

# Japan

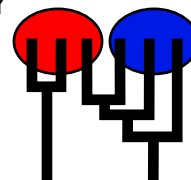
## POPULATION SIZE, MIGRATION, DIVERGENCE, ASSIGNMENT, HISTORY

Bayesian inference using the structured coalescent

Migrate-n version 5.0.2(git:v5.0.2-0-gb89fa60-dirty) [December-1-2021]

Program started at Sat Feb 5 10:31:35 2022

Program finished at Sat Feb 5 10:38:09 2022 [Runtime:0000:00:06:34]



## Options

Datatype: Single nucleotide polymorphism data(Hapmap formatting)

Inheritance multipliers in use for Thetas:

All loci use an inheritance multiplier of 1.0

Random number seed: (with internal timer) 1390658227

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

1 Japan \*

Order of parameters:

1  $\Theta_1$  <displayed>

Mutation rate among loci: Mutation rate is constant for all loci

Analysis strategy: Bayesian inference

-Population size estimation:

Exponential Distribution

## Proposal distributions for parameter

| Parameter         | Proposal            |
|-------------------|---------------------|
| Theta             | Metropolis sampling |
| M                 | Metropolis sampling |
| Divergence        | Metropolis sampling |
| Divergence Spread | Metropolis sampling |
| Genealogy         | Metropolis-Hastings |

## Prior distribution for parameter

| Parameter | Prior            | Minimum  | Mean  | Maximum | Delta | Bins | UpdateFreq |
|-----------|------------------|----------|-------|---------|-------|------|------------|
| 1         | Theta ** Uniform | 0.000000 | 0.050 | 0.100   | 0.010 | 1500 | 0.50000    |

[\* \* means priors were set globally]

## Markov chain settings:

Long chain

|  |         |
|--|---------|
| Number of chains                             | 1       |
| Recorded steps [a]                           | 10000   |
| Increment (record every x step [b])          | 100     |
| Number of concurrent chains (replicates) [c] | 1       |
| Visited (sampled) parameter values [a*b*c]   | 1000000 |
| Number of discard trees per chain (burn-in)  | 1000    |

## Multiple Markov chains:

Static heating scheme

4 chains with temperatures  
 1000000.00 3.00 1.50 1.00  
 Swapping interval is 1

## Print options:

|   |                 |
|---|-----------------|
| Data file:  | infile.hapmap   |
|   | parmfile.hapmap |
| Haplotyping is turned on:                         | NO              |
| Output file:                                      | outfile_hapmap  |
| Posterior distribution raw histogram file:        | bayesfile       |
| Raw data from the MCMC run:                       | bayesallfile.gz |
| Print data:                                       | No              |
| Print genealogies [only some for some data type]: | None            |

## *Data summary*

Data file: infile.hapmap  
 Datatype: SNP data (Hapmap data)  
 Number of loci: 9

### Mutationmodel:

| Locus | Sublocus | Mutationmodel | Mutationmodel parameters |
|-------|----------|---------------|--------------------------|
| 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]        |

### Sites per locus

| Locus | Sites |
|-------|-------|
| 1     | 1     |
| 2     | 1     |
| 3     | 1     |
| 4     | 1     |
| 5     | 1     |
| 6     | 1     |
| 7     | 1     |
| 8     | 1     |
| 9     | 1     |

### 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       |  |
| Population               |   |   | Locus |       | Gene copies |  |
| 1 Japan                  |   |   | 1     | 72    |             |  |
|                          |   |   | 2     | 90    |             |  |
|                          |   |   | 3     | 88    |             |  |
|                          |   |   | 4     | 90    |             |  |
|                          |   |   | 5     | 90    |             |  |
|                          |   |   | 6     | 88    |             |  |
|                          |   |   | 7     | 90    |             |  |
|                          |   |   | 8     | 90    |             |  |
|                          |   |   | 9     | 90    |             |  |
| Total of all populations |   |   | 1     | 72    |             |  |
|                          |   |   | 2     | 90    |             |  |
|                          |   |   | 3     | 88    |             |  |
|                          |   |   | 4     | 90    |             |  |
|                          |   |   | 5     | 90    |             |  |
|                          |   |   | 6     | 88    |             |  |
|                          |   |   | 7     | 90    |             |  |
|                          |   |   | 8     | 90    |             |  |
|                          |   |   | 9     | 90    |             |  |

