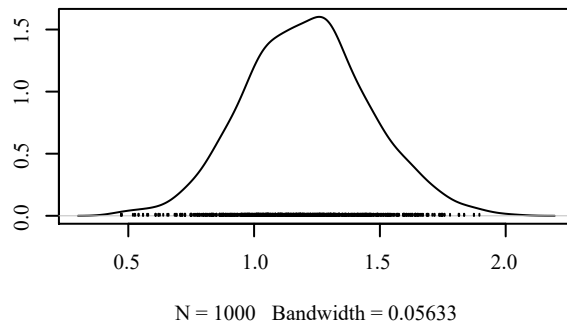


Filoviridae Binomial iCAR memc traceplot

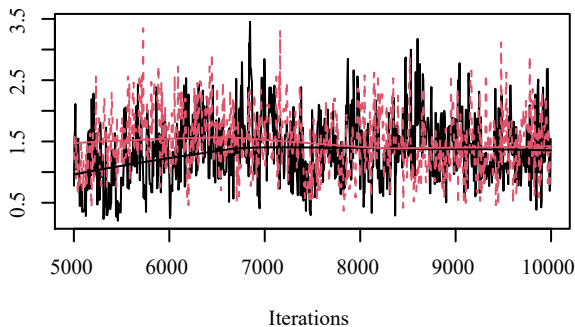
Trace of beta.lc_modi



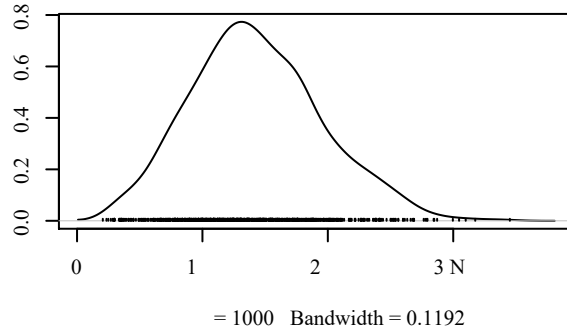
Density of beta.lc_modi



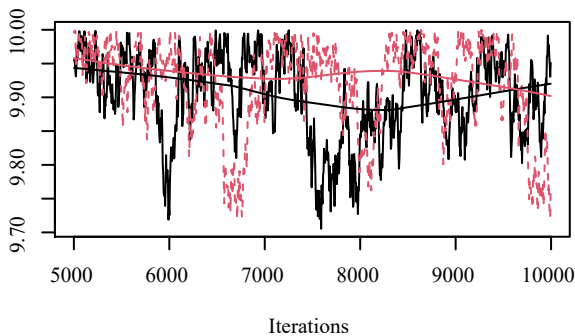
Trace of beta.pop_den



Density of beta.pop_den



Trace of Vrho



Density of Vrho

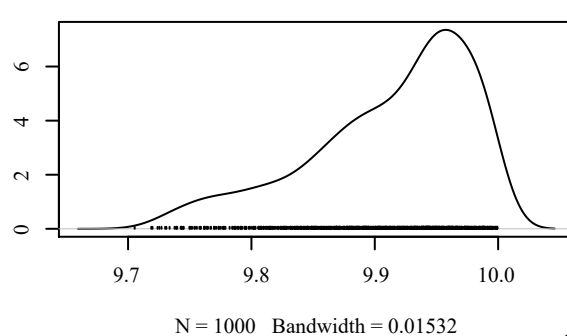
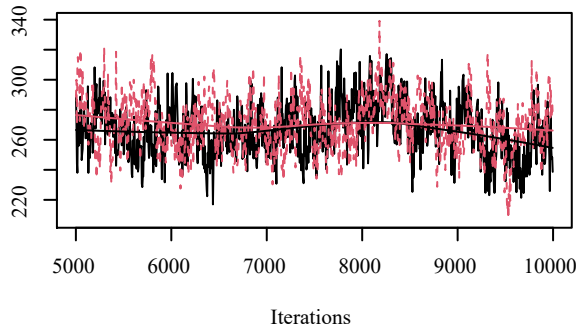


Figure S1: MCMC
traceplots

Trace of Deviance



Density of Deviance

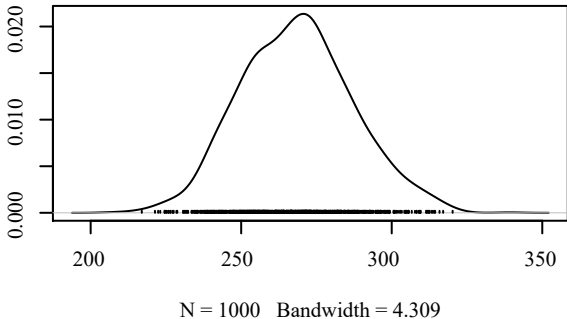
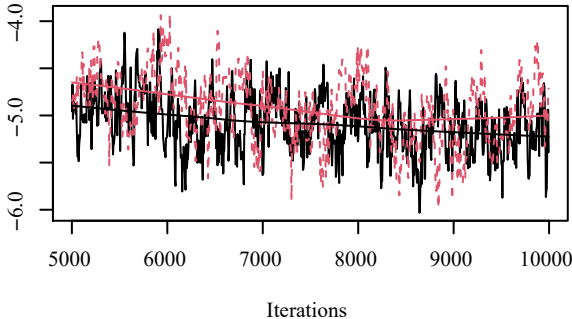
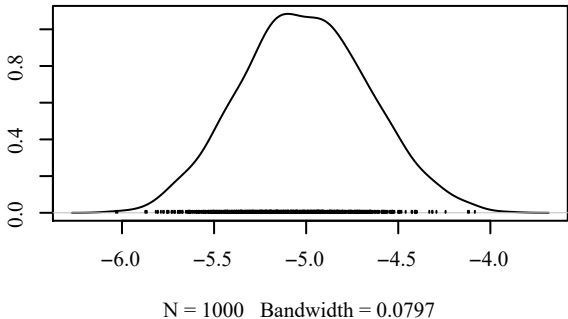


Figure S1: MCMC traceplots

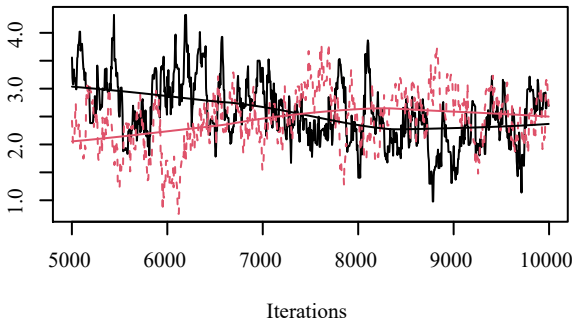
Trace of beta.(Intercept)



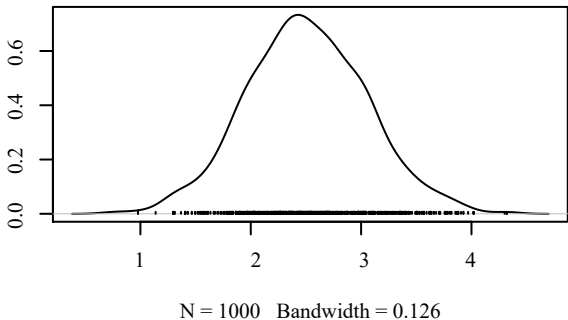
Density of beta.(Intercept)



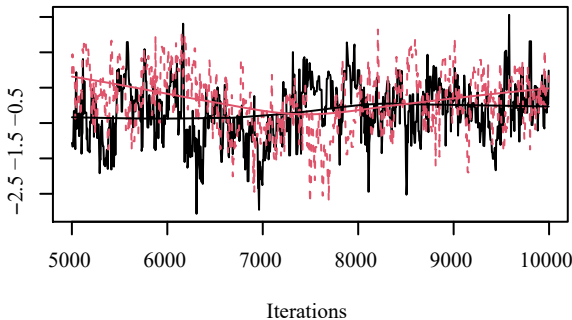
Trace of beta.layer.1



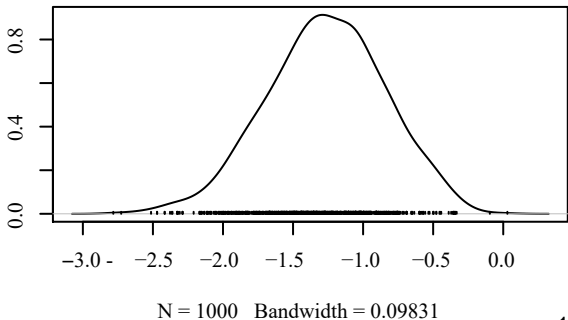
Density of beta.layer.1



Trace of beta.layer.2



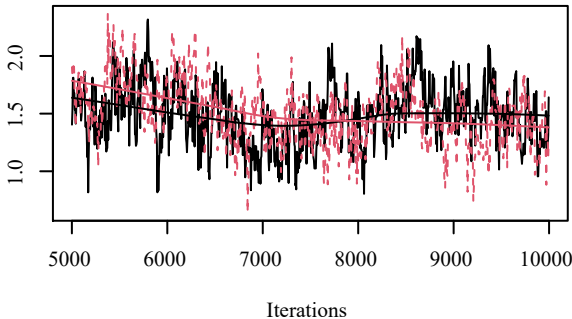
Density of beta.layer.2



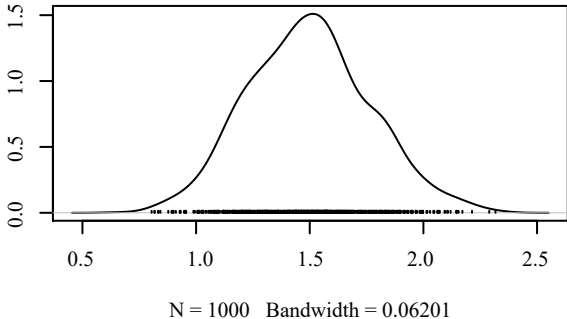
Filoviridae ZIB iCAR memc traceplot

Figure S1: MCMC traceplots

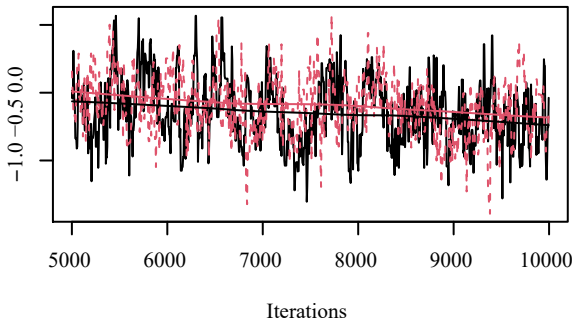
Trace of beta.layer



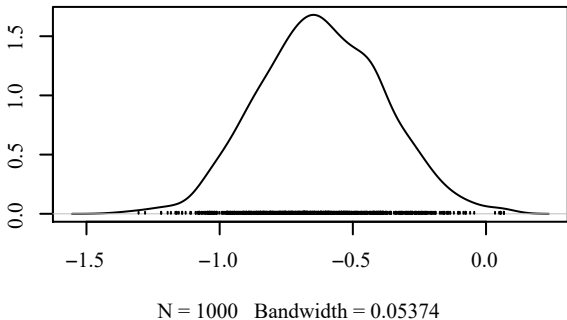
Density of beta.layer



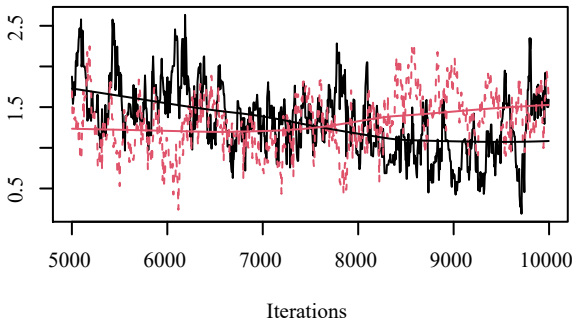
Trace of beta.lc



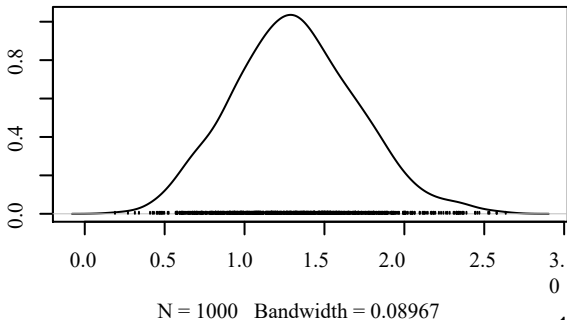
Density of beta.lc



Trace of beta.alt

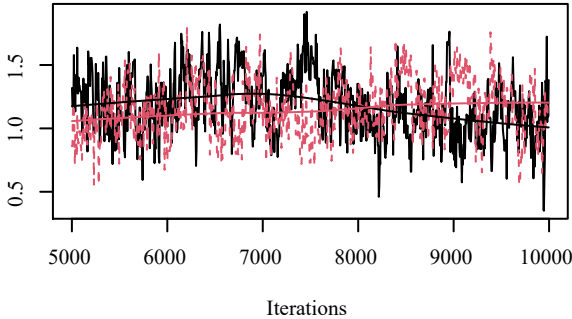


Density of beta.alt

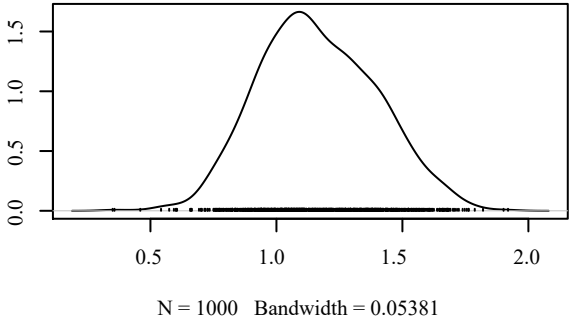


Filoviridae ZIB iCAR mcmc traceplot

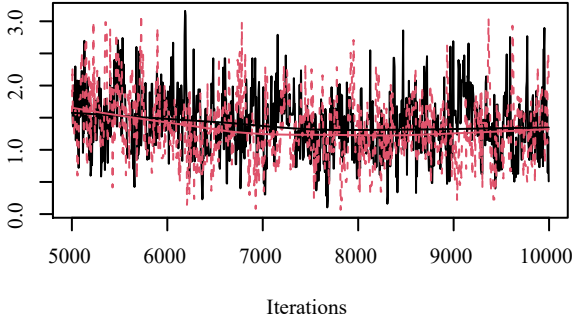
Trace of beta.lc_modi



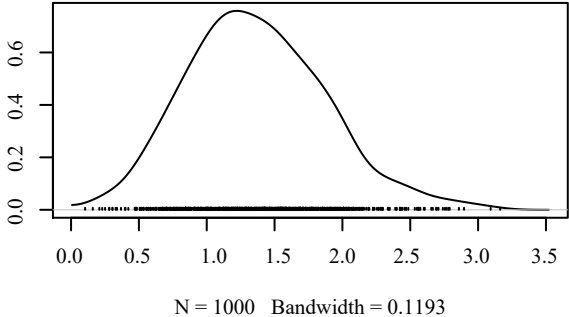
Density of beta.lc_modi



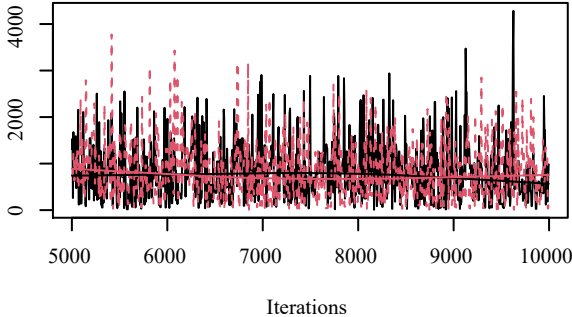
Trace of beta.pop_den



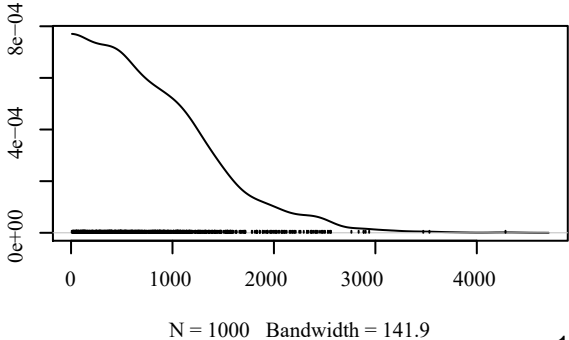
Density of beta.pop_den



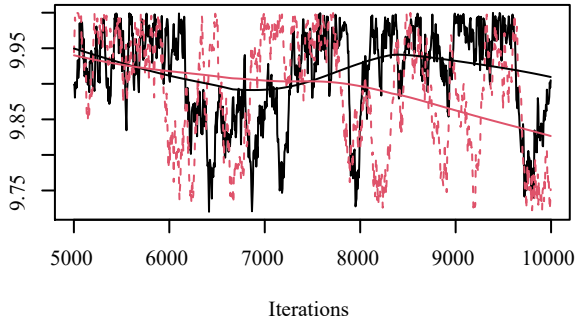
Trace of gamma.(Intercept)



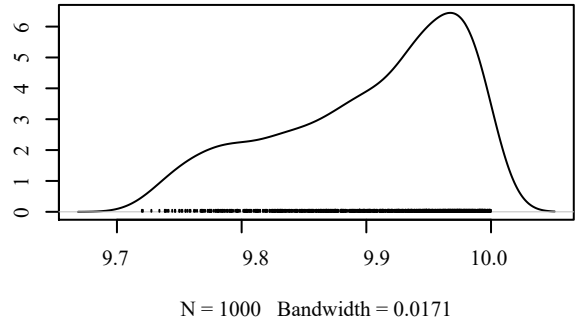
Density of gamma.(Intercept)



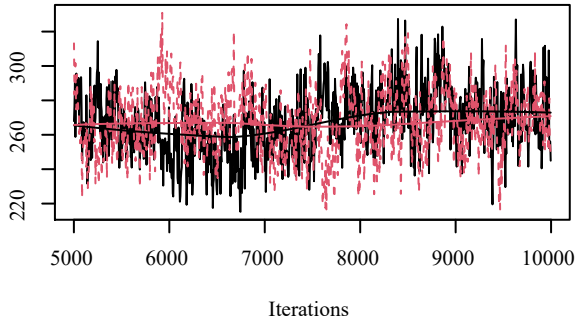
Trace of Vrho



Density of Vrho



Trace of Deviance



Density of Deviance

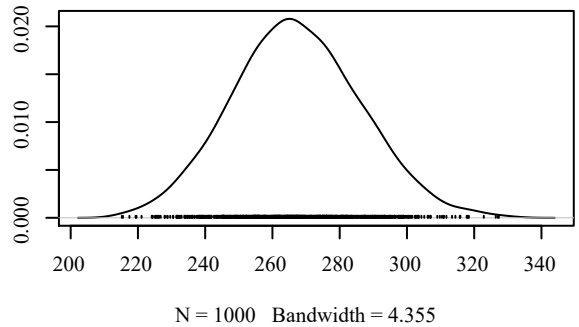
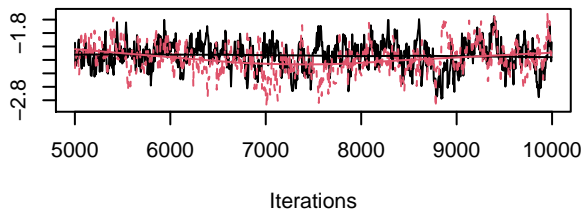
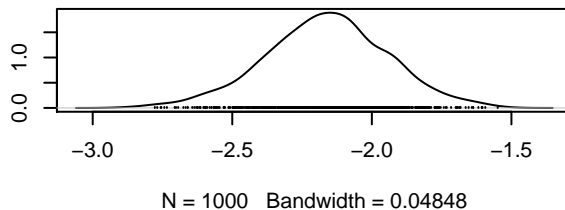


Figure S1: MCMC
traceplots

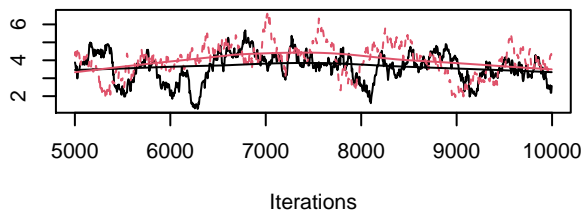
Trace of beta.(Intercept)



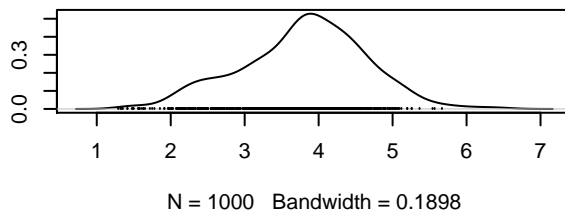
Density of beta.(Intercept)



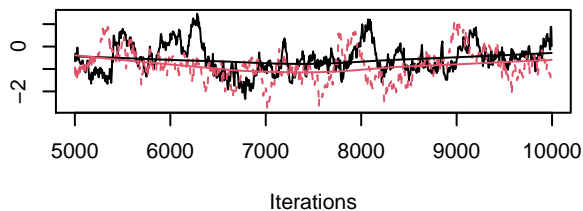
Trace of beta.layer.1



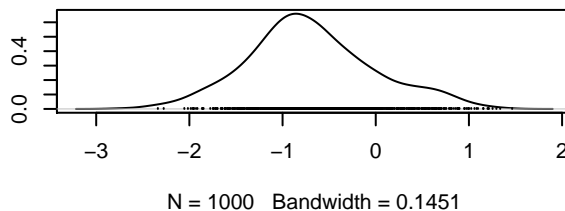
Density of beta.layer.1



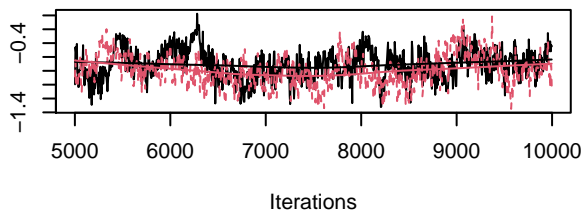
Trace of beta.layer.2



Density of beta.layer.2



Trace of beta.layer



Density of beta.layer

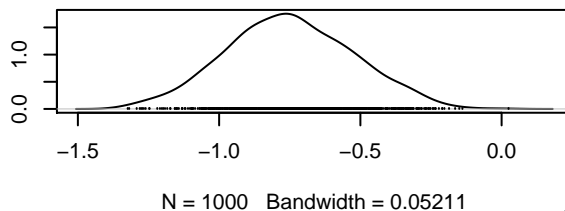
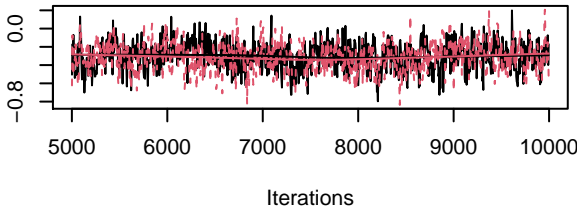
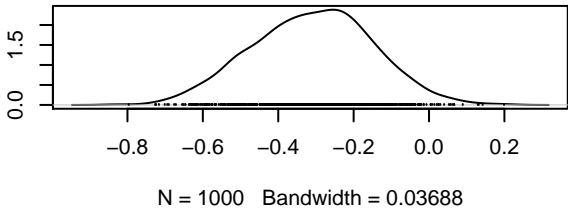


