Supplementary Material

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01/08/2018

Contents

Data

Kinship & social structure

All data was extracted from the D-PLACE Ethnographic atlas github repository. 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.

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## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 1: Table S1: Count of societies in signal test and ancestral state analyses, by language family

	Count
Austronesian	85
Bantu	69
Uto-Aztecan	22

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## kable. kableExtra can customize either HTML or LaTeX outputs. See https://
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Table 2: 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
Crow	27	1	matrilineal	43	3	85
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
Crow	27	1	uni.localresidence	10	1,5,8,9,10	84
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
Hawaiian	27	4	bi.localextendedfamily	8	6,7,8	83
Hawaiian	27	4	absenceofcousinmarriage.permitted	25	10,11,15	79
Hawaiian	27	4	absenceofcousinmarriage.preference	23	7,8,11,12	79
Hawaiian	27	4	bi.localresidence	10	2,11,12	84
Iroquois	27	5	exogamy.unilineal.descent	15	4	78
Iroquois	27	5	uni.linealdescent	43	1,3,4	85
Iroquois	27	5	cross.cousinmarriage.permitted	25	1,6,9	79
Iroquois	27	5	cross.cousinmarriage.preferred	23	1,2,3,5,6,8,12,13,14	79
Iroquois	27	5	high.polygyny	9	3,4,5,6	80
Iroquois	27	5	polygyny	9	2,3,4,5,6	80
Iroquois	27	5	matri.anvunclocalresidence	10	1,5,9	84
Iroquois	27	5	uni.localresidence	10	1,5,8,9,10	84
Omaha	27	6	patrilineal	43	1	
Omaha	27	6	matri.anvunclocalresidence	10	1,5,9	
Omaha	27	6	uni.localresidence	10	1,5,8,9,10	

Co-evolutionary hypotheses and references

terminology	hypotheses	quote
Crow	High polygyny	"Non-sororal polygyny tends to be associated with kinship terminology of the
Crow	Matri-anvunculocal residence	"Crow systems should occur more frequencly in societies which are avunculo
Crow	Matrilineal	"The tables show a strong correlation between Omaha terms and patrilineal u
Crow	Matrilocal	"... there is reason to believe that unilocal patrilocal groupings are the essen
Crow	Polygyny	"Non-sororal polygyny tends to be associated with kinship terminology of the
Crow	Uni-local residence	"In the presence of patrilocal, matri-local or avunculocal residence, separate t
Eskimo	Absence of CM permitted	"Prohibition on cousins vary [in Eskimo-types], but as one might expect, are

terminology	hypotheses	quote
Eskimo	Absence of CM preference	"Prohibition on cousins vary [in Eskimo-types], but as one might expect, are
Eskimo	Bi-lineal descent	"There is a distinct association of Eskimo terms with bilateral [descent] syste
Eskimo	Monogamy	"The following variables are dependent upon diverging devolution (transmissi
Eskimo	Neo-local residence	"Neolocal residence tends to be associated with kinship terminology of the li
Eskimo	Nuclear families	"In the absence of clans and polygamous and extended families, the isolated
Hawaiian	Absence of CM permitted	"Hawaiian [kin] terms . . . are associated with the prohibition on [cross] cousi
Hawaiian	Absence of CM preference	"Hawaiian [kin] terms . . . are associated with the prohibition on [cross] cousi
Hawaiian	Bi-lineal descent	"Bilateral kindreds tend to be associated with kinship terminology of the gen
Hawaiian	Bi-local extended family	"The several types of extended family . . . depend upon the prevailing rule of
Hawaiian	Bi-local residence	"Bilocal residence tends to be associated with kinship terminology of the gen
Iroquois	Cross CM permitted	"Iroquois [kin] terms . . . are associatedd with preferred cross-cousin marriage
Iroquois	Cross CM preferred	"Iroquois [kin] terms . . . are associatedd with preferred cross-cousin marriage
Iroquois	Exogamy & unilineal descent	"In the presence of exogamous matrilineal or patrilineal lineages, sibs, phratri
Iroquois	High polygyny	"Non-sororal polygyny tends to be associated with kinship terminology of the
Iroquois	Matri-anvunculocal residence	"Matrilocal and anvunculocal residence tend to be associated with kinship te
Iroquois	Polygyny	"Non-sororal polygyny tends to be associated with kinship terminology of the
Iroquois	Uni-lineal descent	"The classic but erroneous anthropological view concerning the nature of the
Iroquois	Uni-local residence	"In the presence of patrilocal, matri-local or avunculocal residence, separate t
Omaha	Matri-anvunculocal residence	"Matrilocal and anvunculocal residence tend to be associated with kinship te
Omaha	Patrilineal	"The tables show a strong correlation between Omaha terms and patrilineal
Omaha	Patrilocal	". . . there is reason to believe that unilocal patrilocal groupings are the esse
Omaha	Uni-local residence	"In the presence of patrilocal, matri-local or avunculocal residence, separate t