## *Allele frequency spectra*

### Locus 1

| Allele     | Pop1  | All   |
|------------|-------|-------|
| G          | 0.542 | 0.542 |
| C          | 0.458 | 0.458 |
|            | -     | 0.000 |
|            | -     | 0.000 |
| Alleles    | 0.497 | 0.497 |
| Samplesize | 72    | 72    |
| $H_{exp}$  |       |       |

### Locus 2

| Allele     | Pop1  | All   |
|------------|-------|-------|
| G          | 1.000 | 1.000 |
| A          | -     | 0.000 |
|            | -     | 0.000 |
|            | -     | 0.000 |
| Alleles    | 0.000 | 0.000 |
| Samplesize | 72    | 72    |
| $H_{exp}$  |       |       |

### Locus 3

| Allele     | Pop1  | All   |
|------------|-------|-------|
| C          | 1.000 | 1.000 |
| A          | -     | 0.000 |
|            | -     | 0.000 |
|            | -     | 0.000 |
| Alleles    | 0.000 | 0.000 |
| Samplesize | 72    | 72    |
| $H_{exp}$  |       |       |

### Locus 4

| Allele | Pop1  | All   |
|--------|-------|-------|
| G      | 0.125 | 0.125 |
| A      | 0.875 | 0.875 |
|        | -     | 0.000 |
|        | -     | 0.000 |

| Allele     | Pop1  | All   |
|------------|-------|-------|
| Alleles    | 0.219 | 0.219 |
| Samplesize | 72    | 72    |
| $H_{exp}$  |       |       |
| Locus 5    |       |       |
| Allele     | Pop1  | All   |
| T          | 1.000 | 1.000 |
| C          | -     | 0.000 |
|            | -     | 0.000 |
|            | -     | 0.000 |
| Alleles    | 0.000 | 0.000 |
| Samplesize | 72    | 72    |
| $H_{exp}$  |       |       |
| Locus 6    |       |       |
| Allele     | Pop1  | All   |
| C          | 1.000 | 1.000 |
| T          | -     | 0.000 |
|            | -     | 0.000 |
|            | -     | 0.000 |
| Alleles    | 0.000 | 0.000 |
| Samplesize | 72    | 72    |
| $H_{exp}$  |       |       |
| Locus 7    |       |       |
| Allele     | Pop1  | All   |
| C          | 1.000 | 1.000 |
|            | -     | 0.000 |
|            | -     | 0.000 |
|            | 0.000 | 0.000 |
| Alleles    | 1     | 4     |
| Samplesize | 72    | 72    |
| $H_{exp}$  |       |       |
| Locus 8    |       |       |
| Allele     | Pop1  | All   |
| G          | 1.000 | 1.000 |
| T          | -     | 0.000 |
|            | -     | 0.000 |

| Allele                          | Pop1  | All   |
|---------------------------------|-------|-------|
|                                 | -     | 0.000 |
| Alleles                         | 0.000 | 0.000 |
| Samplesize                      | 72    | 72    |
| $H_{exp}$                       |       |       |
| Locus 9                         |       |       |
| Allele                          | Pop1  | All   |
| A                               | 1.000 | 1.000 |
| G                               | -     | 0.000 |
|                                 | -     | 0.000 |
|                                 | -     | 0.000 |
| Alleles                         | 0.000 | 0.000 |
| Samplesize                      | 72    | 72    |
| $H_{exp}$                       |       |       |
| Average expected heterozygosity |       |       |
|                                 | Pop1  | All   |
| $H_{exp}$                       | 0.079 | 0.079 |

## *Bayesian Analysis: Posterior distribution table*

| Locus | Parameter  | 2.5%    | 25.0%   | Mode    | 75.0%   | 97.5%   | Median  | Mean    |
|-------|------------|---------|---------|---------|---------|---------|---------|---------|
| 1     | $\Theta_1$ | 0.04533 | 0.06967 | 0.08277 | 0.09173 | 0.09993 | 0.07630 | 0.07457 |
| 2     | $\Theta_1$ | 0.03227 | 0.05167 | 0.06437 | 0.07867 | 0.09813 | 0.06437 | 0.06387 |
| 3     | $\Theta_1$ | 0.04927 | 0.06127 | 0.06490 | 0.07027 | 0.09887 | 0.07223 | 0.07287 |
| 4     | $\Theta_1$ | 0.05160 | 0.08453 | 0.09010 | 0.09253 | 0.09993 | 0.07903 | 0.07764 |
| 5     | $\Theta_1$ | 0.05907 | 0.08987 | 0.09343 | 0.09600 | 0.09993 | 0.08090 | 0.08008 |
| 6     | $\Theta_1$ | 0.04787 | 0.07287 | 0.08450 | 0.09447 | 0.09993 | 0.07763 | 0.07586 |
| 8     | $\Theta_1$ | 0.07107 | 0.08040 | 0.08870 | 0.09260 | 0.09993 | 0.08543 | 0.08436 |
| 9     | $\Theta_1$ | 0.05193 | 0.07827 | 0.08877 | 0.09807 | 0.09993 | 0.07997 | 0.07823 |
| All   | $\Theta_1$ | 0.06940 | 0.07853 | 0.08350 | 0.08773 | 0.09793 | 0.08317 | 0.08292 |