Figure S1: MCMC traceplots

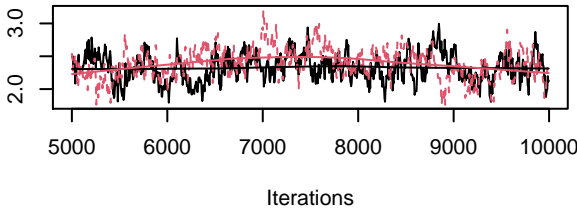
Trace of beta.lc



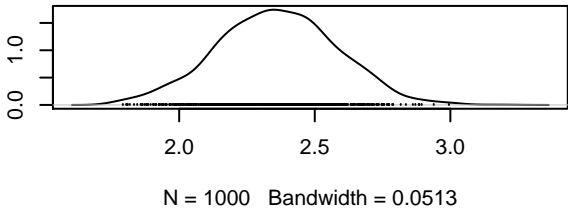
Density of beta.lc



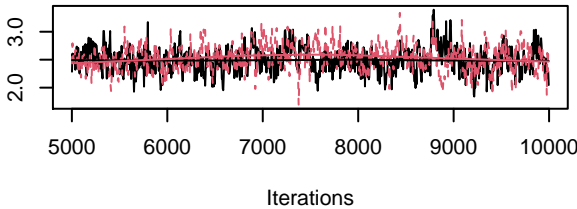
Trace of beta.alt



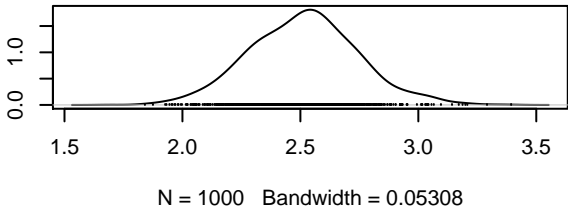
Density of beta.alt



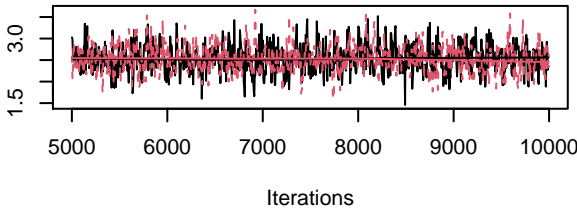
Trace of beta.lc_modi



Density of beta.lc_modi



Trace of beta.pop_den



Density of beta.pop_den

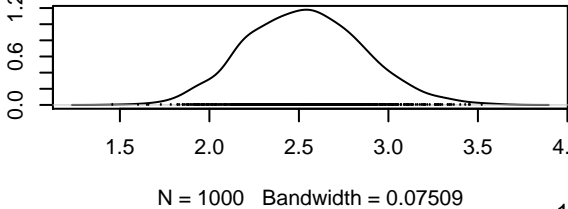
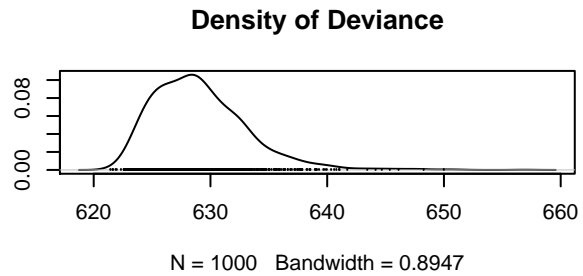
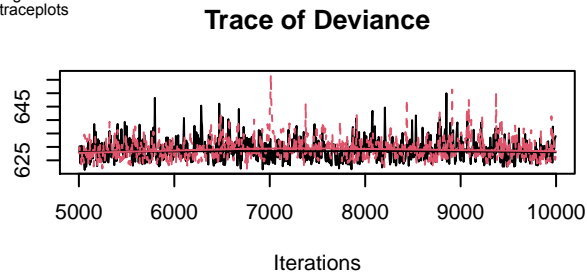
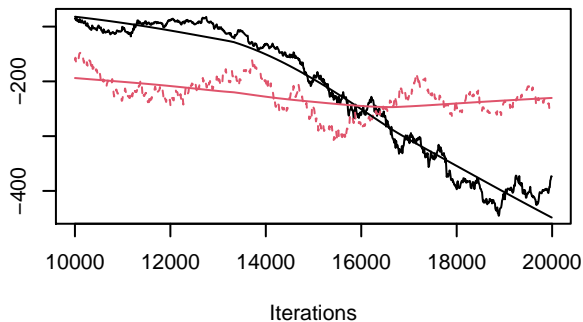


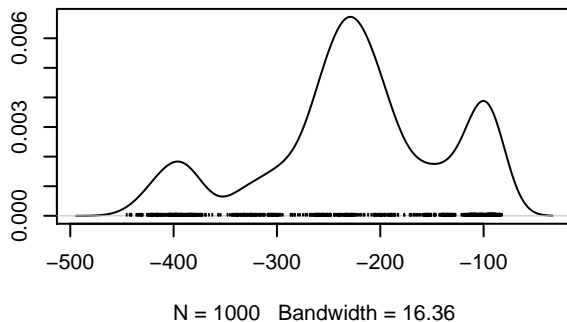
Figure S1: MCMC
traceplots



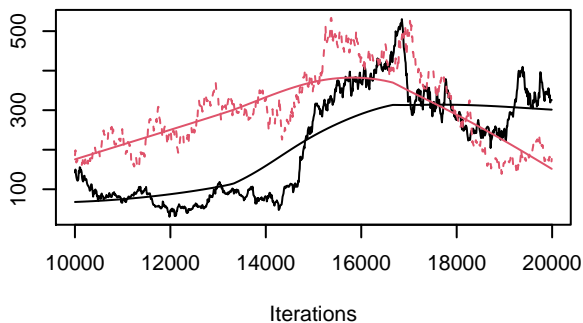
Trace of beta.(Intercept)



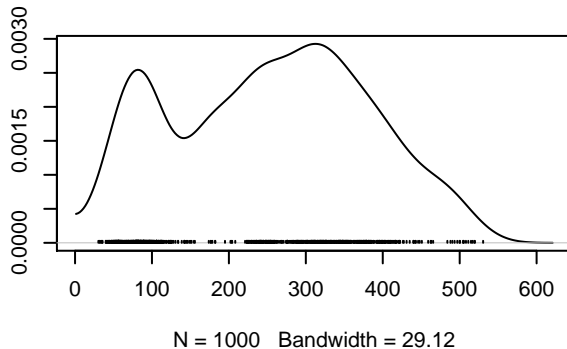
Density of beta.(Intercept)



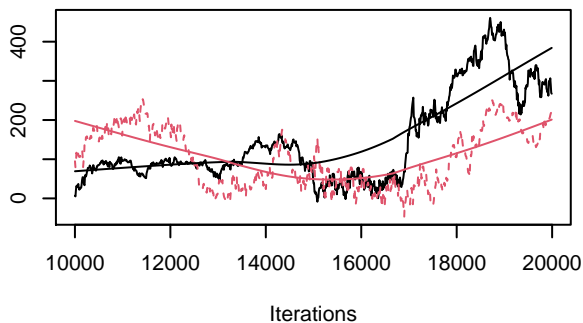
Trace of beta.layer.1



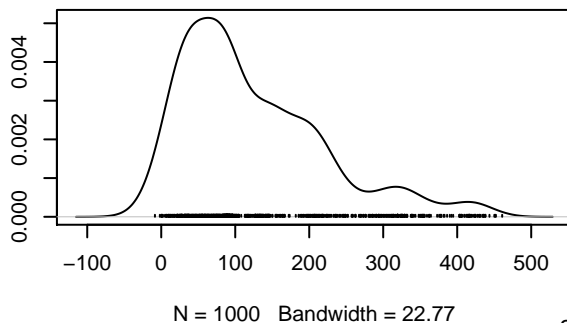
Density of beta.layer.1



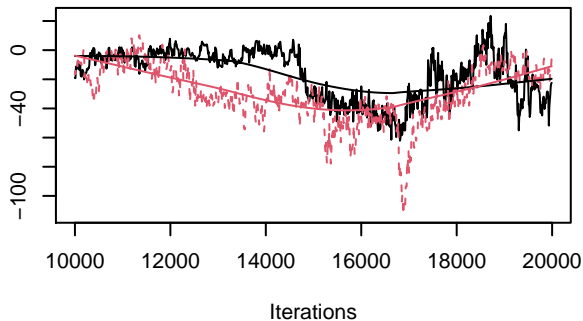
Trace of beta.layer.2



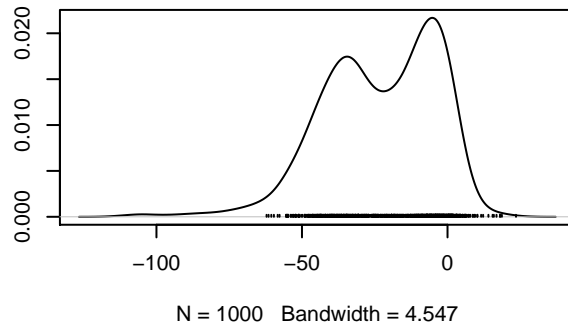
Density of beta.layer.2



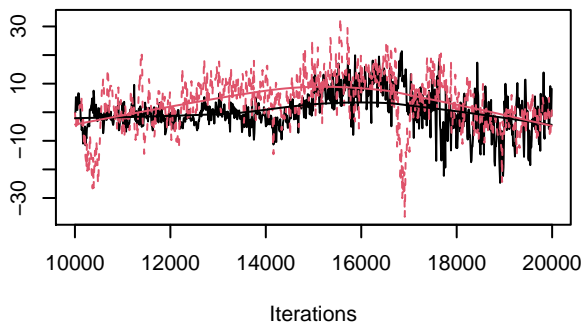
Trace of beta.layer



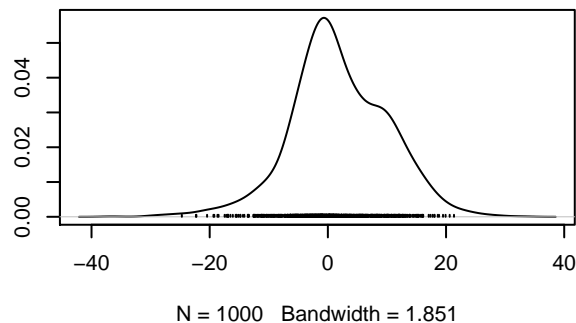
Density of beta.layer



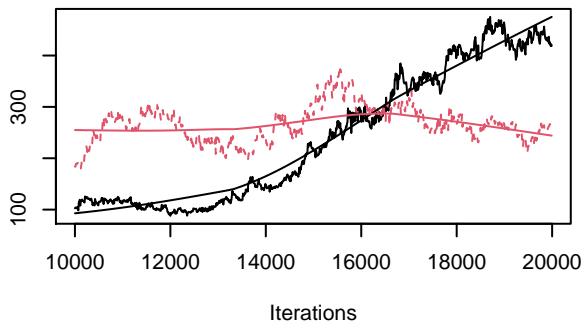
Trace of beta.lc



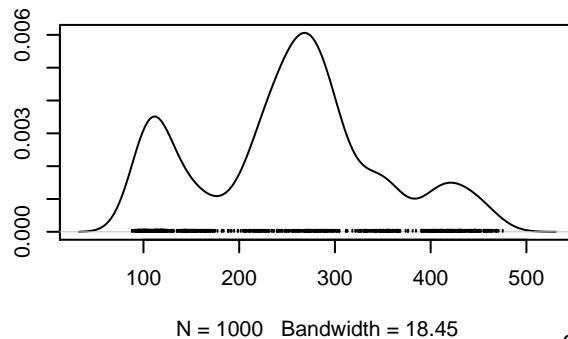
Density of beta.lc



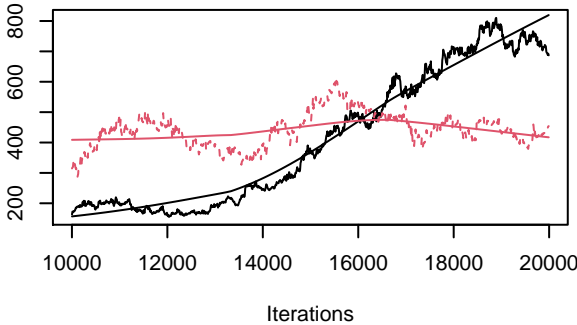
Trace of beta.alt



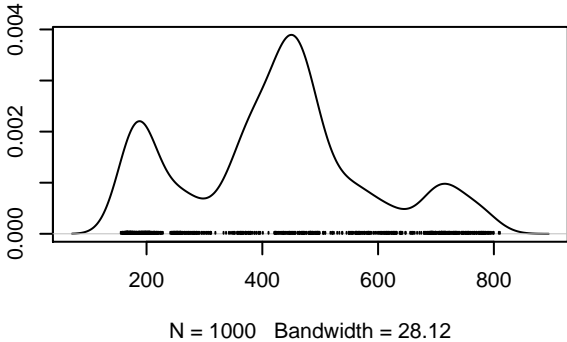
Density of beta.alt



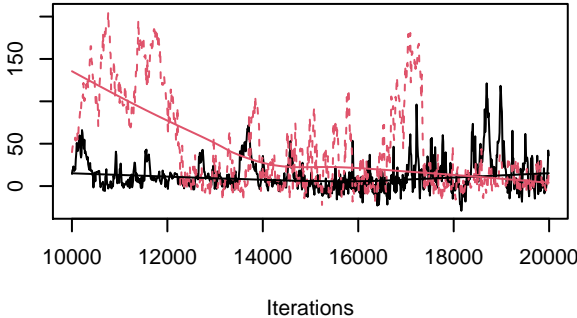
Trace of beta.lc_modi



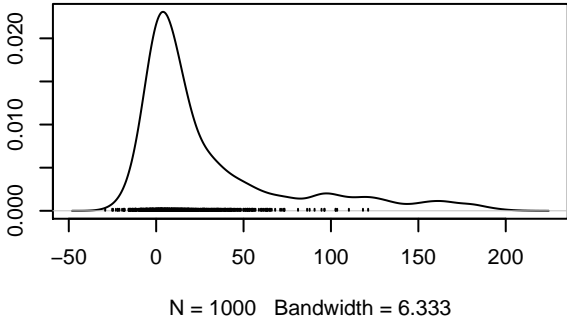
Density of beta.lc_modi



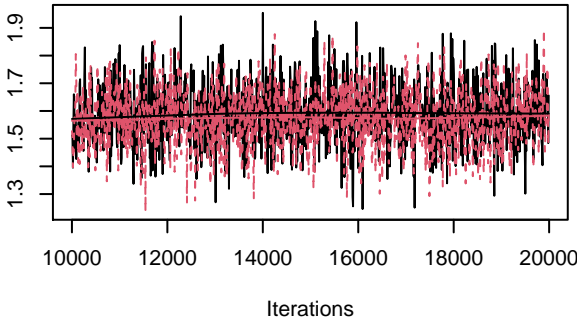
Trace of beta.pop_den



Density of beta.pop_den



Trace of gamma.(Intercept)



Density of gamma.(Intercept)

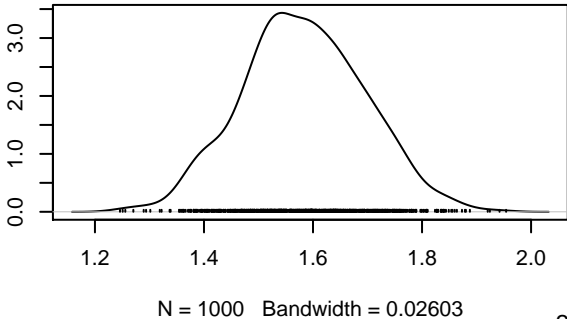
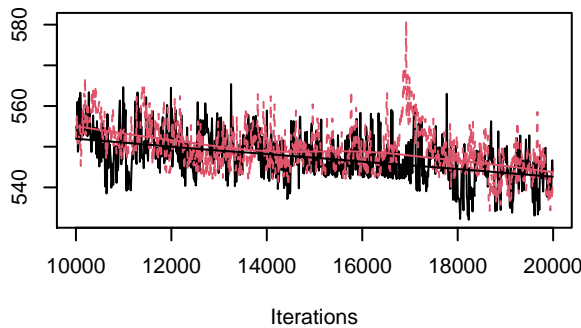
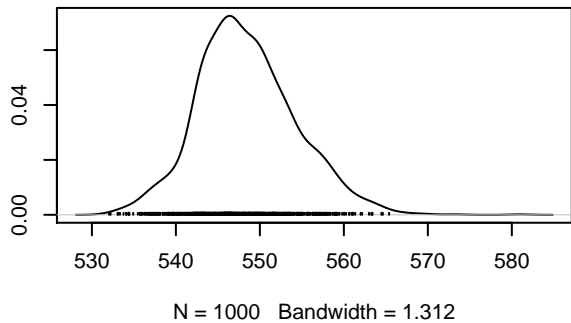


Figure S1: MCMC
traceplots

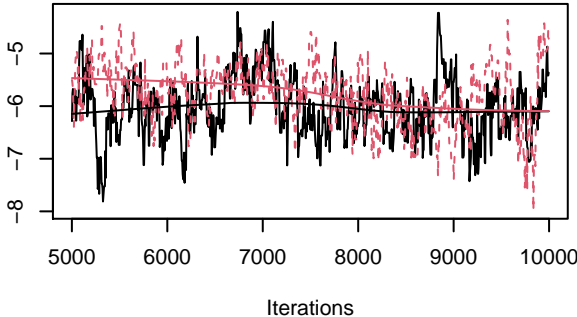
Trace of Deviance



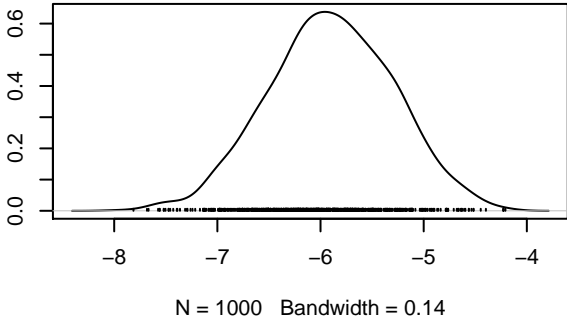
Density of Deviance



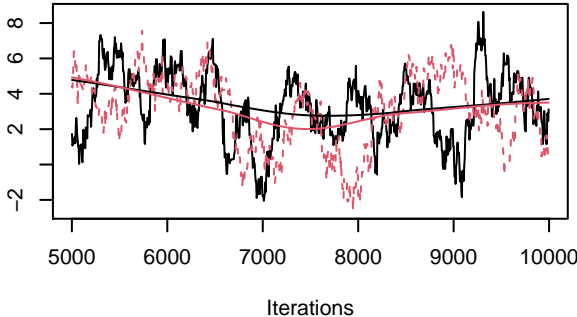
Trace of beta.(Intercept)



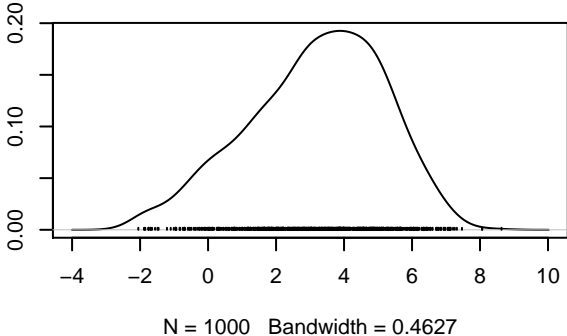
Density of beta.(Intercept)



