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# Data

## Kinship & social structure

All data was extracted from the D-PLACE Ethnographic atlas [github repository](https://github.com/D-PLACE/dplace-data). Counts of the number of societies used for the signal and ancestral state anlyses for each langauges family are in table S1. Question and variable codes are displayed below in table S2. Due to the nature of the analysis, all variables are binary coded. The numbers in the value columns indicate the criteria for a society to have the terminology or social structure coded as present (i.e. 1). For details on what each code indicates, refer to the Ethnographic Atlas codebook or the [D-PLACE github repository](https://github.com/D-PLACE/dplace-data/blob/master/datasets/EA/codes.csv).

Table S1: Count of societies in signal test and ancestral state analyses, by language family

Count

Austronesian

85

Bantu

69

Indo-European

33

Uto-Aztecan

22

Table S2: Data coding taken from D-PLACE & Co-evolutionary analyses data counts

terminology

question code

value code

social structure

question code

value code

AN counts

BT counts

UA counts

Crow

27

1

matrilineal

43

3

85

69

Crow

27

1

high.polygyny

9

3,4,5,6

80

Crow

27

1

polygyny

9

2,3,4,5,6

80

Crow

27

1

matri.anvunclocalresidence

10

1,5,9

84

69

Crow

27

1

uni.localresidence

10

1,5,8,9,10

84

69

Eskimo

27

3

bi.linealdescent

43

2,5,7

85

Eskimo

27

3

uni.linealdescent

43

1,3,4

85

Eskimo

27

3

absenceofcousinmarriage.permitted

25

10,11,15

79

Eskimo

27

3

absenceofcousinmarriage.preference

23

7,8,11,12

79

Eskimo

27

3

monogamy

9

1

80

Eskimo

27

3

neo.localresidence

10

6

84

Eskimo

27

3

nuclear.families

8

1,2

83

Hawaiian

27

4

bi.linealdescent

43

2,5,7

85

69

23

Hawaiian

27

4

bi.localextendedfamily

8

6,7,8

83

69

22

Hawaiian

27

4

absenceofcousinmarriage.permitted

25

10,11,15

79

66

19

Hawaiian

27

4

absenceofcousinmarriage.preference

23

7,8,11,12

79

66

19

Hawaiian

27

4

bi.localresidence

10

2,11,12

84

69

22

Iroquois

27

5

exogamy.unilineal.descent

15

4

78

62

19

Iroquois

27

5

uni.linealdescent

43

1,3,4

85

69

23

Iroquois

27

5

cross.cousinmarriage.permitted

25

1,6,9

79

66

19

Iroquois

27

5

cross.cousinmarriage.preferred

23

1,2,3,5,6,8,12,13,14

79

66

19

Iroquois

27

5

high.polygyny

9

3,4,5,6

80

22

Iroquois

27

5

polygyny

9

2,3,4,5,6

80

Iroquois

27

5

matri.anvunclocalresidence

10

1,5,9

84

69

22

Iroquois

27

5

uni.localresidence

10

1,5,8,9,10

84

69

22

Omaha

27

6

patrilineal

43

1

69

Omaha

27

6

matri.anvunclocalresidence

10

1,5,9

69

Omaha

27

6

uni.localresidence

10

1,5,8,9,10

69

### Co-evolutionary hypotheses and references

Here we show the the location of the original hypotheses of social structure and kinship terminologies.

## Phylogenies

We tested hypotheses across three languages families, where data allowed. This was the Austronesian, Bantu, and Uto-Aztecan language phylogenies. All language to phylogeny pairings were taken from decisions made in (**???**). In Austronesian, we sub-sampled 1000 phylogenies from a posterior sample of 4199 phylogenies developed in (**???**). Austronesian phylogenies were estimated through linguistic data and supported by genetic evidence, and archaeological records. Detailed methods can be found in (**???**). Trees were pruned from the original sample of 400 languages, to 80 languages based on data availability. In Bantu, we sampled 1000 from a posterior sample of 2000 phylogenies developed in (**???**). These were developed using linguistic data and calibrated using the archaeological record. Trees were pruned from the original sample of 425 languages, to 69 languages based on data availability. In Uto-Aztecan, we sampled 1000 phylogenies from a posterior of 10000 phylogenies developed by (**???**). This was developed using linguistic data. Trees were pruned from the original sample of 34 languages, to 19 based on data availability.

# Signal tests

We performed 4 signal tests to assess the hypotheses that shared ancestry was a constraint on kinship diversity. The phylogenetic ‘D’ test uses simulation to determine whether the clustering of binary variables on a phylogeny follow patterns of Brownian motion (D = 0 indicates perfectly Brownian clusters & D < 0 strong clustering) or random clustering (D = 1 indicates complete randomness). To test whether geography may also predict the distribution of terminologies, we used Mantel tests. Mantel tests use random permutation and Pearson’s correlation statistics to determine the correlation between two matrices. Here we compare log geographic distance, calculated with the haversine formula, to a binary similarity matrix of each terminology present in each language family, each over the default setting of 999 permutations. To determine whether phylogenetic or geographic distances best determined the distribution of terminologies, we used partial mantel tests. Partial Mantel tests control for a confounding variable, while comparing matrices. We perform two tests, one between a terminology and geographic distance, controlling for phylogenetic distance, and one between terminology and phylogenetic distance, controlling for geographic distance. Phylogenetic distance is calculated using cophenetic distance, and the cophenetic function in R {stats} (R Core Team 2018). All results in table S3 show the mean result from 1000 phylogenies. Here we show the results of all these tests for all terminologies present within each language family. However, we only consider results viable if the terminology consists of more than 10% of the overall sample. All p-values are bonferonni corrected.

The code for all signal tests can be found in file analysis/signal-tests.R. This file comes with helper functions analysis/signal-functions & analysis/mantel-functions for the D-statistic and Mantel tests respectively.

Table S3: Signal tests for each terminology within each langauge family. Columns 2 & 3 indicate the presence and absence of a terminology. Columns 4 to 6 are outputs from the D-statistic test. Columns 7 to 21 are output from Mantel tests.