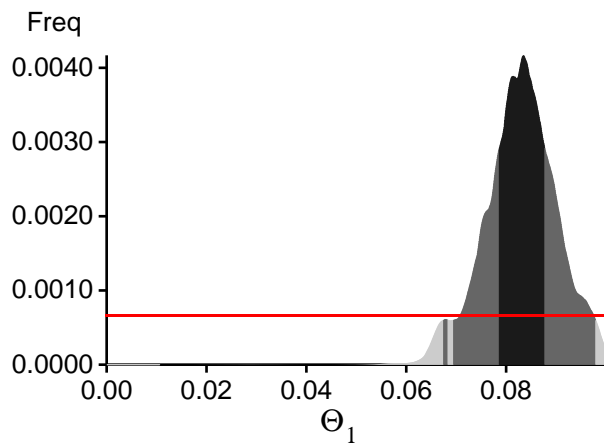
Citation suggestions:

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:

$BF = \text{Exp}[\ln(\text{Prob}(D \mid \text{thisModel}) - \ln(\text{Prob}(D \mid \text{otherModel}))]$

or as  $LBF = 2 (\ln(\text{Prob}(D \mid \text{thisModel}) - \ln(\text{Prob}(D \mid \text{otherModel})))$

shows the support for thisModel]

| Locus | TI(1a)  | BTI(1b) | HS(3)   |
|-------|---------|---------|---------|
| 1     | -61.56  | -40.13  | -15.30  |
| 2     | -8.17   | -8.01   | -8.13   |
| 3     | -43.07  | -35.34  | -16.47  |
| 4     | -34.01  | -31.03  | -18.38  |
| 5     | -16.62  | -16.26  | -16.56  |
| 6     | -16.69  | -16.34  | -15.43  |
| 8     | -24.45  | -23.18  | -14.54  |
| 9     | -29.01  | -27.24  | -20.31  |
| All   | -238.09 | -202.04 | -129.63 |

(1a) TI: Thermodynamic integration:  $\log(\text{Prob}(D|\text{Model}))$ : Good approximation with many temperatures

(1b) BTI: Bezier-approximated Thermodynamic integration: when using few temperatures USE THIS!

(2) SS: Steppingstone Sampling (Xie et al 2011)

(3) HS: Harmonic mean approximation: Overestimates the marginal likelihood, poor variance

[Scaling factor = -4.506571]

Citation suggestions:

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

Palczewski M. and P. Beerli, 2014. Population model comparison using multi-locus datasets.

In M.-H. Chen, L. Kuo, and P. O. Lewis, editors, *Bayesian Phylogenetics: Methods, Algorithms, and Applications*, pages 187-200. CRC Press, 2014.

Xie W., P. O. Lewis, Y. Fan, L. Kuo, and M.-H. Chen. 2011. Improving marginal likelihood estimation for Bayesian phylogenetic model selection. *Systematic Biology*, 60(2):150â 160, 2011.

*Acceptance ratios for all parameters and the genealogies*

| Parameter   | Accepted changes | Ratio   |
|-------------|------------------|---------|
| $\Theta_1$  | 2626935/3999538  | 0.65681 |
| Genealogies | 3342941/4000462  | 0.83564 |

## *MCMC-Autocorrelation and Effective MCMC Sample Size*

| Parameter   | Autocorrelation | Effective Sample Size |
|-------------|-----------------|-----------------------|
| $\Theta_1$  | 0.79149         | 10063.31              |
| Genealogies | 0.79149         | 10063.31              |

## *Average temperatures during the run*

| Chain | Temperatures |
|-------|--------------|
|-------|--------------|

|   |               |
|---|---------------|
| 1 | 1.00000       |
| 2 | 1.50000       |
| 3 | 3.00000       |
| 4 | 1000000.00000 |

Adaptive heating often fails, if the average temperatures are very close together try to rerun using static heating! If you want to compare models using marginal likelihoods then you **MUST** use static heating

## *Potential Problems*

This section reports potential problems with your run, but such reporting is often not very accurate. With 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 whether 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