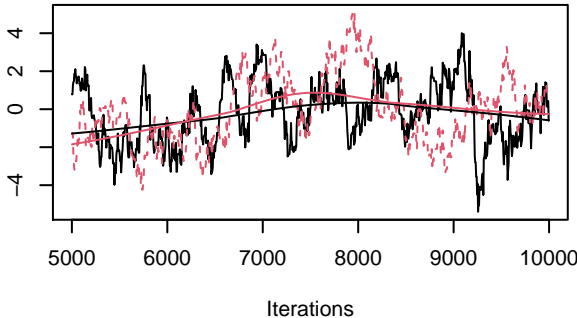
Trace of beta.layer.1



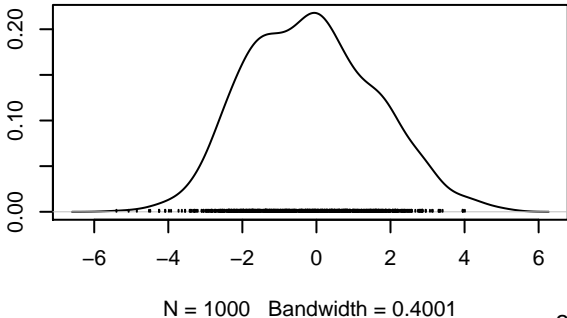
Density of beta.layer.1



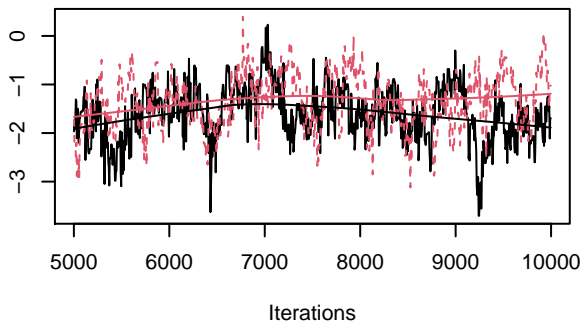
Trace of beta.layer.2



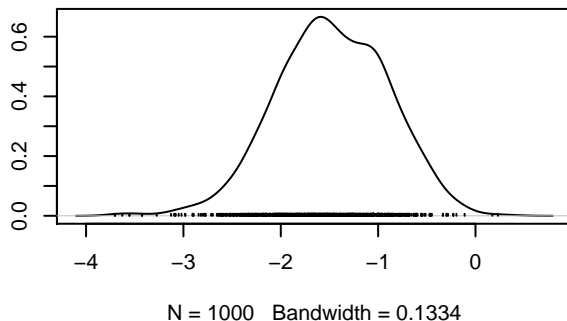
Density of beta.layer.2



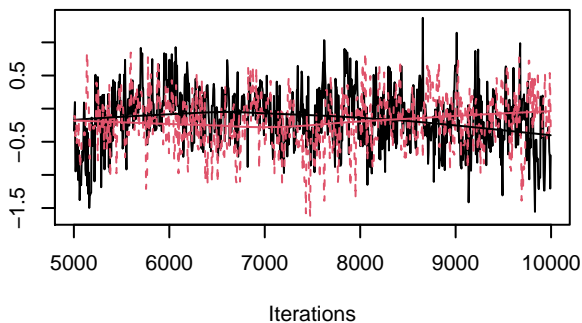
Trace of beta.layer



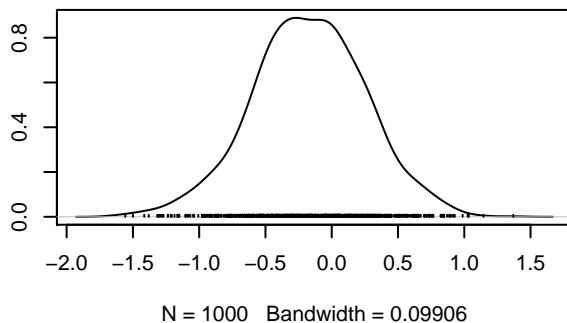
Density of beta.layer



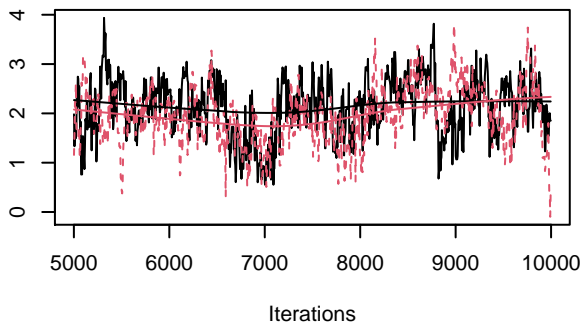
Trace of beta.lc



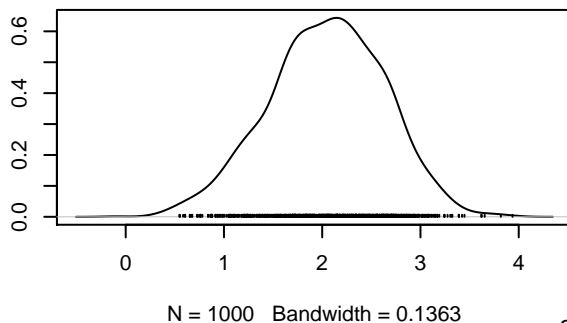
Density of beta.lc



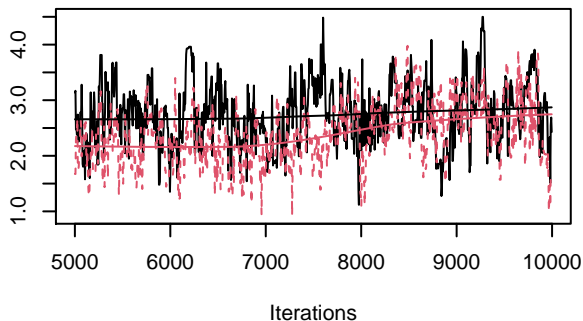
Trace of beta.alt



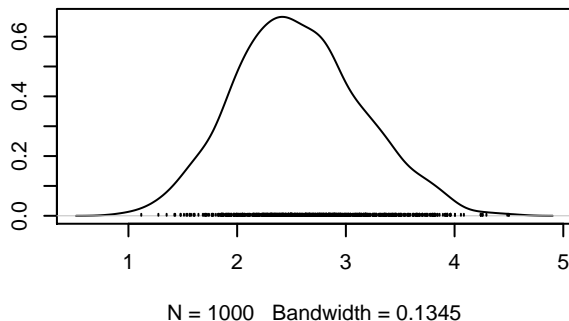
Density of beta.alt



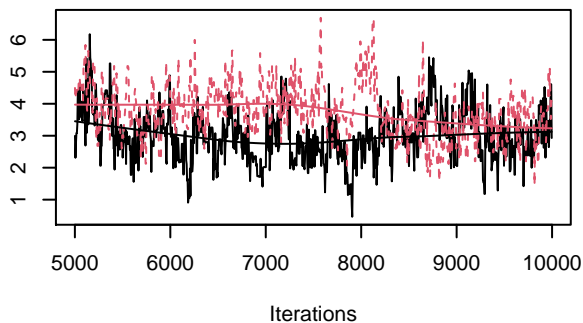
Trace of beta.lc_modi



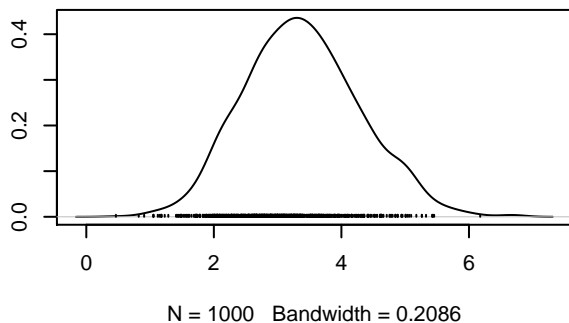
Density of beta.lc_modi



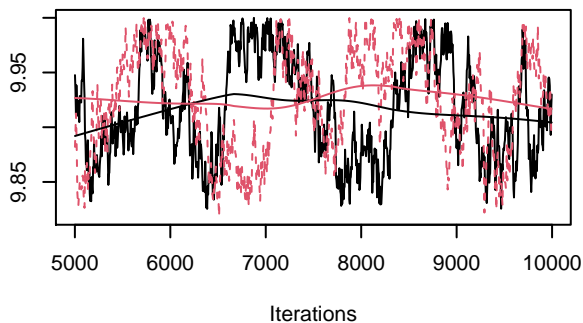
Trace of beta.pop_den



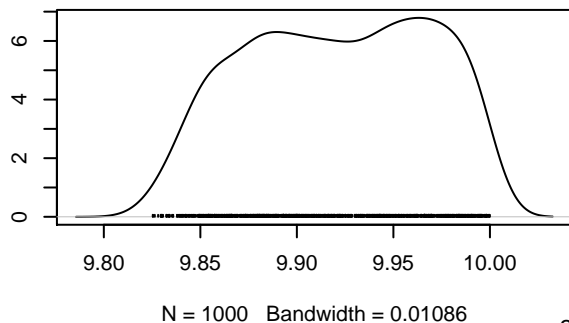
Density of beta.pop_den



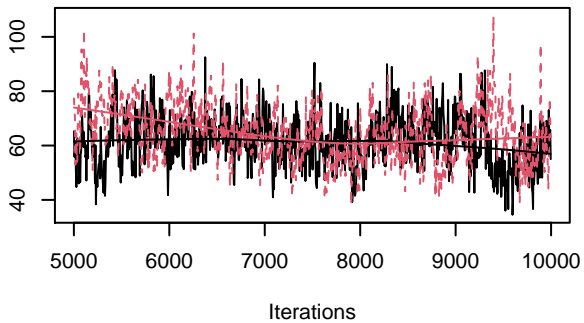
Trace of Vrho



Density of Vrho



Trace of Deviance



Density of Deviance

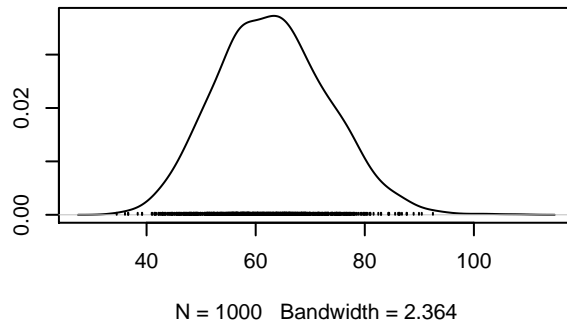
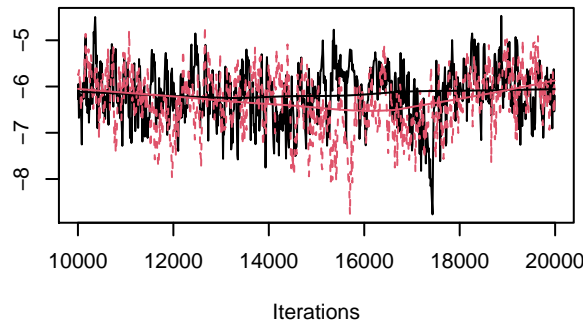
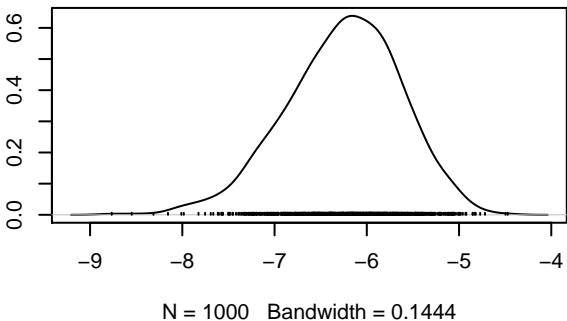


Figure S1: MCMC traceplots

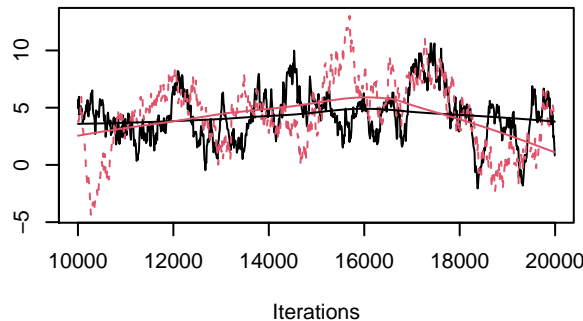
Trace of beta.(Intercept)



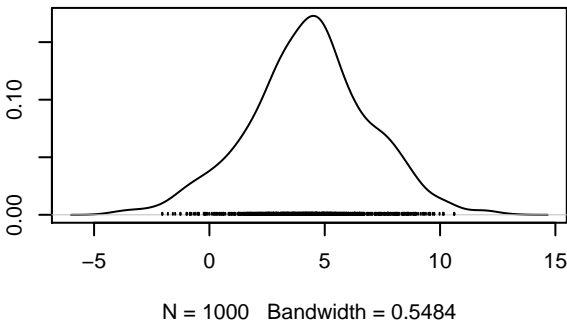
Density of beta.(Intercept)



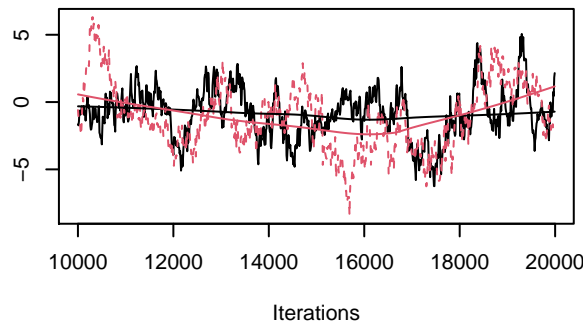
Trace of beta.layer.1



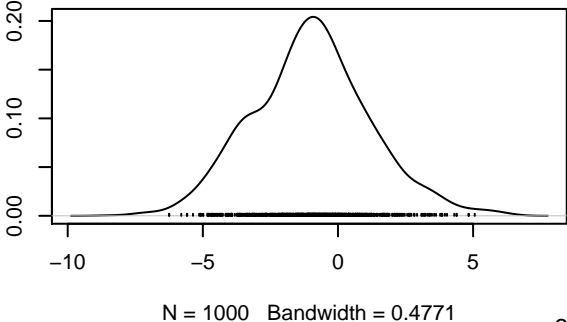
Density of beta.layer.1



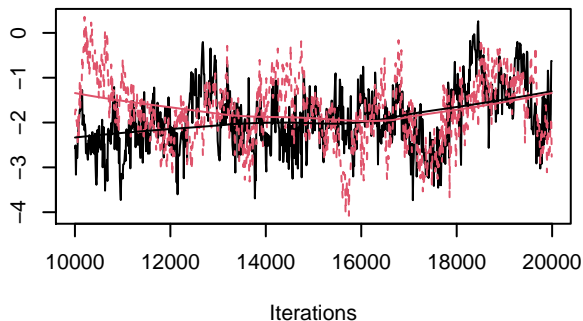
Trace of beta.layer.2



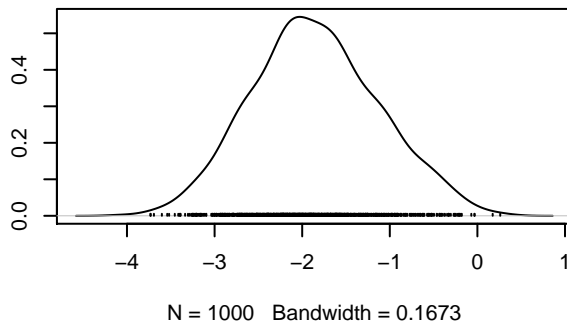
Density of beta.layer.2



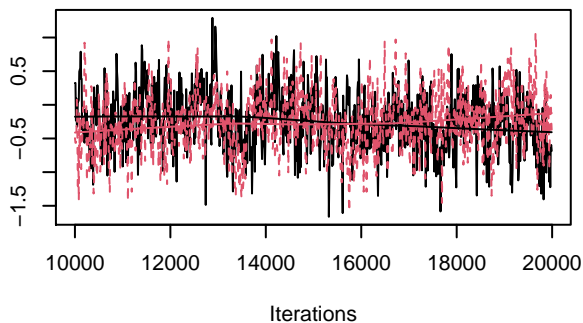
Trace of beta.layer



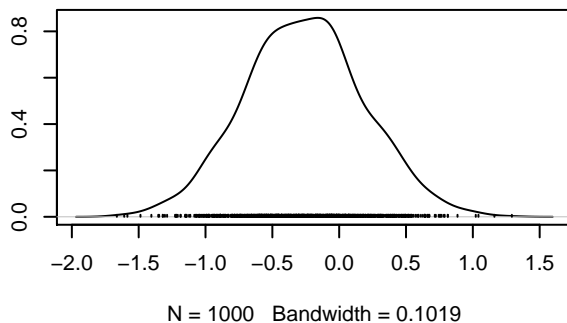
Density of beta.layer



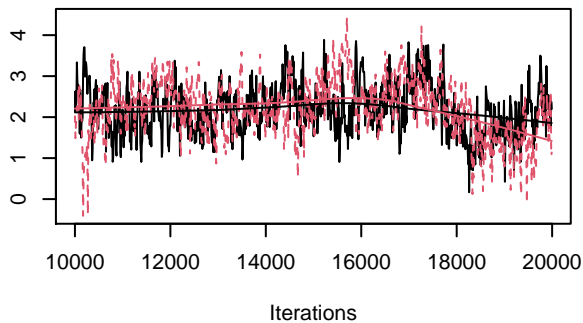
Trace of beta.lc



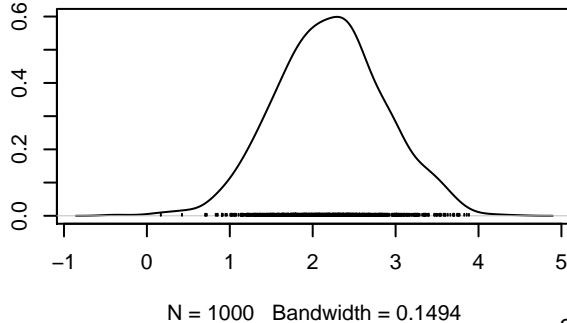
Density of beta.lc



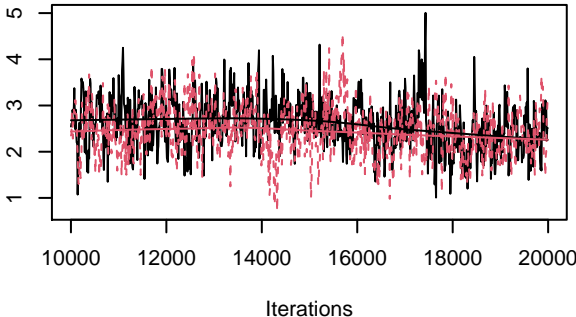
Trace of beta.alt



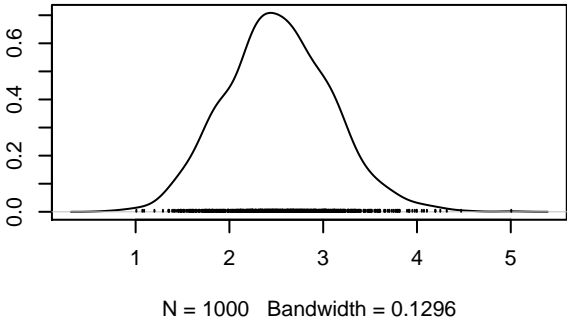
Density of beta.alt



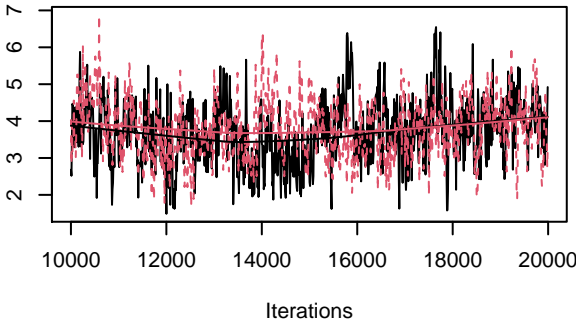
Trace of beta.lc_modi



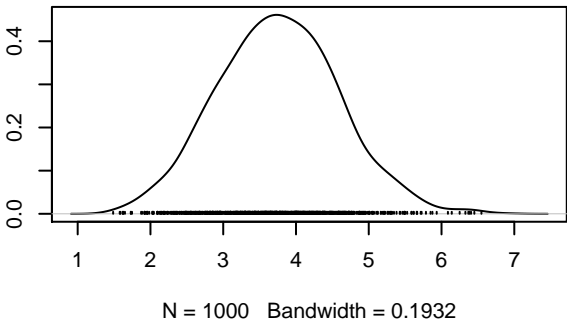
Density of beta.lc_modi



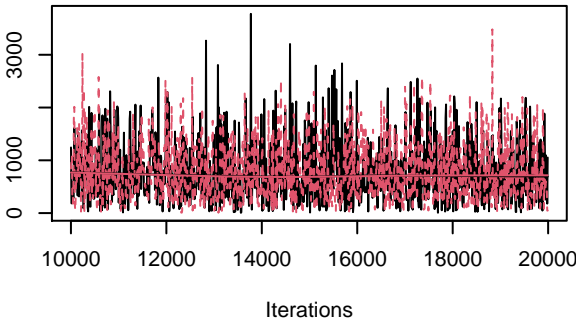
Trace of beta.pop_den



Density of beta.pop_den



Trace of gamma.(Intercept)



Density of gamma.(Intercept)

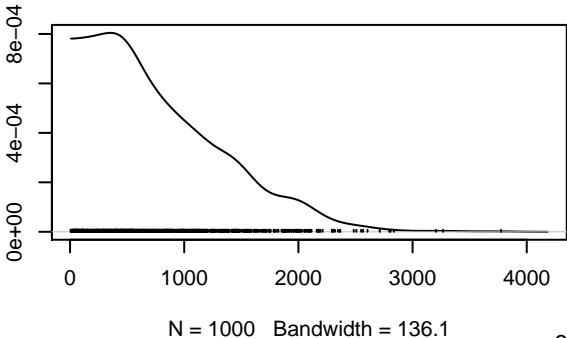
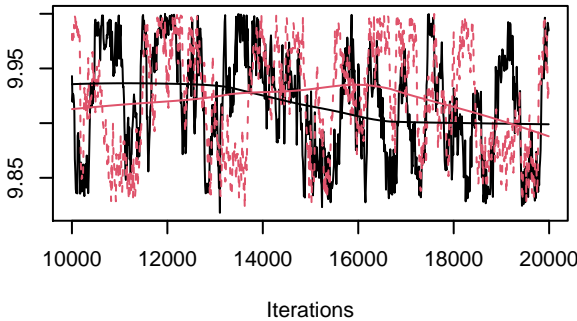
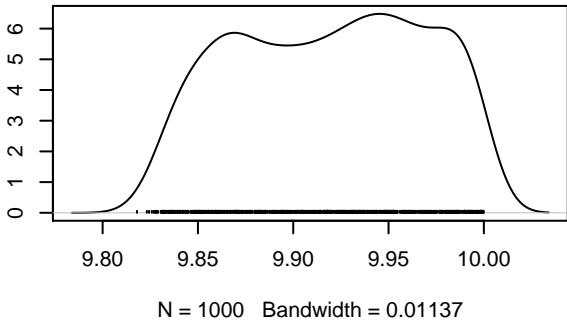


Figure S1: MCMC
traceplots

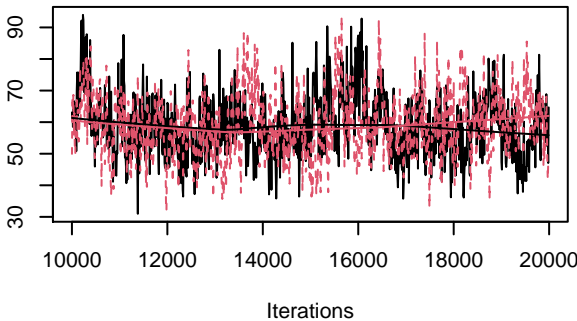
Trace of Vrho



Density of Vrho



Trace of Deviance



Density of Deviance

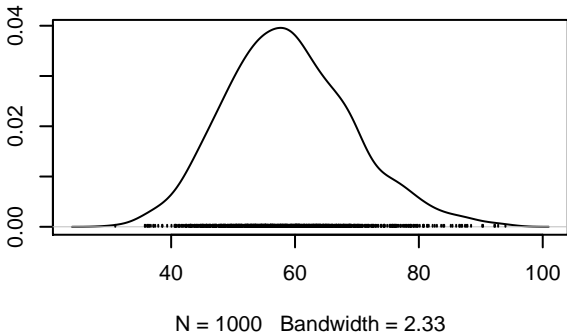
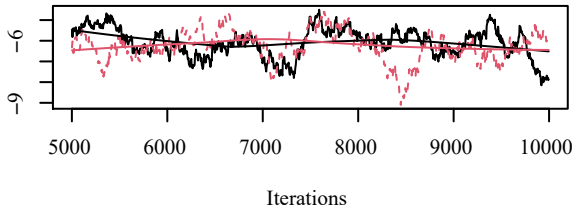
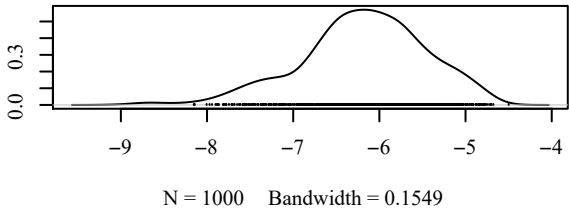


Figure S1: MCMC
traceplots

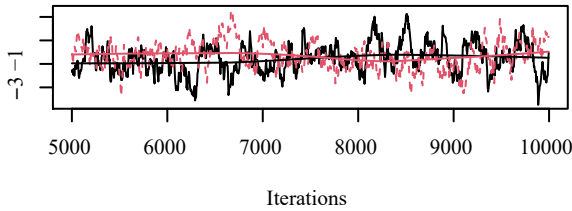
Trace of beta.(Intercept)



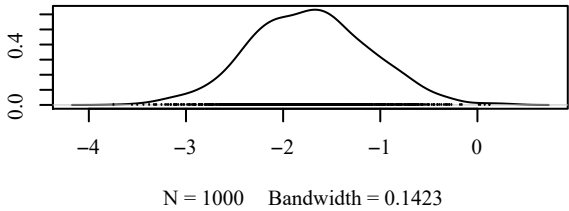
Density of beta.(Intercept)



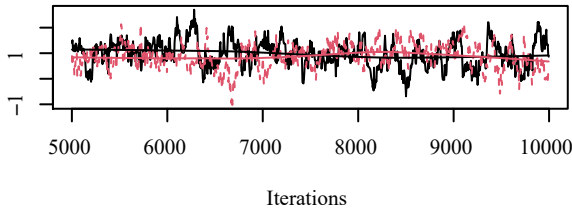
Trace of beta.layer.1



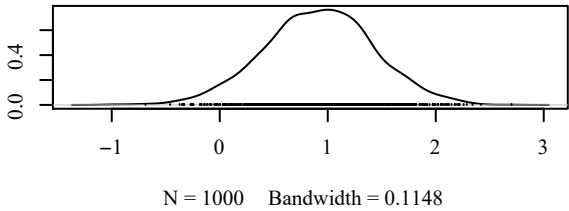
Density of beta.layer.1



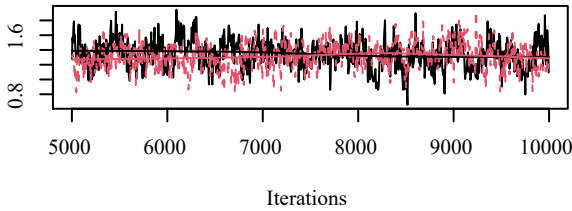
Trace of beta.layer.2



Density of beta.layer.2



Trace of beta.layer



Density of beta.layer

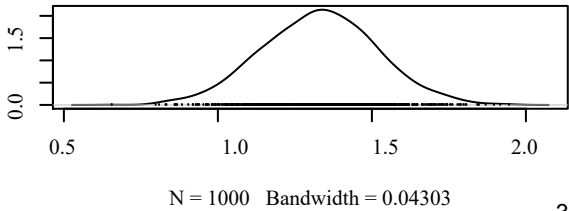
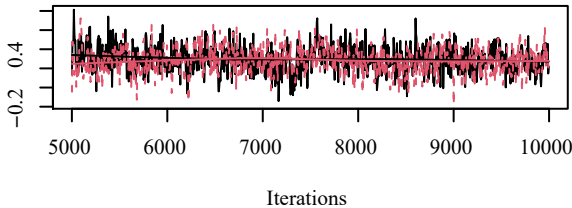
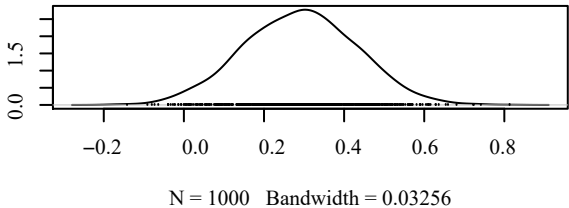