Mantel

Partial Mantel

D-statistic

Geography

Log-Geography

Phylogeny

Log-Geo + Phy

Phy + Log Geo

Terminology

Absent

Present

D

Prob. Brownian

Prob. Random

Z-stat

p-value

corrected-p

Z-stat

p-value

corrected-p

Z-stat

p-value

corrected-p

Statistic

p-value

corrected-p

Statistic

p-value

corrected-p

Austronesian

Crow

79

6

-0.115

0.603

0.036

1752616.53

0.039

0.233

3789.807

0.400

1.000

32.773

0.028

0.167

0.012

0.368

1.000

-0.116

0.977

1.000

Eskimo

71

14

-0.494

0.806

0.000

4905208.29

0.219

1.000

8155.126

0.180

0.985

78.033

0.038

0.229

-0.004

0.500

1.000

0.133

0.031

0.184

Hawaiian

37

48

0.661

0.054

0.081

8021595.70

0.959

1.000

14388.168

0.854

1.000

131.969

0.596

1.000

-0.001

0.446

1.000

-0.010

0.665

1.000

Iroquois

70

15

0.097

0.468

0.007

4216334.11

0.032

0.190

8460.864

0.484

1.000

74.751

0.005

0.030

0.028

0.248

1.000

-0.125

0.997

1.000

Omaha

84

1

2.860

0.230

0.700

430380.25

0.376

1.000

702.380

0.377

1.000

6.328

0.867

1.000

0.044

0.171

0.975

-0.014

0.626

1.000

Sudanese

84

1

-2.063

0.714

0.171

498098.38

0.260

1.000

709.856

0.281

1.000

6.220

0.826

1.000

0.067

0.118

0.710

-0.035

0.674

1.000

Bantu

Crow

65

4

1.105

0.129

0.525

348598.29

0.887

1.000

1823.446

0.857

1.000

15359.566

0.627

1.000

-0.011

0.512

1.000

-0.063

0.670

1.000

Descriptive

68

1

2.941

0.066

0.881

93014.64

0.783

1.000

477.297

0.900

1.000

5417.879

0.233

1.000

-0.031

0.603

1.000

0.136

0.077

0.537

Hawaiian

60

9

0.405

0.297

0.083

792380.62

0.524

1.000

3835.774

0.496

1.000

35032.624

0.542

1.000

0.031

0.284

1.000

0.040

0.288

1.000

Iroquois

25

44

0.166

0.362

0.008

1636008.46

0.023

0.159

7853.277

0.007

0.046

71119.715

0.151

0.892

0.105

0.005

0.038

0.051

0.138

0.863

Mixed

68

1

-2.432

0.834

0.040

116322.82

0.320

1.000

500.446

0.290

1.000

3836.258

0.916

1.000

0.086

0.121

0.844

-0.067

0.854

1.000

Omaha

61

8

0.767

0.140

0.274

733279.95

0.393

1.000

3484.320

0.309

1.000

32352.914

0.396

1.000

0.051

0.197

1.000

0.067

0.218

1.000

Sudanese

67

2

1.051

0.287

0.459

169263.56

0.718

1.000

929.736

0.623

1.000

10075.747

0.223

1.000

-0.066

0.840

1.000

0.148

0.083

0.580

Uto-Aztecan

Crow

21

1

0.243

0.419

0.462

13195.12

0.365

1.000

132.056

0.998

1.000

0.025

0.659

0.990

-0.022

0.484

1.000

0.060

0.341

0.935

Eskimo

21

1

3.253

0.216

0.679

14128.24

0.818

1.000

133.048

0.909

1.000

0.026

0.504

0.974

-0.003

0.355

1.000

0.087

0.255

0.827

Hawaiian

6

16

-0.600

0.798

0.004

70096.07

0.259

0.980

606.534

0.596

1.000

0.114

0.136

0.545

-0.035

0.604

1.000

0.145

0.073

0.291

Iroquois

18

4

-2.343

0.985

0.000

54649.14

0.881

1.000

457.499

0.973

1.000

0.086

0.235

0.840

0.001

0.438

1.000

0.134

0.120

0.479

# Ancestral state

## MCMC review

Ancestral state reconstruction allows us to estimate the probability of a particular terminology at the root of each language phylogeny, as well as estimating the patterns of change between each state. We perform Bayesian reversible-jump MCMC ancestral reconstructions kinship terminologies using BayesTraits V 3.0 Multistate (Pagel and Meade 2017). The advantage of the MCMC approach over a maximum likelihood approach is that it allows the result to be integrated over the sample of trees. Multistate uses a posterior of phylogenies to estimate the probability of each terminology present in the taxa at the phylogeny root, and an estimation of the rate (Q) matrix. The reversible-jump approach searches the model space for an optimal solution by dynamically setting some rate parameters (i.e. transitions from one state to another) to zero. This results in searching the model space where we are confident transition rates are non-zero. The Q matrix shows the likelihood of changing from any state to any other. MCMC chains were run for 109 iterations, sampling every 50 000 iterations with a burn-in of 10 000 iterations, to give a posterior sample of 19 999. Each analysis ran three times to test consistent MCMC convergence using the Gelman-Rubin diagnostic (Gelman and Rubin 1992). Due to uncertainty in the reconstruction of the Bantu ancestral state, each possible taxa was fossilized as the root to estimate likelihoods. We calculate pairwise Bayes factors (BF) to assess the evidence for each response. BF < 2 indicates weak evidence, > 2 positive evidence, 5-10 strong evidence, and >10 very strong evidence. This involves the same process as above, but forcing the model to assume an ancestral state and using model comparison to determine the most likely ancestral state.

Three MCMC chains for the austronesian language family

Lh

Crow

Eskimo

Hawaiian

Iroquois

Omaha

Sudanese

1

-95.169

0.016

0.918

0.004

0.005

0.025

0.032

2

-95.143

0.016

0.920

0.005

0.005

0.024

0.032

3

-95.144

0.016

0.920

0.004

0.005

0.024

0.030

Mean

-95.152

0.016

0.919

0.004

0.005

0.024

0.031

Three MCMC chains for the bantu language family

Lh

Crow

Descriptive

Hawaiian

Iroquois

Omaha

Sudanese

Mixed

1

-82.227

0.105

0.096

0.153

0.324

0.114

0.099

0.110

2

-82.244

0.105

0.097

0.152

0.320

0.114

0.100

0.112

3

-82.219

0.105

0.097

0.152

0.323

0.113

0.099

0.111

Mean

-82.230

0.105

0.097

0.152

0.322

0.114

0.099

0.111

Three MCMC chains for the utoaztecan language family

Lh

Crow

Eskimo

Hawaiian

Iroquois

1

-14.709

0

0

0.999

0.001

2

-14.708

0

0

0.999

0.001

3

-14.695

0

0

0.999

0.001

Mean

-14.704

0

0

0.999

0.001

Gelman-Rubin tests of MCMC convergence for each langauge family

Point est.

Upper C.I.

austronesian

1

1.001

bantu

1

1.000

utoaztecan

1

1.000

### Fossilized Bantu

#### MCMC Review

We fossilize the ancestral state for each possible terminology within Bantu in an attempt to determine the most plausible ancestral state. Below are the MCMC diagnostics for these models and the result with comparisons to an Iroquoian fossilized ancestral state.

Marginal log-likelihood for three runs of each fossilized terminology in Bantu

Crow

Descriptive

Hawaiian

Iroquois

Mixed

Omaha

Sudanese

1

-93.867

-94.056

-92.303

-91.562

-94.748

-94.915

-93.454

2

-92.828

-95.856

-93.706

-90.160

-93.739

-93.824

-94.241

3

-92.440

-94.463

-91.300

-91.131

-94.466

-92.978

-93.329

Mean

-93.041

-94.786

-92.426

-90.947

-94.316

-93.899

-93.673

Gelman-Rubin tests of MCMC convergence for each each fossilized model

Point est.

Upper C.I.

Crow

1

1.000

Descriptive

1

1.000

Hawaiian

1

1.001

Iroquois

1

1.000

Mixed

1

1.000

Omaha

1

1.000

Sudanese

1

1.000

#### Bayes factor model comparison

Bayes factor calculations show that there is some evidence for a Iroquoian root over a Hawaiian root (BF = 2.957). The table below shows comparisons to the fossilized Iroquois root to all other fossilized roots.

Pariwise Bayes factor between Iroquois and all other possible states.

terminology

Bayes’ Factor

Crow

4.188

Descriptive

7.677

Hawaiian

2.957

Iroquois

0.000

Mixed

6.737

Omaha

5.904

Sudanese

5.452

## Transition rates

RJ ancestral state analysis also estimates the rate of transition between kinship terminological types. The model constrains the number of parameters estimated, forcing some parameters to be zero, and then estimates and appropriate number of parameters for accurately represent the model. By looking at which parameters are set to zero across the MCMC chain, we can see which transition rates the model believes to be important. We consider transition rates to be important if they are set to zero in less than 1% of models. That is, the model considered these transitions important in 99% of the iterations. Transition rates are coded by numerical codes, which are:

Kin terminologies and their numerical codes.

1

Crow

2

Descriptive

3

Eskimo

4

Hawaiian

5

Iroquois

6

Omaha

7

Sudanese

8

Mixed

Transition rates between kin terminologies in the austronesian language family.

transition

parameterized

zero

percentage

q34

9999

1

0.000

q45

9908

92

0.009

q14

9036

964

0.096

q54

7688

2312

0.231

q15

7639

2361

0.236

q64

7174

2826

0.283

q41

7023

2977

0.298

q74

6958

3042

0.304

q16

6809

3191

0.319

q61

6573

3427

0.343

q51

6500

3500

0.350

q65

6497

3503

0.350

q67

6479

3521

0.352

q17

6235

3765

0.376

q71

6223

3777

0.378

q76

6161

3839

0.384

q75

6134

3866

0.387

q73

5717

4283

0.428

q63

5492

4508

0.451

q37

4734

5266

0.527

q13

4625

5375

0.538

q56

4399

5601

0.560

q46

3899

6101

0.610

q57

3687

6313

0.631

q53

2532

7468

0.747

q36

2250

7750

0.775

q31

2163

7837

0.784

q35

2114

7886

0.789

q47

2052

7948

0.795

q43

2037

7963

0.796

Transition rates between kin terminologies in the bantu language family.

transition

parameterized

zero

percentage

q56

7786

2214

0.221

q65

7715

2285

0.228

q54

7418

2582

0.258

q15

7008

2992

0.299

q17

6968

3032

0.303

q14

6889

3111

0.311

q62

6839

3161

0.316

q71

6824

3176

0.318

q45

6725

3275

0.328

q64

6561

3439

0.344

q41

6547

3453

0.345

q75

6342

3658

0.366

q26

6341

3659

0.366

q74

6302

3698

0.370

q85

6156

3844

0.384

q24

6148

3852

0.385

q25

6134

3866

0.387

q61

6099

3901

0.390

q84

6079

3921

0.392

q76

6018

3982

0.398

q16

5988

4012

0.401

q21

5938

4062

0.406

q86

5921

4079

0.408

q28

5800

4200

0.420

q81

5776

4224

0.422

q27

5723

4277

0.428

q67

5698

4302

0.430

q78

5654

4346

0.435

q87

5541

4459

0.446

q72

5502

4498

0.450

q82

5357

4643

0.464

q18

5284

4716

0.472

q46

5061

4939

0.494

q12

4927

5073

0.507

q68

4867

5133

0.513

q51

4229

5771

0.577

q47

4189

5811

0.581

q48

3597

6403

0.640

q42

3045

6955

0.696

q57

1781

8219

0.822

q58

628

9372

0.937

q52

531

9469

0.947

Transition rates between kin terminologies in the utoaztecan language family.

transition

parameterized

zero

percentage

q43

9970

30

0.003

q45

9969

31

0.003

q41

9932

68

0.007

q34

5470

4530

0.453

q54

5335

4665

0.466

q14

5334

4666

0.467

q13

5157

4843

0.484

q31

5156

4844

0.484

q15

5044

4956

0.496

q51

4996

5004

0.500

q53

4979

5021

0.502

q35

4973

5027

0.503

## Guillon & Mace comparison

Previous research performed by Guillon and Mace, using similar methods, found support for a Hawaiian root, with some evidence of an Iroquoian root within the Bantu langauge family. This is the inverse of our result, which found most support for an Iroquoian root, with some support for Hawaiian. This discrepancy is concerning considering the terminological data for both analysis come from the same source. The analysis here uses a more recently developed phylogeny, but more importantly, Guillon and Mace include missing data, where we exclude it. We re-analysed our data including missing data and found no change in our previous conclusions. Suggesting that the improved phylogeny is driving the change in results. Efforts were made to contact the authors to make more direct comparisons, but with no response.

