# Example: sequence data set wit two loci [simula

MIGRATION RATE AND POPULATION SIZE ESTIMATION using the coalescent and maximum likelihood or Bayesian inference Migrate-n version 3.2.16 [1920] Compiled for a SYMMETRIC MULTIPROCESSORS Program started at Tue Jan 29 09:43:29 2013 Program finished at Tue Jan 29 11:41:40 2013



## Options

Datatype:					DNA	A sequence data
Inheritance scale [Each Theta uses Random number Start parameters	rs in use fo s the (true) seed: :	nce] (with internal timer)	1352947789			
Theta values wer	e generate	d			from the	FST-calculation
M values were ge	enerated				from the	FST-calculation
Connection type where m = aver s = symmetric M * = free to vary, Population 1 BAJA 2 MIDR	matrix: age (averag 1, S = symn Thetas are 1 * *	ge ov netric on c 2 0 *	ver a group of The c 4Nm, 0 = zero, liagonal 3 0 0	tas or M, and not estimated,		
3 MAIN	*	×	×			
Order of parame	eters:					
1	$\Theta_1$			<displayed></displayed>		
2	$\Theta_2$			<displayed></displayed>		
3	$\Theta_3$			<displayed></displayed>		
6	M <sub>1-&gt;2</sub>			<displayed></displayed>		
8	M <sub>1-&gt;3</sub>			<displayed></displayed>		