Figure S1: MCMC traceplots

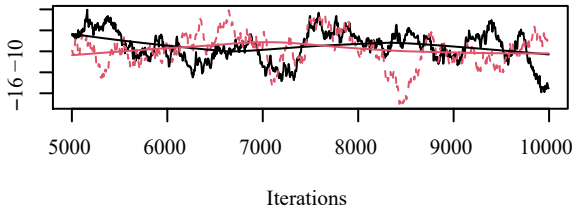
Trace of beta.lc



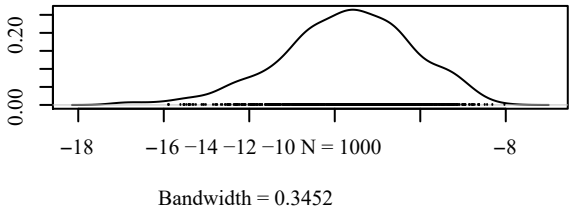
Density of beta.lc



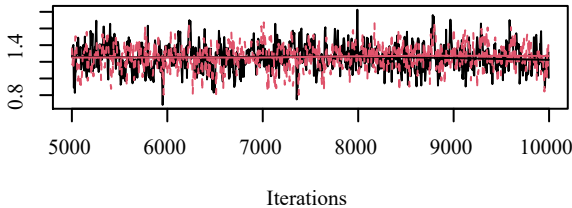
Trace of beta.alt



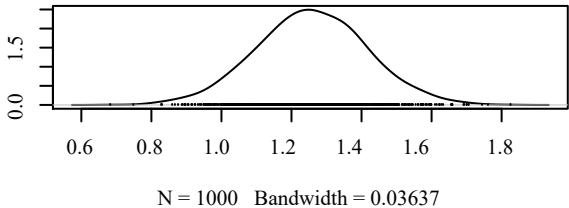
Density of beta.alt



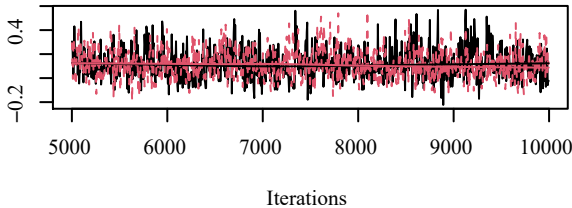
Trace of beta.lc_modi



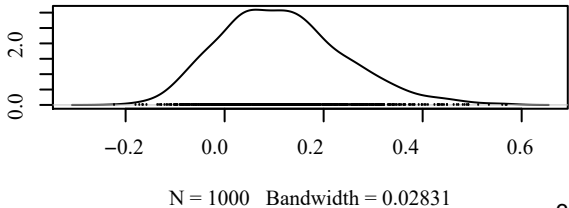
Density of beta.lc_modi



Trace of beta.pop_den



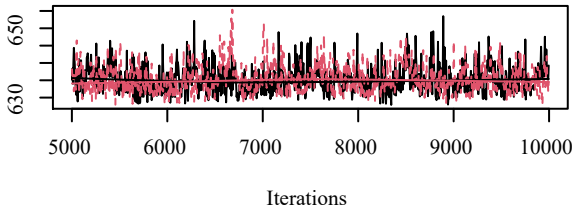
Density of beta.pop_den



Henipavirus Binomial mcmc traceplot

Figure S1: MCMC traceplots

Trace of Deviance



Density of Deviance

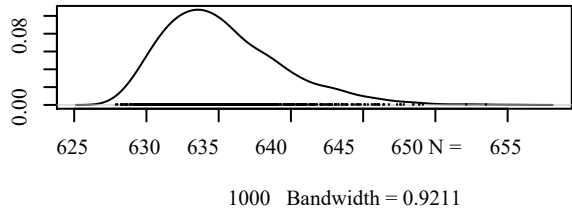
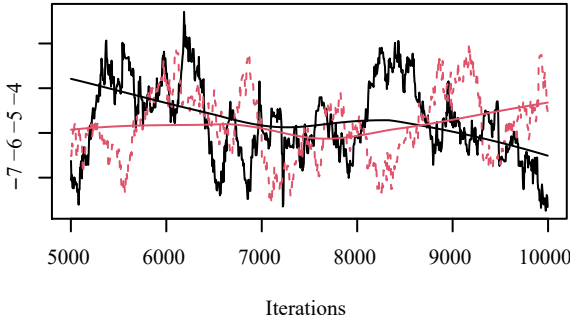
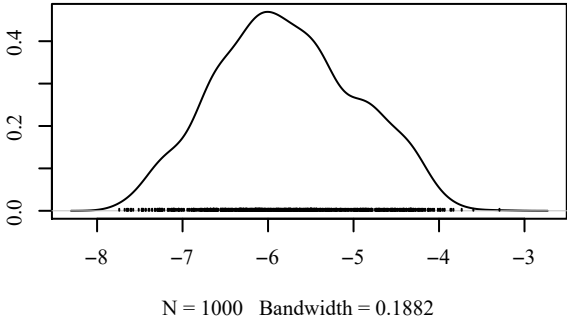


Figure S1: MCMC traceplots

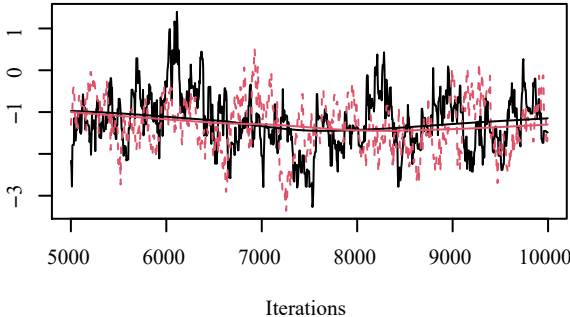
Trace of beta.(Intercept)



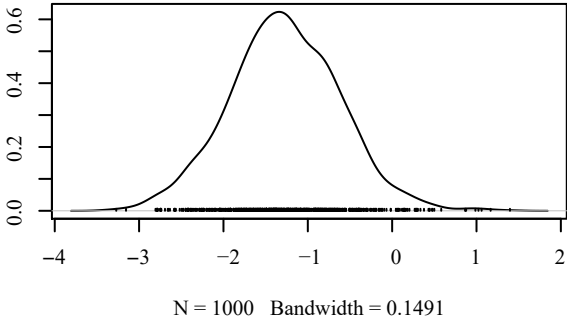
Density of beta.(Intercept)



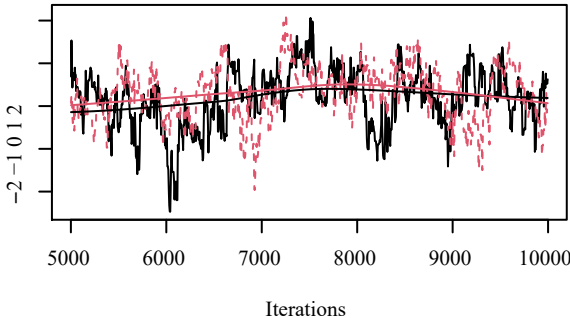
Trace of beta.layer.1



Density of beta.layer.1



Trace of beta.layer.2



Density of beta.layer.2

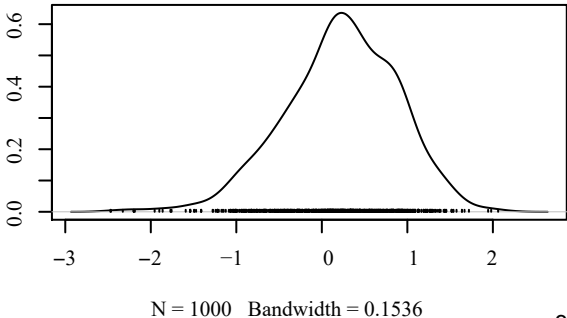
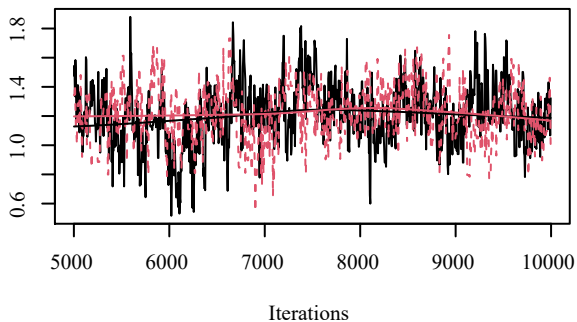
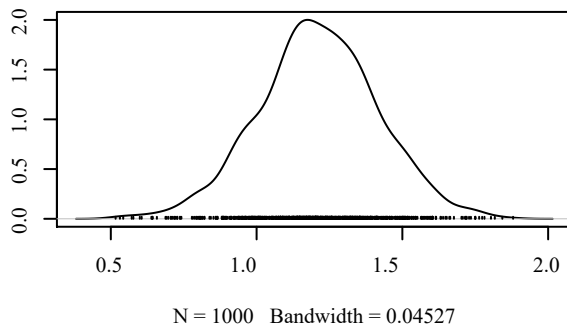


Figure S1: MCMC
traceplots

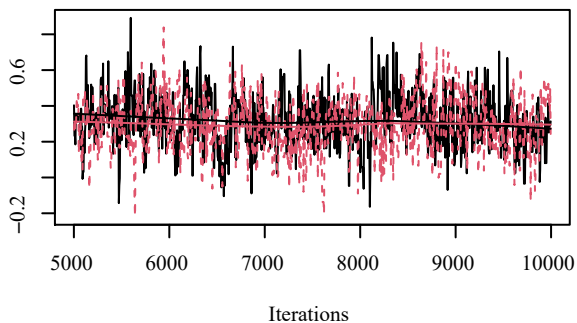
Trace of beta.layer



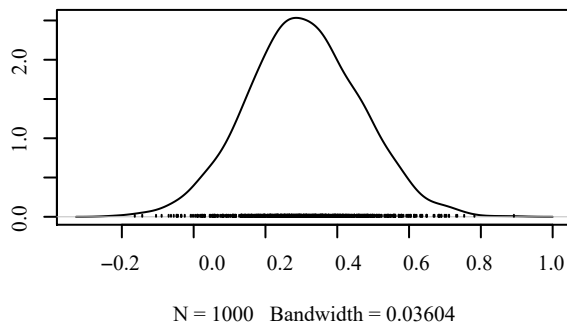
Density of beta.layer



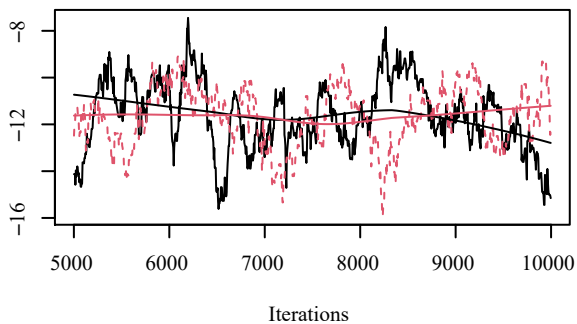
Trace of beta.lc



Density of beta.lc



Trace of beta.alt



Density of beta.alt

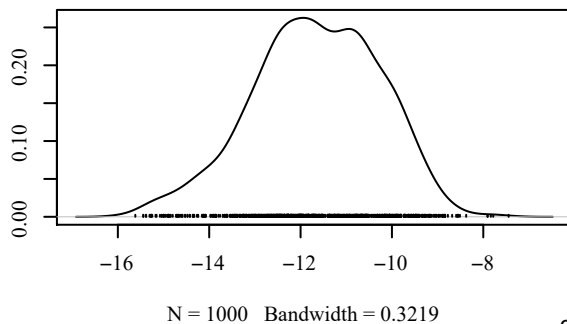
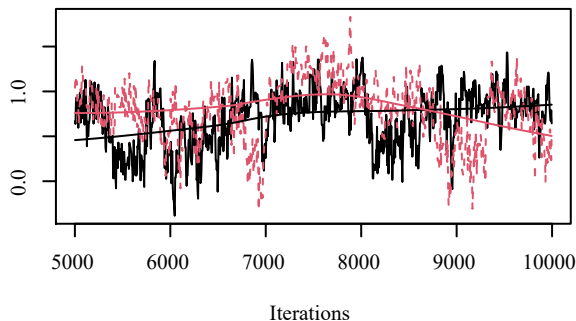
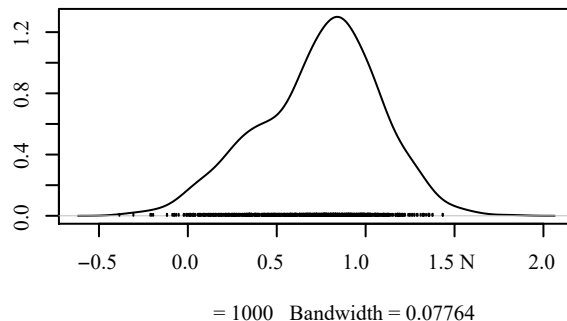


Figure S1: MCMC
traceplots

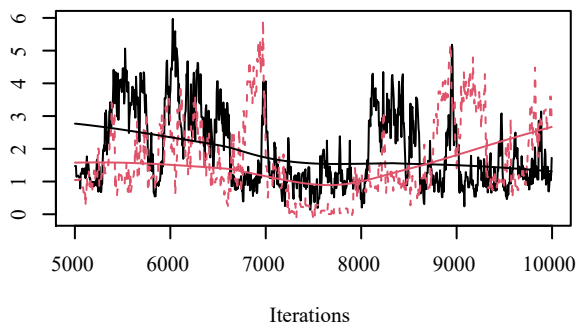
Trace of beta.lc_modi



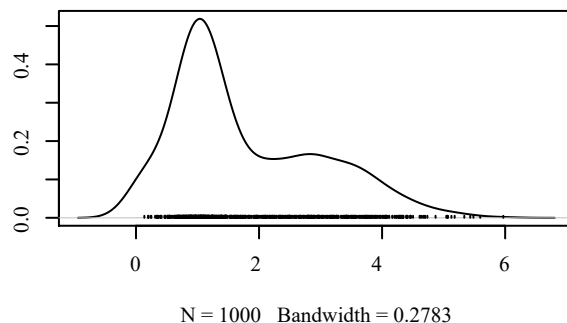
Density of beta.lc_modi



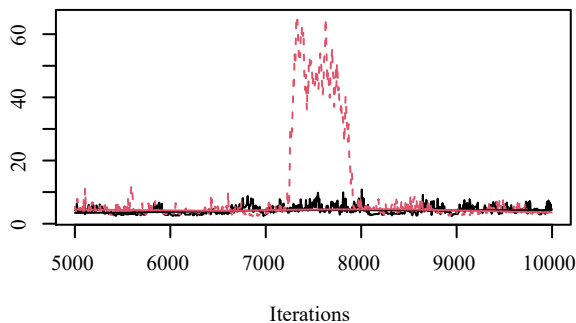
Trace of beta.pop_den



Density of beta.pop_den



Trace of gamma.(Intercept)



Density of gamma.(Intercept)

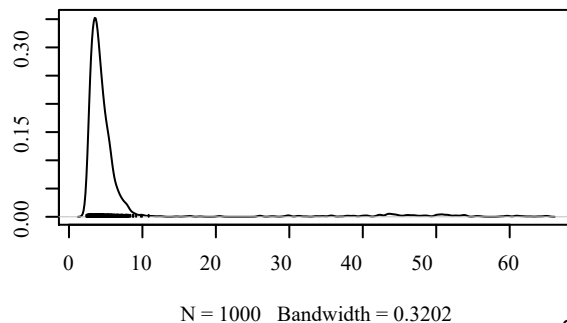
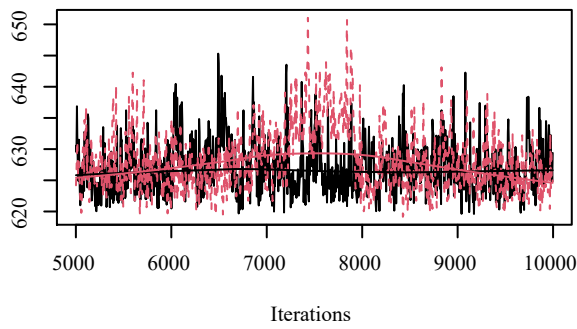
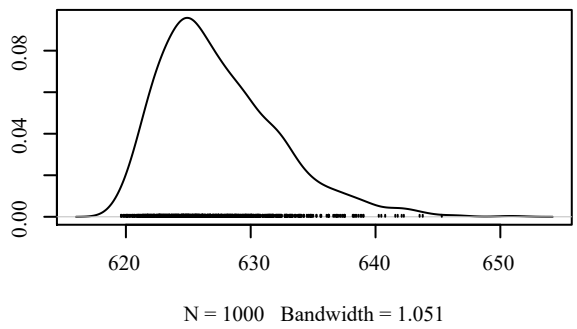


Figure S1: MCMC
traceplots

Trace of Deviance



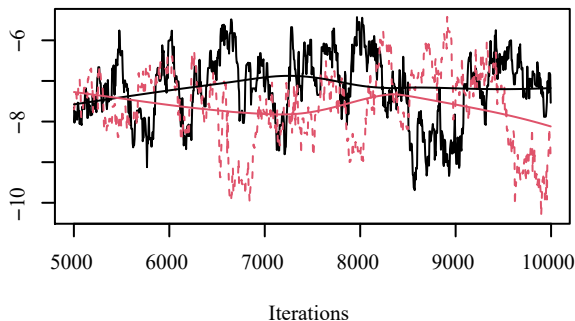
Density of Deviance



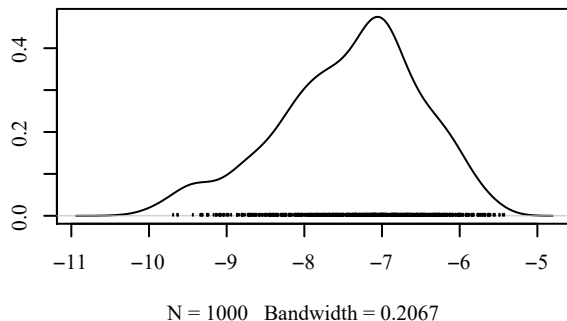
Henipavirus ZIB memc traceplot

Figure S1: MCMC traceplots

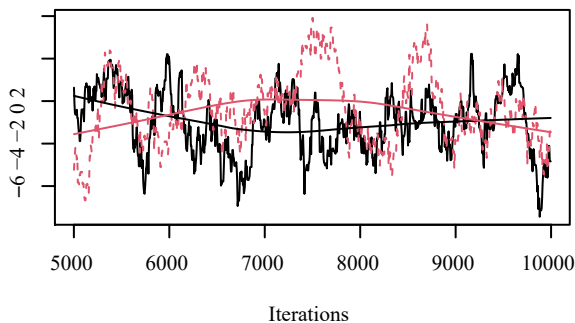
Trace of beta.(Intercept)



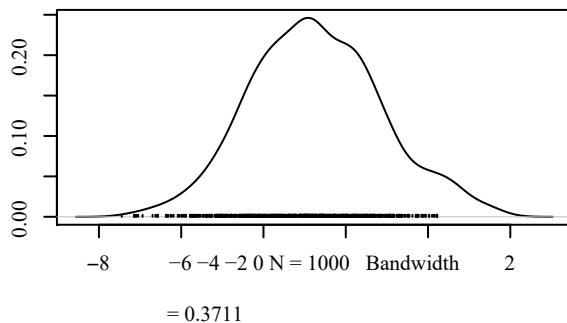
Density of beta.(Intercept)



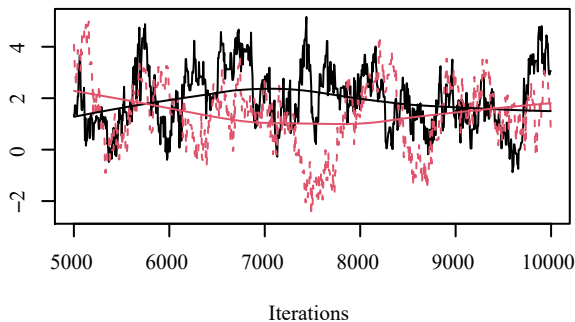
Trace of beta.layer.1



Density of beta.layer.1



Trace of beta.layer.2



Density of beta.layer.2

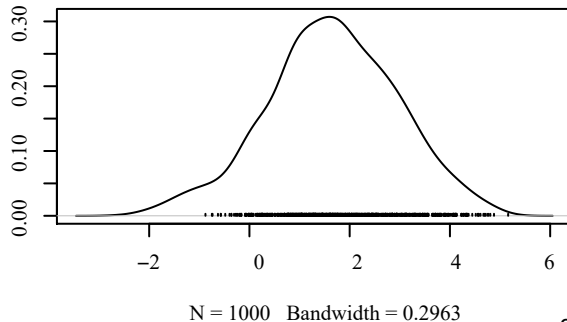
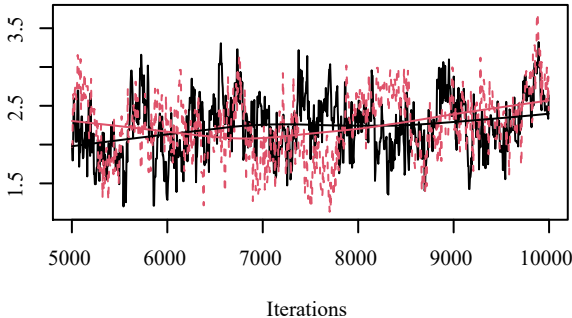
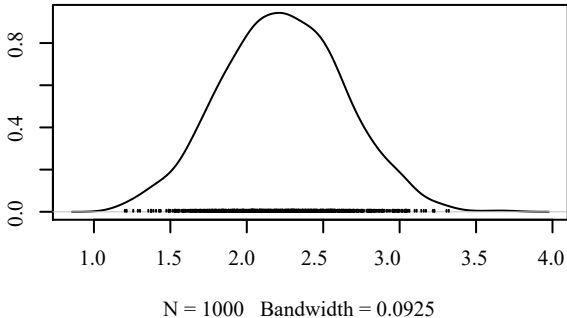


Figure S1: MCMC
traceplots

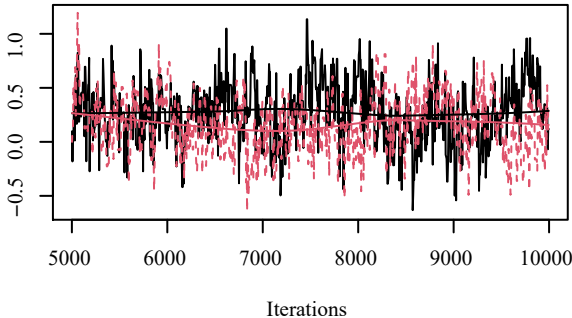
Trace of beta.layer



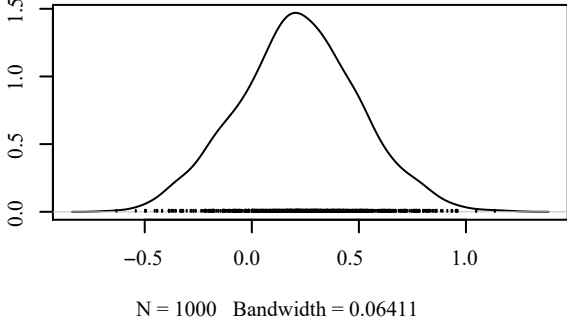
Density of beta.layer



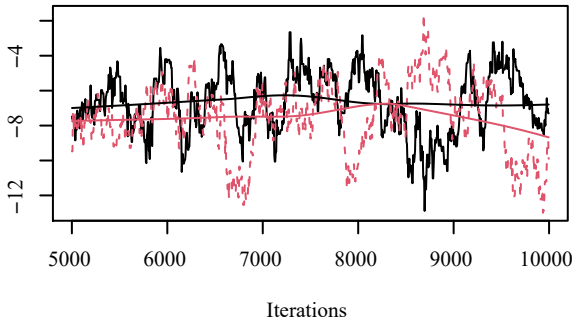
Trace of beta.lc



Density of beta.lc



Trace of beta.alt



Density of beta.alt

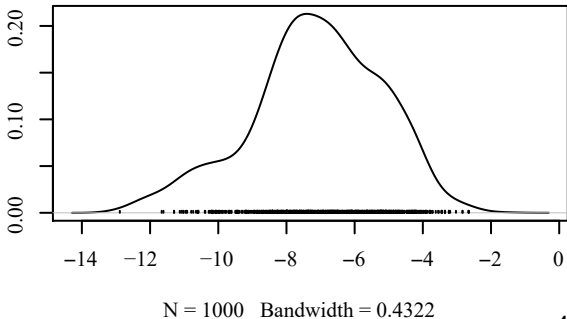
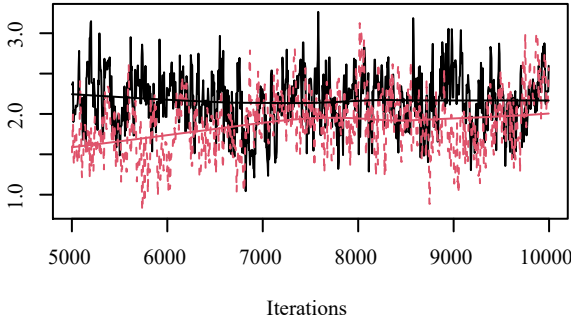
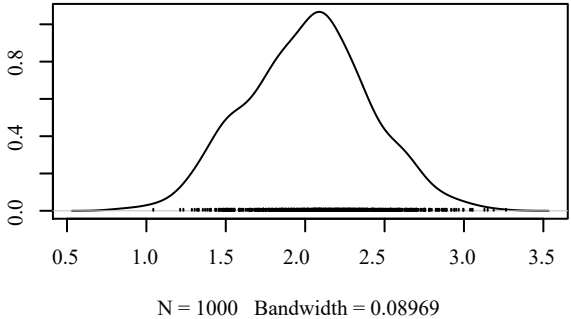