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 Kirby et al. (2016). In Austronesian, we sub-sampled 1000 phylogenies from a posterior sample of 4199 phylogenies developed in Gray, Drummond, and Greenhill (2009). Austronesian phylogenies were estimated through linguistic data and supported by genetic evidence, and archaeological records. Detailed methods can be found in Gray, Drummond, and Greenhill (2009). 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 Grollemund et al. (2015). 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 Levinson et al. (2011) 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.

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## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.

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## format in kable. kableExtra can customize either HTML or LaTeX outputs. See
## https://haozhu233.github.io/kableExtra/ for details.

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## format in kable. kableExtra can customize either HTML or LaTeX outputs. See
## https://haozhu233.github.io/kableExtra/ for details.

## Warning in group_rows(., "Uto-Aztecan", groups[2] + 1, groups[3]): Please
## specify format in kable. kableExtra can customize either HTML or LaTeX
## outputs. See https://haozhu233.github.io/kableExtra/ for details.

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## or LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
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Table 4: Table S3: Signal tests for each langauge family. Columns 2 & 3 indicate of a terminology. Columns 4 to 6 are ou test. Columns 7 to 21 are output from I bonferonni corrected values shown

Terminology	Absent	Present	D	Prob. Brownian	Prob. Random	Z-stat	p-value	bonf-p	Z-stat
Crow	79	6	-0.115	0.603	0.036	1752616.53	0.039	0.233	3789.807
Eskimo	71	14	-0.494	0.806	0.000	4905208.29	0.219	1.000	8155.126
Hawaiian	37	48	0.661	0.054	0.081	8021595.70	0.959	1.000	14388.168
Iroquois	70	15	0.097	0.468	0.007	4216334.11	0.032	0.190	8460.864
Omaha	84	1	2.860	0.230	0.700	430380.25	0.376	1.000	702.380
Sudanese	84	1	-2.063	0.714	0.171	498098.38	0.260	1.000	709.856
Crow	65	4	1.105	0.129	0.525	348598.29	0.887	1.000	1823.446
Descriptive	68	1	2.941	0.066	0.881	93014.64	0.783	1.000	477.297
Hawaiian	60	9	0.405	0.297	0.083	792380.62	0.524	1.000	3835.774
Iroquois	25	44	0.166	0.362	0.008	1636008.46	0.023	0.159	7853.277
Mixed	68	1	-2.432	0.834	0.040	116322.82	0.320	1.000	500.446
Omaha	61	8	0.767	0.140	0.274	733279.95	0.393	1.000	3484.320
Sudanese	67	2	1.051	0.287	0.459	169263.56	0.718	1.000	929.736
Crow	21	1	0.243	0.419	0.462	13195.12	0.365	1.000	132.056

Terminology	Absent	Present	D	Prob. Brownian	Prob. Random	Z-stat	p-value	bonf-p	Z-stat
Eskimo	21	1	3.253	0.216	0.679	14128.24	0.818	1.000	133.048
Hawaiian	6	16	-0.600	0.798	0.004	70096.07	0.259	0.980	606.534
Iroquois	18	4	-2.343	0.985	0.000	54649.14	0.881	1.000	457.499

Ancestral state

MCMC review

Ancestral state inference 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 state inference 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 10^9 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 inference 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 < 3 indicates weak evidence, >3 positive 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.