Example: sequence data set wit two loci [simulated data] -- 2

9	9 M <sub>2-&gt;3</sub>			<di< th=""><th>isplayed&gt;</th><th></th><th></th><th></th></di<>	isplayed>			
Mutation rate	among loc	i:					Mutati	on rate is constant
Analysis stra	tegy:							Bayesian inference
Proposal dist Parameter Theta M	ributions for	r parameter	Pro Slice sa Slice sa	oposal mpling mpling				
Prior distribu	tion for para	ameter						
Parameter Theta M	Prior Uniform Uniform	Minimum 0.000000 0.000000	50.00 37500.00	Mean* )0000 )0000	Maximum 100.000000 75000.000000	10. 7500.	Delta .000000 .000000	Bins 1500 1500
Markov chair Number of ch Recorded Increment Number of Visited (sa Number of	n settings: nains steps [a] (record eve concurrent mpled) para discard tre	ry x step [b] chains (replic ameter values es per chain (	cates) [c] s [a*b*c] (burn-in)					Long chain 1 50000 100 1 5000000 2500000
Multiple Mark Static heat 0 2.10	ov chains: ing scheme 2.00	1.95	1.80	1.65	5 1.50	1.40	20 chains 1.25 Swa	with temperatures 1.10 1.00 apping interval is 1
Print options: Data file: Output file: Posterior c Print data: Print gene	: listribution r alogies [onlı	aw histogram y some for so	ı file: ıme data ty	′pe]:			MR MRO_I	O_NGulf_direc.seq NGulf_Direc2_run1 bayesfile No None
	9 Mutation rate Analysis strat Proposal dist Parameter Theta M Prior distribut Parameter Theta M Markov chair Number of ch Recorded Increment Number of Visited (sa Number of Visited (sa Number of Visited (sa Number of Visited (sa Number of Print options Data file: Output file Posterior c Print data: Print gene	9M2-Mutation rate among locAnalysis strategy:Proposal distributions for ParameterThetaMPrior distribution for para ParameterPrior distribution for para ParameterPrior distribution for para ParameterMUniformMMarkov chain settings:Number of chains Recorded steps [a] Increment (record eve Number of concurrent Visited (sampled) para Number of discard treeMultiple Markov chains: Static heating scheme D2.102.00Print options: Data file: Output file: Print data: Print genealogies [online]	9       M         Putation rate among loci:         Analysis strategy:         Proposal distributions for parameter         Parameter         Theta         M         Prior distribution for parameter         Parameter         Prior distribution for parameter         Parameter         Prior distribution for parameter         Parameter         Prior Minimum         Theta         M         Visited Uniform         Number of chains         Recorded steps [a]         Increment (record every x step [b]         Number of concurrent chains (replice         Visited (sampled) parameter values         Number of discard trees per chain (effect)         Multiple Markov chains:         Static heating scheme         D       2.10       2.00       1.95         Print options:         Data file:         Output file:       Posterior distribution raw histogram         Print data:       Print genealogies [only some for sc	9       M         2->3         Mutation rate among loci:         Analysis strategy:         Proposal distributions for parameter         Parameter       Pro         Theta       Slice sail         M       Slice sail         Prior distribution for parameter         Parameter       Prior         Prior distribution for parameter         Parameter       Prior         Mutation in the uniform       0.000000         M       Uniform         Output of chains       Recorded steps [a]         Increment (record every x step [b]       Number of concurrent chains (replicates) [c]         Visited (sampled) parameter values [a*b*c]       Number of discard trees per chain (burn-in)         Multiple Markov chains:       Static heating scheme         D       2.10       2.00       1.95       1.80         Print options:       Data file:       Output file:       Posterior distribution raw histogram file:       Print data:         Print genealogies [only some for some data ty       Print genealogies [only some for some data ty	9       M       2->3 <di>         Mutation rate among loci:       Analysis strategy:         Proposal distributions for parameter       Parameter       Proposal         Parameter       Proposal       Slice sampling         M       Slice sampling         Prior distribution for parameter       Parameter         Parameter       Prior       Minimum         Parameter       Prior       Minimum         Prior distribution for parameter       Parameter       Parameter         Parameter       Prior       Minimum       Mean*         Theta       Uniform       0.000000       50.000000         M       Uniform       0.000000       37500.000000         Markov chain settings:       Number of chains       Recorded steps [a]       Increment (record every x step [b]         Number of concurrent chains (replicates) [c]       Visited (sampled) parameter values [a*b*c]       Number of discard trees per chain (burn-in)         Multiple Markov chains:       Static heating scheme       2       2.10       2.00       1.95       1.80       1.65         Print options:       Data file:       Output file:       Posterior distribution raw histogram file:       Print data:         Print genealogies [only some for some data type]:</di>	9       M       2->3 <displayed>         Mutation rate among loci:       Analysis strategy:       Proposal distributions for parameter         Parameter       Proposal       Theta       Slice sampling         M       Slice sampling       M       Slice sampling         Prior distribution for parameter       Parameter       Prior distribution for parameter         Parameter       Prior       Minimum       Mean*       Maximum         Theta       Uniform       0.000000       50.000000       100.000000         M       Uniform       0.000000       37500.000000       75000.000000         Markov chain settings:       Number of chains       Recorded steps [a]       Increment (record every x step [b]         Number of concurrent chains (replicates) [c]       Visited (sampled) parameter values [a*b*c]       Number of discard trees per chain (burn-in)         Multiple Markov chains:       Static heating scheme       2.10       2.00       1.95       1.80       1.65       1.50         Print options:       Data file:       Output file:       Posterior distribution raw histogram file:       Print data:       Print genealogies [only some for some data type]:</displayed>	9       M       2->3 <displayed>         Mutation rate among loci:       Analysis strategy:         Proposal distributions for parameter       Proposal         Parameter       Proposal         Theta       Slice sampling         M       Slice sampling         Prior distribution for parameter       Prameter         Parameter       Prior         Parameter       Prior         Parameter       Prior         Mutation no.000000       50.000000         M       Uniform         0.000000       37500.000000         Markov chain settings:         Number of chains         Recorded steps [a]         Increment (record every x step [b]         Number of discard trees per chain (burn-in)         Mutiple Markov chains:         Static heating scheme         0       2.10       2.00       1.95       1.80       1.65       1.50       1.40         Print options:       Data file:       Output file:       Print data:       Print genealogies [only some for some data type]:       Print genealogies [only some for some data type]:</displayed>	9       M       23 <displayed>         Mutation rate among loci:       Mutati         Analysis strategy:       Proposal       Mutati         Proposal distributions for parameter       Proposal       Mutati         Prior distribution for parameter       Proposal       Mutati         Prior distribution for parameter       Prarameter       Prior distribution for parameter         Parameter       Prior Minimum       Mean*       Maximum         Theta       Uniform       0.000000       50.000000       100.000000         M       Uniform       0.000000       37500.000000       75000.000000       7500.000000         Markov chain settings:       Number of chains       Recorded steps [a]       Increment (record every x step [b]       Number of discard trees per chain (burn-in)         Multiple Markov chains:       Static heating scheme       20 chains:         0       2.10       2.00       1.95       1.80       1.65       1.50       1.40       1.25         Sw:       Print options:      </displayed>