Ancestral state of Bantu with missing data included

probability

Crow

0.124

Descriptive

0.117

Hawaiian

0.139

Iroquois

0.259

Omaha

0.124

Sudanese

0.119

Mixed

0.118

# Co-evolution tests

## MCMC settings

All co-evolutionary analyses was performed in BayesTraits v3.1 using Discrete models (**???**). For all models we used an Reversible Jump MCMC approach, and tested an independent and dependent model of evolution. In an independent model, a trait can change, regardless of the state of the other trait. In a dependent model, a trait change is dependent on the state of the second trait. If co-evolution has occurred, the data should fit a dependent model better than it fits an independent model. Analyses were run between 10010000 and 65000000 iterations, with burn-ins ranging between 10000 and 55000000, and sampling every 1000 iterations. This results is a posteriot of 10000 iterations, approximately 10 iterations per tree. A stepping stone sampler was used to estimate the marginal likelihood. We used 100 stones sampled every 1000 iterations. For details of the prior and other settings for each hypotheses, see table S2.

Table S2: MCMC settings for both dependent and independent analyses

hypotheses

exponential mean

scaled branch length

iterations

sampling

burn-in

posterior size

austronesian-crow-high.polygyny

10

Yes

10050000

1000

50000

10000

austronesian-crow-matri.anvunclocalresidence

10

Yes

10050000

1000

50000

10000

austronesian-crow-matrilineal

10

Yes

10050000

1000

50000

10000

austronesian-crow-polygyny

10

Yes

10050000

1000

50000

10000

austronesian-crow-matrilocal

10

Yes

10010000

1000

10000

10000

austronesian-crow-uni.localresidence

10

Yes

10010000

1000

10000

10000

austronesian-eskimo-absenceofcousinmarriage.permitted

10

Yes

65000000

1000

55000000

10000

austronesian-eskimo-absenceofcousinmarriage.preference

10

Yes

65000000

1000

55000000

10000

austronesian-eskimo-bi.linealdescent

10

Yes

10010000

1000

10000

10000

austronesian-eskimo-monogamy

10

Yes

10050000

1000

50000

10000

austronesian-eskimo-neo.localresidence

10

Yes

65000000

1000

55000000

10000

austronesian-eskimo-inheritancetobothsex.restricted

10

Yes

10010000

1000

10000

10000

austronesian-eskimo-nuclear.families

10

Yes

10010000

1000

10000

10000

austronesian-eskimo-inheritancetobothsex

10

Yes

10010000

1000

10000

10000

austronesian-eskimo-uni.linealdescent

10

Yes

10010000

1000

10000

10000

austronesian-hawaiian-absenceofcousinmarriage.permitted

10

Yes

10050000

1000

50000

10000

austronesian-hawaiian-absenceofcousinmarriage.preference

10

Yes

10010000

1000

10000

10000

austronesian-hawaiian-bi.linealdescent

10

Yes

10010000

1000

10000

10000

austronesian-hawaiian-bi.localextendedfamily

10

Yes

10010000

1000

10000

10000

austronesian-hawaiian-first&secondcousinforbidden

10

Yes

10050000

1000

50000

10000

austronesian-hawaiian-bi.localresidence

10

Yes

10050000

1000

50000

10000

austronesian-iroquois-cross.cousinmarriage.permitted

10

Yes

10010000

1000

10000

10000

austronesian-iroquois-cross.cousinmarriage.preferred

10

Yes

10010000

1000

10000

10000

austronesian-iroquois-exogamy.unilineal.descent

10

Yes

10010000

1000

10000

10000

austronesian-iroquois-high.polygyny

10

Yes

10010000

1000

10000

10000

austronesian-iroquois-matri.anvunclocalresidence

10

Yes

10010000

1000

10000

10000

austronesian-iroquois-polygyny

10

Yes

10010000

1000

10000

10000

austronesian-iroquois-uni.linealdescent

10

Yes

10010000

1000

10000

10000

austronesian-iroquois-uni.localresidence

10

Yes

10050000

1000

50000

10000

bantu-crow-matri.anvunclocalresidence

10

Yes

10010000

1000

10000

10000

bantu-crow-matrilineal

10

Yes

10010000

1000

10000

10000

bantu-crow-matrilocal

10

Yes

10050000

1000

50000

10000

bantu-crow-uni.localresidence

10

Yes

10010000

1000

10000

10000

bantu-hawaiian-absenceofcousinmarriage.permitted

10

Yes

10010000

1000

10000

10000

bantu-hawaiian-absenceofcousinmarriage.preference

10

Yes

10010000

1000

10000

10000

bantu-hawaiian-bi.linealdescent

10

Yes

10010000

1000

10000

10000

bantu-hawaiian-bi.localextendedfamily

10

Yes

10010000

1000

10000

10000

bantu-hawaiian-first&secondcousinforbidden

10

Yes

10050000

1000

50000

10000

bantu-hawaiian-bi.localresidence

10

Yes

10010000

1000

10000

10000

bantu-iroquois-cross.cousinmarriage.permitted

10

Yes

10010000

1000

10000

10000

bantu-iroquois-cross.cousinmarriage.preferred

10

Yes

10010000

1000

10000

10000

bantu-iroquois-exogamy.unilineal.descent

10

Yes

10010000

1000

10000

10000

bantu-iroquois-matri.anvunclocalresidence

10

Yes

10010000

1000

10000

10000

bantu-iroquois-uni.linealdescent

10

Yes

10010000

1000

10000

10000

bantu-iroquois-uni.localresidence

10

Yes

10010000

1000

10000

10000

bantu-omaha-matri.anvunclocalresidence

10

Yes

10010000

1000

10000

10000

bantu-omaha-patrilineal

10

Yes

10010000

1000

10000

10000

bantu-omaha-patrilocal

10

Yes

10010000

1000

10000

10000

bantu-omaha-uni.localresidence

10

Yes

10010000

1000

10000

10000

uto-hawaiian-absenceofcousinmarriage.permitted

10

Yes

10010000

1000

10000

10000

uto-hawaiian-absenceofcousinmarriage.preference

10

Yes

10010000

1000

10000

10000

uto-hawaiian-bi.linealdescent

10

Yes

10010000

1000

10000

10000

uto-hawaiian-bi.localextendedfamily

10

Yes

10010000

1000

10000

10000

uto-hawaiian-first&secondcousinforbidden

10

Yes

10010000

1000

10000

10000

uto-hawaiian-bi.localresidence

10

Yes

10010000

1000

10000

10000

uto-iroquois-cross.cousinmarriage.permitted

10

Yes

10010000

1000

10000

10000

uto-iroquois-cross.cousinmarriage.preferred

10

Yes

10010000

1000

10000

10000

uto-iroquois-exogamy.unilineal.descent

10

Yes

10010000

1000

10000

10000

uto-iroquois-high.polygyny

10

Yes

10010000

1000

10000

10000

uto-iroquois-matri.anvunclocalresidence

10

Yes

10010000

1000

10000

10000

uto-iroquois-uni.linealdescent

10

Yes

10010000

1000

10000

10000

uto-iroquois-uni.localresidence

10

Yes

10010000

1000

10000

10000

ie-eskimo-absenceofcousinmarriage.permitted

10

Yes

10010000

1000

10000

10000

ie-eskimo-absenceofcousinmarriage.preference

10

Yes

10010000

1000

10000

10000

ie-eskimo-bi.linealdescent

10

Yes

10010000

1000

10000

10000

ie-eskimo-inheritancetobothsex

10

Yes

10010000

1000

10000

10000

ie-eskimo-monogamy

10

Yes

10010000

1000

10000

10000

ie-eskimo-neo.localresidence

10

Yes

10010000

1000

10000

10000

ie-eskimo-nuclear.families

10

Yes

10010000

1000

10000

10000

ie-eskimo-uni.linealdescent

10

Yes

10010000

1000

10000

10000

ie-hawaiian-absenceofcousinmarriage.permitted

10

Yes

10010000

1000

10000

10000

ie-hawaiian-absenceofcousinmarriage.preference

10

Yes

10010000

1000

10000

10000

ie-hawaiian-bi.linealdescent

10

Yes

10010000

1000

10000

10000

ie-hawaiian-bi.localextendedfamily

10

Yes

10010000

1000

10000

10000

ie-hawaiian-bi.localresidence

10

Yes

10010000

1000

10000

10000

ie-hawaiian-first&secondcousinforbidden

10

Yes

10010000

1000

10000

10000

ie-hawaiian-first&secondcousinforbidden

10

Yes

10010000

1000

10000

10000

ie-eskimo-inheritancetobothsex.restricted

10

Yes

10010000

1000

10000

10000

## MCMC review & Bayes Factors

Here we show the results of MCMC chains and respective tests. The first table for each hypotheses is a review of the MCMC chains. Each row shows the marginal log-likelihood and averaged transition rates for the dependent and independent models for a single chain. There are three MCMC chains run for each hypotheses to ensure the model is reaching the same conclusion each time. The penultimate row shows the mean across the three runs. The final row tests which model was more appropriate for the data. We calculate a Bayes-factor, which compares the log marginal likelihood between the dependent and independent models, as explained in (**???**). Following common practice we interpret Bayes factors of less than two as no support for co-evolution. Between two and five as positive support, between five and ten as strong support and above ten as very strong support.