Table 5: Three MCMC chains for the austronesian language family

	Lh	Global Rate	Crow	Eskimo	Hawaiian	Iroquois	Omaha	Sudanese
1	-95.225	38.740	0.029	0.850	0.009	0.012	0.043	0.057
2	-95.215	37.444	0.028	0.855	0.008	0.011	0.043	0.055
3	-95.217	36.975	0.028	0.857	0.008	0.011	0.042	0.054
Mean	-95.219	37.720	0.028	0.854	0.008	0.011	0.043	0.055

Table 6: Three MCMC chains for the bantu language family

	Lh	Global Rate	Crow	Descriptive	Hawaiian	Iroquois	Omaha	Sudanese	Mixed
1	-80.992	30.195	0.089	0.078	0.156	0.398	0.101	0.081	0.098
2	-80.970	32.177	0.091	0.080	0.156	0.388	0.102	0.084	0.099
3	-80.995	32.282	0.091	0.080	0.154	0.388	0.102	0.084	0.099
Mean	-80.986	31.551	0.090	0.079	0.155	0.391	0.102	0.083	0.099

Table 7: Three MCMC chains for the utoaztecan language family

	Lh	Global Rate	Crow	Eskimo	Hawaiian	Iroquois
1	-13.157	12.844	0.079	0.080	0.756	0.085

	Lh	Global Rate	Crow	Eskimo	Hawaiian	Iroquois
2	-13.124	12.465	0.079	0.078	0.761	0.081
3	-13.143	11.890	0.078	0.080	0.762	0.080
Mean	-13.141	12.400	0.079	0.079	0.760	0.082

Table 8: Gelman-Rubin tests of MCMC convergence for each language family

	Point est.	Upper C.I.
austronesian	1.000	1.000
bantu	1.000	1.000
utoaztecan	1.001	1.002

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.

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## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 9: 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

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 10: 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 weak 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.

```
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```

Table 11: 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 5% of models. That is, the model considered these transitions important in 95% of the iterations. Transition rates are coded by numerical codes, which are:

```
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```

Table 12: Kin terminologies and their numerical codes.

1	Crow
2	Descriptive
3	Eskimo
4	Hawaiian
5	Iroquois
6	Omaha
7	Sudanese
8	Mixed

```
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```

Table 13: Transition rates between kin terminologies in the austronesian-st language family.

transition	parameterized	zero	percentage
q34	9930	70	0.007
q45	9571	429	0.043
q14	9367	633	0.063
q54	7926	2074	0.207
q15	7476	2524	0.252
q64	7343	2657	0.266
q74	7321	2679	0.268
q51	6809	3191	0.319
q61	6796	3204	0.320
q65	6785	3215	0.322
q67	6719	3281	0.328
q16	6424	3576	0.358
q71	6422	3578	0.358
q75	6273	3727	0.373
q76	6272	3728	0.373
q17	5930	4070	0.407
q73	5636	4364	0.436
q63	5510	4490	0.449
q41	5467	4533	0.453
q56	4264	5736	0.574
q13	4184	5816	0.582
q57	3367	6633	0.663
q37	3232	6768	0.677
q46	2508	7492	0.749
q53	1805	8195	0.820
q31	1488	8512	0.851
q36	1435	8565	0.856
q35	1280	8720	0.872
q47	1244	8756	0.876
q43	1169	8831	0.883

```
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## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 14: Transition rates between kin terminologies in the bantu-st language family.

transition	parameterized	zero	percentage
q56	9294	706	0.071
q54	8279	1721	0.172
q62	8116	1884	0.188
q17	7639	2361	0.236
q65	7294	2706	0.271
q14	7034	2966	0.297
q71	6943	3057	0.306
q41	6860	3140	0.314
q64	6476	3524	0.352
q74	6359	3641	0.364

transition	parameterized	zero	percentage
q15	6312	3688	0.369
q61	6225	3775	0.378
q67	6181	3819	0.382
q26	6117	3883	0.388
q84	5915	4085	0.408
q76	5843	4157	0.416
q24	5835	4165	0.416
q45	5821	4179	0.418
q75	5701	4299	0.430
q86	5645	4355	0.436
q16	5609	4391	0.439
q21	5587	4413	0.441
q81	5487	4513	0.451
q78	5436	4564	0.456
q68	5413	4587	0.459
q85	5405	4595	0.460
q18	5374	4626	0.463
q28	5345	4655	0.466
q27	5337	4663	0.466
q25	5258	4742	0.474
q72	5219	4781	0.478
q87	5191	4809	0.481
q51	5159	4841	0.484
q82	5037	4963	0.496
q12	4815	5185	0.518
q46	4284	5716	0.572
q47	4166	5834	0.583
q48	3616	6384	0.638
q42	2791	7209	0.721
q57	1825	8175	0.818
q58	346	9654	0.965
q52	163	9837	0.984

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## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 15: Transition rates between kin terminologies in the utoaztecan-st language family.

transition	parameterized	zero	percentage
q43	7291	2709	0.271
q34	6767	3233	0.323
q31	6576	3424	0.342
q35	6461	3539	0.354
q15	6362	3638	0.364
q13	6354	3646	0.365
q14	6236	3764	0.376
q41	6030	3970	0.397
q45	5984	4016	0.402
q51	4984	5016	0.502
q53	4709	5291	0.529

transition	parameterized	zero	percentage
q54	4654	5346	0.535

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.