Figure S1: MCMC
traceplots

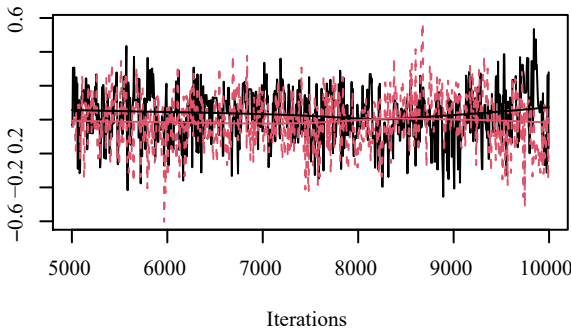
Trace of beta.lc_modi



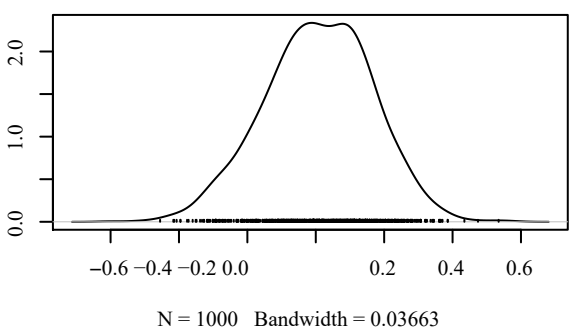
Density of beta.lc_modi



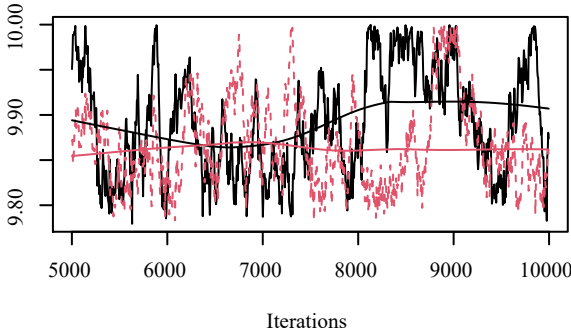
Trace of beta.pop_den



Density of beta.pop_den



Trace of Vrho



Density of Vrho

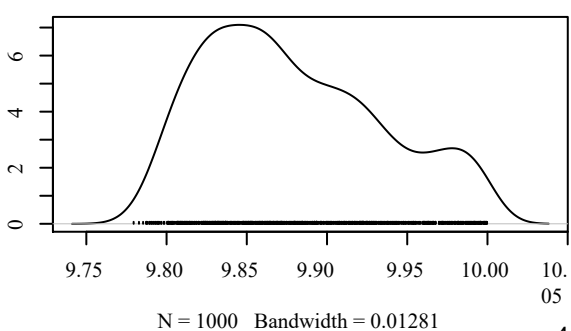
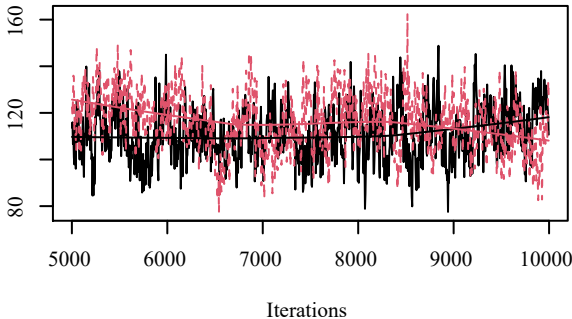


Figure S1: MCMC
traceplots

Trace of Deviance



Density of Deviance

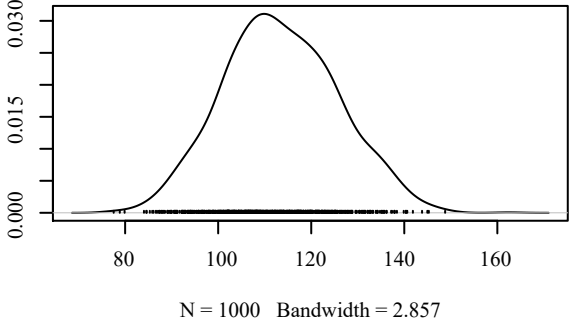
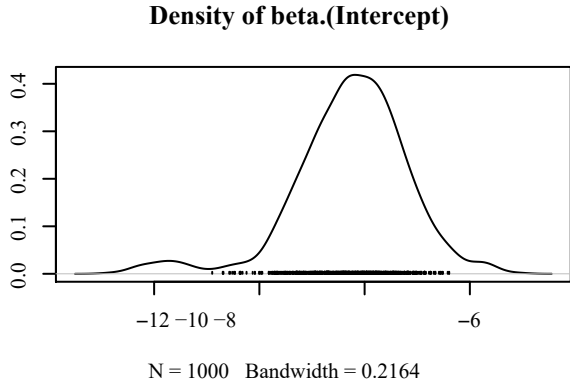
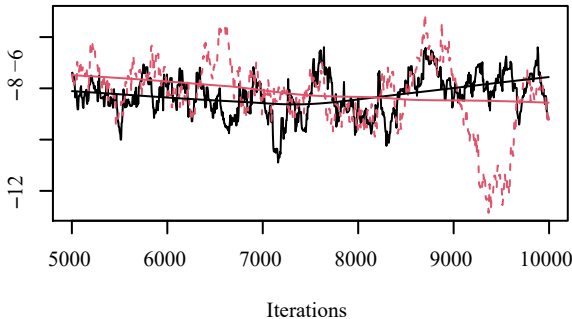
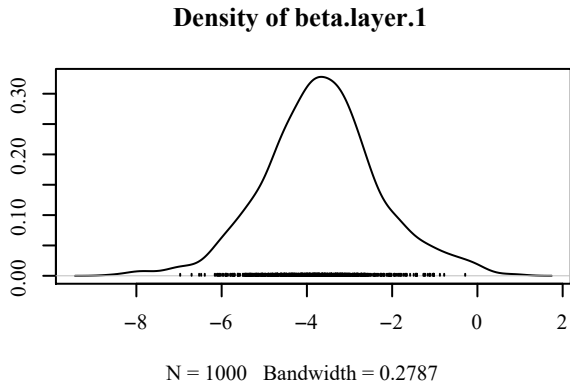
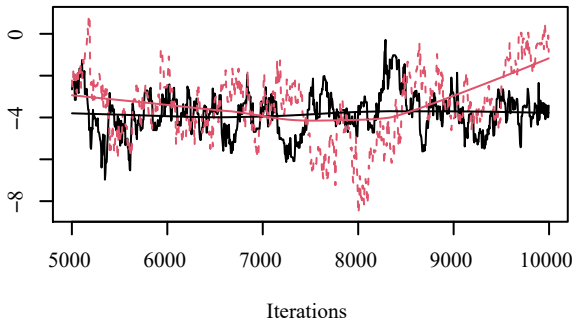


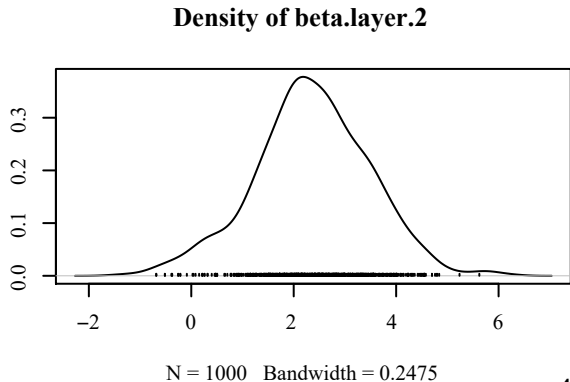
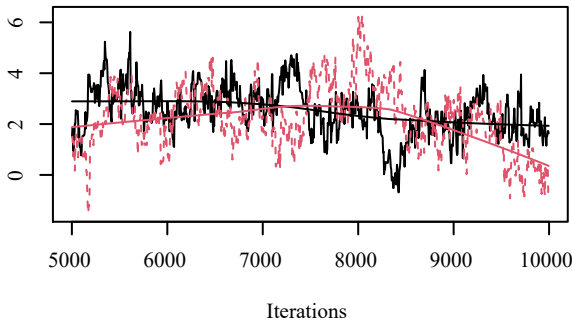
Figure S1: MCMC Trace of beta.(Intercept)
traceplots



Trace of beta.layer.1



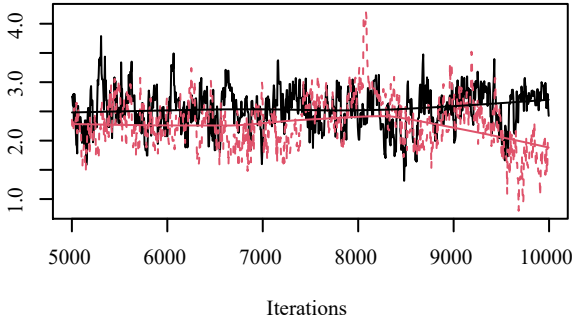
Trace of beta.layer.2



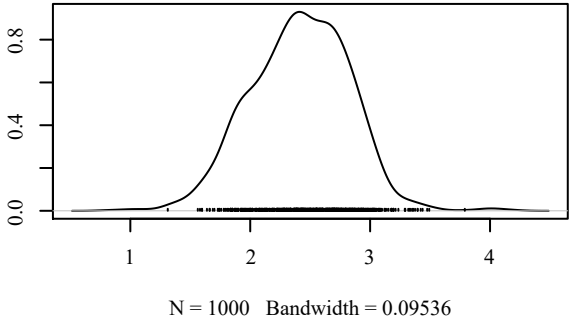
Henipavirus ZIB iCAR memc traceplot

Figure S1: MCMC
traceplots

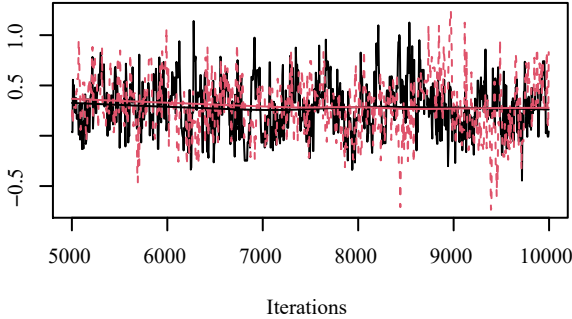
Trace of beta.layer



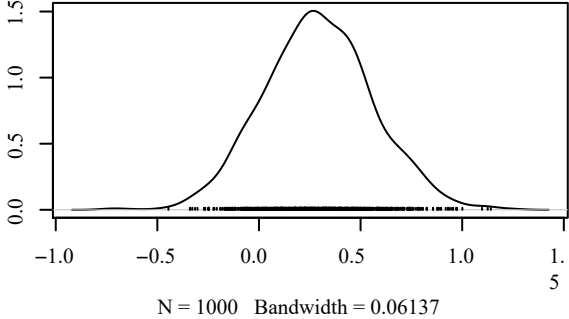
Density of beta.layer



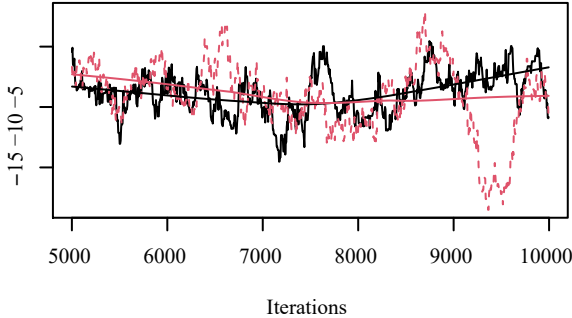
Trace of beta.lc



Density of beta.lc



Trace of beta.alt



Density of beta.alt

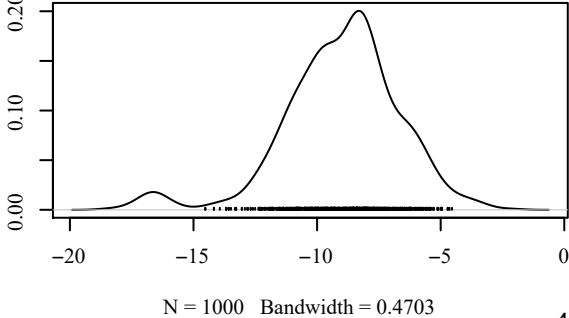
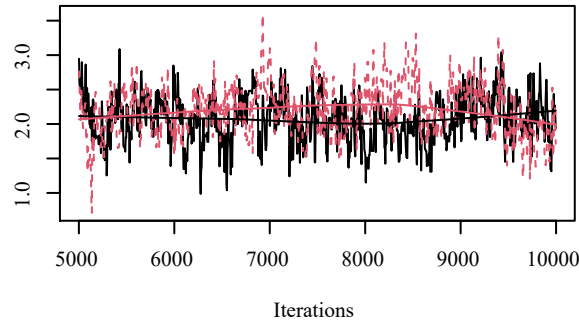
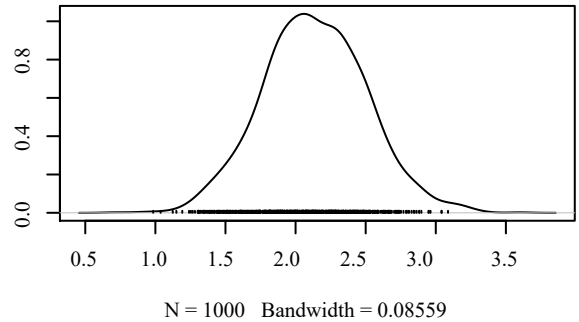


Figure S1: MCMC
traceplots

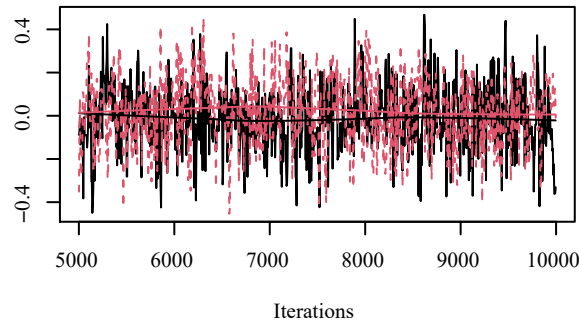
Trace of beta.lc_modi



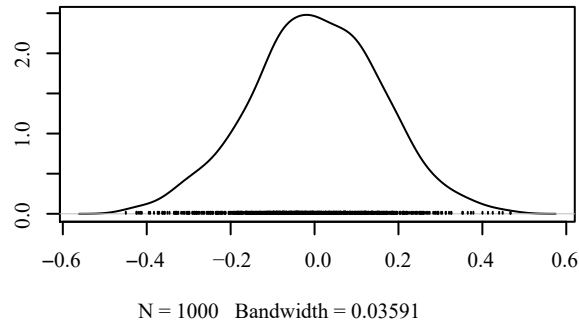
Density of beta.lc_modi



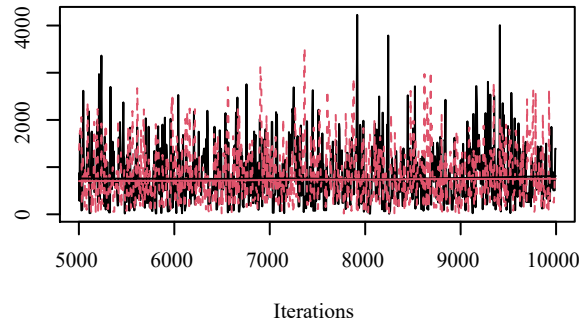
Trace of beta.pop_den



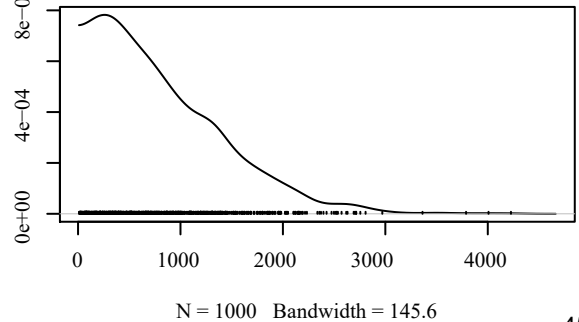
Density of beta.pop_den



Trace of gamma.(Intercept)



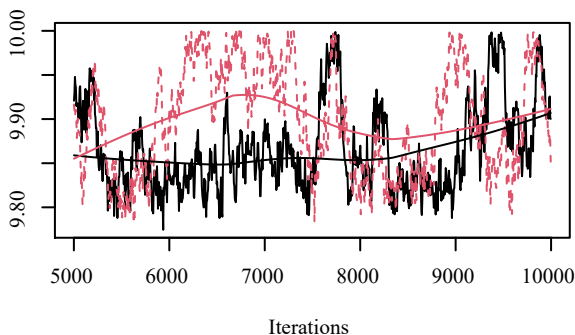
Density of gamma.(Intercept)



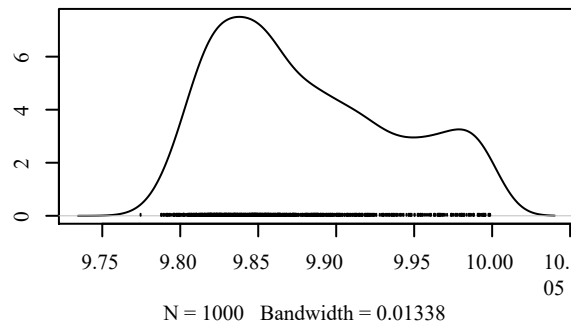
Henipavirus ZIB iCAR memc traceplot

Figure S1: MCMC traceplots

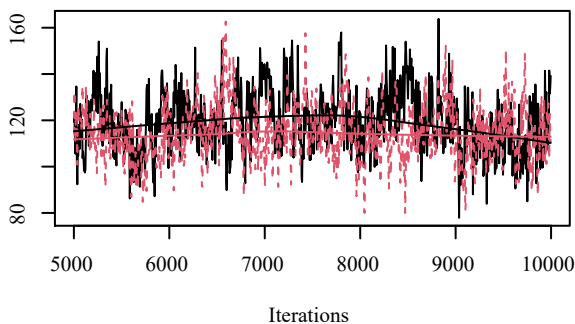
Trace of V_{rho}



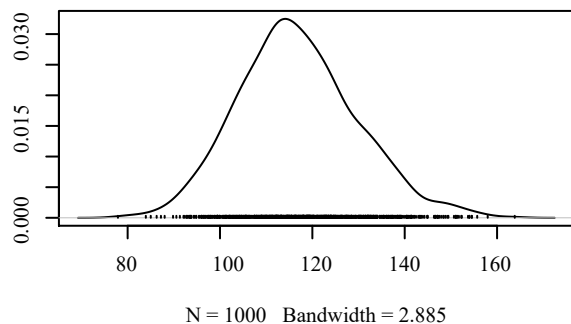
Density of V_{rho}



Trace of Deviance



Density of Deviance



Iterations = 5001:9996 Thinning
interval = 5 Number of chains = 2
Sample size per chain = 1000

**1. Empirical mean and standard deviation for each variable,
plus standard error of the mean:**

	Mean	SD	Naive SE	Time-series SE
beta.(Intercept)	-5.0585	0.38275	0.008558	0.035358
beta.layer.1	2.8126	0.63396	0.014176	0.091549
beta.layer.2	-1.2756	0.43896	0.009815	0.044785
beta.layer	1.5379	0.28266	0.006321	0.020456
beta.lc	-0.4537	0.23741	0.005309	0.016624
beta.alt		0.42220	0.009441	0.043218
beta. lc_modi	1.2101	0.24662	0.005515	0.019175
beta.pop_den	1.4288	0.52485	0.011736	0.028831
Vrho	9.9117	0.06608	0.001478	0.009067
Deviance	268.5234	18.59034	0.415693	1.368309

2. Quantiles for each variable:

	2.5%	25%	50%	75%	97.5%
beta.(Intercept)	-5.9281	-5.2883	-5.0267	-4.8015	-4.377118
beta.layer.1	1.6322	2.3601	2.8213	3.2370	4.093664
beta.layer.2	-2.1452	-1.5521	-1.2730	-0.9835	-0.416579
beta.layer	0.9906	1.3403	1.5413	1.7226	2.083984
beta.lc	-0.9343	-0.6152	-0.4509	-0.2934	-0.008502
beta.alt	1.2272	1.5100	1.8304	2.359139	0.7510
beta.lc_modi	1.2039	1.3657	1.720882	0.4723	1.0645
beta.pop_den	1.7538	2.541129			1.3920
Vrho	9.7524	9.8724	9.9292	9.9623	9.995419
Deviance	234.5247	255.2666	268.5496	280.7599	307.406395

Potential scale reduction factors:

	Point est.	Upper C.I.
beta.(Intercept)	1.08	1.11
beta.layer.1	1.05	1.13
beta.layer.2	1.10	1.18
beta.layer	1.04	1.16
beta.lc	1.01	1.03
beta.alt	1.04	1.17
beta.lc_modi	1.02	1.10
beta.pop_den	1.03	1.12
Vrho	1.03	1.15
Deviance	1.02	1.08

Multivariate psrf **1.01**

Filoviridae- ZIB model

Iterations = 5001:9996 Thinning
interval = 5 Number of chains = 2
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable, plus standard error of the mean:

	Mean	SD	Naive SE	Time-series SE
beta.(Intercept)	-2.4360	0.2005	0.004483	0.014305
beta.layer.1	3.0160	0.3328	0.007443	0.027527
beta.layer.2	-1.4385	0.2119	0.004739	0.010294
beta.layer	1.4636	0.1627	0.003638	0.007255
beta.lc	-0.5116	0.1397	0.003124	0.005707
beta.alt			0.2289	0.005119
beta.lc_modi	0.9691	0.1217	0.002721	0.004821
beta.pop_den	1.4301	0.3510	0.007849	0.011363
Deviance	839.2431	3.9822	0.089046	0.202869

2. Quantiles for each variable:

	2.5%	25%	50%	75%	97.5%
beta.(Intercept)	-2.8509	-2.5694	-2.4249	-2.2968	-2.0594
beta.layer.1	2.4301	2.7740	3.0153	3.2328	3.6853
beta.layer.2	-1.8613	-1.5798	-1.4316	-1.2940	-1.0319
beta.layer	1.1559	1.3522	1.4624	1.5733	1.7776
beta.lc	-0.7829	-0.6050	-0.5106	-0.4143	-0.2414
beta.alt	1.4303	1.7023	1.8535	2.0087	2.3234
beta.lc_modi	0.8872	0.9675	1.0515	1.2153	1.4161
beta.pop_den	0.7658	0.9675	1.0515	1.2153	1.4161
Deviance	833.5560	836.3873	838.5348	841.3827	848.7955

Potential scale reduction factors:

	Point est.	Upper C.I.
beta.(Intercept)	1.01	1.04
beta.layer.1	1.02	1.09
beta.layer.2	1.00	1.01
beta.layer	1.00	1.00
beta.lc	1.00	1.00
beta.alt	1.00	1.00
beta.lc_modi	1.00	1.06
beta.pop_den	1.00	1.01
Deviance	1.00	1.00
	1.01	1.02

Multivariate psrf

1.02

Filoviridae- Binomial iCAR model

Iterations = 5001:9996 Thinning
interval = 5 Number of chains = 2
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable, plus standard error of the mean:

	Mean	SD	Naive SE	Time-series SE
beta.(Intercept)	-68.584	20.47129	0.4578	6.285113
beta.layer.1	184.727	76.96106	1.7209	20.970875
beta.layer.2	-161.274	66.52704	1.4876	17.530246
beta.layer	146.552	56.67100	1.2672	14.934569
beta.lc	26.221	21.29192	0.4761	3.294789
beta.alt	86.114	34.51012	0.7717	5.069096
beta.lc_modi	20.336	9.84002	0.2200	0.985933
beta.pop_den	270.768	183.23397	4.0972	53.637638
gamma.(Intercept)	1.062	0.08945	0.0020	0.002459
Deviance	764.375	4.91207	0.1098	0.291679

2. Quantiles for each variable:

	2.5%	25%	50%	75%	97.5%
beta.(Intercept)	-122.6578	-77.441	-67.79	-55.346	-36.732
beta.layer.1	74.0126	127.148	162.59	241.215	321.694
beta.layer.2	-278.9760	-212.217	-143.69	-110.954	-64.301
beta.layer	61.0214	105.083	132.25	201.442	243.409
beta.lc	-1.9518	10.361	17.84	41.800	69.142
beta.alt	33.5277	58.772	81.14	115.079	152.069
beta.lc_modi	6.2491	12.448	18.53	27.078	42.176
beta.pop_den	129.690	186.50	394.954	634.447	
gamma.(Intercept)	0.8874	1.003	1.06	1.119	1.241
Deviance	756.7407	760.864	763.77	767.172	775.737

Potential scale reduction factors:

	Point est.	Upper C.I.
beta.(Intercept)	1.42	2.38
beta.layer.1	3.17	8.29
beta.layer.2	3.15	8.13
beta.layer	3.20	7.61
beta.lc	2.51	8.71
beta.alt	2.84	6.25
beta.lc_modi	2.16	4.73
beta.pop_den	2.90	12.15
gamma.(Intercept)	1.00	1.01
Deviance	1.06	1.23

Multivariate psrf 2.17

Iterations = 5001:9996 Thinning
interval = 5 Number of chains = 2
Sample size per chain = 1000

**1. Empirical mean and standard deviation for each variable,
plus standard error of the mean:**

	Mean	SD	Naive SE	Time-series SE
beta.(Intercept)	-5.0058	0.34385	0.007689	0.02988
beta.layer.1	2.5048	0.54371	0.012158	0.06129
beta.layer.2	-1.2656	0.42426	0.009487	0.03501
beta.layer	1.4961	0.26798	0.005992	0.02517
beta.lc	-0.6177	0.23187	0.005185	0.01600
beta.alt	1.3166	0.38944	0.008708	0.04137
beta.lc_modi	1.1634	0.23215	0.005191	0.01679
beta.pop_den	1.3672	0.51480	0.011511	0.02824
gamma.(Intercept)	814.8946	620.53149	13.875506	19.42589
Vrho	9.9018	0.07377	0.001649	Deviance
267.1366	19.03855	0.425715		1.65344