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30

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### Data summary

Datatype: Number of loci:		Sequence of	lata 1
Population	Locus	Gene copies	
1 BAJA	1	30	
2 MIDR	1	30	

1

1

3 MAIN

Total of all populations

# Bayesian Analysis: Posterior distribution table

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	$\Theta_1$	0.00000	0.00000	0.03333	0.53333	1.40000	0.56667	0.00736
1	$\Theta_2$	1.00000	40.06667	45.83333	47.20000	48.00000	49.63334	49.98975
1	$\Theta_3$	81.20000	97.06667	98.30000	98.93333	99.13333	50.03333	49.93806
1	M <sub>1-&gt;2</sub>	4050.0	6800.0	8675.0	10850.0	17050.0	9525.0	10032.4
1	M <sub>1-&gt;3</sub>	3200.0	10550.0	18775.0	33050.0	65450.0	28025.0	30690.1
1	M <sub>2-&gt;3</sub>	15450.0	30650.0	48975.0	56750.0	74900.0	44375.0	44198.1



### Bayesian Analysis: Posterior distribution over all loci

Migrate 3.2.16: (http://popgen.sc.fsu.edu) [program run on 09:43:29]

Migrate 3.2.16: (http://popgen.sc.fsu.edu) [program run on 09:43:29]

## Log-Probability of the data given the model (marginal likelihood) Use this value for Bayes factor calculations: BF = Exp[ In(Prob(D I thisModel) - In( Prob( D I otherModel) or as LBF = 2 (In(Prob(D | thisModel) - In( Prob( D | otherModel)) shows the support for thisModel] Method In(Prob(DIModel)) Notes Thermodynamic integration -2661.014048 (1a) -2658.636834 (1b) Harmonic mean -2513.071104 (2) (1a, 1b and 2) is an approximation to the marginal likelihood, make sure the program run long enough! (1a, 1b) and (2) should give a similar result, (2) is considered more crude than (1), but (1) needs heating with several well-spaced chains, (1b) is using a Bezier-curve to get better approximations for runs with low number of heated chains

### Acceptance ratios for all parameters and the genealogies

Parameter	Accepted changes	Ratio
$\Theta_1$	624587/624587	1.00000
$\Theta_2^{-1}$	625395/625395	1.00000
$\Theta_3$	625200/625200	1.00000
M <sub>1-&gt;2</sub>	624409/624409	1.00000
$M_{1->3}^{1>2}$	625542/625542	1.00000
$M_{2->3}^{1>3}$	626232/626232	1.00000
Genealogies	493698/2498912	0.19757

### MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
$\Theta_1$	0.36828	23084.65
$\Theta_2^{-1}$	0.00592	49411.09
$\Theta_{3}$	-0.00749	50755.05
$M_{1-2}^{2}$	0.50259	16551.69
$M_{1-3}^{1-2}$	0.45867	18555.64
M $_{2-3}^{2-3}$	0.48218	17468.08
Ln[Prob(DIG)]	0.53727	15050.49

#### Potential Problems

This section reports potential problems with your run, but such reporting is often not very accurate. Whith many parameters in a multilocus analysis, it is very common that some parameters for some loci will not be very informative, triggering suggestions (for example to increase the prior range) that are not sensible. This suggestion tool will improve with time, therefore do not blindly follow its suggestions. If some parameters are flagged, inspect the tables carefully and judge wether an action is required. For example, if you run a Bayesian inference with sequence data, for macroscopic 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 routes 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.

