# Current protocols example dataset

POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY

Bayesian inference using the structured coalescent

Migrate-n version 4.4.3(git:) [March-21-2019]

Using Intel AVX (Advanced Vector Extensions)

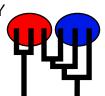
Compiled for PARALLEL computer architectures

One master and 8 compute nodes are available.

Compiled for a SYMMETRIC multiprocessors (Grandcentral)

Program started at Sat Jun 1 22:18:00 2019

Program finished at Sat Jun 1 22:21:28 2019 [Runtime:0000:00:03:28]



### **Options**

Inheritance scalers in use for Thetas:

All loci use an inheritance scaler of 1.0

[The locus with a scaler of 1.0 used as reference]

Random number seed: (with internal timer) 2298936202

Start parameters:

Theta values were generated Using a percent value of the prior

M values were generated Using a percent value of the prior

Connection matrix:

m = average (average over a group of Thetas or M,

s = symmetric migration M, S = symmetric 4Nm,

0 = zero, and not estimated,

\* = migration free to vary, Thetas are on diagonal

d = row population split off column population, D = split and then migration

Population 1 2 3 1 Arbon\_1 \* \* \* 2 Berg\_2 \* \* \* 3 Chur\_3 \* \* \*

Order of parameters:

						ounon p	10100010 0710	inple dataset 2
1	$\Theta_1$			<displa< td=""><td>yed&gt;</td><td></td><td></td><td></td></displa<>	yed>			
2	$\Theta_2$			<displa< td=""><td>yed&gt;</td><td></td><td></td><td></td></displa<>	yed>			
3	$\Theta_3^2$			<displa< td=""><td>yed&gt;</td><td></td><td></td><td></td></displa<>	yed>			
4	N /	->1		<displa< td=""><td>yed&gt;</td><td></td><td></td><td></td></displa<>	yed>			
5	NΛ	->1		<displa< td=""><td>yed&gt;</td><td></td><td></td><td></td></displa<>	yed>			
6	NΛ	->2		<displa< td=""><td>yed&gt;</td><td></td><td></td><td></td></displa<>	yed>			
7	N/I	->2		<displa< td=""><td>yed&gt;</td><td></td><td></td><td></td></displa<>	yed>			
8	NΛ	->3		<displa< td=""><td>yed&gt;</td><td></td><td></td><td></td></displa<>	yed>			
9	N/I	->3		<displa< td=""><td>yed&gt;</td><td></td><td></td><td></td></displa<>	yed>			
	2	75						
Mutation	n rate among lo	ci:				Mutatio	n rate is con	stant for all loci
Analysis	s strategy:						Baye	esian inference
1	ation size estima	ation:					-	tial Distribution
-	ow estimation:							tial Distribution
							•	
Proposa	al distributions fo	or paramete	er					
Paramete	er		Prop	osal				
Theta		M	letropolis sam	pling				
M		M	letropolis sam	pling				
Divergen	ce	M	letropolis sam	pling				
Divergen	ce Spread	M	letropolis sam	pling				
Genealog	<b>ду</b>	M	letropolis-Has	tings				
Dui a u ali a	4							
	tribution for par		Minimo	M*		Dalta	Dia a I	la dete Essa
Paramete		Prior	Minimum	MeanMa		Delta		JpdateFreq
1	Theta **	Uniform	0.000000	0.050	0.100	0.010	1500	0.05556
2	meta	Uniform	0.000000 0.000000	0.050 0.050	0.100	0.010 0.010	1500 1500	0.05556 0.05556
3	meta	Uniform			0.100			
4	M ** M **	Uniform Uniform	0.000000 0.000000	2500.	5000. 5000.	500.0	1500 1500	0.05556
5	IVI M **			2500.		500.0		0.05556
6	IVI M **	Uniform Uniform	0.000000	2500.	5000.	500.0	1500 1500	0.05556
7			0.000000	2500.	5000.	500.0		0.05556 0.05556
8	171	Uniform	0.000000	2500.	5000.	500.0	1500	
9 [* * maa	M ** ns priors were :	Uniform	0.000000	2500.	5000.	500.0	1500	0.05556
l Illea	ns phors were :	set globally	I					
Markov	chain settings:							Long chain
Number	of chains							1
Recor	ded steps [a]							5000
Increr	nent (record ev	ery x step [l	b]					10
Numb	er of concurren	nt chains (re	plicates) [c]					1
Visite	d (sampled) par	rameter val	ues [a*b*c]					50000
Numb	er of discard tre	ees per cha	in (burn-in)					5000