2. Quantiles for each variable:

	2.5%	25%	50%	75%	97.5%
beta.(Intercept)	-5.6722	-5.2418	-5.0128	-4.7700	-4.3141
beta.layer.1	1.4060	2.1420	2.4936	2.8745	3.6247
beta.layer.2	-2.1314	-1.5475	-1.2646	-0.9791	-0.4775
beta.layer	1.0052	1.3065	1.4921	1.6650	2.0475
beta.lc	-1.0441	-0.7742	-0.6215	-0.4535	-0.1562
beta.alt	0.5948	1.0561	1.3028	1.5745	2.1356
beta.lc_modi	0.7507	0.9962	1.1450	1.3280	1.6362
beta.pop_den	0.4781	1.0035	1.3313	1.7039	2.4967
gamma.(Intercept)	37.1924	339.1505	694.1825	1159.6324	2390.2706
Vrho	9.9203	9.9646	9.9957		
Deviance	231.4583	254.5566	266.4477	279.7336	305.0297

Potential scale reduction factors:

	Point est.	Upper C.I.
beta.(Intercept)	1.12	1.43
beta.layer.1	1.03	1.12
beta.layer.2	1.05	1.22
beta.layer	1.00	1.01
beta.lc	1.02	1.09
beta.alt	1.02	1.02
beta.lc_modi	1.01	1.04
beta.pop_den	1.01	1.03
gamma.(Intercept)	1.00	1.00
Vrho	1.05	1.18

Deviance	1.00	1.00
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Multivariate psrf

1.12

Model Deviance Perc

1	NULL	1891.4073	0
2	env	764.3752	69
3	binomial	839.2431	65
4	binomial.icar	268.5234	100
5	ZIB.icar	267.1366	100

"masTSS"	"OA"	"prob"
0.99 1	0.66	

Coronaviridae- Binomial model

Iterations = 5001:9996 Thinning
interval = 5 Number of chains = 2
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable,
plus standard error of the mean:

	Mean	SD	Naive SE	Time-series SE
beta.(Intercept)	-2.1638	0.2205	0.004929	0.015419
beta.layer.1	3.7979	0.8500	0.019007	0.141365
beta.layer.2	-0.6954	0.6879	0.015382	0.106804
beta.layer	-0.7493	0.2248	0.005027	0.028991
beta.lc	-0.3097	0.1591	0.003557	0.006269
beta.alt			0.2213	0.004948
beta.lc_modi	2.5148	0.2299	0.005142	0.011551
beta.pop_den	2.5332	0.3239	0.007244	0.011723
Deviance	629.1162		4.1161	0.092039
				0.156460

2. Quantiles for each variable:

	2.5%	25%	50%	75%
beta.(Intercept)	-2.6155	-2.3058	-2.1630	-2.0255
beta.layer.1	2.0819	3.2633	3.8563	4.3605
beta.layer.2	-1.9724	-1.1275	-0.7602	-0.2885
beta.layer	-1.1868	-0.9021	-0.7542	-0.5926
beta.lc	-0.6217	-0.4195	-0.3057	-0.1974
beta.alt		2.2091	2.3555	2.5068
beta.lc_modi	2.0629	2.3564	2.5175	2.6632
beta.pop_den	1.9309	2.3045	2.5273	2.7513
Deviance	623.3048	626.1436	628.5594	631.3158
	97.5%			
beta.(Intercept)	-1.73494			
beta.layer.1	5.34437			
beta.layer.2	0.76732			
beta.layer	-0.31073			
beta.lc	-0.01345			
beta.alt	2.77599			
beta.lc_modi	3.00822			
beta.pop_den	3.19233			
Deviance	638.75865			

Potential scale reduction factors:

	Point est.	Upper C.I.
beta.(Intercept)	1.02	1.09
beta.layer.1	1.11	1.42
beta.layer.2	1.09	1.35
beta.layer	1.06	1.24

beta.lc	1.00	1.01
beta.alt	1.04	1.18
beta.lc_modi	1.01	1.07
beta.pop_den	1.00	1.00
Deviance	1.01	1.04

Multivariate psrf

1.07

Coronaviridae- ZIB model

Iterations = 10001:19991 Thinning
interval = 10 Number of chains = 2
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable,
plus standard error of the mean:

	Mean	SD	Naive SE	Time-series SE
beta.(Intercept)	-224.637	88.0989	1.969952	5.998e+01
beta.layer.1	255.155	125.6389	2.809370	6.025e+ 01
beta.layer.2	124.343	98.5342	2.203292	3.987e+ 01
beta.layer	-23.198	19.6178	0.438668	5.455e+00
beta.lc	1.894	8.3197	0.186035	1.131e+00
beta.alt	253.489	95.1583	2.127805	5.831e+01
beta.lc_modi	425.926	161.5253	3.611816	1.114e+02
beta.pop_den	29.792	45.2351	1.011489	8.569e+00
gamma.(Intercept)	1.582	0.1125	0.002515	2.656e-03
Deviance	548.472	5.8761	0.131393	6.678e-01

2. Quantiles for each variable:

	2.5%	25%	50%	75%
beta.(Intercept)	-414.5339	-260.954	-224.749	-166.357
beta.layer.1	52.8548	158.580	259.036	348.230
beta.layer.2	0.6359	48.964	92.950	180.589
beta.layer	-63.0630	-37.165	-21.297	-6.601
beta.lc	-15.3978	-3.038	1.023	7.661
beta.alt	97.7189	193.783	260.491	300.421
beta.lc_modi	166.9442	333.225	436.017	495.776
beta.pop_den	-12.3879	1.657	11.688	38.266
gamma.(Intercept)	1.3712	1.508	1.581	1.658
Deviance	537.3869	544.428	547.923	552.011

beta.(Intercept) -89.949
beta.layer.1 485.966
beta.layer.2 386.439
beta.layer 4.337
beta.lc17.872
beta.alt445.758
beta.lc_modi 759.543
beta.pop_den 164.533 gamma.
(Intercept) 1.802 Deviance
561.017

Potential scale reduction factors:

	Point est.	Upper C.I.
beta.(Intercept)	1.25	1.30

beta.layer.1	1.29	1.98
beta.layer.2	1.14	1.47
beta.layer1.25		1.83
beta.lc	1.11	1.36
beta.alt	1.26	1.82
beta.lc_modi	1.25	1.54
beta.pop_den	1.42	3.32
gamma.(Intercept)	1.01	1.04
Deviance	1.06	1.24

Multivariate psrf

1.38

Iterations = 5001:9996 Thinning
interval = 5 Number of chains = 2
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable,
plus standard error of the mean:

	Mean	SD	Naive SE	Time-series SE
beta.(Intercept)	-5.8993	0.60388	0.013503	0.054930
beta. layer. 1	3.1738	1.99638	0.044640	0.388036
beta. layer. 2	-0.1431	1.72627	0.038600	0.302624
beta. layer	-1.4755	0.57547	0.012868	0.069770
beta.lc	-0.1733	0.42810	0.009573	0.022948
beta.alt		0.58802	0.013149	0.055892
beta. lc_modi	2.5623	0.58561	0.013095	0.040325
beta. pop_den	3.3864	0.90664	0.020273	0.080053
Vrho	0.9211	0.04686	0.001048	0.007787
Deviance	63.0917	10.20057	0.228092	0.805057

2. Quantiles for each variable:

	2.5%	25%	50%	75%	97.5%
beta.(Intercept)	-7.057	-6.2937	-5.9007	-5.4734	-4.7317
beta.layer.1	1.8136	3.3688	4.6736	6.4875	
beta.layer.2	-0.1816	1.0283	3.2976		
beta.layer	-1.0505	-0.4358		-1.059	-0.4522
beta.lc	0.6530				
beta.alt		0.837	1.6606	2.0643	2.4616
beta.lc_modi	1.497	2.1540	2.5237	2.9314	3.7982
beta.pop_den	1.745	2.7541	3.3471	3.9601	5.1832

Vrho	0.839	9.8821	9.9220	9.9619	9.9956
Deviance	44.653	55.9676	62.6950	69.8488	83.9747

Potential scale reduction factors:

	Point est.	Upper C.I.
beta.(Intercept)	1.09	1.34
beta.layer.1	1.01	1.02
beta.layer.2	1.01	1.02
beta.layer	1.10	1.38
beta.lc	1.01	1.03
beta.alt	1.04	1.16
beta.lc_modi	1.22	1.73
beta.pop_den	1.44	2.30
Vrho	1.01	1.06
Deviance	1.05	1.18

Multivariate psrf	1.4
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Iterations = 10001:19991 Thinning
interval = 10 Number of chains = 2
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable,
plus standard error of the mean:

	Mean	SD	Naive SE beta.
(Intercept)	-6.257	0.62276	0.013925
beta.layer.1	4.312	2.63169	0.058846
beta.layer.2	-0.990	2.19117	0.048996
beta.layer	-1.849	0.72472	0.016205
beta.lc	-0.262	0.44891	0.010038
beta.alt	2.206	0.65840	0.014722
beta.lc_modi	2.522	0.56494	0.012632
beta.pop_den	3.755	0.83355	0.018639
gamma.(Intercept)	776.973	587.09236	13.127784

Vrho Deviance	9.919	0.04903	0.001096
	59.005	10.23167	0.228787

Time-series SE

beta.(Intercept)	0.044082
beta.layer.1	0.532657
beta.layer.2	0.382394
beta.layer	0.093402
beta.lc	0.023349
beta.alt	0.099156
beta.lc_modi	0.030517
beta.pop_den	0.059244
gamma.(Intercept)	14.200550
Vrho	0.006272
Deviance	0.721394

2. Quantiles for each variable:

	2.5%	25%	50%	75%
beta.(Intercept)	-7.5764	-6.6587	-6.2157	-5.81767
beta.layer.1	-1.0942	2.7539	4.3463	5.92397
beta.layer.2	-5.0734	-2.4187	-0.9744	0.33959
beta.layer	-3.2070	-2.3339	-1.8875	-1.36643
beta.lc	-1.1423	-0.5646	-0.2654	0.02459
beta.alt	1.7687	2.2031	2.63256	
beta.lc_modi	1.4749	2.1512	2.5048	2.90040
beta.pop_den	2.1531	3.1863	3.7472	4.30956
gamma.(Intercept)	38.1536	320.4527	639.2747	1123.56527
Vrho	9.8351	9.8755	9.9217	9.96113
Deviance	40.7212	51.9276	58.3373	65.39818
	97.5%			
beta.(Intercept)	-5.1221			
beta.layer.1	9.3579			
beta.layer.2	3.5601			
beta.layer	-0.3798			

beta.lc 0.6421
beta.alt 3.5145
beta.lc_modi 3.6880
beta.pop_den 5.4344
gamma.(Intercept) 2115.2218
Vrho 9.9968
Deviance 81.1050

Potential scale reduction factors:

	Point est. Upper C.I.	
beta.(Intercept)	1.03	1.11
beta.layer.1	1.05	1.05
beta.layer.2	1.05	1.07
beta.layer.beta.lc	1.02	1.10
beta.alt	1.00	1.00
beta.lc_modi	1.01	1.02
beta.pop_den	1.03	1.15
	1.01	1.03
gamma.(Intercept)	1.00	1.00
Vrho Deviance	1.00	1.02
Multivariate psrf	1.00	1.00
	1.17	

	Model	Deviance	Perc
1	NULL	1889.17448	0
2	env	548.47170	74
3	binomial	629.11621	69
4	binomial.icar	63.09174	100
5	ZIB.icar	67.01016	100

"masTSS"	"OA"	"prob"
1	1	0.65

Henipavirus- Binomial model

Iterations = 5001:9996 Thinning
interval = 5 Number of chains = 2
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable, plus standard error of the mean:

	Mean	SD	Naive SE	Time-series SE
beta.(Intercept)	-7.42157	0.91838	0.020536	0.148278
beta.layer.1	-2.72411	1.60108	0.035801	0.270781
beta.layer.2	1.65097	1.30463	0.029172	0.215200
beta.layer	2.23412	0.39907	0.008923	0.046655
beta.lc		0.21787	0.28018	0.006265
beta.alt	-7.12888	1.92968	0.043149	0.308019
beta. lc_modi	2.01717	0.38696	0.008653	0.026624
beta.pop_den	0.00701	0.15813	0.003536	0.007293
Vrho	9.87936	0.05526	0.001236	0.008422
Deviance	113.44166			
	12.32776	0.275657	0.945002	

2. Quantiles for each variable:

	2.5%	25%	50%	75%	97.5%
beta.(Intercept)	-9.4726	-8.00068	-7.29651	-6.8059	-5.8840
beta.layer.1	-5.7679	-3.82144	-2.80242	-1.6734	0.6095
beta.layer.2	-1.1103	0.82618	1.65468	2.5389	4.1226
beta.layer	1.4294	1.96110	2.23344	2.5053	3.0142
beta.lc			0.03295	0.21572	0.4036
beta.alt	-11.3713	-8.22921	-7.05425	-5.7307	-3.9039
beta.lc_modi	1.2865	1.75444	2.03407	2.2744	2.7566
beta.pop_den	-0.3128	-0.09765	0.01136	0.1141	0.2983
Vrho	9.7971	9.83454	9.86940	9.9186	9.9928
Deviance	90.6080	104.71929	112.90177	122.1287	138.1282

Potential scale reduction factors:

	Point est.	Upper C.I.
beta.(Intercept)	1.13	1.46
beta.layer.1	1.08	1.31
beta.layer.2	1.11	1.42
beta.layer	1.00	1.01
beta.lc		
beta.alt	1.06	1.25
beta.lc_modi	1.10	1.36
beta.pop_den	1.33	2.03
Vrho		
Deviance	1.02	1.10
	1.10	1.37
	1.09	1.33

Multivariate psrf 1.57

Henipavirus- ZIB model

Iterations = 5001:9996 Thinning
interval = 5 Number of chains = 2
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable, plus standard error of the mean:

	Mean	SD	Naive SE	Time-series SE
beta.(Intercept)	-6.1898	0.7317	0.016362	0.133905
beta.layer.1	-1.7241	0.6138	0.013725	0.060312
beta.layer.2	0.9176	0.5074	0.011346	0.042359
beta.layer	1.3295	0.1863	0.004165	0.012484
beta.lc	0.2903	0.1405	0.003141	0.005599
beta.alt	-11.7266	1.5390	0.034413	0.301332
beta. lc_modi	1.2574	0.1581	0.003536	0.005924
beta. pop_den	0.1164	0.1256	0.002808	0.003849
Deviance	635.2810	4.0968	0.091607	0.197628

2. Quantiles for each variable:

	2.5%	25%	50%	75%	97.5%
beta.(Intercept)	-7.77453	-6.59967	-6.1525	-5.7043	-4.9017
beta.layer.1	-2.91079	-2.14856	-1.7303	-1.3177	-0.5201
beta.layer.2	-0.08586	0.59115	0.9290	1.2549	1.9092
beta.layer	0.96104	1.20545	1.3335	1.4542	1.6975
beta.lc	0.01660	0.19248	0.2918	0.3849	0.5634
beta.alt	-15.08253	-12.66530	-11.6315	-10.6695	-9.0201
beta.lc_modi	0.94251	1.15159	1.2567	1.3619	1.5712
beta.pop_den	-0.09433	0.02814	0.1078	0.1918	0.3981
Deviance	629.32335	632.25033	634.6044	637.5753	645.0544

Potential scale reduction factors:

	Point est.	Upper C.I.
beta.(Intercept)	1.02	1.11
beta.layer.1	1.02	1.08
beta.layer.2	1.02	1.07
beta.layer	1.01	1.05
beta.lc	1.00	1.02
beta.alt	1.00	1.02
beta.lc_modi	1.02	1.08
beta.pop_den	1.00	1.00
Deviance	1.00	1.00
	1.00	1.00

Multivariate psrf

1.04

Henipavirus- Binomial iCAR model

Iterations = 5001:9996 Thinning
interval = 5 Number of chains = 2
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable, plus standard error of the mean:

	Mean	SD	Naive SE	Time-series SE
beta.(Intercept)	-5.7849	0.8117	0.018151	0.157069
beta.layer.1	-1.2758	0.6525	0.014590	0.067635
beta.layer.2	0.2252	0.6628	0.014820	0.084433
beta.layer	1.2112	0.2052	0.004588	0.017493
beta.lc	0.3060	0.1564	0.003498	0.006503
beta.alt	-11.6670	1.3888	0.031054	0.238654
beta.lc_modi	0.7398	0.3380	0.007558	0.045304
beta.pop_den	1.7751	1.2008	0.026851	0.197678
gamma.(Intercept)	6.9297	10.3305	0.230997	2.579533
Deviance	627.4858	4.7735	0.106739	0.475115

2. Quantiles for each variable:

	2.5%	25%	50%	75%	97.5%
beta.(Intercept)	-7.27209	-6.3586	-5.8325	-5.2327	-4.25214
beta.layer.1	-2.56459	-1.7053	-1.2951	-0.8435	0.06333
beta.layer.2	-1.14806	-0.1876	0.2455	0.7096	1.40811
beta.layer	0.79719	1.0828	1.2055	1.3445	1.60444
beta.lc	0.01016	0.2008	0.3048	0.4091	0.61377
beta.alt	-14.60397	-12.5680	-11.6711	-10.6569	-9.26813
beta.lc_modi	0.03019	0.5245	0.7775	0.9734	1.32638
beta.pop_den	0.10213	0.9022	1.3065	2.6855	4.41259
gamma.(Intercept)	2.69122	3.4291	4.0987	5.2802	47.80220
Deviance	620.68101	624.0309	626.6045	630.1071	639.03774

Potential scale reduction factors:

	Point est.	Upper C.I.
beta.(Intercept)	1.01	1.04
beta.layer.1	1.01	1.03
beta.layer.2	1.02	1.08
beta.layer	1.00	1.01
beta.lc	1.00	1.01
beta.alt	1.01	1.03
beta.lc_modi	1.01	1.03
beta.pop_den	1.01	1.01
	1.03	1.14
	1.02	1.10
gamma.(Intercept)	1.36	3.62
Deviance	1.04	1.12

Multivariate psrf 1.08

Henipavirus- ZIB iCAR model

Iterations = 5001:9996 Thinning
interval = 5 Number of chains = 2
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable, plus standard error of the mean:

	Mean	SD	Naive SE	Time-series SE
beta.(Intercept)	-8.271041	1.10538	0.024717	0.245798
beta.layer.1	-3.651963	1.37054	0.030646	0.196258
beta.layer.2	2.353747	1.13634	0.025409	0.176039
beta.layer	2.413694	0.41139	0.009199	0.040010
beta.lc	0.291016	0.26851	0.006004	0.015301
beta.alt	-9.052617	2.42205	0.054159	0.534230
beta.lc_modi	2.135840	0.36923	0.008256	0.025867
beta.pop_den	0.003795	0.15525	0.003472	0.006192
gamma.(Intercept)	817.584802	628.33554	14.050010	18.905331
Vrho	9.881421	0.05772	0.001291	0.009663
Deviance	12.93415	0.289216	0.828173	116.763581

2. Quantiles for each variable:

	2.5%	25%	50%	75%
beta.(Intercept)	-11.53154	-8.83573	-8.194535	-7.5847
beta.layer.1	-6.26383	-4.49145	-3.666831	-2.8802
beta.layer.2	-0.02205	1.66728	2.354603	3.0980
beta.layer	1.61763	2.13063	2.427338	2.7051
beta.lc			0.11038	0.289858
beta.alt				0.4652
beta.lc_modi	-16.27392	-10.31546	-8.840097	-7.5964
	1.41220	1.88832	2.125123	2.3858
beta.pop_den	-0.30820	-0.09714	0.003661	0.1105
gamma.(Intercept)	51.19336	321.06399	676.766416	1198.1010
Vrho	9.79906	9.83378	9.867952	9.9227
Deviance	93.46029	107.92418	115.857036	124.5996
	97.5%			
beta.(Intercept)	-6.3486			
beta.layer.1	-	0.6572		
beta.layer.2		4.5281		
beta.layer		3.1192		
beta.lc		0.8251		
beta.alt		-4.9500		
beta.lc_modi		2.8822		
beta.pop_den		0.3041		
gamma.(Intercept)		2297.7514		
Vrho		9.9944		
Deviance		144.9087		

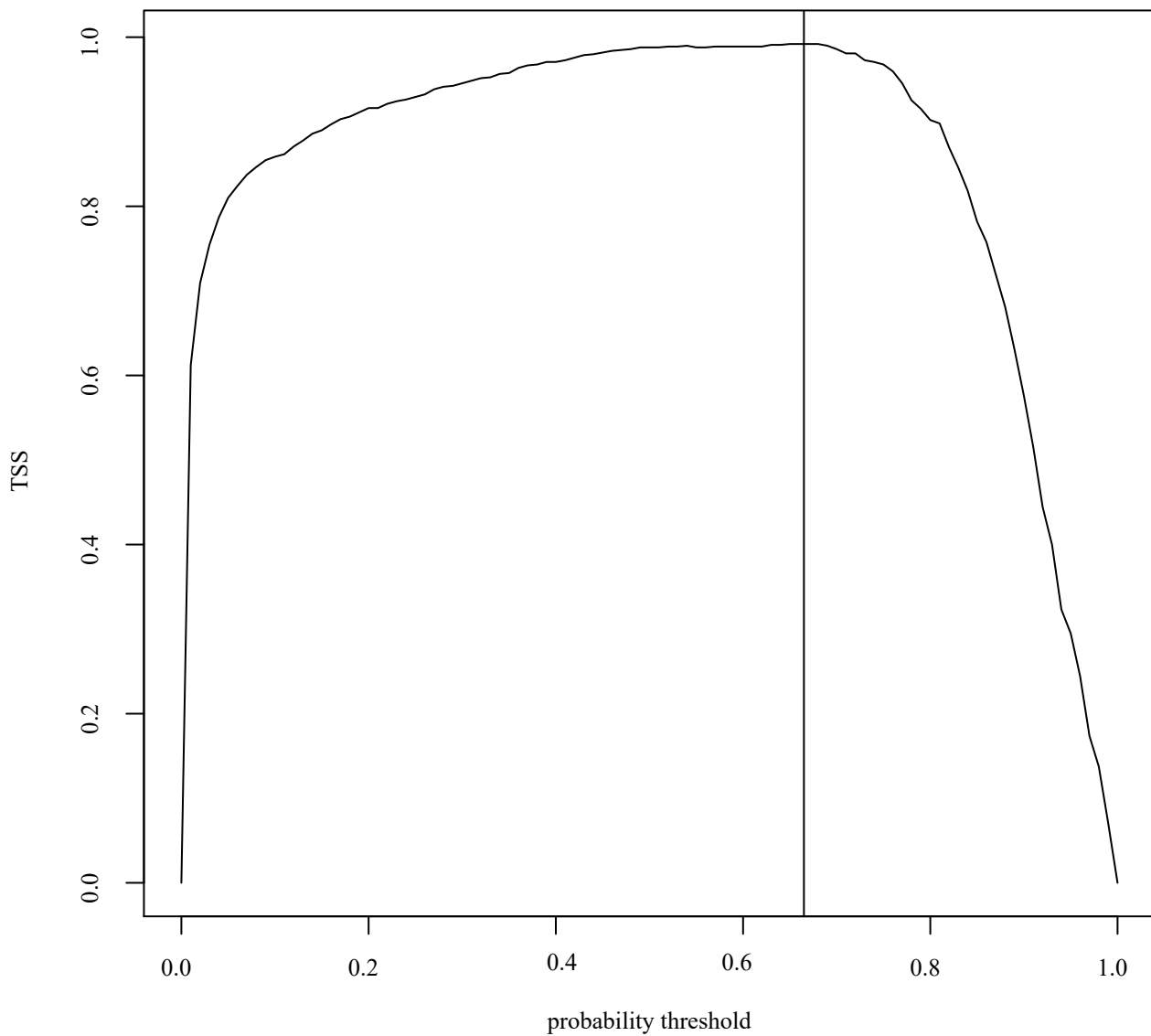
Potential scale reduction factors:

	Point est. Upper C.I.	
beta.(Intercept)	1.10	1.10
beta.layer.1	1.11	1.25
beta.layer.2	1.06	1.15
beta.layer	1.20	1.38
beta.lc	1.01	1.01
beta.lc_modi	1.10	1.14
beta.pop_den	1.08	1.20
	1.02	1.08
gamma.(Intercept)	1.00	1.00
Vrho Deviance	1.18	1.33
Multivariate psrf	1.07	1.27

1.18

	Model	Deviance	Perc
1	NULL	1862.7433	0
2	env	627.4858	71
3	binomial	635.2810	70
4	binomial.icar	113.4417	100
5	ZIB.icar	116.7636	100