A second table shows the results of a Gelman-Rubin diagnostic testing, to test for any significant differences between chains (**???**). A value of 1 indicates no difference, and a rule of thumb suggests point-estimates of less than 1.1 indicate negligible differences between chains.

Austronesian : Crow High.polygyny

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-62.369

0.598

0.59

0.435

0.418

0.497

0.468

0.356

0.367

-61.254

0.596

0.631

0.601

0.626

2

-62.689

0.602

0.595

0.473

0.385

0.466

0.472

0.342

0.365

-61.265

0.609

0.63

0.617

0.626

3

-62.621

0.594

0.587

0.415

0.382

0.476

0.5

0.352

0.419

-61.286

0.601

0.62

0.611

0.618

Mean

-62.56

0.598

0.591

0.441

0.395

0.48

0.48

0.35

0.384

-61.268

0.602

0.627

0.61

0.623

BF

-2.23

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1.001

1.002

Independent

1.007

1.008

Austronesian : Crow Matri.anvunclocalresidence

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-70.689

2.005

0.001

2.708

2.263

1.356

1.837

2.028

2.46

-76.921

1.518

19.171

1.571

2.073

2

-70.264

1.988

0.018

2.688

2.261

1.512

2.032

2.2

2.446

-75.832

1.49

18.7

1.543

2.039

3

-70.699

1.997

0.004

2.7

2.287

1.325

1.818

2.07

2.471

-76.481

1.495

18.63

1.557

2.041

Mean

-70.551

1.997

0.008

2.699

2.27

1.398

1.896

2.099

2.459

-76.411

1.501

18.834

1.557

2.051

BF

12.464

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1.001

1.002

Independent

1.001

1.002

Austronesian : Crow Matrilineal

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-54.971

0.029

0.003

0.753

25.7

25.736

25.481

26.098

25.998

-65.046

0.831

5.906

0.83

4.8

2

-55.688

0.038

0.005

0.598

25.963

25.941

25.385

26.186

26.015

-65.203

0.815

5.809

0.816

4.595

3

-55.674

0.039

0.004

0.891

25.498

25.462

25.221

25.901

25.794

-65.892

0.81

5.578

0.809

4.499

Mean

-55.444

0.035

0.004

0.747

25.72

25.713

25.362

26.062

25.936

-65.38

0.819

5.764

0.818

4.631

BF

20.151

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1.003

1.007

Independent

1.001

1.004

Austronesian : Crow Polygyny

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-68.705

3.499

3.288

1.712

1.259

26.294

9.579

12.996

7.033

-67.451

2.099

24.247

3.301

1.778

2

-68.799

3.471

3.293

1.713

1.232

26.339

9.718

13.028

6.977

-67.63

2.121

24.489

3.178

1.759

3

-68.711

3.529

3.301

1.723

1.253

26.507

9.638

12.928

6.971

-67.578

2.09

24.236

3.29

1.774

Mean

-68.738

3.5

3.294

1.716

1.248

26.38

9.645

12.984

6.994

-67.553

2.103

24.324

3.256

1.77

BF

-2.509

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1.000

Independent

1

1.001

Austronesian : Crow Matrilocal

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-47.68

0.05

0.034

3.197

19.97

19.132

13.441

20.535

20.154

-50.737

0.425

1.234

0.425

1.144

2

-48.203

0.073

0.066

3.346

18.897

18.154

12.646

19.531

18.918

-50.628

0.43

1.382

0.43

1.282

3

-47.952

0.055

0.043

3.591

19.274

18.417

13.065

19.954

19.524

-50.718

0.43

1.418

0.429

1.269

Mean

-47.945

0.059

0.048

3.378

19.38

18.568

13.051

20.007

19.532

-50.694

0.428

1.345

0.428

1.232

BF

6.114

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1.001

1.002

Independent

1.000

1.000

Austronesian : Crow Uni.localresidence

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-80.295

3.554

0.002

3.291

2.533

3.704

3.482

5.586

0.909

-83.262

2.62

29.298

3.464

3.465

2

-80.644

3.61

0.003

3.343

2.517

3.662

3.388

5.358

0.887

-83.358

2.595

29.095

3.555

3.554

3

-80.738

3.624

0.005

3.375

2.561

3.724

3.508

5.54

0.911

-84.408

2.604

29.252

3.498

3.498

Mean

-80.559

3.596

0.003

3.336

2.537

3.697

3.459

5.495

0.902

-83.676

2.606

29.215

3.506

3.506

BF

5.932

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1.000

1.001

Independent

1.001

1.003

Austronesian : Eskimo Absenceofcousinmarriage.permitted

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-79.508

17.212

2.843

4.475

0.555

6.771

8.987

4.507

7.653

-79.276

0.399

3.764

16.2

5.685

2

-79.522

17.302

2.856

4.458

0.544

6.833

8.987

4.51

7.721

-79.281

0.4

3.762

16.016

5.586

3

-79.16

17.177

2.813

4.509

0.547

6.69

9.16

4.588

7.782

-79.368

0.401

3.791

16.151

5.625

Mean

-79.397

17.23

2.837

4.481

0.549

6.765

9.045

4.535

7.719

-79.308

0.4

3.772

16.122

5.632

BF

-0.465

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1

Independent

1

1

Austronesian : Eskimo Absenceofcousinmarriage.preference

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-70.788

5.077

0.566

21.49

1.762

3.671

1.501

15.58

16.282

-69.578

0.414

3.836

4.427

22.76

2

-70.685

5.081

0.542

21.585

1.777

3.646

1.543

15.334

16.426

-69.833

0.404

3.806

4.379

22.617

3

-70.767

5.119

0.54

21.53

1.714

3.632

1.515

15.506

16.188

-69.704

0.402

3.804

4.383

22.559

Mean

-70.747

5.092

0.549

21.535

1.751

3.65

1.52

15.473

16.299

-69.705

0.407

3.815

4.396

22.645

BF

-2.419

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1

Independent

1

1

Austronesian : Eskimo Bi.linealdescent

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-90.796

3.344

0.47

3.578

0.096

3.455

0.689

2.962

2.707

-88.847

0.023

2.854

2.784

2.867

2

-91.31

3.303

0.478

3.545

0.062

3.442

0.683

2.772

2.779

-89.238

0.027

2.864

2.781

2.884

3

-90.53

3.335

0.492

3.561

0.061

3.45

0.696

2.788

2.762

-89.294

0.016

2.856

2.795

2.872

Mean

-90.879

3.327

0.48

3.561

0.073

3.449

0.689

2.841

2.749

-89.126

0.022

2.858

2.787

2.874

BF

-3.899

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1.001

1.001

Independent

1.013

1.022

Austronesian : Eskimo Monogamy

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-69.397

0.029

0.001

7.018

0.521

0.592

7.394

7.247

7.273

-74.416

0.431

1.67

1.555

1.628

2

-68.392

0.049

0.002

6.854

0.665

0.727

7.327

7.187

7.197

-74.04

0.439

1.666

1.547

1.632

3

-69.269

0.036

0.002

6.935

0.583

0.67

7.354

7.198

7.213

-74.053

0.429

1.672

1.556

1.625

Mean

-69.019

0.038

0.002

6.936

0.59

0.663

7.358

7.211

7.228

-74.17

0.433

1.669

1.553

1.628

BF

10.04

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1.001

1.002

Independent

1.001

1.002

Austronesian : Eskimo Neo.localresidence

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-50.333

0.287

0.3

11.559

10.432

3.207

3.409

11.184

13.452

-51.09

0.285

3.471

0.568

8.816

2

-50.058

0.283

0.301

11.449

10.594

3.265

3.377

11.128

13.557

-51.11

0.291

3.49

0.572

8.873

3

-50.307

0.287

0.296

11.476

10.705

3.207

3.392

11.207

13.455

-51.222

0.289

3.476

0.581

8.983

Mean

-50.233

0.286

0.299

11.495

10.577

3.226

3.393

11.173

13.488

-51.141

0.288

3.479

0.574

8.891

BF

1.513

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1.000

1.000

Independent

1.001

1.003

Austronesian : Eskimo Inheritancetobothsex.restricted

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-54.276

2.83

0.008

5.225

3.409

1.636

4.308

4.602

5.017

-57.776

1.353

2.173

2.054

2.243

2

-54.57

2.771

0.008

5.371

3.418

1.677

4.538

4.74

5.196

-57.908

1.352

2.168

2.05

2.249

3

-54.751

2.713

0.008

5.358

3.311

1.617

4.553

4.79

5.236

-58.016

1.365

2.19

2.055

2.276

Mean

-54.532

2.771

0.008

5.318

3.379

1.643

4.466

4.711

5.15

-57.9

1.357

2.177

2.053

2.256

BF

7

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1.000

1.000

Independent

1.001

1.002

Austronesian : Eskimo Nuclear.families

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-88.016

3.707

0.002

3.691

3.443

3.013

3.363

3.423

3.607

-87.216

0.042

3.33

3.349

3.344

2

-88.268

3.714

0.002

3.694

3.448

3.018

3.371

3.442

3.615

-87.677

0.035

3.322

3.34

3.33

3

-87.584

3.72

0.002