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## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 16: 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 (Pagel and Meade 2006). 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.

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## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
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Table 17: Table S2: MCMC settings for both dependent and independent analyses

hypotheses	exponential mean	scaled branch length	iterations	samplin
austronesian-crow-high.polygyny	10	Yes	10050000	100
austronesian-crow-matri.anvunclocalresidence	10	Yes	10050000	100
austronesian-crow-matrilineal	10	Yes	10050000	100
austronesian-crow-polygyny	10	Yes	10050000	100
austronesian-crow-matrilocal	10	Yes	10010000	100
austronesian-crow-uni.localresidence	10	Yes	10010000	100
austronesian-eskimo-absenceofcousinmarriage.permitted	10	Yes	65000000	100
austronesian-eskimo-absenceofcousinmarriage.preference	10	Yes	65000000	100
austronesian-eskimo-bi.linealdescent	10	Yes	10010000	100
austronesian-eskimo-monogamy	10	Yes	10050000	100
austronesian-eskimo-neo.localresidence	10	Yes	65000000	100
austronesian-eskimo-inheritancetobothsex.restricted	10	Yes	10010000	100
austronesian-eskimo-nuclear.families	10	Yes	10010000	100
austronesian-eskimo-inheritancetobothsex	10	Yes	10010000	100
austronesian-eskimo-uni.linealdescent	10	Yes	10010000	100
austronesian-hawaiian-absenceofcousinmarriage.permitted	10	Yes	10050000	100
austronesian-hawaiian-absenceofcousinmarriage.preference	10	Yes	10010000	100
austronesian-hawaiian-bi.linealdescent	10	Yes	10010000	100
austronesian-hawaiian-bi.localextendedfamily	10	Yes	10010000	100
austronesian-hawaiian-first&secondcousinforbidden	10	Yes	10050000	100
austronesian-hawaiian-bi.localresidence	10	Yes	10050000	100
austronesian-iroquois-cross.cousinmarriage.permitted	10	Yes	10010000	100
austronesian-iroquois-cross.cousinmarriage.preferred	10	Yes	10010000	100
austronesian-iroquois-exogamy.unilineal.descent	10	Yes	10010000	100
austronesian-iroquois-high.polygyny	10	Yes	10010000	100
austronesian-iroquois-matri.anvunclocalresidence	10	Yes	10010000	100
austronesian-iroquois-polygyny	10	Yes	10010000	100
austronesian-iroquois-uni.linealdescent	10	Yes	10010000	100
austronesian-iroquois-uni.localresidence	10	Yes	10050000	100
bantu-crow-matri.anvunclocalresidence	10	Yes	10010000	100
bantu-crow-matrilineal	10	Yes	10010000	100
bantu-crow-matrilocal	10	Yes	10050000	100
bantu-crow-uni.localresidence	10	Yes	10010000	100
bantu-hawaiian-absenceofcousinmarriage.permitted	10	Yes	10010000	100
bantu-hawaiian-absenceofcousinmarriage.preference	10	Yes	10010000	100
bantu-hawaiian-bi.linealdescent	10	Yes	10010000	100
bantu-hawaiian-bi.localextendedfamily	10	Yes	10010000	100
bantu-hawaiian-first&secondcousinforbidden	10	Yes	10050000	100
bantu-hawaiian-bi.localresidence	10	Yes	10010000	100
bantu-iroquois-cross.cousinmarriage.permitted	10	Yes	10010000	100
bantu-iroquois-cross.cousinmarriage.preferred	10	Yes	10010000	100
bantu-iroquois-exogamy.unilineal.descent	10	Yes	10010000	100
bantu-iroquois-matri.anvunclocalresidence	10	Yes	10010000	100
bantu-iroquois-uni.linealdescent	10	Yes	10010000	100
bantu-iroquois-uni.localresidence	10	Yes	10010000	100
bantu-omaha-matri.anvunclocalresidence	10	Yes	10010000	100
bantu-omaha-patrilineal	10	Yes	10010000	100
bantu-omaha-patrilocal	10	Yes	10010000	100
bantu-omaha-uni.localresidence	10	Yes	10010000	100