"masTSS"	"OA"	"prob"
0.99	1	0.48

Filoviridae- Evolution of TSS

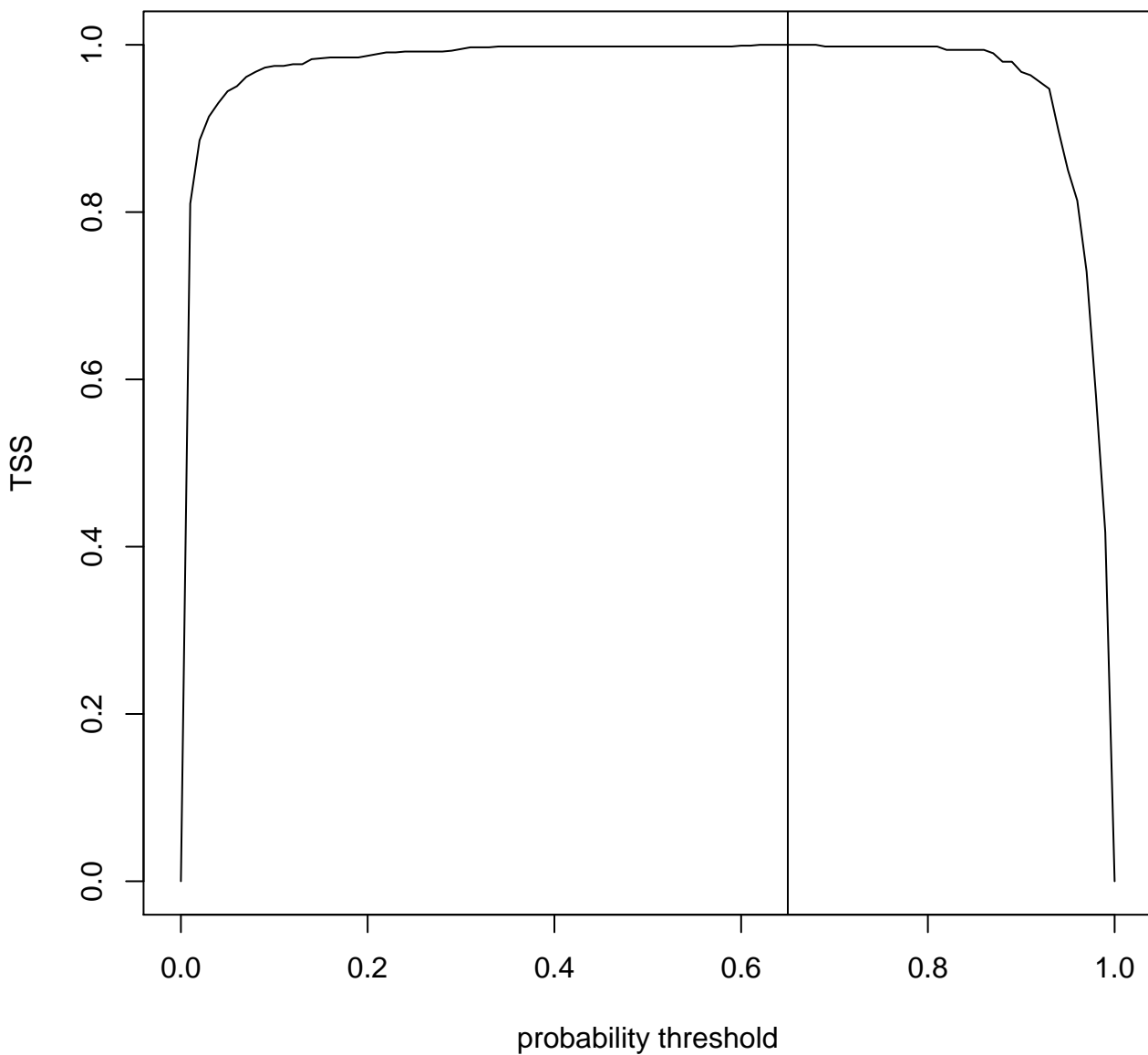
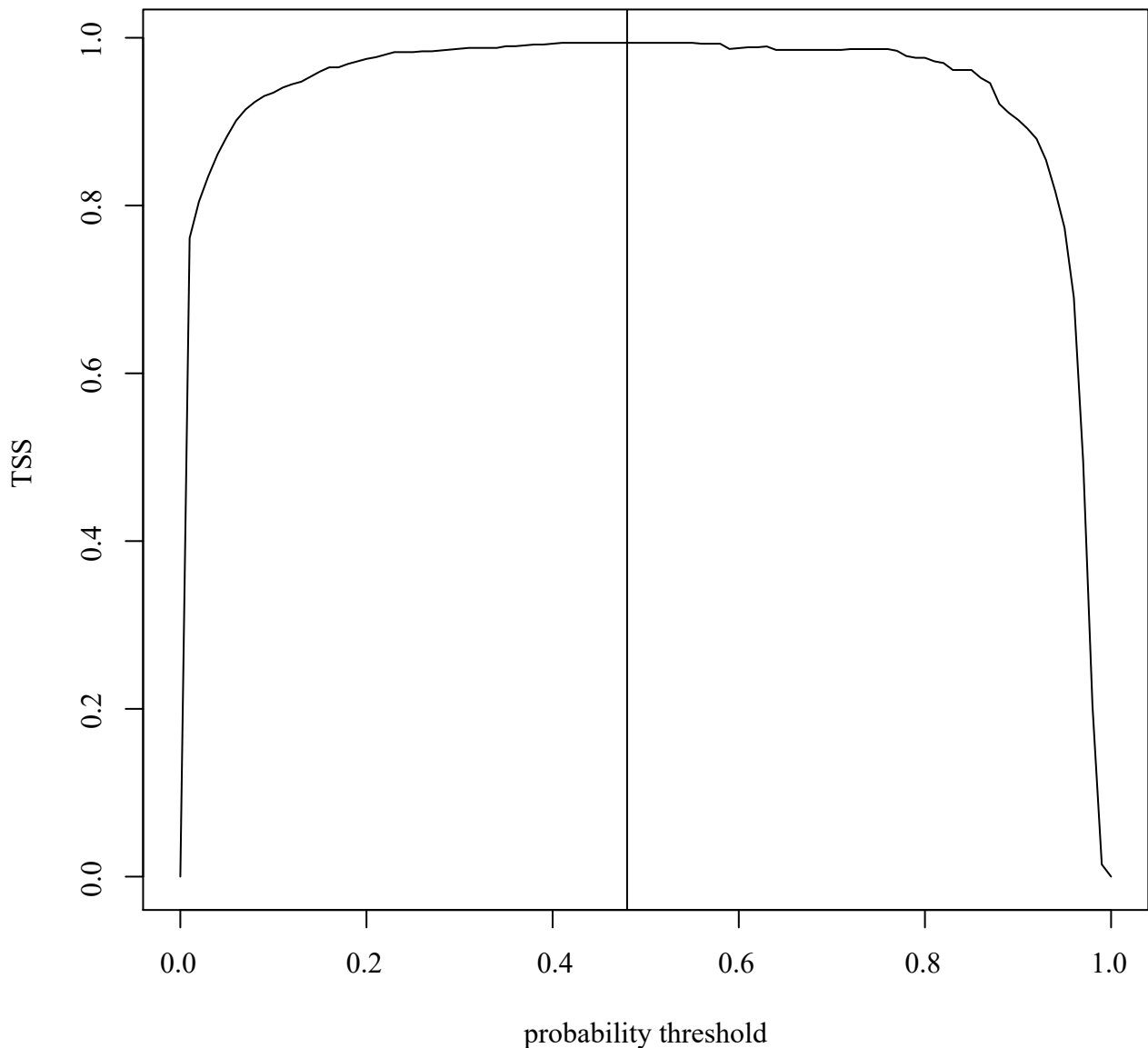
Coronaviridae- Evolution of TSS