3.695

3.435

3.027

3.372

3.41

3.618

-86.673

0.042

3.34

3.358

3.35

Mean

-87.956

3.714

0.002

3.693

3.442

3.019

3.369

3.425

3.613

-87.189

0.04

3.331

3.349

3.341

BF

-1.601

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1.000

1.001

Independent

1.004

1.008

Austronesian : Eskimo Uni.linealdescent

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-83.952

2.859

0.31

2.966

0.094

3.016

0.46

3.194

2.737

-84.789

0.069

2.652

2.216

2.643

2

-85.021

2.917

0.277

2.998

0.085

3.057

0.427

3.16

2.804

-84.345

0.083

2.653

2.186

2.647

3

-83.308

2.85

0.291

2.968

0.113

3.027

0.463

3.274

2.754

-86.124

0.092

2.671

2.138

2.67

Mean

-84.094

2.875

0.293

2.977

0.097

3.033

0.45

3.209

2.765

-85.086

0.081

2.659

2.18

2.653

BF

1.674

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1.002

1.005

Independent

1.006

1.012

Austronesian : Hawaiian Absenceofcousinmarriage.permitted

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-103.568

3.145

5.599

1.904

6.869

6.466

6.919

6.858

4.581

-104.165

10.021

9.989

10.458

4.301

2

-102.917

3.246

5.661

2.05

6.943

6.545

6.978

6.919

4.504

-104.031

10.049

10.023

10.515

4.333

3

-103.157

3.047

5.497

1.774

6.775

6.471

6.81

6.754

4.688

-104.176

10.188

10.156

10.773

4.376

Mean

-103.214

3.146

5.586

1.909

6.862

6.494

6.902

6.844

4.591

-104.124

10.086

10.056

10.582

4.337

BF

1.195

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1.001

Independent

1

1.000

Austronesian : Hawaiian Absenceofcousinmarriage.preference

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-94.106

11.891

12.711

12.753

12.21

12.397

0.102

12.859

12.907

-94.813

11.095

11.088

4.613

23.603

2

-93.864

11.936

12.651

13.038

12.234

12.262

0.152

13.153

13.065

-94.997

10.647

10.643

4.583

23.521

3

-93.762

11.766

12.583

12.783

12.19

12.265

0.119

12.956

13.013

-95.213

10.921

10.916

4.599

23.514

Mean

-93.911

11.864

12.648

12.858

12.211

12.308

0.124

12.989

12.995

-95.008

10.888

10.882

4.598

23.546

BF

1.414

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1.002

1.003

Independent

1.000

1.001

Austronesian : Hawaiian Bi.linealdescent

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-114.801

1.07

6.139

5.957

6.333

6.838

6.243

5.337

5.988

-115.672

4.647

4.645

4.578

4.61

2

-114.664

0.883

6.146

5.756

6.249

6.694

6.176

5.43

5.908

-115.645

4.627

4.625

4.54

4.572

3

-114.726

0.694

6.032

5.553

6.133

6.499

6.06

5.486

5.809

-115.653

4.561

4.559

4.496

4.536

Mean

-114.73

0.882

6.106

5.755

6.238

6.677

6.16

5.418

5.902

-115.657

4.612

4.61

4.538

4.573

BF

1.741

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1.001

Independent

1

1.000

Austronesian : Hawaiian Bi.localextendedfamily

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-115.025

3.462

6.387

5.612

8.09

6.717

7.347

7.748

7.133

-112.373

5.853

5.851

5.837

5.843

2

-114.787

3.015

6.447

5.193

7.867

6.745

7.377

7.57

7.108

-112.409

5.834

5.831

5.83

5.835

3

-114.946

2.873

6.398

5.159

7.796

6.718

7.321

7.463

7.03

-112.385

5.875

5.871

5.866

5.873

Mean

-114.919

3.117

6.411

5.321

7.918

6.727

7.348

7.594

7.09

-112.389

5.854

5.851

5.844

5.85

BF

-5.303

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1.002

Independent

1

1.000

Austronesian : Hawaiian Bi.localresidence

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-103.465

6.047

15.787

13.139

12.354

15.697

2.524

9.715

16.854

-100.34

10.545

10.541

4.644

23.336

2

-103.184

5.748

15.579

13.037

12.268

15.453

2.722

9.832

16.771

-101.264

10.289

10.286

4.645

23.422

3

-102.074

5.763

15.812

12.792

12.275

15.728

2.704

9.537

16.853

-100.666

10.272

10.267

4.628

23.348

Mean

-102.908

5.853

15.726

12.989

12.299

15.626

2.65

9.695

16.826

-100.757

10.369

10.365

4.639

23.369

BF

-6.249

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1.000

1.001

Independent

1.001

1.002

Austronesian : Iroquois Cross.cousinmarriage.permitted

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-69.605

2.263

0.368

16.051

15.89

4.522

5.739

6.188

13.738

-73.423

1.171

2.907

1.171

3.402

2

-70.348

2.413

0.331

16.949

15.373

4.503

5.389

5.878

13.482

-73.686

1.182

2.913

1.181

3.345

3

-69.288

2.276

0.368

16.337

15.743

4.69

6.06

6.049

13.747

-73.654

1.148

2.778

1.147

3.262

Mean

-69.747

2.317

0.356

16.446

15.669

4.572

5.729

6.038

13.656

-73.588

1.167

2.866

1.166

3.336

BF

7.634

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1.001

Independent

1

1.000

Austronesian : Iroquois Cross.cousinmarriage.preferred

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-89.271

4.051

0.001

4.056

4.04

2.799

3.514

3.148

4.025

-95.949

2.224

8.119

9.97

9.972

2

-89.27

4.064

0

4.068

4.052

2.817

3.555

3.139

4.046

-96.033

2.267

8.315

10.069

10.074

3

-88.333

4.041

0

4.042

4.033

2.8

3.532

3.144

4.03

-96.255

2.254

8.212

10.171

10.174

Mean

-88.958

4.052

0

4.055

4.042

2.805

3.534

3.144

4.034

-96.079

2.248

8.215

10.07

10.073

BF

13.355

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1.001

Independent

1

1.000

Austronesian : Iroquois Exogamy.unilineal.descent

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-56.276

0.603

0.665

2.175

2.609

0.905

0.887

1.506

2.585

-55.028

0.618

0.761

0.613

1.554

2

-56.533

0.614

0.638

2.123

2.664

0.83

0.761

1.324

2.62

-55.125

0.617

0.77

0.614

1.603

3

-56.537

0.615

0.658

2.225

2.822

0.88

0.863

1.467

2.83

-54.79

0.616

0.795

0.612

1.625

Mean

-56.449

0.611

0.654

2.174

2.698

0.872

0.837

1.432

2.678

-54.981

0.617

0.775

0.613

1.594

BF

-2.498

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1.001

1.003

Independent

1.000

1.001

Austronesian : Iroquois High.polygyny

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-71.032

0.66

0.54

7.624

4.862

1.585

7.201

7.383

7.657

-69.358

0.928

1.245

0.929

1.258

2

-71.246

0.719

0.608

6.616

4.423

1.579

6.111

6.449

6.556

-69.249

0.935

1.312

0.935

1.322

3

-70.397

0.781

0.667

5.993

3.969

1.812

5.588

5.709

5.956

-69.33

0.935

1.286

0.935

1.303

Mean

-70.892

0.72

0.605

6.744

4.418

1.659

6.3

6.514

6.723

-69.312

0.933

1.281

0.933

1.294

BF

-3.347

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1.001

Independent

1

1.000

Austronesian : Iroquois Matri.anvunclocalresidence

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-84.634

1.777

0.971

1.874

1.625

1.617

0.221

1.077

0.628

-84.295

1.262

1.478

1.267

1.491

2

-84.71

1.779

0.956

1.86

1.625

1.614

0.224

0.983

0.578

-84.284

1.265

1.467

1.269

1.484

3

-84.928

1.756

0.975

1.815

1.602

1.591

0.22

0.915

0.517

-84.29

1.265

1.48

1.271

1.486

Mean

-84.757

1.771

0.967

1.85

1.617

1.607

0.222

0.992

0.574

-84.29

1.264

1.475

1.269

1.487

BF

-0.678

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1.001

Independent

1

1.000

Austronesian : Iroquois Polygyny

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-75.66

0.773

0.146

1.163

1.163

0.606

0.885

0.843

1.136

-75.768

1.086

1.104

1.089

1.087

2

-76.132

0.771

0.14

1.161

1.161

0.624

0.892

0.842

1.134

-75.775

1.091

1.106

1.092

1.093

3

-75.959

0.765

0.133

1.164

1.164

0.609

0.889

0.852

1.135

-75.771

1.089

1.106

1.087

1.09

Mean

-75.917

0.77

0.14

1.163

1.163

0.613

0.889

0.846

1.135

-75.771

1.089

1.105

1.089

1.09

BF

0.217

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1.000

1.000

Independent

1.001

1.003

Austronesian : Iroquois Uni.linealdescent

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-90.088

2.195

0.111

3.159

3.455

2.236

2.837

2.908

3.386

-91.098

1.482

1.602

1.49

1.61

2

-89.454

2.157