hypotheses	exponential mean	scaled branch length	iterations	samplin
uto-hawaiian-absenceofcousinmarriage.permitted	10	Yes	10010000	100
uto-hawaiian-absenceofcousinmarriage.preference	10	Yes	10010000	100
uto-hawaiian-bi.linealdescent	10	Yes	10010000	100
uto-hawaiian-bi.localextendedfamily	10	Yes	10010000	100
uto-hawaiian-first&secondcousinforbidden	10	Yes	10010000	100
uto-hawaiian-bi.localresidence	10	Yes	10010000	100
uto-iroquois-cross.cousinmarriage.permitted	10	Yes	10010000	100
uto-iroquois-cross.cousinmarriage.preferred	10	Yes	10010000	100
uto-iroquois-exogamy.unilineal.descent	10	Yes	10010000	100
uto-iroquois-high.polygyny	10	Yes	10010000	100
uto-iroquois-matri.anvunclocalresidence	10	Yes	10010000	100
uto-iroquois-uni.linealdescent	10	Yes	10010000	100
uto-iroquois-uni.localresidence	10	Yes	10010000	100
ie-eskimo-absenceofcousinmarriage.permitted	10	Yes	10010000	100
ie-eskimo-absenceofcousinmarriage.preference	10	Yes	10010000	100
ie-eskimo-bi.linealdescent	10	Yes	10010000	100
ie-eskimo-inheritancetobothsex	10	Yes	10010000	100
ie-eskimo-monogamy	10	Yes	10010000	100
ie-eskimo-neo.localresidence	10	Yes	10010000	100
ie-eskimo-nuclear.families	10	Yes	10010000	100
ie-eskimo-uni.linealdescent	10	Yes	10010000	100
ie-hawaiian-absenceofcousinmarriage.permitted	10	Yes	10010000	100
ie-hawaiian-absenceofcousinmarriage.preference	10	Yes	10010000	100
ie-hawaiian-bi.linealdescent	10	Yes	10010000	100
ie-hawaiian-bi.localextendedfamily	10	Yes	10010000	100
ie-hawaiian-bi.localresidence	10	Yes	10010000	100
ie-hawaiian-first&secondcousinforbidden	10	Yes	10010000	100
ie-hawaiian-first&secondcousinforbidden	10	Yes	10010000	100
ie-eskimo-inheritancetobothsex.restricted	10	Yes	10010000	100

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 Pagel and Meade (2006). Following common practice we interpret Bayes factors of less than 3 indicated weak evidence, greater than 3 as positive evidence, 5-10 as strong evidence, and greater than 10 very strong evidence

A second table shows the results of a Gelman-Rubin diagnostic testing, to test for any significant differences between chains (Gelman and Rubin 1992). 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.