Multiple Markov chains: Static heating scheme	1000000.00	4 chains with temperatures 3.00 1.50 1.00 Swapping interval is 1
Print options: Data file: Haplotyping is turned on: Output file: Posterior distribution raw histogram file: Raw data from the MCMC run: Print data: Print genealogies [only some for some data type]:		infile NO outfile_short bayesfile bayesallfile.gz No None

### Data summary

Data file:	infile
Datatype:	Haplotype data
Number of loci:	10

Mutationmodel parameters

Mutationmodel:	
Locus Sublocus	

1	1	Jukes-Cantor	[Basefreq: =0.25]
2	1	Jukes-Cantor	[Basefreq: =0.25]
3	1	Jukes-Cantor	[Basefreq: =0.25]
4	1	Jukes-Cantor	[Basefreq: =0.25]
5	1	Jukes-Cantor	[Basefreq: =0.25]
6	1	Jukes-Cantor	[Basefreq: =0.25]
7	1	Jukes-Cantor	[Basefreq: =0.25]
8	1	Jukes-Cantor	[Basefreq: =0.25]
9	1	Jukes-Cantor	[Basefreq: =0.25]
10	1	Jukes-Cantor	[Basefreq: =0.25]

Mutationmodel

#### Sites per locus

Locus	Sites
1	1000
2	1000
3	1000
4	1000
5	1000
6	1000
7	1000
8	1000
9	1000
10	1000

Site rate variation and probabilities:

Locus Sublocus Region type Rate of change Probability Patch size

1	1	1	1.000	1.000	1.000
2	1	1	1.000	1.000	1.000
3	1	1	1.000	1.000	1.000
4	1	1	1.000	1.000	1.000
5	1	1	1.000	1.000	1.000
6	1	1	1.000	1.000	1.000

7	1	1	1.000	1.000	1.000		
8	1	1	1.000	1.000	1.000		
9	1	1	1.000	1.000	1.000		
10	1	1	1.000	1.000	1.000		
Populatio		'	1.000	1.000	Locus	Gene c	onies
i opaiatio					20003	data	(missing)
1 Arbon_	1				1	10	(missing)
17(15011_	•				2	10	
					3	10	
					4	10	
					5	10	
					6	10	
					7	10	
					8	10	
					9	10	
0.0					10	10	
2 Berg_2					1	10	
					2	10	
					3	10	
					4	10	
					5	10	
					6	10	
					7	10	
					8	10	
					9	10	
					10	10	
3 Chur_3					1	10	
					2	10	
					3	10	
					4	10	
					5	10	
					6	10	
					7	10	
					8	10	
					9	10	
					10	10	
Total of a	ıll popula	ations			1	30	(0)
					2	30	(0)
					3	30	(0)
					4	30	(0)
					5	30	(0)
					6	30	(0)
					7	30	(0)
					8	30	(0)
					9	30	(0)
							ζ-/

Curr	Current protocols example dataset 6		
10	30	(0)	