Param 3 (Locus 1): Upper prior boundary seems too low!

# Example: sequence data set wit two loci [simula

MIGRATION RATE AND POPULATION SIZE ESTIMATION using the coalescent and maximum likelihood or Bayesian inference Migrate-n version 3.2.16 [1920] Compiled for a SYMMETRIC MULTIPROCESSORS Program started at Tue Jan 29 15:26:57 2013 Program finished at Thu Jan 31 09:59:52 2013



## Options

Datatype:					DNA se	equence data
Inheritance scaler [Each Theta uses Random number Start parameters:	rs in use fo the (true) seed:	r The	etas: 1.00 ance scalar of the	first locus as a referen	ce] (with internal timer)	996106619
Theta values wer	e generate	d			from the FS	ST-calculation
M values were ge	enerated				from the FS	ST-calculation
Connection type if where m = avera s = symmetric M * = free to vary, Population 1 BAJA 2 MIDR 3 MAIN	matrix: age (averag l, S = symn Thetas are 1 * *	ge ov netric on c 2 0 *	rer a group of Thet 2 4Nm, 0 = zero, a iagonal 3 0 0 *	as or M, and not estimated,		
Order of parame	eters:					
1	$\Theta_1$			<displayed></displayed>		
2	$\Theta_2$			<displayed></displayed>		
3	$\Theta_3$			<displayed></displayed>		
6	M <sub>1-&gt;2</sub>			<displayed></displayed>		
8	M <sub>1-&gt;3</sub>			<displayed></displayed>		

Example: sequence data set wit two loci [simulated data] -- 2

	9	M <sub>2-</sub>	->3		-di	splayed>			
	Mutation rate	among loc	i:					Mutati	ion rate is constant
	Analysis stra	tegy:							Bayesian inference
	Proposal dist Parameter Theta M	ributions for	r parameter	Propo Slice samp Slice samp	osal ling lling				
	Prior distribu	tion for pare	ameter						
	Parameter Theta M	Prior Uniform Uniform	Minimum 0.000000 0.000000	ме 50.0000 37500.0000	an* )00 )00	Maximum 100.000000 75000.000000	10. 7500.	Delta 000000 000000	Bins 1500 1500
	Markov chair Number of ch Recorded Increment Number of Visited (sa Number of	n settings: nains steps [a] (record eve concurrent mpled) para discard tre	ry x step [b] chains (replic ameter values es per chain (	cates) [c] s [a*b*c] (burn-in)					Long chain 1 50000 100 1 5000000 2500000
2.4	Multiple Mark Static heat D 2.10	ov chains: ing scheme 2.00	1.95	1.80	1.65	5 1.50	1.40	20 chains 1.25 Swa	with temperatures 1.10 1.00 apping interval is 1
	Print options: Data file: Output file: Posterior d Print data: Print genea	aw histogram y some for so	i file: ime data type	]:			MR MRO_	O_NGulf_direc.seq NGulf_Direc2_run2 bayesfile No None	

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### Data summary

Datatype: Number of loci:		Sequence d	ata 1
Population	Locus	Gene copies	
1 BAJA	1	30	
2 MIDR	1	30	

1

1

3 MAIN

Total of all populations

# Bayesian Analysis: Posterior distribution table

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	$\Theta_1$	0.00000	0.00000	0.03333	0.53333	1.40000	0.56667	0.00752
1	$\Theta_2$	3.00000	25.60000	26.96667	29.40000	46.06667	50.10000	50.09869
1	$\tilde{\Theta_3}$	29.26667	30.13333	32.03333	33.80000	44.66667	49.90000	50.03272
1	М <sub>1-&gt;2</sub>	4100.0	6700.0	8525.0	10700.0	16700.0	9425.0	9930.3
1	M <sub>1-&gt;3</sub>	2550.0	10150.0	20275.0	30900.0	61850.0	26125.0	28985.9
1	M <sub>2-&gt;3</sub>	15750.0	34950.0	46125.0	60650.0	75000.0	46075.0	45358.6