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
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## Warning in add_header_above(., c(` ` = 1, Dependent = 9, Independent = 5)):
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```

```
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 18: Austronesian : Crow <-> High.polygyny

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	62.369	0.58	0.573	0.5	0.478	0.529	0.518	0.434	0.45	61.254	0.58	0.582	0.583	0.582
2	62.689	0.583	0.578	0.535	0.47	0.522	0.519	0.419	0.433	61.265	0.596	0.601	0.603	0.601
3	62.621	0.578	0.576	0.493	0.452	0.525	0.536	0.423	0.485	61.286	0.584	0.587	0.59	0.587
Mean	62.56	0.58	0.576	0.509	0.467	0.525	0.524	0.425	0.456	61.268	0.587	0.59	0.592	0.59
BF	-2.23													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
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```

Table 19: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.001	1.002
Independent	1.007	1.008

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
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```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
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```

Table 20: Austronesian : Crow <-> Matri.anvunclocalresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	70.689	1.872	0	1.911	1.909	0	1.576	1.587	1.909	76.921	1.449	18.964	1.479	1.521
2	70.264	1.86	0	1.896	1.889	0	1.577	1.588	1.891	75.832	1.428	18.508	1.458	1.508
3	70.699	1.877	0	1.914	1.914	0	1.58	1.608	1.91	76.481	1.431	18.548	1.461	1.512
Mean	70.551	1.87	0	1.907	1.904	0	1.578	1.594	1.903	76.411	1.436	18.673	1.466	1.514
BF	12.464													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 21: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.001	1.002
Independent	1.001	1.002

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
## Please specify format in kable. kableExtra can customize either HTML or
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```

Table 22: Austronesian : Crow <-> Matrilineal

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	54.971	0	0	0	26.603	26.643	26.584	26.675	26.611	65.046	0.667	4.315	0.667	1.055
2	55.688	0	0	0	26.577	26.601	26.521	26.645	26.564	65.203	0.662	4.095	0.662	0.931
3	55.674	0	0	0	26.559	26.574	26.547	26.612	26.552	65.892	0.656	3.567	0.656	0.892
Mean	55.444	0	0	0	26.58	26.606	26.551	26.644	26.576	65.38	0.662	3.992	0.662	0.959
BF	20.151													

Table 23: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.003	1.007
Independent	1.001	1.004

Table 24: Austronesian : Crow <-> Polygyny

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	68.705	2.65	2.471	1.493	0.927	24.571	6.823	9.869	5.017	67.451	1.719	21.709	2.515	1.553
2	68.799	2.585	2.51	1.489	0.924	24.592	7.052	9.781	4.982	67.63	1.722	22.155	2.509	1.551
3	68.711	2.652	2.501	1.507	0.923	24.732	6.997	9.68	4.962	67.578	1.726	21.892	2.55	1.549
Mean	68.738	2.629	2.494	1.496	0.925	24.632	6.957	9.777	4.987	67.553	1.722	21.919	2.525	1.551
BF	-2.509													

Table 25: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

Table 26: Austronesian : Crow <-> Matrilocal

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	47.68	0	0	0	20.673	20.335	10.146	20.859	20.731	50.737	0.389	0.399	0.389	0.399
2	48.203	0	0	0	19.807	19.43	9.487	20.104	19.869	50.628	0.394	0.402	0.393	0.402
3	47.952	0	0	0	20.121	19.593	9.876	20.419	20.267	50.718	0.394	0.402	0.394	0.402
Mean	47.945	0	0	0	20.2	19.786	9.836	20.461	20.289	50.694	0.392	0.401	0.392	0.401
BF	6.114													

Table 27: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.001	1.002
Independent	1.000	1.000

Table 28: Austronesian : Crow <-> Uni.localresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	80.295	2.862	0	2.786	2.552	2.488	2.478	2.868	0	83.262	2.568	28.749	2.787	2.787
2	80.644	2.874	0	2.787	2.547	2.498	2.475	2.857	0	83.358	2.55	28.568	2.796	2.796
3	80.738	2.886	0	2.823	2.582	2.535	2.521	2.881	0	84.408	2.578	28.669	2.804	2.804
Mean	80.559	2.874	0	2.799	2.56	2.507	2.491	2.869	0	83.676	2.565	28.662	2.796	2.796
BF	5.932													

Table 29: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.000	1.001

	Point est.	Upper C.I.
Independent	1.001	1.003

```
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```

Table 30: Austronesian : Eskimo <-> Absenceofcousinmarriage.permitted

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	79.508	14.848	1.708	3.726	0.326	5.408	6.785	3.251	5.59	79.276	0.224	3.457	14.028	4.869
2	79.522	14.972	1.698	3.781	0.317	5.457	6.708	3.215	5.703	79.281	0.218	3.447	13.731	4.825
3	79.16	14.92	1.731	3.766	0.318	5.365	7.012	3.278	5.792	79.368	0.219	3.461	13.896	4.823
Mean	79.397	14.913	1.712	3.758	0.32	5.41	6.835	3.248	5.695	79.308	0.22	3.455	13.885	4.839
BF	-0.465													

```
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```

Table 31: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

```
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```

Table 32: Austronesian : Eskimo <-> Absenceofcousinmarriage.preference

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta
1	70.788	4.326	0.327	18.699	1.09	3.271	0.944	12.128	13.217	69.578	0.216	3.483	3.745	19.9
2	70.685	4.36	0.311	19.107	1.067	3.265	0.94	11.898	13.193	69.833	0.222	3.476	3.756	19.9
3	70.767	4.362	0.31	18.826	1.046	3.259	0.926	11.976	13.108	69.704	0.22	3.46	3.772	20.1
Mean	70.747	4.349	0.316	18.877	1.068	3.265	0.937	12.001	13.173	69.705	0.219	3.473	3.758	20.0
BF	-2.419													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
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## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
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```