# Bayesian Analysis: Posterior distribution table

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	$\Theta_1$	0.00600	0.00600	0.00637	0.00647	0.00673	0.01050	0.02178
1	$\Theta_2$	0.00300	0.00620	0.00630	0.00640	0.00680	0.00597	0.00686
1	$\Theta_3$	0.00127	0.00187	0.00203	0.00247	0.00247	0.00550	0.00713
1	M <sub>2-&gt;1</sub>	300.000	430.000	435.000	443.333	650.000	471.667	493.864
1	M <sub>3-&gt;1</sub>	633.333	683.333	688.333	700.000	723.333	715.000	776.383
1	M <sub>1-&gt;2</sub>	240.000	370.000	378.333	383.333	560.000	395.000	405.354
1	$M_{3->2}$	46.667	143.333	148.333	163.333	296.667	175.000	179.888
1	M <sub>1-&gt;3</sub>	373.333	373.333	381.667	386.667	520.000	418.333	432.091
1	M <sub>2-&gt;3</sub>	393.333	396.667	401.667	403.333	433.333	668.333	693.716
2	$\Theta_1$	0.00060	0.00133	0.00203	0.00207	0.00500	0.00263	0.00305
2	$\Theta_2$	0.00287	0.00287	0.00303	0.00307	0.00433	0.00397	0.00501
2	$\Theta_3$	0.00193	0.00487	0.00503	0.00513	0.00787	0.00470	0.00503
2	M <sub>2-&gt;1</sub>	460.000	496.667	501.667	506.667	533.333	828.333	891.312
2	M <sub>3-&gt;1</sub>	413.333	413.333	418.333	420.000	463.333	465.000	498.153
2	M <sub>1-&gt;2</sub>	846.667	870.000	875.000	880.000	890.000	938.333	985.438
2	$M_{3->2}$	246.667	266.667	271.667	273.333	283.333	365.000	401.998
2	M <sub>1-&gt;3</sub>	10.000	123.333	128.333	136.667	323.333	175.000	186.374
2	M <sub>2-&gt;3</sub>	183.333	400.000	405.000	406.667	533.333	425.000	456.665
3	$\Theta_1$	0.00160	0.00333	0.00343	0.00347	0.00500	0.00383	0.00411
3	$\Theta_2$	0.00227	0.00567	0.00583	0.00620	0.01153	0.00663	0.00783
3	$\Theta_3$	0.00893	0.00967	0.00990	0.01007	0.01127	0.01250	0.01596
3	M <sub>2-&gt;1</sub>	123.333	150.000	155.000	156.667	160.000	221.667	355.669
3	M <sub>3-&gt;1</sub>	133.333	136.667	145.000	153.333	156.667	251.667	294.016
3	M <sub>1-&gt;2</sub>	536.667	550.000	555.000	563.333	563.333	521.667	535.871
3	M <sub>3-&gt;2</sub>	23.333	120.000	138.333	160.000	340.000	208.333	233.454
3	M <sub>1-&gt;3</sub>	193.333	460.000	471.667	473.333	476.667	468.333	518.729
3	$M_{2->3}$	93.333	316.667	328.333	333.333	366.667	325.000	353.936
4	$\Theta_1$	0.00193	0.00340	0.00363	0.00380	0.00667	0.00463	0.00498
4	$\Theta_2$	0.00160	0.00473	0.00483	0.00487	0.00827	0.00463	0.00507
4	$\Theta_3^-$	0.00393	0.00780	0.00790	0.00793	0.01120	0.00850	0.00933
4	M <sub>2-&gt;1</sub>	193.333	250.000	255.000	256.667	256.667	425.000	457.728
4	M <sub>3-&gt;1</sub>	403.333	456.667	461.667	466.667	583.333	441.667	447.923
4	M <sub>1-&gt;2</sub>	200.000	353.333	358.333	360.000	480.000	375.000	395.857