### Bayesian Analysis: Posterior distribution over all loci

Migrate 3.2.16: (http://popgen.sc.fsu.edu) [program run on 15:26:57]

Migrate 3.2.16: (http://popgen.sc.fsu.edu) [program run on 15:26:57]

# Log-Probability of the data given the model (marginal likelihood) Use this value for Bayes factor calculations: BF = Exp[ In(Prob(D I thisModel) - In( Prob( D I otherModel) or as LBF = 2 (In(Prob(D | thisModel) - In( Prob( D | otherModel)) shows the support for thisModel] Method In(Prob(DIModel)) Notes Thermodynamic integration -2660.566050 (1a) -2658.266866 (1b) Harmonic mean -2517.504887 (2) (1a, 1b and 2) is an approximation to the marginal likelihood, make sure the program run long enough! (1a, 1b) and (2) should give a similar result, (2) is considered more crude than (1), but (1) needs heating with several well-spaced chains, (1b) is using a Bezier-curve to get better approximations for runs with low number of heated chains

### Acceptance ratios for all parameters and the genealogies

Parameter	Accepted changes	Ratio
$\Theta_1$	624973/624973	1.00000
$\Theta_2^{-1}$	626521/626521	1.00000
$\Theta_3$	625271/625271	1.00000
$M_{1-2}^{2}$	623554/623554	1.00000
$M_{1-3}^{1-3}$	625061/625061	1.00000
$M_{2-3}^{2}$	624369/624369	1.00000
Genealogies	491264/2501306	0.19640

### MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ	0.40862	20991.32
$\Theta_2^{-1}$	0.00082	49917.72
$\Theta_{3}^{-}$	0.00272	49728.94
M <sub>1-&gt;2</sub>	0.47700	17704.76
M $_{1-3}^{1-2}$	0.47190	17939.59
M $_{2-3}^{2}$	0.50422	16479.62
Ln[Prob(DIG)]	0.54818	14591.84

#### Potential Problems

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No warning was recorded during the run

# Example: sequence data set wit two loci [simula

MIGRATION RATE AND POPULATION SIZE ESTIMATION using the coalescent and maximum likelihood or Bayesian inference Migrate-n version 3.2.16 [1920] Compiled for a SYMMETRIC MULTIPROCESSORS Program started at Thu Jan 31 23:00:16 2013 Program finished at Fri Feb 1 00:58:35 2013

0												
Options												
Datatype:										D	NA sec	quence data
Inheritance scalers in [Each Theta uses the Random number seed Start parameters:	use fo (true) :	or The ineri	etas: 1. ance s	00 calar of tl	he first	t locus	s as a re	eferenc	ce] (with inter	nal timer)		599348375
Theta values were ger	nerate	d								from t	he FS	T-calculation
M values were genera	ted									from t	he FS	T-calculation
Connection type matrix where m = average (a s = symmetric M, S = * = free to vary, Theta	x: avera symr as are	ge ov netric on c	ver a gr c 4Nm, liagona	oup of Th 0 = zero I	hetas c b, and i	or M, not es	stimated	ł,				
Population 1 BAJA 2 MIDR 3 MAIN	1 * *	2 0 *	3 0 0 *									

Order of parameters:

1	$\Theta_1$	<displayed></displayed>
2	$\Theta_2$	<displayed></displayed>
3	$\Theta_3$	<displayed></displayed>
6	M <sub>1-&gt;2</sub>	<displayed></displayed>
8	M 1->3	<displayed></displayed>

Migrate 3.2.16: (http://popgen.sc.fsu.edu) [program run on ]