0.12

3.188

3.454

2.287

2.893

2.939

3.375

-91.07

1.48

1.627

1.489

1.631

3

-90.644

2.147

0.118

3.154

3.542

2.375

2.974

3.023

3.446

-91.105

1.475

1.607

1.481

1.611

Mean

-90.062

2.166

0.116

3.167

3.484

2.299

2.901

2.957

3.402

-91.091

1.479

1.612

1.487

1.617

BF

2.022

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1.000

1.001

Independent

1.001

1.002

Austronesian : Iroquois Uni.localresidence

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-91.308

3.107

0.009

3.107

3.089

2.059

2.628

2.765

3.083

-93.127

1.134

2.882

2.885

2.884

2

-90.397

3.107

0.011

3.105

3.086

2.106

2.654

2.755

3.081

-93.345

1.131

2.88

2.913

2.91

3

-90.488

3.102

0.015

3.103

3.075

2.071

2.63

2.756

3.065

-92.745

1.149

2.862

2.88

2.883

Mean

-90.731

3.105

0.012

3.105

3.083

2.079

2.637

2.759

3.076

-93.072

1.138

2.875

2.893

2.892

BF

3.637

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1.000

Independent

1

1.001

Bantu : Crow Matri.anvunclocalresidence

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-67.638

2.578

0.089

2.582

2.345

2.079

2.256

2.798

3.354

-68.086

1.566

17.046

6.198

6.438

2

-68.188

2.538

0.103

2.555

2.333

2.204

2.437

2.979

3.468

-68.711

1.568

17.258

6.286

6.525

3

-67.908

2.557

0.089

2.552

2.337

2.11

2.207

2.719

3.361

-67.8

1.57

17.228

5.995

6.253

Mean

-67.911

2.558

0.094

2.563

2.338

2.131

2.3

2.832

3.394

-68.199

1.568

17.177

6.16

6.405

BF

0.897

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1.001

Independent

1

1.001

Bantu : Crow Matrilineal

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-66.04

2.145

0.365

2.593

2.179

5.275

3.998

4.743

4.621

-66.264

1.354

14.363

2.559

2.879

2

-66.204

2.165

0.353

2.613

2.208

4.904

3.879

4.593

4.443

-66.316

1.322

13.89

2.459

2.784

3

-66.366

2.196

0.324

2.603

2.229

4.799

3.58

4.37

4.406

-65.72

1.374

14.563

2.526

2.841

Mean

-66.203

2.169

0.347

2.603

2.205

4.993

3.819

4.569

4.49

-66.1

1.35

14.272

2.515

2.835

BF

0.447

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1.000

1.001

Independent

1.001

1.002

Bantu : Crow Matrilocal

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-39.476

0.44

0.45

3.908

3.115

3.85

3.14

3.978

3.838

-38.169

0.679

6.041

0.679

6.097

2

-39.103

0.47

0.459

3.328

2.235

3.142

2.192

2.85

2.894

-36.892

0.694

6.324

0.694

6.376

3

-40.354

0.473

0.462

3.686

2.843

3.632

2.662

3.736

3.628

-37.782

0.635

5.258

0.635

5.332

Mean

-39.644

0.461

0.457

3.641

2.731

3.541

2.665

3.521

3.453

-37.614

0.669

5.874

0.669

5.935

BF

-2.613

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1.002

1.004

Independent

1.001

1.002

Bantu : Crow Uni.localresidence

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-48.038

0.454

0.363

0.591

0.592

0.525

0.541

0.715

0.622

-47.094

0.619

1.065

0.92

0.62

2

-48.377

0.457

0.387

0.592

0.598

0.629

0.583

0.807

0.719

-47.099

0.613

1.05

0.876

0.616

3

-48.105

0.506

0.394

0.599

0.6

0.672

0.64

0.836

0.749

-47.003

0.612

1.058

0.877

0.614

Mean

-48.173

0.472

0.381

0.594

0.597

0.609

0.588

0.786

0.697

-47.065

0.615

1.058

0.891

0.617

BF

-1.888

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1.001

1.002

Independent

1.000

1.001

Bantu : Hawaiian Absenceofcousinmarriage.permitted

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-56.076

0.634

0.502

0.819

0.818

0.444

0.49

0.566

0.724

-54.82

0.813

0.818

0.816

0.813

2

-56.289

0.638

0.486

0.818

0.818

0.432

0.49

0.567

0.718

-54.767

0.816

0.836

0.833

0.816

3

-56.211

0.635

0.492

0.819

0.818

0.43

0.471

0.555

0.723

-54.841

0.812

0.819

0.821

0.813

Mean

-56.192

0.636

0.493

0.819

0.818

0.435

0.484

0.563

0.722

-54.809

0.814

0.824

0.823

0.814

BF

-2.511

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1

Independent

1

1

Bantu : Hawaiian Absenceofcousinmarriage.preference

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-54.678

0.797

0.796

0.652

0.312

0.412

0.182

0.617

0.579

-55.109

0.78

0.893

0.779

0.954

2

-55.43

0.796

0.795

0.616

0.307

0.417

0.19

0.619

0.574

-55.16

0.779

0.893

0.779

0.942

3

-54.583

0.797

0.797

0.635

0.31

0.417

0.181

0.628

0.582

-55.186

0.779

0.882

0.779

0.925

Mean

-54.897

0.797

0.796

0.634

0.31

0.415

0.184

0.621

0.578

-55.152

0.779

0.889

0.779

0.94

BF

0.862

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1

Independent

1

1

Bantu : Hawaiian Bi.linealdescent

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-61.391

0.886

0.877

0.879

0.745

0.858

0.633

0.554

0.565

-59.655

0.928

1.342

0.928

1.368

2

-61.68

0.896

0.866

0.945

0.8

0.835

0.655

0.602

0.674

-59.648

0.929

1.37

0.929

1.386

3

-60.881

0.918

0.87

1.049

0.924

0.859

0.678

0.731

0.746

-59.747

0.936

1.424

0.936

1.446

Mean

-61.317

0.9

0.871

0.958

0.823

0.851

0.655

0.629

0.662

-59.683

0.931

1.379

0.931

1.4

BF

-3.473

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1.000

Independent

1

1.001

Bantu : Hawaiian Bi.localextendedfamily

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-75.898

2.966

1.158

5.859

2.805

3.269

3.614

3.895

4.868

-74.228

1.94

4.266

2.028

4.279

2

-75.305

3.257

1.058

6.552

3.167

3.422

3.902

4.345

5.613

-74.508

1.936

4.309

2.042

4.319

3

-75.599

3.534

0.98

7.374

3.553

3.686

4.298

5.059

6.375

-74.55

1.873

3.969

1.95

3.99

Mean

-75.601

3.252

1.065

6.595

3.175

3.459

3.938

4.433

5.619

-74.429

1.916

4.181

2.007

4.196

BF

-3.341

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1.003

1.011

Independent

1.000

1.002

Bantu : Hawaiian Bi.localresidence

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-51.207

0.717

0.717

0.407

0.252

0.51

0.202

0.508

0.509

-51.27

0.684

0.69

0.684

0.693

2

-51.062

0.719

0.719

0.396

0.25

0.523

0.198

0.509

0.512

-51.271

0.682

0.69

0.682

0.693

3

-51.283

0.72

0.721

0.413

0.25

0.524

0.203

0.506

0.503

-51.235

0.685

0.698

0.685

0.699

Mean

-51.184

0.719

0.719

0.405

0.251

0.519

0.201

0.508

0.508

-51.259

0.684

0.693

0.684

0.695

BF

0.127

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1.000

Independent

1

1.001

Bantu : Iroquois Cross.cousinmarriage.permitted

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-73.224

0.058

1.422

0.896

1.293

1.754

1.743

1.719

1.522

-75.395

1.593

1.608

1.469

2.097

2

-73.879

0.056

1.434

0.898

1.301

1.764

1.746

1.723

1.531

-74.917

1.57

1.587

1.456

2.1

3

-73.213

0.044

1.423

0.868

1.279

1.752

1.735

1.715

1.498

-74.844

1.57

1.587

1.461

2.123

Mean

-73.439

0.053

1.426

0.887

1.291

1.757

1.741

1.719

1.517

-75.052

1.578

1.594

1.462

2.107

BF

4.342

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1.001

Independent

1

1.001

Bantu : Iroquois Cross.cousinmarriage.preferred

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-83.128

1.493

1.619

5.821

5.223

4.4

5.617

3.66

2.469

-84.598

2.512

2.529

2.529

2.53

2

-83.355

1.388

1.431

5.517

4.94

4.256

5.348

3.437

2.528

-84.593

2.533

2.549

2.555

2.553

3

-83.315

1.43

1.592

5.569

5.003

4.432

5.424

3.495

2.533

-84.627

2.52

2.529

2.531

2.528

Mean

-83.266

1.437

1.547

5.636

5.055

4.363

5.463

3.531

2.51

-84.606

2.522

2.536

2.538

2.537

BF

2.94

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1.001

Independent

1

1.001

Bantu : Iroquois Exogamy.unilineal.descent

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-71.982

1.718

1.248

1.863

1.59

1.799

1.46

0.99

1.819

-71.213

1.723

1.741

1.576

2.501

2

-72.769

1.817

1.385

1.999

1.748

1.931

1.444

1.098

1.927

-70.627

1.747

1.757

1.578

2.537

3

-71.796

1.827

1.372

1.999

1.731

1.933

1.443