.ocus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
4	M <sub>3-&gt;2</sub>	230.000	230.000	235.000	236.667	243.333	185.000	210.122
4	M <sub>1-&gt;3</sub>	200.000	200.000	205.000	206.667	206.667	478.333	488.052
4	M <sub>2-&gt;3</sub>	83.333	90.000	95.000	96.667	96.667	195.000	205.937
5	$\Theta_1$	0.00340	0.00340	0.00350	0.00373	0.00380	0.02143	0.03230
5	$\Theta_2$	0.00147	0.00327	0.00350	0.00380	0.00540	0.00343	0.00355
5	$\Theta_3$	0.00960	0.01147	0.01157	0.01160	0.01253	0.01810	0.02527
5	M <sub>2-&gt;1</sub>	1343.333	1356.667	1368.333	1370.000	1376.667	1445.000	1508.224
5	M <sub>3-&gt;1</sub>	416.667	536.667	541.667	546.667	623.333	675.000	704.797
5	M <sub>1-&gt;2</sub>	230.000	293.333	298.333	300.000	360.000	385.000	405.235
5	M <sub>3-&gt;2</sub>	473.333	476.667	481.667	483.333	490.000	811.667	837.139
5	M <sub>1-&gt;3</sub>	783.333	810.000	815.000	820.000	820.000	871.667	878.581
5	M <sub>2-&gt;3</sub>	700.000	786.667	791.667	800.000	833.333	691.667	706.514
6	$\Theta_1$	0.00233	0.00273	0.00283	0.00287	0.00693	0.00430	0.00452
6	$\Theta_2$	0.00253	0.00253	0.00263	0.00287	0.00293	0.00497	0.00747
6	$\Theta_3$	0.01360	0.01427	0.01437	0.01440	0.01520	0.01397	0.01610
6	M <sub>2-&gt;1</sub>	43.333	350.000	355.000	356.667	396.667	278.333	334.218
6	M <sub>3-&gt;1</sub>	146.667	170.000	178.333	180.000	443.333	338.333	415.296
6	M <sub>1-&gt;2</sub>	666.667	710.000	715.000	716.667	726.667	848.333	886.493
6	$M_{3->2}$	493.333	503.333	508.333	510.000	510.000	605.000	631.007
6	M <sub>1-&gt;3</sub>	70.000	106.667	128.333	150.000	296.667	201.667	255.050
6	M <sub>2-&gt;3</sub>	160.000	226.667	235.000	240.000	356.667	291.667	318.485
7	$\Theta_1$	0.01027	0.01033	0.01043	0.01053	0.01060	0.00937	0.01027
7	$\Theta_2$	0.00120	0.00187	0.00223	0.00247	0.00813	0.00510	0.00639
7	$\Theta_3$	0.00520	0.00527	0.00537	0.00540	0.00540	0.03237	0.03910
7	M <sub>2-&gt;1</sub>	463.333	470.000	478.333	483.333	486.667	481.667	487.949
7	M <sub>3-&gt;1</sub>	433.333	453.333	458.333	460.000	463.333	561.667	573.345
7	M <sub>1-&gt;2</sub>	423.333	756.667	781.667	783.333	800.000	718.333	752.283
7	M <sub>3-&gt;2</sub>	43.333	133.333	138.333	143.333	306.667	198.333	214.624
7	M <sub>1-&gt;3</sub>	1753.333	1766.667	1771.667	1773.333	1780.000	1988.333	2034.149
7	M <sub>2-&gt;3</sub>	0.000	0.000	5.000	6.667	10.000	115.000	142.649
8	$\Theta_1$	0.00140	0.00200	0.00210	0.00220	0.00593	0.00370	0.00392
8	$\Theta_2$	0.00293	0.00473	0.00503	0.00513	0.00813	0.00643	0.00720
8	$\Theta_3$	0.00467	0.00467	0.00503	0.00507	0.00507	0.00877	0.01251
8	M <sub>2-&gt;1</sub>	366.667	493.333	505.000	506.667	576.667	555.000	576.374
8	M <sub>3-&gt;1</sub>	283.333	286.667	291.667	296.667	503.333	451.667	467.961
8	M <sub>1-&gt;2</sub>	230.000	373.333	381.667	383.333	476.667	375.000	386.159
-						853.333	738.333	759.456