Table 33: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

```
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```

Table 34: Austronesian : Eskimo <-> Bi.linealdescent

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	90.796	3.397	0	3.451	0	3.407	0	3.165	3.171	88.847	0	2.771	2.742	2.776
2	91.31	3.39	0	3.446	0	3.4	0	3.179	3.204	89.238	0	2.774	2.728	2.776
3	90.53	3.413	0	3.456	0	3.43	0	3.181	3.204	89.294	0	2.763	2.732	2.763
Mean	90.879	3.4	0	3.451	0	3.412	0	3.175	3.193	89.126	0	2.769	2.734	2.772
BF	-3.899													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 35: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.001	1.001
Independent	1.013	1.022

```
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```

Table 36: Austronesian : Eskimo <-> Monogamy

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	69.397	0	0	7.171	0	0	7.273	7.211	7.225	74.416	0	1.602	1.513	1.552
2	68.392	0	0	7.133	0	0	7.236	7.182	7.197	74.04	0	1.597	1.498	1.546
3	69.269	0	0	7.153	0	0	7.256	7.197	7.209	74.053	0	1.597	1.505	1.544
Mean	69.019	0	0	7.152	0	0	7.255	7.197	7.21	74.17	0	1.599	1.505	1.547

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
BF	10.04													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
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```

Table 37: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.001	1.002
Independent	1.001	1.002

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
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```
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```

Table 38: Austronesian : Eskimo <-> Neo.localresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	50.333	0.18	0.175	8.575	8.13	2.951	2.427	9.04	11.088	51.09	0.158	3.267	0.414	7.018
2	50.058	0.176	0.177	8.549	8.346	3.003	2.437	9.017	11.238	51.11	0.161	3.269	0.414	7.054
3	50.307	0.176	0.172	8.508	8.411	2.988	2.443	9.084	11.194	51.222	0.164	3.255	0.42	7.108
Mean	50.233	0.177	0.175	8.544	8.296	2.981	2.436	9.047	11.173	51.141	0.161	3.264	0.416	7.06
BF	1.513													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
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```

Table 39: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.000	1.000
Independent	1.001	1.003

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
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```
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```

Table 40: Austronesian : Eskimo <-> Nuclear.families

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	88.016	3.516	0	3.517	3.462	3.291	3.451	3.443	3.488	87.216	0	3.296	3.304	3.302
2	88.268	3.523	0	3.526	3.459	3.286	3.443	3.443	3.486	87.677	0	3.294	3.303	3.301
3	87.584	3.53	0	3.531	3.462	3.302	3.455	3.44	3.493	86.673	0	3.304	3.31	3.308
Mean	87.956	3.523	0	3.525	3.461	3.293	3.45	3.442	3.489	87.189	0	3.298	3.306	3.304
BF	-1.601													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
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```

Table 41: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.000	1.001
Independent	1.004	1.008

```
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```

Table 42: Austronesian : Hawaiian <-> Absenceofcousinmarriage.permitted

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	103.568	0	4.998	0	5.409	5.275	5.422	5.401	4.786	104.165	6.975	6.965	7.379	3.371
2	102.917	0	5.018	0	5.415	5.288	5.429	5.404	4.735	104.031	7.09	7.067	7.534	3.419
3	103.157	0	4.971	0	5.397	5.287	5.401	5.386	4.829	104.176	7.063	7.033	7.598	3.413
Mean	103.214	0	4.996	0	5.407	5.283	5.417	5.397	4.783	104.124	7.043	7.022	7.504	3.401
BF	1.195													

```
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```

Table 43: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
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```

Table 44: Austronesian : Hawaiian <-> Absenceofcousinmarriage.preference

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	94.106	8.75	9.22	9.312	8.945	9.038	0	9.406	9.513	94.813	6.261	6.255	4.34	22.166
2	93.864	8.749	9.196	9.579	9.009	9.005	0	9.681	9.692	94.997	6.149	6.146	4.298	22.183
3	93.762	8.729	9.155	9.434	8.952	9.026	0	9.537	9.664	95.213	6.177	6.177	4.332	22.094
Mean	93.911	8.743	9.19	9.442	8.969	9.023	0	9.541	9.623	95.008	6.196	6.193	4.323	22.148
BF	1.414													

Table 45: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.002	1.003
Independent	1.000	1.001