1.095

1.897

-70.834

1.708

1.722

1.57

2.48

Mean

-72.182

1.787

1.335

1.954

1.69

1.888

1.449

1.061

1.881

-70.891

1.726

1.74

1.575

2.506

BF

-1.539

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1.001

1.003

Independent

1.000

1.000

Bantu : Iroquois Matri.anvunclocalresidence

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-87.586

0.845

2.727

3.681

3.595

3.577

3.774

2.68

2.945

-89.436

2.505

2.509

2.503

2.524

2

-87.682

0.775

2.737

3.661

3.63

3.527

3.808

2.749

2.985

-89.464

2.51

2.517

2.511

2.528

3

-87.416

0.783

2.707

3.622

3.565

3.519

3.778

2.701

2.914

-89.397

2.503

2.509

2.505

2.524

Mean

-87.561

0.801

2.724

3.655

3.597

3.541

3.787

2.71

2.948

-89.432

2.506

2.512

2.506

2.525

BF

3.7

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1.001

Independent

1

1.001

Bantu : Iroquois Uni.linealdescent

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-81.009

1.281

0.91

1.487

1.615

1.565

1.684

1.707

1.506

-78.803

1.616

1.625

1.777

1.517

2

-80.949

1.203

0.856

1.457

1.591

1.474

1.628

1.691

1.516

-78.83

1.599

1.603

1.744

1.511

3

-81.043

1.168

0.831

1.431

1.561

1.446

1.604

1.661

1.512

-78.834

1.606

1.616

1.796

1.519

Mean

-81

1.217

0.866

1.458

1.589

1.495

1.639

1.686

1.511

-78.822

1.607

1.615

1.772

1.516

BF

-4.413

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1.000

Independent

1

1.001

Bantu : Iroquois Uni.localresidence

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-73.838

0.729

0.751

0.974

1.417

1.28

1.334

1.567

1.422

-72.652

1.354

1.367

1.395

1.313

2

-74.152

0.761

0.758

0.991

1.445

1.31

1.328

1.584

1.421

-72.636

1.351

1.367

1.393

1.311

3

-74.48

0.748

0.771

0.997

1.437

1.293

1.347

1.579

1.415

-72.634

1.356

1.369

1.387

1.311

Mean

-74.157

0.746

0.76

0.987

1.433

1.294

1.336

1.577

1.419

-72.641

1.354

1.368

1.392

1.312

BF

-2.372

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1

Independent

1

1

Bantu : Omaha Matri.anvunclocalresidence

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-71.612

1.451

2.943

3.266

0.007

3.385

0.298

1.894

3.109

-76.23

1.411

6.036

4.486

4.835

2

-71.629

1.529

2.964

3.347

0.008

3.5

0.297

1.992

3.189

-76.055

1.372

5.665

4.356

4.717

3

-71.979

1.464

2.968

3.329

0.004

3.442

0.283

1.932

3.173

-76.018

1.393

5.901

4.408

4.746

Mean

-71.74

1.481

2.958

3.314

0.006

3.442

0.293

1.939

3.157

-76.101

1.392

5.867

4.417

4.766

BF

9.234

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1

Independent

1

1

Bantu : Omaha Patrilineal

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-73.797

2.7

0.004

2.571

2.674

1.403

1.965

2.301

2.674

-76.938

1.619

8.666

7.673

7.689

2

-73.435

2.697

0.005

2.581

2.674

1.428

2.01

2.306

2.682

-76.993

1.638

8.825

7.813

7.837

3

-73.136

2.673

0.004

2.555

2.659

1.398

1.945

2.289

2.66

-77.002

1.612

8.802

7.853

7.873

Mean

-73.456

2.69

0.004

2.569

2.669

1.41

1.973

2.299

2.672

-76.978

1.623

8.764

7.78

7.8

BF

6.282

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1.001

Independent

1

1.000

Bantu : Omaha Patrilocal

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-71.037

2.985

0

3.026

2.946

2.534

2.701

2.501

0.65

-77.163

1.849

11.241

9.874

9.92

2

-70.765

2.991

0.001

3.056

2.948

2.537

2.715

2.527

0.623

-77.113

1.84

11.32

10.13

10.171

3

-70.961

2.973

0

3.031

2.933

2.498

2.668

2.471

0.67

-77.213

1.825

11.23

9.928

9.973

Mean

-70.921

2.983

0

3.038

2.942

2.523

2.695

2.5

0.648

-77.163

1.838

11.264

9.977

10.021

BF

12.251

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1

Independent

1

1

Bantu : Omaha Uni.localresidence

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-54.633

0.512

0.218

0.768

0.768

0.545

0.641

0.639

0.32

-54.368

0.756

0.937

0.913

0.757

2

-54.805

0.499

0.223

0.768

0.768

0.527

0.634

0.625

0.325

-54.412

0.765

1.005

0.983

0.765

3

-54.668

0.504

0.226

0.767

0.767

0.536

0.625

0.636

0.33

-54.475

0.764

1.005

0.983

0.764

Mean

-54.702

0.505

0.222

0.768

0.768

0.536

0.633

0.633

0.325

-54.418

0.762

0.982

0.96

0.762

BF

-0.531

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1.001

Independent

1

1.001

Uto : Hawaiian Absenceofcousinmarriage.permitted

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-15.093

15.323

15.927

9.33

13.266

11.164

14.836

23.662

23.878

-14.521

21.555

22.037

21.764

22.058

2

-14.98

15.237

16.042

9.501

13.14

11.398

15.347

23.794

24.028

-14.529

21.533

22.078

21.801

22.062

3

-14.78

15.153

15.767

9.528

13.293

11.428

15.43

23.722

23.93

-14.51

22.089

22.573

22.258

22.576

Mean

-14.951

15.238

15.912

9.453

13.233

11.33

15.204

23.726

23.945

-14.52

21.726

22.229

21.941

22.232

BF

-1.144

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1.000

Independent

1

1.001

Uto : Hawaiian Absenceofcousinmarriage.preference

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-15.238

7.454

11.044

11.548

13.131

18.169

18.188

9.781

11.407

-14.662

17.193

17.662

17.532

17.482

2

-15.285

7.629

11.292

11.724

13.232

18.406

18.488

9.79

11.307

-14.792

17.138

17.534

17.422

17.358

3

-15.394

7.712

11.293

11.758

13.394

18.445

18.538

9.801

11.41

-15.238

16.993

17.495

17.384

17.304

Mean

-15.306

7.598

11.21

11.677

13.252

18.34

18.405

9.791

11.375

-14.897

17.108

17.564

17.446

17.381

BF

-1.153

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1

Independent

1

1

Uto : Hawaiian Bi.linealdescent

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-15.411

7.719

12.174

13.401

15.481

20.973

20.623

10.507

12.133

-15.433

18.618

19.364

19.005

19.023

2

-15.416

7.493

12.136

13.189

15.421

20.932

20.512

10.551

12.2

-15.283

18.464

19.133

18.808

18.857

3

-15.275

7.476

12.109

13.337

15.462

20.949

20.564

10.408

12.073

-15.341

18.449

19.115

18.807

18.843

Mean

-15.367

7.563

12.14

13.309

15.455

20.951

20.566

10.489

12.135

-15.352

18.51

19.204

18.873

18.908

BF

0.045

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1.000

Independent

1

1.001

Uto : Hawaiian Bi.localextendedfamily

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-34.559

54.139

38.497

50.312

35.084

51.038

60.355

39.414

46.133

-33.044

51.27

52.76

52.877

52.477

2

-35.039

48.922

34.303

45.169

32.689

47.497

53.968

34.712

39.627

-33.098

51.708

53.01

53.125

52.662

3

-34.405

48.899

33.785

44.805

32.892

47.522

53.614

34.395

39.069

-33.121

51.568

52.946

53.098

52.729

Mean

-34.668

50.653

35.528

46.762

33.555

48.686

55.979

36.174

41.61

-33.088

51.515

52.905

53.033

52.623

BF

-3.029

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1.026

1.087

Independent

1.000

1.000

Uto : Hawaiian Bi.localresidence

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-22.208

8.802

14.818

16.336

19.67

26.074

26.158

13.874

16.292

-22.114

23.492

24.256

24.156

24.002

2

-22.345

8.687

14.968

16.088

18.9

25.828

25.834

13.569

16.145

-22.057

23.335

23.964

23.903

23.689

3

-22.004

8.683

14.952

16.332

19.31

26.201

26.235

13.852

16.089

-22.314

23.545

24.27

24.229

24.05

Mean

-22.186

8.724

14.913

16.252

19.293

26.034

26.076

13.765

16.175

-22.162

23.457

24.163

24.096

23.914

BF

-0.187

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1.001

Independent

1

1.001

Uto : Iroquois Cross.cousinmarriage.permitted

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-12.543

13.655

13.606

8.74

6.747

7.907

5.762

8.891

8.594

-12.258

13.147

13.074

13.145

13.08

2

-12.461

13.578

13.534

8.863

6.723

7.718

5.808

8.893

8.566

-12.188

13.034

13.005

13.048

12.991

3

-12.575

13.727

13.747

8.916

6.881