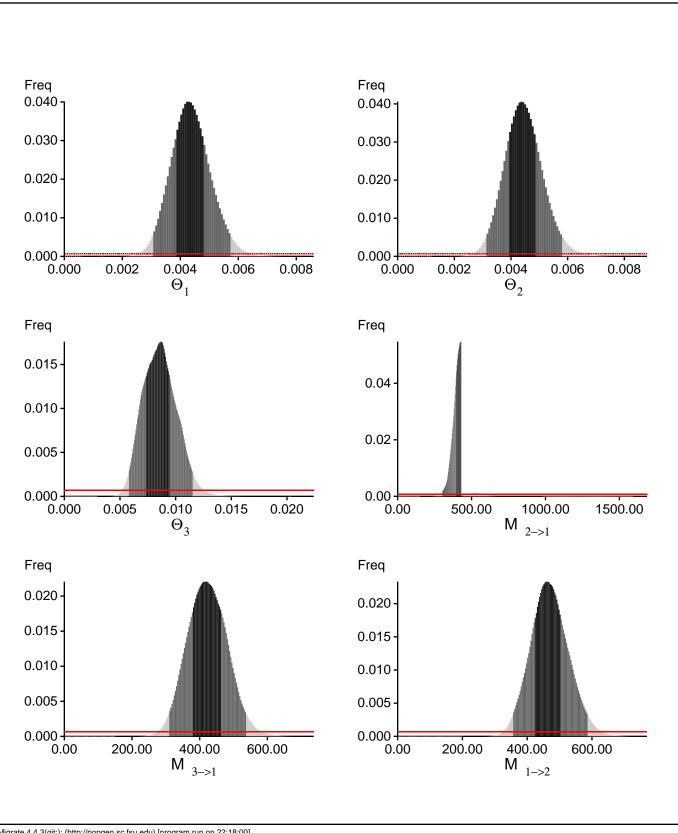
Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
8	M <sub>1-&gt;3</sub>	346.667	376.667	381.667	386.667	386.667	451.667	475.097
8	M <sub>2-&gt;3</sub>	370.000	373.333	378.333	380.000	380.000	778.333	937.721
9	Θ1	0.00200	0.00320	0.00330	0.00400	0.00847	0.00810	0.01052
9	$\Theta_2$	0.00487	0.00487	0.00497	0.00500	0.00573	0.00557	0.00648
9	$\Theta_3^2$	0.01487	0.01607	0.01617	0.01620	0.01687	0.01897	0.02311
9	M <sub>2-&gt;1</sub>	330.000	610.000	615.000	616.667	786.667	535.000	545.360
9	M <sub>3-&gt;1</sub>	296.667	393.333	411.667	430.000	643.333	495.000	515.910
9	M <sub>1-&gt;2</sub>	176.667	290.000	298.333	300.000	453.333	351.667	363.230
9	M <sub>3-&gt;2</sub>	343.333	343.333	351.667	353.333	356.667	398.333	418.876
9	M <sub>1-&gt;3</sub>	110.000	200.000	208.333	213.333	330.000	215.000	218.592
9	M <sub>2-&gt;3</sub>	116.667	306.667	318.333	330.000	386.667	288.333	290.088
10	$\Theta_1$	0.00333	0.00333	0.00363	0.00393	0.00593	0.00417	0.00481
10	$\Theta_2$	0.00360	0.00607	0.00623	0.00640	0.00907	0.00643	0.00699
10	$\Theta_3$	0.03133	0.03153	0.03163	0.03167	0.03173	0.04497	0.04768
10	M <sub>2-&gt;1</sub>	1270.000	1270.000	1291.667	1300.000	1406.667	1385.000	1390.792
10	M <sub>3-&gt;1</sub>	66.667	250.000	255.000	256.667	420.000	241.667	252.949
10	M <sub>1-&gt;2</sub>	413.333	660.000	665.000	670.000	833.333	668.333	685.455
10	M <sub>3-&gt;2</sub>	186.667	276.667	281.667	323.333	560.000	361.667	375.127
10	M <sub>1-&gt;3</sub>	463.333	470.000	481.667	483.333	483.333	615.000	623.137
10	M <sub>2-&gt;3</sub>	1030.000	1033.333	1038.333	1040.000	1043.333	811.667	847.946
All	$\Theta_1$	0.00300	0.00380	0.00423	0.00480	0.00573	0.00443	0.00437
All	$\Theta_2$	0.00307	0.00387	0.00437	0.00487	0.00580	0.00450	0.00445
All	$\Theta_3^-$	0.00573	0.00727	0.00870	0.00947	0.01153	0.00863	0.00861
All	M <sub>2-&gt;1</sub>	300.000	393.333	425.000	430.000	430.000	405.000	397.818
All	M <sub>3-&gt;1</sub>	306.667	376.667	421.667	463.333	536.667	425.000	422.848
All	M <sub>1-&gt;2</sub>	353.333	420.000	458.333	503.333	586.667	471.667	469.855
All	$M_{3->2}$	223.333	280.000	321.667	356.667	426.667	328.333	325.538
All	M <sub>1-&gt;3</sub>	226.667	296.667	338.333	376.667	440.000	338.333	335.272
All	M <sub>2-&gt;3</sub>	263.333	316.667	348.333	380.000	453.333	358.333	357.729