Example: sequence data set wit two loci [simulated data] -- 2

9 M <sub>2-&gt;3</sub>			<di:< th=""><th>splayed&gt;</th><th></th><th></th><th></th></di:<>	splayed>				
Mutation rate	among loc	i:					Mutati	ion rate is constant
Analysis stra	tegy:							Bayesian inference
Proposal dist Parameter Theta M	ributions for	r parameter	Pro Slice sa Slice sa	oposal mpling mpling				
Prior distribu	tion for pare	ameter						
Parameter Theta M	Prior Uniform Uniform	Minimum 0.000000 0.000000	50.00 37500.00	Mean* )0000 )0000	Maximum 100.000000 75000.000000	10. 7500.	Delta 000000 000000	Bins 1500 1500
Markov chair Number of ch Recorded Increment Number of Visited (sa Number of	n settings: nains steps [a] (record eve concurrent mpled) para discard tre	ry x step [b] chains (replic ameter values es per chain (	cates) [c] s [a*b*c] (burn-in)					Long chain 1 50000 100 1 5000000 2500000
Multiple Mark Static heat 0 2.10	ov chains: ing scheme 2.00	1.95	1.80	1.65	1.50	1.40	20 chains 1.25 Swa	with temperatures 1.10 1.00 apping interval is 1
Print options: Data file: Output file: Posterior c Print data: Print gene	: listribution r alogies [onl	aw histogram y some for so	file: me data ty	′pe]:			MR MRO_I	O_NGulf_direc.seq NGulf_Direc2_run1 bayesfile No None
	9 Mutation rate Analysis stra Proposal dist Parameter Theta M Prior distribut Parameter Theta M Markov chair Number of ch Recorded Increment Number of Visited (sa Number of Visited (sa Number of Visited (sa Number of Visited (sa Number of Print options Data file: Output file Posterior c Print data: Print gene	9M2-Mutation rate among lociAnalysis strategy:Proposal distributions for ParameterThetaMPrior distribution for para ParameterPrior distribution for para ParameterPrior distribution for para ParameterMarkov chain settings:Number of chains Recorded steps [a] Increment (record eve Number of concurrent Visited (sampled) para Number of discard treeMultiple Markov chains: Static heating scheme 02.102.00Print options: Data file: Output file: Print data: Print genealogies [online]	9 M <sub>2-&gt;3</sub> Mutation rate among loci: Analysis strategy: Proposal distributions for parameter Parameter Theta M Prior distribution for parameter Parameter Prior Minimum Theta Uniform 0.000000 M Uniform 0.000000 Markov chain settings: Number of chains Recorded steps [a] Increment (record every x step [b] Number of concurrent chains (replic Visited (sampled) parameter values Number of discard trees per chain ( Multiple Markov chains: Static heating scheme D 2.10 2.00 1.95 Print options: Data file: Output file: Posterior distribution raw histogram Print data: Print genealogies [only some for so	9 M <sub>2-&gt;3</sub> Mutation rate among loci: Analysis strategy: Proposal distributions for parameter Parameter Prior Minimum Slice sau M Slice sau Prior distribution for parameter Parameter Prior Minimum Slice Theta Uniform 0.000000 50.00 M Uniform 0.000000 37500.00 Markov chain settings: Number of chains Recorded steps [a] Increment (record every x step [b] Number of concurrent chains (replicates) [c] Visited (sampled) parameter values [a*b*c] Number of discard trees per chain (burn-in) Multiple Markov chains: Static heating scheme 2.10 2.00 1.95 1.80 Print options: Data file: Output file: Posterior distribution raw histogram file: Print data: Print genealogies [only some for some data ty	9 M <sub>2-&gt;3</sub> <di (burn-in)="" (record="" 0.000000="" 1.65="" 1.80="" 1.95="" 2.00="" 2.10="" 37500.000000="" 50.000000="" [a]="" [b]="" [only="" among="" analysis="" chain="" chains="" chains:="" d="" data="" data:="" discard="" distribution="" distributions="" every="" file:="" for="" genealogies="" heating="" histogram="" increment="" loci:="" m="" markov="" mean*="" minimum="" multiple="" mutation="" number="" of="" options:="" output="" parameter="" per="" posterior="" print="" prior="" proposal="" rate="" raw="" recorded="" sampling="" scheme="" settings:="" slice="" some="" static="" step="" steps="" strategy:="" td="" theta="" trees="" type]:<="" uniform="" x=""><td>9 M <sub>2-&gt;3</sub> <displayed></displayed></td><td>9 M <sub>2-×3</sub> <displayed> Mutation rate among loci: Analysis strategy: Proposal distributions for parameter Parameter Proposal Theta Slice sampling M Slice sampling M Slice sampling M Outform 0.000000 50.000000 100.000000 10. M Uniform 0.000000 37500.000000 75000.000000 7500. Markov chain settings: Number of chains Recorded steps [a] Increment (record every x step [b] Number of concurrent chains (replicates) [c] Visited (sampled) parameter values [a*b*c] Number of discard trees per chain (burn-in) Multiple Markov chains: Static heating scheme D 2.10 2.00 1.95 1.80 1.65 1.50 1.40 Print options: Data file: Output file: Posterior distribution raw histogram file: Print genealogies [only some for some data type]:</displayed></td><td>9       M       23       <displayed>         Mutation rate among loci:       Mutati       Mutati         Analysis strategy:       Proposal distributions for parameter       Parameter       Proposal         Theta       Slice sampling       M       Slice sampling         M       Slice sampling       M       Delta         Prior distribution for parameter       Parameter       Prior distribution for parameter         Parameter       Prior Minimum       Mean*       Maximum       Delta         Theta       Uniform       0.000000       50.000000       100.000000       7500.000000         M       Uniform       0.000000       37500.000000       7500.000000       7500.000000         Markov chain settings:       Number of chains       Recorded steps [a]       Increment (record every x step [b]       Number of concurrent chains (replicates) [c]       Visited (sampled) parameter values [a*b*c]       Number of discard trees per chain (burn-in)         Mutiple Markov chains:       Static heating scheme       20 chainse       20 chainse         2.10       2.00       1.95       1.80       1.65       1.50       1.40       1.25         Sw       Print options:       Data file:       MRO_       MRO_       Posterior distribution raw histogram f</displayed></td></di>	9 M <sub>2-&gt;3</sub> <displayed></displayed>	9 M <sub>2-×3</sub> <displayed> Mutation rate among loci: Analysis strategy: Proposal distributions for parameter Parameter Proposal Theta Slice sampling M Slice sampling M Slice sampling M Outform 0.000000 50.000000 100.000000 10. M Uniform 0.000000 37500.000000 75000.000000 7500. Markov chain settings: Number of chains Recorded steps [a] Increment (record every x step [b] Number of concurrent chains (replicates) [c] Visited (sampled) parameter values [a*b*c] Number of discard trees per chain (burn-in) Multiple Markov chains: Static heating scheme D 2.10 2.00 1.95 1.80 1.65 1.50 1.40 Print options: Data file: Output file: Posterior distribution raw histogram file: Print genealogies [only some for some data type]:</displayed>	9       M       23 <displayed>         Mutation rate among loci:       Mutati       Mutati         Analysis strategy:       Proposal distributions for parameter       Parameter       Proposal         Theta       Slice sampling       M       Slice sampling         M       Slice sampling       M       Delta         Prior distribution for parameter       Parameter       Prior distribution for parameter         Parameter       Prior Minimum       Mean*       Maximum       Delta         Theta       Uniform       0.000000       50.000000       100.000000       7500.000000         M       Uniform       0.000000       37500.000000       7500.000000       7500.000000         Markov chain settings:       Number of chains       Recorded steps [a]       Increment (record every x step [b]       Number of concurrent chains (replicates) [c]       Visited (sampled) parameter values [a*b*c]       Number of discard trees per chain (burn-in)         Mutiple Markov chains:       Static heating scheme       20 chainse       20 chainse         2.10       2.00       1.95       1.80       1.65       1.50       1.40       1.25         Sw       Print options:       Data file:       MRO_       MRO_       Posterior distribution raw histogram f</displayed>