7.915

5.899

8.813

8.655

-12.096

13.026

12.952

13.022

12.98

Mean

-12.526

13.653

13.629

8.84

6.784

7.847

5.823

8.866

8.605

-12.181

13.069

13.01

13.072

13.017

BF

-0.569

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1.000

1.001

Independent

1.001

1.002

Uto : Iroquois Cross.cousinmarriage.preferred

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-14.306

18.801

18.676

11.871

8.753

10.483

7.587

12.106

11.818

-14.059

17.479

17.386

17.545

17.379

2

-14.142

18.831

18.694

11.948

8.708

10.518

7.708

12.156

11.94

-14.236

17.376

17.311

17.432

17.312

3

-14.63

18.545

18.389

11.616

8.613

10.319

7.499

11.981

11.633

-14.618

17.569

17.517

17.66

17.512

Mean

-14.359

18.726

18.586

11.812

8.691

10.44

7.598

12.081

11.797

-14.304

17.475

17.405

17.546

17.401

BF

-0.493

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1.001

1.002

Independent

1.000

1.001

Uto : Iroquois Exogamy.unilineal.descent

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-11.011

13.568

13.531

8.831

6.644

7.709

5.837

8.777

8.613

-10.841

12.908

12.832

12.885

12.833

2

-11.054

13.569

13.547

8.642

6.728

7.787

5.745

8.873

8.511

-10.791

12.984

12.902

12.94

12.913

3

-11.191

13.529

13.52

8.775

6.82

7.848

5.75

8.675

8.396

-10.626

12.91

12.848

12.905

12.861

Mean

-11.085

13.555

13.533

8.749

6.731

7.781

5.777

8.775

8.507

-10.753

12.934

12.861

12.91

12.869

BF

-0.34

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1

Independent

1

1

Uto : Iroquois High.polygyny

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-20.347

25.487

18.389

18.424

15.983

14.2

21.67

15.331

20.815

-19.029

23.549

23.523

23.806

23.522

2

-20.105

25.617

18.426

18.276

16.346

14.253

21.516

15.206

20.933

-19.185

23.411

23.342

23.653

23.325

3

-19.767

25.766

18.326

18.365

16.326

14.254

21.543

15.248

20.941

-19.029

23.633

23.558

23.848

23.57

Mean

-20.073

25.623

18.38

18.355

16.218

14.236

21.576

15.262

20.896

-19.081

23.531

23.474

23.769

23.472

BF

-2.635

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1.001

Independent

1

1.001

Uto : Iroquois Matri.anvunclocalresidence

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-25.058

36.654

35.441

36.896

11.178

13.578

12.4

23.071

22.762

-25.177

31.051

31.091

31.413

31.44

2

-25.346

35.888

34.781

36.108

11.259

13.312

11.807

22.297

21.998

-25.272

30.723

30.716

31.072

31.091

3

-25.621

35.5

34.529

35.747

11.275

13.219

11.982

21.869

21.377

-25.243

30.997

31.009

31.357

31.416

Mean

-25.342

36.014

34.917

36.25

11.237

13.37

12.063

22.412

22.046

-25.231

30.924

30.939

31.281

31.316

BF

0.238

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1.001

Independent

1

1.001

Uto : Iroquois Uni.linealdescent

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-12.711

19.161

7.038

15.663

17.425

10.842

12.745

8.584

8.608

-12.497

15.065

15.051

15.168

14.996

2

-12.928

19.005

7

15.62

17.202

10.926

12.59

8.466

8.552

-12.259

15.156

15.123

15.237

15.069

3

-12.532

19.053

6.834

15.9

17.307

11.083

12.46

8.164

8.088

-12.364

14.957

14.897

15.012

14.86

Mean

-12.724

19.073

6.957

15.728

17.311

10.95

12.598

8.405

8.416

-12.373

15.059

15.024

15.139

14.975

BF

-0.428

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1.001

Independent

1

1.001

Uto : Iroquois Uni.localresidence

Dependent

Independent

run

MLL

q12

q13

q21

q24

q31

q34

q42

q43

MLL

alpha1

beta1

alpha2

beta2

1

-25.946

36.328

10.751

39.613

37.319

24.447

25.634

13.011

12.472

-25.969

33.235

33.197

33.461

33.695

2

-25.702

36.719

10.47

39.864

37.596

24.525

25.557

12.955

12.698

-25.927

33.446

33.469

33.777

34.034

3

-25.622

36.423

10.801

39.566

37.294

24.564

25.241

13.228

12.537

-26.023

33.492

33.47

33.786

34.093

Mean

-25.757

36.49

10.674

39.681

37.403

24.512

25.477

13.065

12.569

-25.973

33.391

33.379

33.675

33.941

BF

0.046

Gelman-Rubin MCMC chain diagnostic test

Point est.

Upper C.I.

Dependent

1

1

Independent

1

1

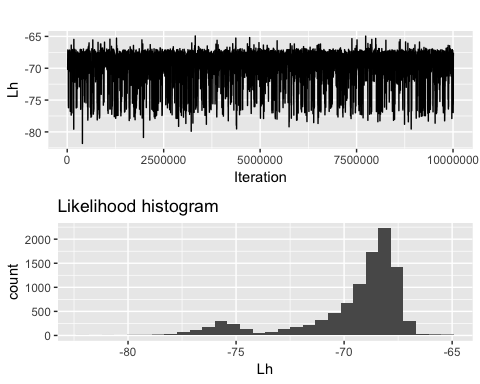
### Multi-solution models

Some of the hypotheses did not converge satisfactorily despite passing the Gelman-Rubin tests. These often are switching between two possible solutions. Extending burn-in to 2332763595 iterations had no effect of convergence. Therefore we conclude that these two solutions are equally likely and we explore the impact of these here.

#### Austronesian

###### Crow & Matri-anvunculocal residence

There is evidence of two solutions in this model. The most likely model has a likelihood of ~69 (model 1), and a second with a likelihood of ~76 (model 2). The ancestral states are similar, but model 1 shows changes are occurring approximately half as fast as model 2. Under model 1 changes from Crow terminologies to not Crow would occur 200 times every ten years, which seems unlikely. Therefore, we qualitatively choose model 2 as the most likely model. This means that the likelihood should approximately be -76, which is what the stepping stone sampler chose, therefore not effecting our results.



Ancestral states for model 1 and model 2

Root - P(0,0)

Root - P(0,1)

Root - P(1,0)

Root - P(1,1)

model 1

0.933

0.043

0.014

0.010

model 2

0.989

0.008

0.000

0.002

Independent rates for model 1 and model 2

alpha1

beta1

alpha2

beta2

model 1

1.578

20.959

1.629

2.179

model 2

0.910

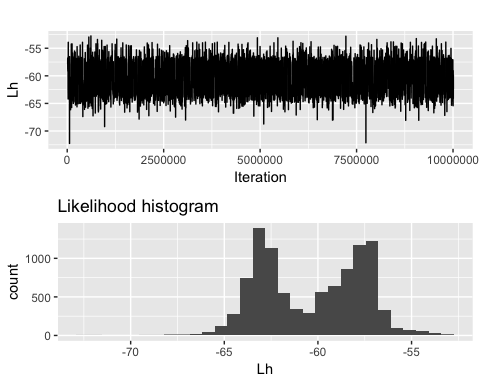
1.067

0.981

0.996

###### Crow & Matrilineal

The independent model of this hypotheses is multimodel, as shown in the figure below. Increasing the burn-in and chain length did not increase the preference of one model over the other. We look at the average model for each of these peaks, defining model 1 as the model with a likelihood of approximately -58, and model 2 with a likelihood of approximately -63. The models show similar ancestral states, but a large difference in the rate of change. Beta1 and Beta2 for model 1 are exceptionally high. Beta1 the rate at which societies change from Crow to not Crow is approximately 986 times per 100 years, and Beta2 indicates the rate at which societies loose matrilineal descent is approximately 798 times per 100 years. These rates seem improbable, and lead us to qualitatively prefer model 2. The stepping stone sampler has already shown a value close to this peak is preferable, and this has no change to our conclusion that these two phenomena show signs of co-evolution.



Ancestral states for model 1 and model 2

Root - P(0,0)

Root - P(0,1)

Root - P(1,0)

Root - P(1,1)

model 1

0.786

0.144

0.016

0.054

model 2

0.993

0.005

0.001

0.002

Independent rates for model 1 and model 2

alpha1

beta1

alpha2

beta2

model 1

1.005

9.866

1.002

7.984

model 2

0.622

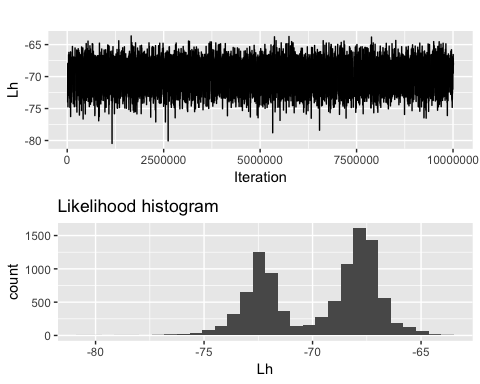
1.151

0.623

0.977

###### Eskimo & Monogamy

This hypotheses is multi-modal and running the chain longer made no decision between the two. In this instance we have two competeing solutions, model one suggests it is likely that Eskimo type is the most likely ancestral state, but is split between whether monogamy was also present. And model two suggests that an Eskimo system was not the ancestral state, and neither was monogamy. Other analysis in this paper suggests that Eskimo is very likely to be the ancestral state in Austronesia, so we take model one as the most likely model. The stepping stone sampler already prefers this model, therefore this makes no changes to our results.



Ancestral states for model 1 and model 2

Root - P(0,0)

Root - P(0,1)

Root - P(1,0)

Root - P(1,1)

model 1

0.001

0.001

0.426

0.572

model 2

0.679

0.227

0.032

0.063

Independent rates for model 1 and model 2

alpha1

beta1

alpha2

beta2

model 1

0.008

1.962

1.814

1.892

model 2

1.051

1.242

1.177

1.242