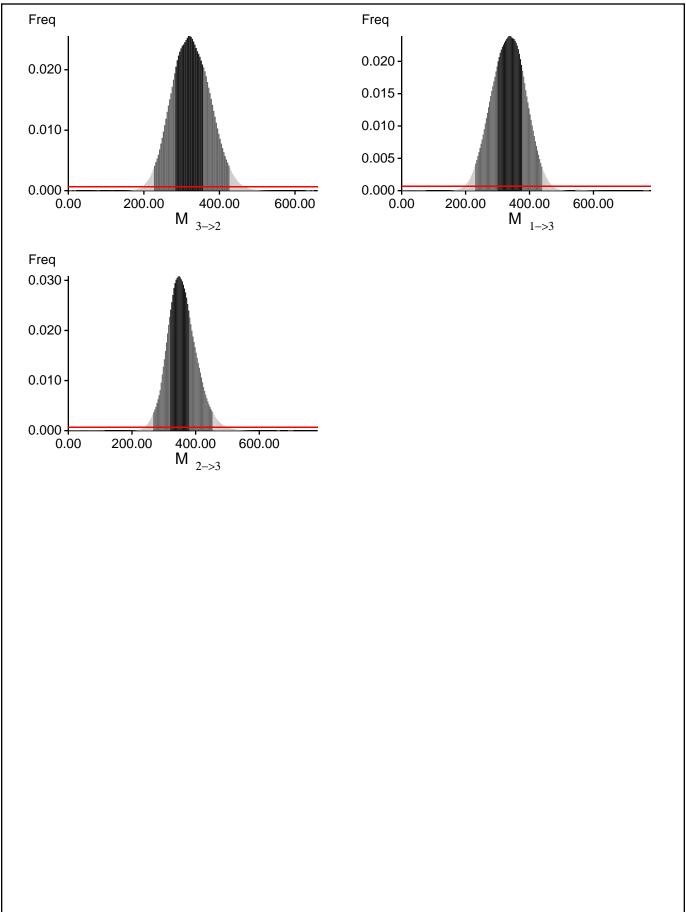
Citation suggestions:

Beerli P., 2006. Comparison of Bayesian and maximum-likelihood inference of population genetic parameters. Bioinformatics 22:341-345

Beerli P., 2009. How to use MIGRATE or why are Markov chain Monte Carlo programs difficult to use? In Population Genetics for Animal Conservation, G. Bertorelle, M. W. Bruford, H. C. Hauffe, A. Rizzoli, and C. Vernesi, eds., vol. 17 of Conservation Biology, Cambridge University Press, Cambridge UK, pp. 42-79.