5

30

90

### Data summary

Datatype: Number of loci:		Sequence d	ata 1
Population	Locus	Gene copies	
1 BAJA	1	30	
2 MIDR	1	30	

1

1

3 MAIN

Total of all populations

# Bayesian Analysis: Posterior distribution table

Locus	Parameter	2.5%	25.0%	Mode	75.0%	97.5%	Median	Mean
1	$\Theta_1$	0.00000	0.00000	0.03333	0.53333	1.40000	0.56667	0.00748
1	$\Theta_2^{\dagger}$	0.00000	0.00000	0.03333	4.73333	29.73333	49.70000	49.80238
1	$\tilde{\Theta_3}$	1.00000	6.60000	8.90000	11.26667	43.80000	49.76667	49.90507
1	M <sub>1-&gt;2</sub>	4250.0	7000.0	8775.0	11000.0	17400.0	9725.0	10251.9
1	M <sub>1-&gt;3</sub>	2950.0	10200.0	20975.0	32200.0	64450.0	27475.0	30287.4
1	M <sub>2-&gt;3</sub>	14950.0	32600.0	45475.0	57850.0	75000.0	44625.0	44230.9



### Bayesian Analysis: Posterior distribution over all loci

Migrate 3.2.16: (http://popgen.sc.fsu.edu) [program run on 23:00:16]

## Log-Probability of the data given the model (marginal likelihood) Use this value for Bayes factor calculations: BF = Exp[ In(Prob(D I thisModel) - In( Prob( D I otherModel) or as LBF = 2 (In(Prob(D | thisModel) - In( Prob( D | otherModel)) shows the support for thisModel] Method In(Prob(DIModel)) Notes Thermodynamic integration -2660.905427 (1a) -2658.464366 (1b) Harmonic mean -2515.794262 (2) (1a, 1b and 2) is an approximation to the marginal likelihood, make sure the program run long enough! (1a, 1b) and (2) should give a similar result, (2) is considered more crude than (1), but (1) needs heating with several well-spaced chains, (1b) is using a Bezier-curve to get better approximations for runs with low number of heated chains

### Acceptance ratios for all parameters and the genealogies

Parameter	Accepted changes	Ratio
$\Theta_1$	625435/625435	1.00000
$\Theta_2^{-1}$	624793/624793	1.00000
$\Theta_3$	625019/625019	1.00000
M <sub>1-&gt;2</sub>	625290/625290	1.00000
$M_{1->3}$	624017/624017	1.00000
$M_{2-3}$	626584/626584	1.00000
Genealogies	492370/2499774	0.19697

### MCMC-Autocorrelation and Effective MCMC Sample Size

Parameter	Autocorrelation	Effective Sampe Size
Θ	0.38129	22395.87
$\Theta_2^{-1}$	0.02018	48021.49
$\Theta_{3}$	-0.00076	50076.32
$M_{1-2}^{2}$	0.47159	17953.89
$M_{1-3}^{1-2}$	0.47816	17651.48
M $_{2-3}^{2-3}$	0.50152	16599.39
Ln[Prob(DIG)]	0.53923	14967.64

#### Potential Problems

This section reports potential problems with your run, but such reporting is often not very accurate. Whith many parameters in a multilocus analysis, it is very common that some parameters for some loci will not be very informative, triggering suggestions (for example to increase the prior range) that are not sensible. This suggestion tool will improve with time, therefore do not blindly follow its suggestions. If some parameters are flagged, inspect the tables carefully and judge wether an action is required. For example, if you run a Bayesian inference with sequence data, for macroscopic 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 routes 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