Figure S2: True Skill Statistic (TSS) plots

Henipavirus - Evolution of TSS



Filoviridae- ZIB iCAR model Random effects

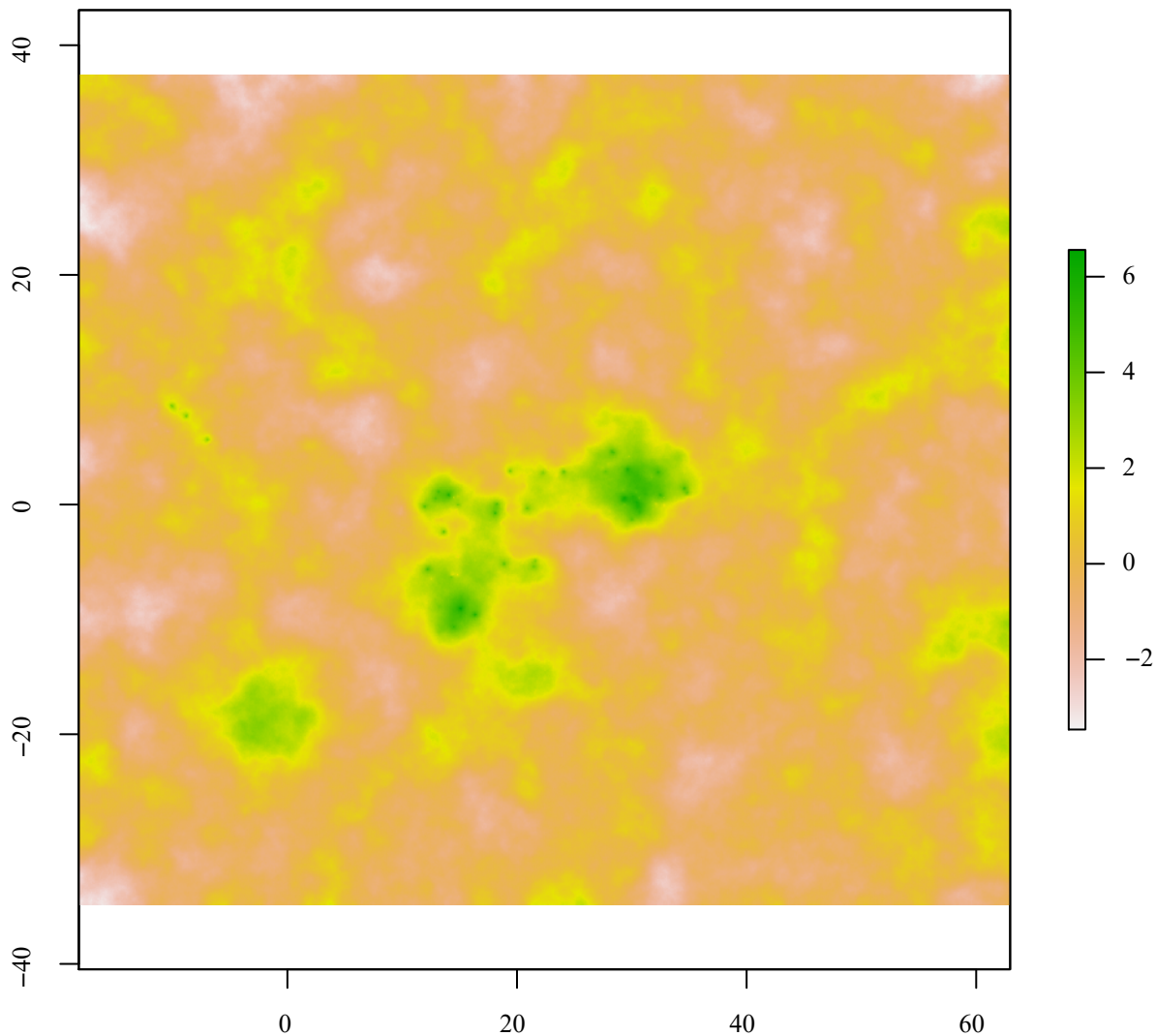


Figure S3: ZIB
iCAR random effects

Coronaviridae- ZIB iCAR model Random effects
Inclusion of SARS CoV 2 origins

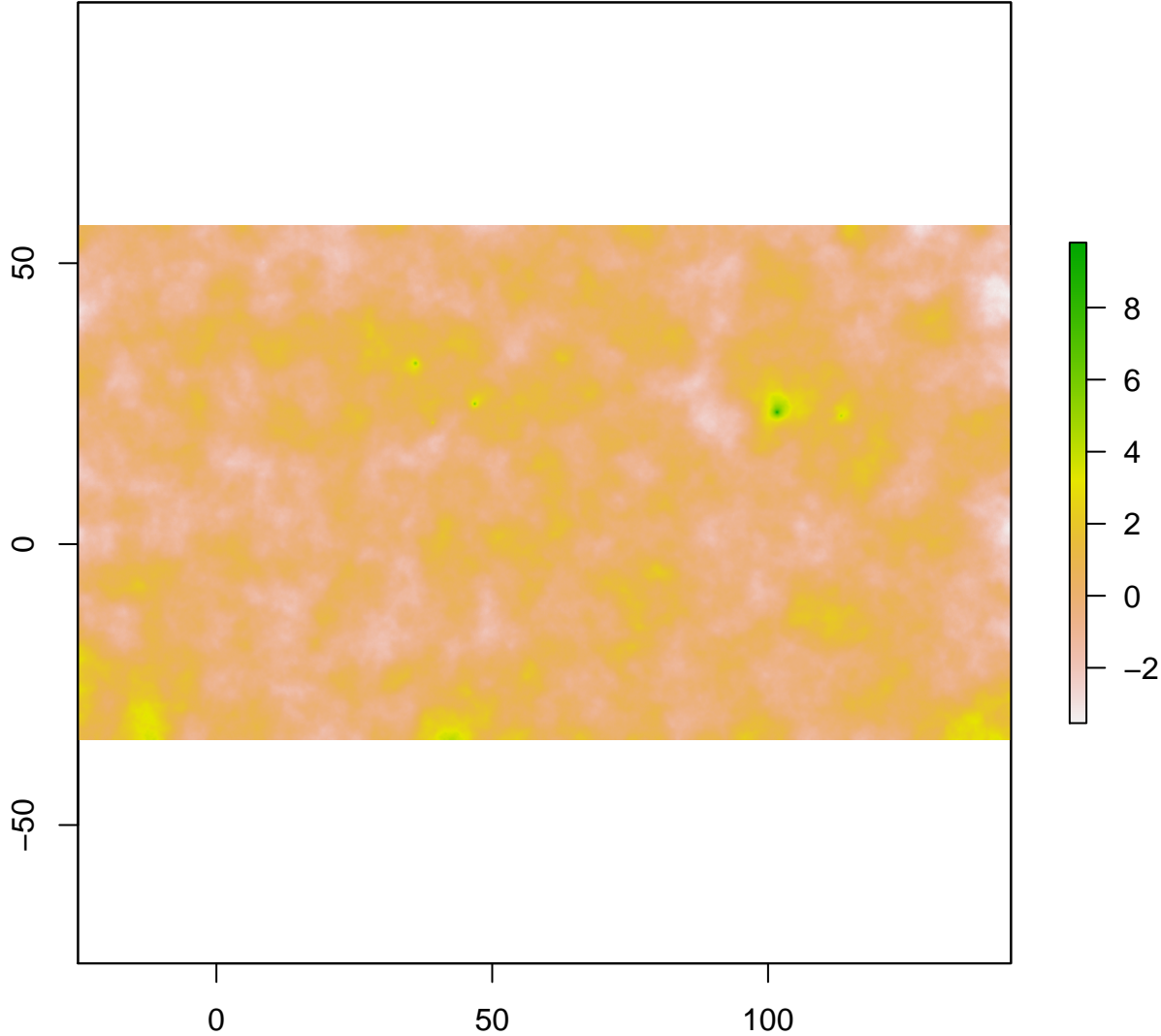


Figure S3: ZIB
iCAR random effects

Henipavirus- ZIB iCAR model Random effects

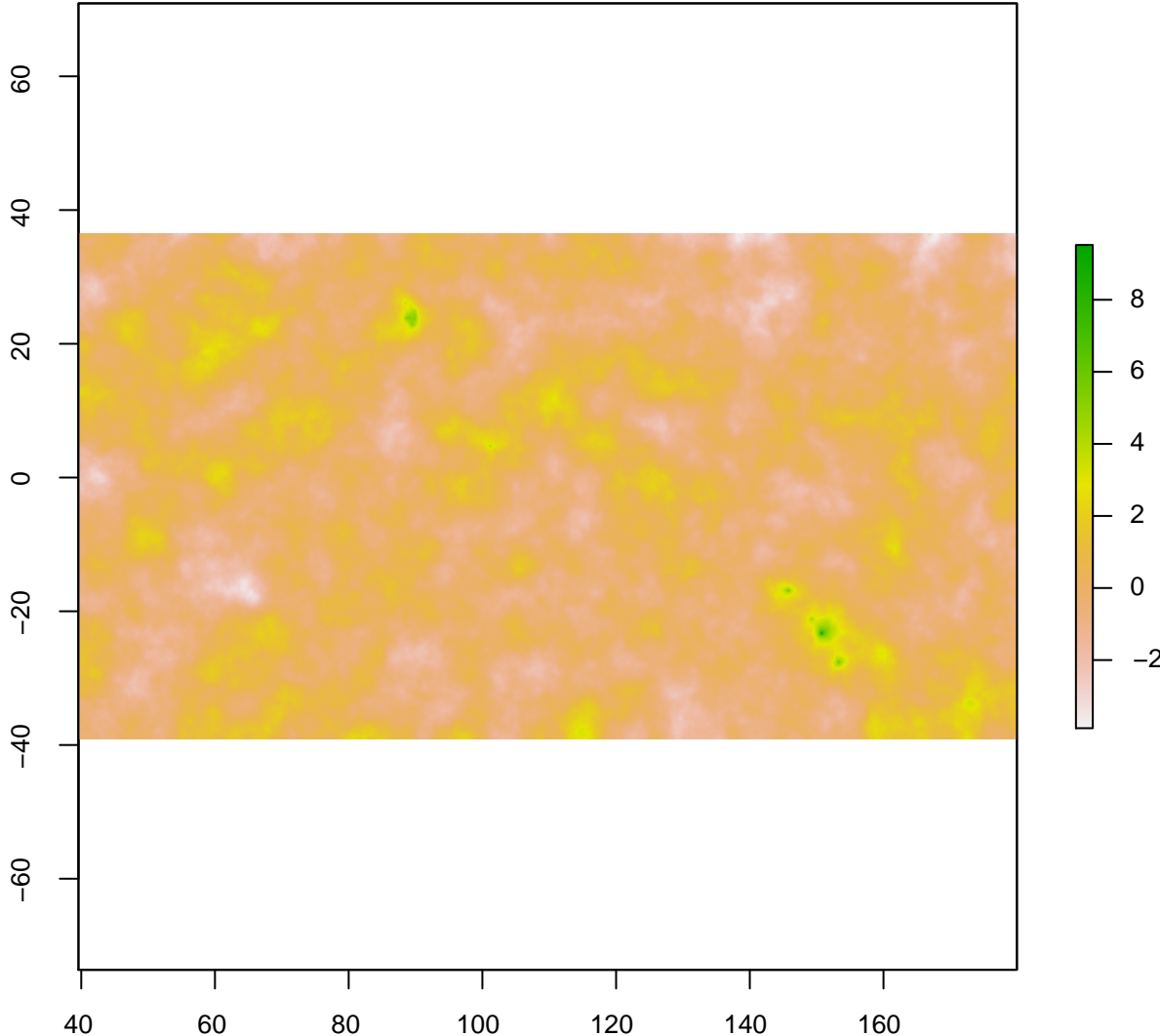


Figure S4: Significant hotspots based on TSS

Filoviridae hotspots with detection >TSS threshold

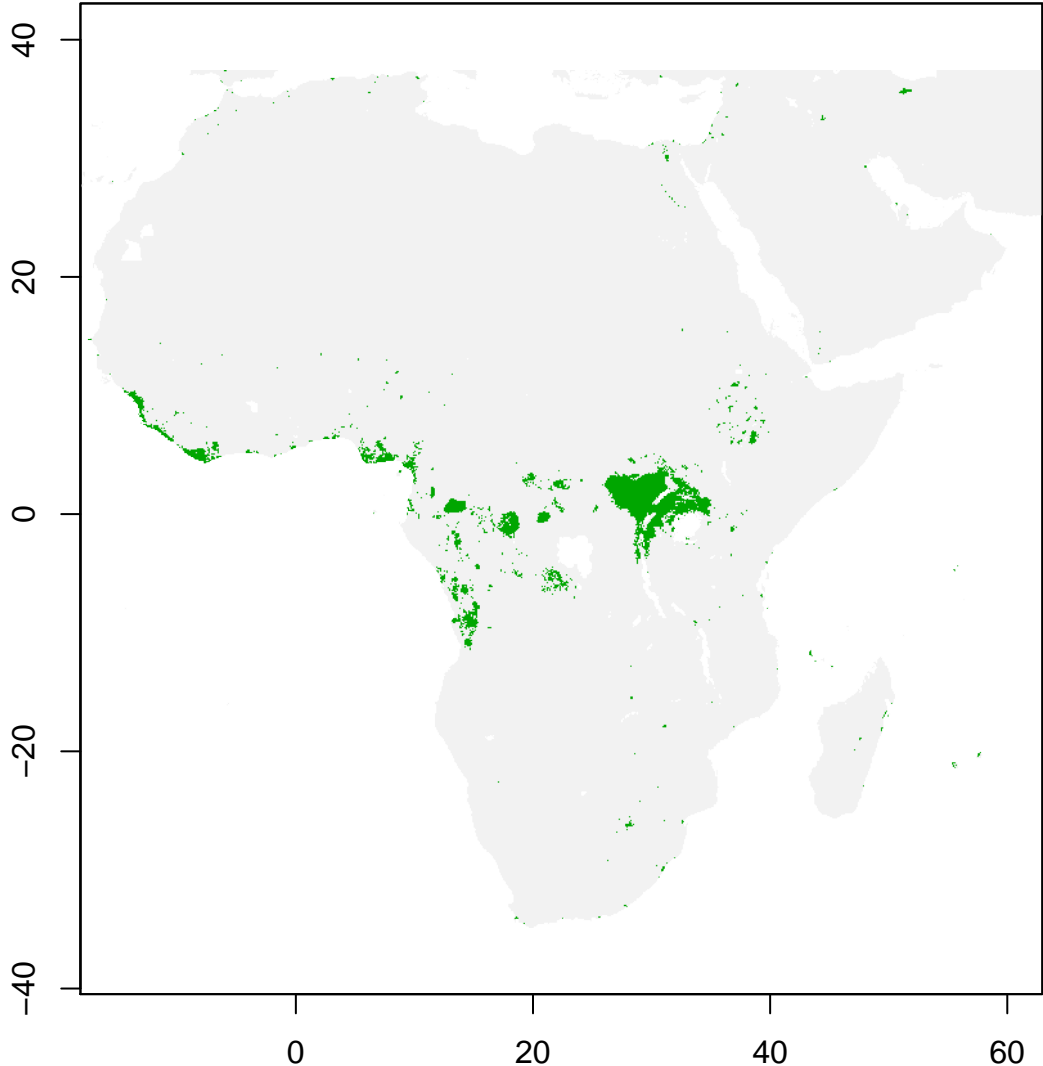


Figure S4: Significant hotspots based on TSS

Coronaviridae hotspots with detection >TSS threshold

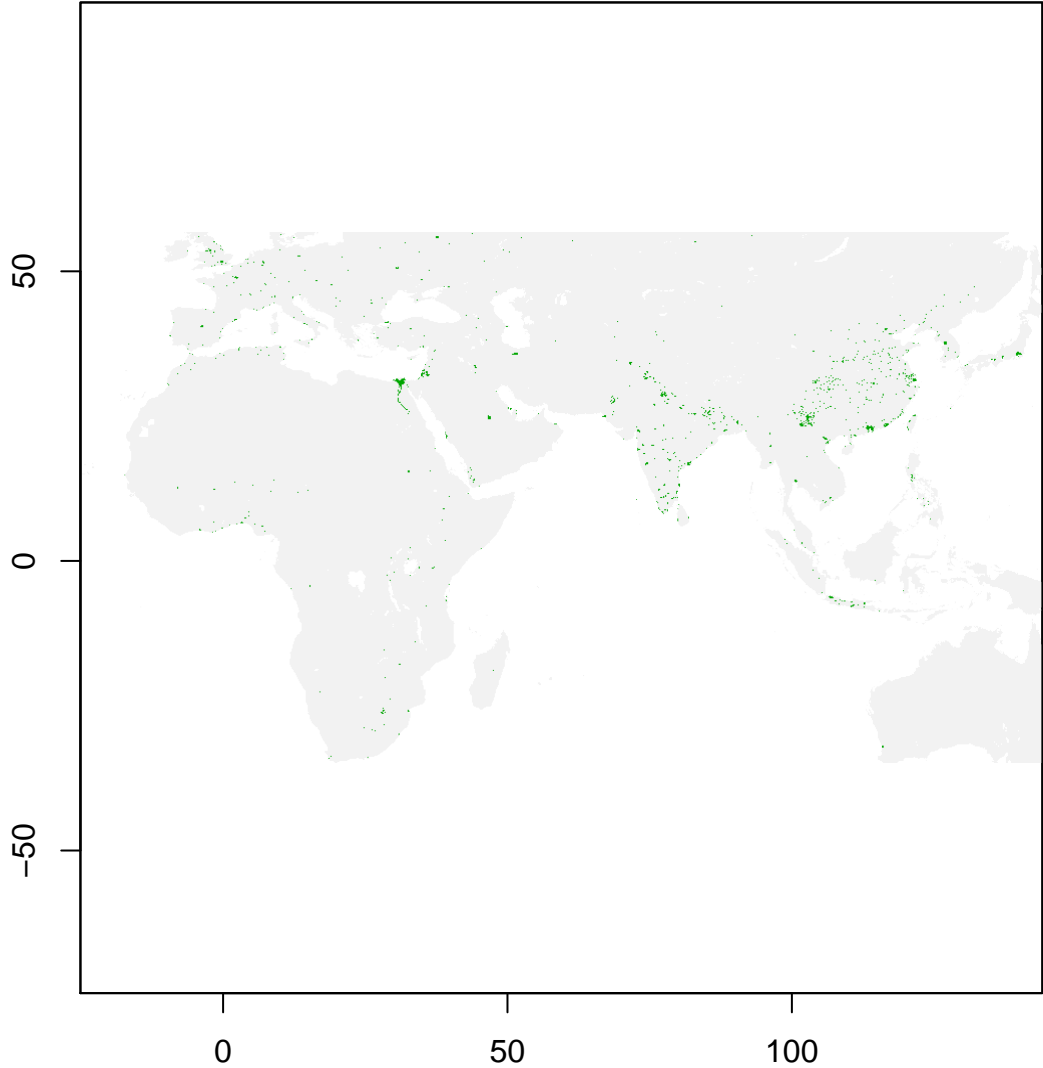
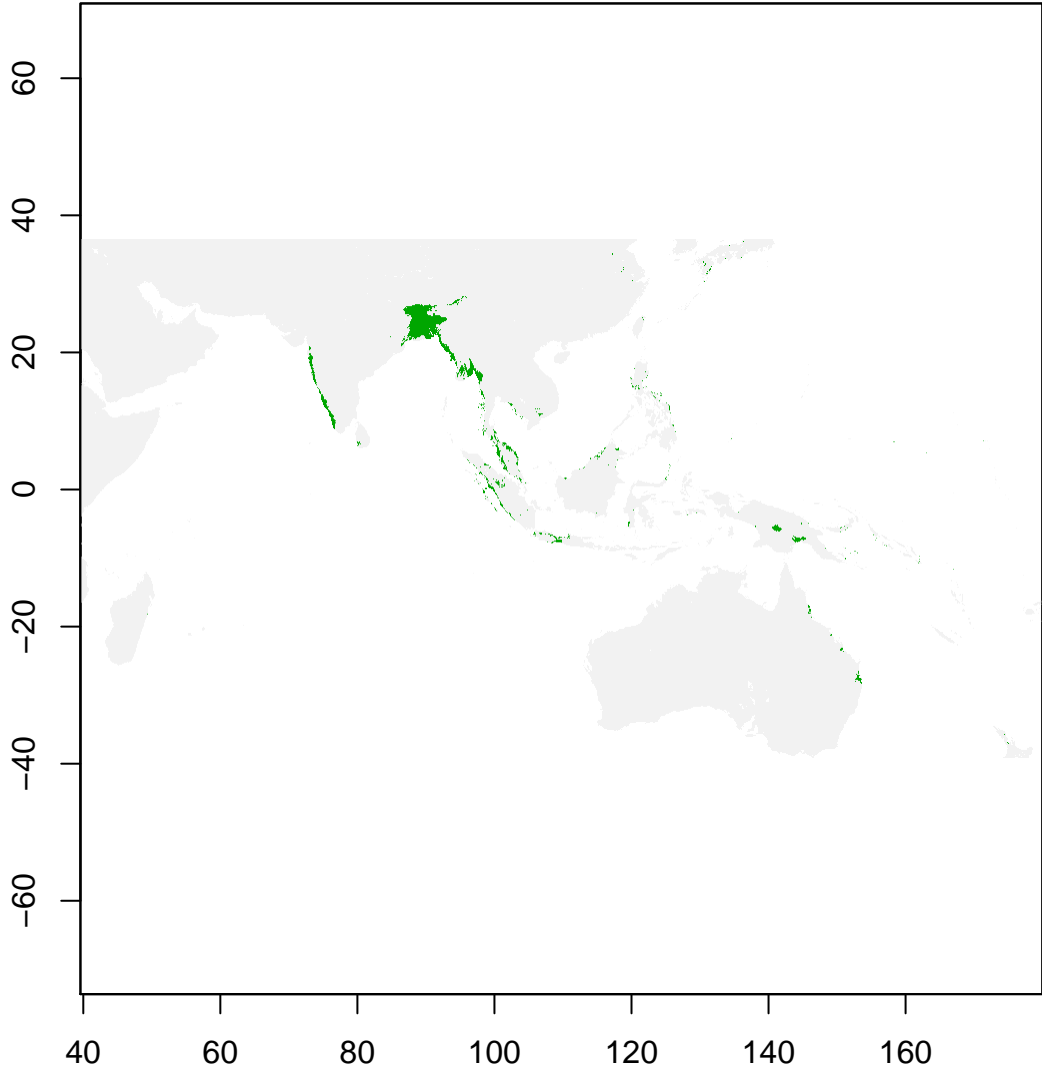


Figure S4: Significant hotspots based on TSS

Henpavirus hotspots with detection >TSS threshold



Supplementary Table 1: Reservoirs of diseases analyzed in the study

Virus	Reservoir	Binomial
MERS	serotine bat	Neoromicia_zuluensis
MERS	Egyptian tomb bat	Taphozous_perforatus
MERS	bat	Rhinopoma_microphyllum
MERS	bat	Pipistrellus_kuhlii
MERS	bat	Eptesicus_bottae
MERS	bat	Eidolon_helvum
MERS	bat	Rousettus_aegyptiacus
Henipavirus	fruit bats/ flying foxes	Pteropus_anetianus
Henipavirus	fruit bats/ flying foxes	Pteropus_aruensis
Henipavirus	fruit bats/ flying foxes	Pteropus_caniceps
Henipavirus	fruit bats/ flying foxes	Pteropus_capistratus
Henipavirus	fruit bats/ flying foxes	Pteropus_chrysoproctus
Henipavirus	fruit bats/ flying foxes	Pteropus_cognatus
Henipavirus	fruit bats/ flying foxes	Pteropus_conspicillatus
Henipavirus	fruit bats/ flying foxes	Pteropus_dasymallus
Henipavirus	fruit bats/ flying foxes	Pteropus_faunulus
Henipavirus	fruit bats/ flying foxes	Pteropus_fundatus
Henipavirus	fruit bats/ flying foxes	Pteropus_giganteus
Henipavirus	fruit bats/ flying foxes	Pteropus_gilliardorum
Henipavirus	fruit bats/ flying foxes	Pteropus_griseus
Henipavirus	fruit bats/ flying foxes	Pteropus_howensis
Henipavirus	fruit bats/ flying foxes	Pteropus_hypomelanus

Henipavirus	fruit bats/ flying foxes	Pteropus_intermedius
Henipavirus	fruit bats/ flying foxes	Pteropus_keyensis
Henipavirus	fruit bats/ flying foxes	Pteropus_leucopterus
Henipavirus	fruit bats/ flying foxes	Pteropus_livingstonii
Henipavirus	fruit bats/ flying foxes	Pteropus_lombocensis
Henipavirus	fruit bats/ flying foxes	Pteropus_loochoensis
Henipavirus	fruit bats/ flying foxes	Pteropus_leyi
Henipavirus	fruit bats/ flying foxes	Pteropus_macrotis
Henipavirus	fruit bats/ flying foxes	Pteropus_mahaganus
Henipavirus	fruit bats/ flying foxes	Pteropus_mariannus
Henipavirus	fruit bats/ flying foxes	Pteropus_melanopogon
Henipavirus	fruit bats/ flying foxes	Pteropus_melanotus
Henipavirus	fruit bats/ flying foxes	Pteropus_molossinus
Henipavirus	fruit bats/ flying foxes	Pteropus_neohibernicus
Henipavirus	fruit bats/ flying foxes	Pteropus_niger
Henipavirus	fruit bats/ flying foxes	Pteropus_nitendiensis
Henipavirus	fruit bats/ flying foxes	Pteropus_ocularis
Henipavirus	fruit bats/ flying foxes	Pteropus_ornatus
Henipavirus	fruit bats/ flying foxes	Pteropus_pelewensis
Henipavirus	fruit bats/ flying foxes	Pteropus_personatus
Henipavirus	fruit bats/ flying foxes	Pteropus_pohlei
Henipavirus	fruit bats/ flying foxes	Pteropus_poliocephalus
Henipavirus	fruit bats/ flying foxes	Pteropus_pselaphon
Henipavirus	fruit bats/ flying foxes	Pteropus_pumilus

Henipavirus	fruit bats/ flying foxes	Pteropus_rayneri
Henipavirus	fruit bats/ flying foxes	Pteropus_rennelli
Henipavirus	fruit bats/ flying foxes	Pteropus_rodricensis
Henipavirus	fruit bats/ flying foxes	Pteropus_rufus
Henipavirus	fruit bats/ flying foxes	Pteropus_samoensis
Henipavirus	fruit bats/ flying foxes	Pteropus_scapulatus
Henipavirus	fruit bats/ flying foxes	Pteropus_seychellensis
Henipavirus	fruit bats/ flying foxes	Pteropus_speciosus
Henipavirus	fruit bats/ flying foxes	Pteropus_temminckii
Henipavirus	fruit bats/ flying foxes	Pteropus_tonganus
Henipavirus	fruit bats/ flying foxes	Pteropus_tuberculatus
Henipavirus	fruit bats/ flying foxes	Pteropus_ualanus
Henipavirus	fruit bats/ flying foxes	Pteropus_vampyrus
Henipavirus	fruit bats/ flying foxes	Pteropus_vetulus
Henipavirus	fruit bats/ flying foxes	Pteropus_voeltzkowi
Henipavirus	fruit bats/ flying foxes	Pteropus_woodfordi
EVD	Greater Long-fingered bat	Miniopterus_inflatus
EVD	Franquet's epauletted fruit bat	Epomops_franqueti
EVD	hammer-headed fruit bat	Hypsignathus_monstrosus
EVD	little collared fruit bats	Myonycteris_torquata
MVD	Egyptian fruit bat	Rousettus_aegyptiacus
SARS	Greater horseshoe bat	Rhinolophus_ferrumequinum
SARS	civet	Paguma_larvata

Coronaviridae- Binomial model Inclusion of SARS CoV-2 origin

Iterations = 5001:9996 Thinning
interval = 5 Number of chains = 2
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable, plus standard error of the mean:

	Mean	SD	Naive SE	Time-series SE	
beta.(Intercept)	-4.7390	0.28041	0.0062701		0.034669
beta.layer.1	3.5341	0.97653	0.0218358		0.169654
beta.layer.2	-2.4537	0.86143	0.0192622		0.146552
beta.layer	-0.9982	0.45390	0.0101494		0.058780 0.4306
beta.lc	0.27230	0.0060888	0.015987	0.7419	0.33981
beta.alt	0.0075984	0.032927			
beta. lc_modi	1.2297	0.25588	0.0057216		0.016796
beta. pop_den	0.6959	0.38004	0.0084979		0.018124
Vrho	9.9363	0.04228	0.0009454		0.006303
Deviance	167.5602	20.00579	0.4473430		4.263603

2. Quantiles for each variable:

	2.5%	25%	50%	75%	97.5%	
beta.(Intercept)	-5.29025	-4.9219	-4.7412	-4.5516	-4.1893	
beta.layer.1	1.95791	2.8337	3.4249	4.0775	5.8057	
beta.layer.2	-4.54382	-3.0043	-2.3280	-1.8164	-1.1100	
beta.layer	-1.94214	-1.2997	-0.9614	-0.6568	-0.1935	beta.lc
-0.06632	0.2348	0.4243	0.6151	0.9767	beta.alt	0.04202
0.5225	0.7425	0.9846	1.3649	beta.lc_modi	0.75666	1.0526
1.2249	1.3973	1.7489	beta.pop_den	0.03395	0.4101	0.6681
0.9602	1.4821					
Vrho	9.84410	9.9070	9.9430	9.9710	9.9968	
Deviance	134.46400	153.4041	165.3311	179.1117	213.7345	

Potential scale reduction factors:

	Point est.	Upper C.I.
beta.(Intercept)	1.16	1.56
beta.layer.1	1.15	1.52
beta.layer.2	1.10	1.37
beta.layer	1.24	1.78
beta.lc	1.31	1.98
beta.alt	1.01	1.04
beta.lc_modi	1.01	1.03
beta.pop_den	1.01	1.01
Vrho	1.01	1.01
Deviance	1.27	1.95

Multivariate psrf 1.69

Coronaviridae- ZIB model

Inclusion of SARS CoV-2 origin

Iterations = 5001:9996 Thinning
interval = 5 Number of chains = 2
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable, plus standard error of the mean:

	Mean	SD	Naive SE	Time-series SE
beta.(Intercept)	-1.0375	0.08718	0.001949	0.003691
beta.layer.1	2.5893	0.38003	0.008498	0.058296
beta.layer.2	-1.7417	0.33506	0.007492	0.048560
beta.layer	-0.6705	0.15486	0.003463	0.015303
beta.lc	0.10546	0.002358	0.003524	0.9007
beta.alt	0.002467	0.008849		0.11034
beta.lc_modi				
beta.pop_den	1.2216	0.10344	0.002313	0.003691
Deviance	0.8019	0.24268	0.005427	0.007636
	1285.5064	4.31098	0.096397	0.279522

2. Quantiles for each variable:

	2.5%	25%	50%	75%
beta.(Intercept)	-1.2049	-1.0953	-1.0379	-0.9791
beta.layer.1	1.8054	2.3529	2.5974	2.8567
beta.layer.2	-2.3346	-1.9802	-1.7525	-1.5269
beta.layer	-0.9784	-0.7766	-0.6667	-0.5633
beta.lc	0.1132	0.2431	0.3184	0.3861
beta.alt	0.6775	0.8264	0.9014	0.9764
beta.lc_modi	1.0218	1.1541	1.2215	1.2889
beta.pop_den	0.3647	0.6365	0.7873	0.9641
Deviance	1279.4800	1282.4205	1284.7211	1287.7234
97.5%beta.				
(Intercept)	-0.8671			
beta.layer.1	3.2889			
beta.layer.2	-1.0756			
beta.layer	-0.3737			
beta.lc	0.5219			
beta.alt	1.1200			
beta.lc_modi				
beta.pop_den	1.4294			
Deviance	1.2899			
	1296.0396			

Potential scale reduction factors:

	Point est.	Upper C.I.
beta.(Intercept)	1.01	1.02
beta.layer.1	1.08	1.19
beta.layer.2	1.07	1.16
beta.layer	1.04	1.11

beta.lc	1.00	1.02
beta.alt	1.01	1.05
beta.lc_modi	1.00	1.01
beta.pop_den	1.00	1.00
Deviance	1.02	1.06

Multivariate psrf

1.03

Coronaviridae- Binomial iCAR model

Inclusion of SARS CoV-2 origin

Iterations = 5001:9996 Thinning
interval = 5 Number of chains = 2
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable, plus standard error of the mean:

	Mean	SD	Naive SE	Time-series SE
beta.(Intercept)	1.3221	0.5269	0.011782	0.083936
beta.layer.1	1.9397	0.5659	0.012655	0.094587
beta.layer.2	-0.9727	0.5200	0.011628	0.089489
beta.layer	0.2343	0.005239	0.027425	0.2138
beta.lc	0.003044	0.006156	1.0704	0.1692
beta.alt	0.012079			0.003782
beta.lc_modi				
beta.pop_den	1.3130	0.2429	0.005431	0.012950
	10.2581	2.1242	0.047498	0.333385
gamma.(Intercept)	1.3278	0.2088	0.004668	0.015005
Deviance	1238.1997	4.4458	0.099410	0.267020

2. Quantiles for each variable:

	2.5%	25%	50%	75%
beta.(Intercept)	0.40655	0.9159	1.2808	1.7086
beta.layer.1	1.00704	1.5414	1.8677	2.2640
beta.layer.2	-2.20851	-1.2713	-0.9190	-0.6073
beta.layer	-1.12968	-0.7879	-0.6301	-0.4853
beta.lc	-0.04953	0.1216	0.2082	0.3038
beta.alt	0.77241	0.9495	1.0595	1.1823
beta.lc_modi	0.90714	1.1365	1.2941	1.4625
beta.pop_den	6.63048	8.5868	10.2018	11.8183
gamma.(Intercept)	0.94351	1.1814	1.3156	1.4658
Deviance	1231.78006	1234.8944	1237.4213	1240.6048
97.5%				
beta.(Intercept)	2.3746			
beta.layer.1	3.2386			
beta.layer.2	-0.0914			
beta.layer	-	0.2172		
beta.lc		0.4888		
beta.alt	1.4167			
beta.lc_modi	1.8656			
beta.pop_den	14.4870			
gamma.(Intercept)	1.7759			
Deviance	1248.8583			

Potential scale reduction factors:

	Point est.	Upper C.I.
beta.(Intercept)	1.04	1.19

beta.layer.1	1.10	1.37
beta.layer.2	1.07	1.27
beta.layer	1.04	1.18
beta.lc	1.00	1.00
beta.alt	1.09	1.33
beta.lc_modi	1.00	1.01
beta.pop_den	1.04	1.18
gamma.(Intercept)	1.04	1.15
Deviance	1.01	1.03

Multivariate psrf

1.15

Coronaviridae- ZIB iCAR model

Inclusion of SARS CoV-2 origin

Iterations = 5001:9996 Thinning
interval = 5 Number of chains = 2
Sample size per chain = 1000

1. Empirical mean and standard deviation for each variable, plus standard error of the mean:

	Mean	SD	Naive SE	Time-series SE
beta.(Intercept)	-4.5484	0.27529	6.156e-03	0.019618
beta.layer.1	3.4225	0.87309	1.952e- 02	0.147034
beta.layer.2	-2.5347	0.77196	1.726e-02	0.129692
beta.layer	- 0.9393	0.34825	7.787e-03	0.033309
beta.lc	0.3537	0.23934	5.352e-03	0.013159
beta.alt	0.32173	7.194e-03	0.028046	
beta.lc_modi	1.2559	0.22885	5.117e- 03	0.011594
beta.pop_den	0.5832	0.36399	8.139e- 03	0.018234
gamma.(Intercept)	796.8551	592.53081	1.325e+01	18.721051
Vrho	9.9046	0.04366	9.762e-04	0.006487
Deviance	3.728e-01	1.387722		171.2733
				16.67269

2. Quantiles for each variable:

	2.5%	25%	50%	75%	97.5%
beta.(Intercept)	-5.05525	-4.7544	-4.5593	-4.3546	-4.0053
beta.layer.1	1.59953	2.8593	3.4294	3.9959	5.0928
beta.layer.2	-3.96861	-3.0312	-2.5386	-2.0806	-0.9069
beta.layer	-1.63615	-1.1788	-0.9465	-0.7072	-0.2656
beta.lc	-0.11484	0.1942	0.3636	0.5142	0.8201
beta.alt	0.11748	0.5173	0.7243	0.9253	1.4216
beta.lc_modi	0.81031	1.1000	1.2535	1.4090	1.7086
beta.pop_den	-0.04103	0.3189	0.5609	0.8082	1.3255
gamma.(Intercept)	32.10191	337.8567	680.9352	1127.1751	2216.3527
Vrho	9.9007	9.9356	9.9891		
Deviance	140.04840	159.1466	170.8898	182.8275	204.5376

Potential scale reduction factors:

	Point est.	Upper C.I.
beta.(Intercept)	1.02	1.09
beta.layer.1	1.05	1.08
beta.layer.2	1.15	1.53
beta.layer.1.02		1.03
beta.lc	1.09	1.36
beta.alt	1.06	1.24
beta.lc_modi	1.05	1.21
beta.pop_den	1.01	1.02
gamma.(Intercept)	1.00	1.00
Vrho	1.00	1.00

Deviance	1.03	1.07
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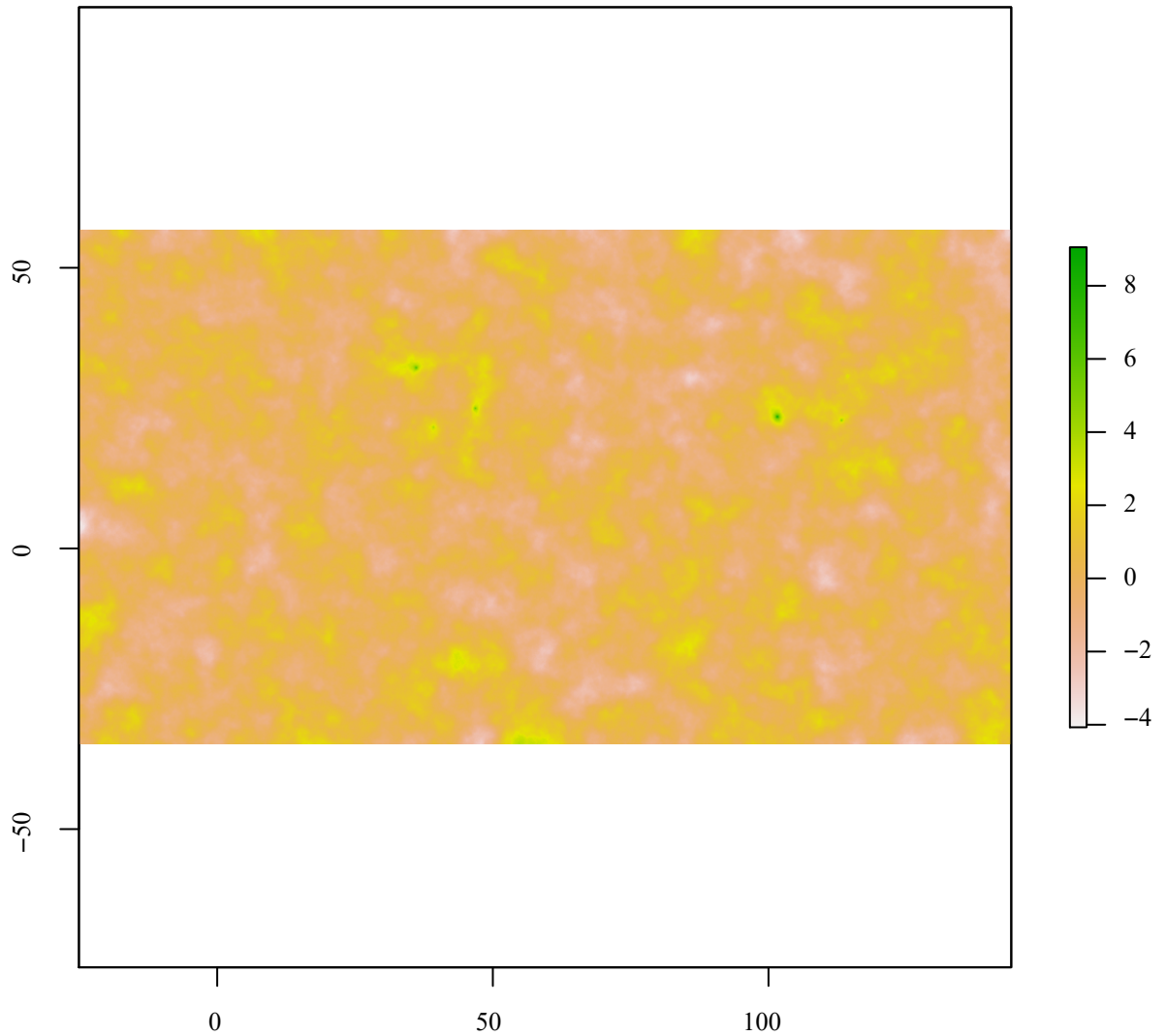
Multivariate psrf

1.15

	Model	Deviance	Perc
1	NULL	1896.61687	0
2	env	571.05392	73
3	binomial	587.76539	72
4	binomial.icar	77.34814	100
5	ZIB.icar	74.03859	100

	"masTSS"	"OA"	"prob"
1	1	0.44	

Coronaviridae- ZIB iCAR model Random effects



Coronaviridae hotspots with detection >TSS threshold
Inclusion of SARS CoV-2 origins