### Bayesian Analysis: Posterior distribution over all loci





#### Log-Probability of the data given the model (marginal likelihood)

Use this value for Bayes factor calculations:

BF = Exp[ In(Prob(D | thisModel) - In( Prob( D | otherModel) or as LBF = 2 (In(Prob(D | thisModel) - In( Prob( D | otherModel)) shows the support for thisModel]

Locus	Raw thermodynamic score(1a)	Bezier approximation score(1b)	Harmonic mean(2)
1	-3424.00	-2499.78	-2300.61
2	-2867.88	-2117.59	-1969.81
3	-3136.14	-2287.23	-2129.59
4	-3563.41	-2480.05	-2239.92
5	-3238.54	-2365.30	-2191.39
6	-3160.48	-2454.94	-2315.60
7	-3127.22	-2358.31	-2200.64
8	-3463.93	-2435.97	-2237.37
9	-3536.33	-2483.11	-2282.97
10	-2956.38	-2284.81	-2163.61
All	-32357.56	-23650.33	-21914.76

(1a, 1b and 2) are approximations to the marginal likelihood, make sure that the program run long enough! (1a, 1b) and (2) should give similar results, in principle.

But (2) is overestimating the likelihood, it is presented for historical reasons and should not be used (1a, 1b) needs heating with chains that span a temperature range of 1.0 to at least 100,000.

(1b) is using a Bezier-curve to get better approximations for runs with low number of heated chains [Scaling factor = 116.746701]

Citation suggestions:

Beerli P. and M. Palczewski, 2010. Unified framework to evaluate panmixia and migration direction among multiple sampling locations, Genetics, 185: 313-326.

## Acceptance ratios for all parameters and the genealogies

Parameter	Accepted changes	Ratio
$\Theta_1$	13051/27861	0.46843
$\Theta_2$	12560/27876	0.45057
$\Theta_3^2$	13386/27803	0.48146
$M_{2\rightarrow 1}$	11531/27766	0.41529
$M_{3->1}$	12942/27731	0.46670
$M_{1\rightarrow 2}$	13169/27725	0.47499
$M_{3->2}$	12784/27875	0.45862
$M_{1->3}$	11037/27916	0.39536
$M_{2->3}$	9666/27592	0.35032
Genealogies	29706/249855	0.11889

## MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
$\Theta_1$	0.92616	2534.81
$\Theta_2^{r}$	0.93987	2195.13
$\Theta_3^2$	0.91106	3485.00
$M_{2->1}^{3}$	0.92958	2469.34
$M_{3->1}^{2}$	0.91408	3168.42
$M_{1->2}$	0.89374	4162.73
$M_{3->2}$	0.90616	3414.71
$M_{1->3}$	0.91657	3085.53
$M_{2->3}$	0.92413	3009.46
Genealogies	0.90095	4063.80

#### Potential Problems

This section reports potential problems with your run, but such reporting is often not very accurate. Whith many parameters in a multilocus analysi s, it is very common that some parameters for some loci will not be very informative, triggering suggestions (for example to increase the prior ran ge) that are not sensible. This suggestion tool will improve with time, therefore do not blindly follow its suggestions. If some parameters are fla

gged, inspect the tables carefully and judge wether an action is required. For example, if you run a Bayesian inference with sequence data, for mac roscopic species there is rarely the need to increase the prior for Theta beyond 0.1; but if you use microsatellites it is rather common that your prior distribution for Theta should have a range from 0.0 to 100 or more. With many populations (>3) it is also very common that some migration rou						
tes are estimated poorly because the data contains little or no information for that route. Increasing the range will						
not help in such situations, reducing number of parameters may help in such situations.						
No warning was recorded during the run						