Table 46: Austronesian : Hawaiian <-> Bi.linealdescent

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	114.801	0	5.28	5.082	5.34	5.472	5.355	5.081	5.276	115.672	3.93	3.929	3.904	3.92
2	114.664	0	5.294	5.05	5.336	5.441	5.35	5.111	5.25	115.645	3.902	3.901	3.877	3.893
3	114.726	0	5.268	4.972	5.315	5.417	5.316	5.13	5.232	115.653	3.915	3.913	3.886	3.903
Mean	114.73	0	5.281	5.035	5.33	5.443	5.34	5.107	5.253	115.657	3.916	3.914	3.889	3.905
BF	1.741													

Table 47: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

Table 48: Austronesian : Hawaiian <-> Bi.localextendedfamily

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	115.025	0	5.495	4.649	6.279	5.61	6.026	6.086	5.875	112.373	5.066	5.062	5.055	5.06
2	114.787	0	5.579	4.509	6.22	5.689	6.046	6.046	5.892	112.409	5.075	5.073	5.069	5.08
3	114.946	0	5.542	4.541	6.14	5.657	6.018	5.992	5.85	112.385	5.067	5.065	5.06	5.065
Mean	114.919	0	5.539	4.566	6.213	5.652	6.03	6.041	5.872	112.389	5.069	5.067	5.061	5.068
BF	-5.303													

Table 49: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.002
Independent	1	1.000

Table 50: Austronesian : Hawaiian <-> Bi.localresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2
1	103.465	2.981	13.667	11.506	9.124	13.619	1.549	4.892	14.874	100.34	5.799	5.796	4.374
2	103.184	2.849	13.504	11.172	8.925	13.461	1.804	4.979	14.798	101.264	5.597	5.596	4.348
3	102.074	2.823	13.515	10.814	9.121	13.483	1.772	4.846	14.775	100.666	5.626	5.626	4.363
Mean	102.908	2.884	13.562	11.164	9.057	13.521	1.708	4.906	14.816	100.757	5.674	5.673	4.362
BF	-6.249												

Table 51: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.000	1.001

	Point est.	Upper C.I.
Independent	1.001	1.002

```
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```

Table 52: Austronesian : Iroquois <-> Cross.cousinmarriage.permitted

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	69.605	1.948	0	14.48	14.835	1.668	1.467	1.526	13.425	73.423	0.902	0.91	0.901	0.916
2	70.348	2.031	0	14.923	14.344	1.808	1.408	1.528	13.11	73.686	0.901	0.908	0.901	0.913
3	69.288	1.93	0	14.749	14.753	1.727	1.549	1.455	13.46	73.654	0.892	0.897	0.892	0.903
Mean	69.747	1.97	0	14.717	14.644	1.734	1.475	1.503	13.332	73.588	0.898	0.905	0.898	0.911
BF	7.634													

```
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```

Table 53: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

```
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```

Table 54: Austronesian : Iroquois <-> Cross.cousinmarriage.preferred

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	89.271	3.667	0	3.67	3.662	3.014	3.511	3.281	3.655	95.949	1.726	5.877	7.085	7.089
2	89.27	3.678	0	3.677	3.672	3.021	3.531	3.277	3.665	96.033	1.754	5.941	7.054	7.056
3	88.333	3.683	0	3.684	3.683	3.01	3.533	3.296	3.677	96.255	1.751	5.838	7.113	7.116
Mean	88.958	3.676	0	3.677	3.672	3.015	3.525	3.285	3.666	96.079	1.744	5.885	7.084	7.087
BF	13.355													

```
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Table 55: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

```
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```

Table 56: Austronesian : Iroquois <-> Exogamy.unilineal.descent

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	56.276	0.564	0.573	0.534	0.515	0.492	0.557	0.472	0.51	55.028	0.584	0.59	0.581	0.593
2	56.533	0.566	0.566	0.533	0.516	0.482	0.552	0.466	0.511	55.125	0.584	0.59	0.581	0.591
3	56.537	0.57	0.576	0.541	0.524	0.495	0.563	0.469	0.513	54.79	0.582	0.588	0.58	0.591
Mean	56.449	0.567	0.572	0.536	0.518	0.49	0.557	0.469	0.511	54.981	0.583	0.589	0.581	0.592
BF	-2.498													

```
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```

Table 57: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.001	1.003
Independent	1.000	1.001

```
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```

Table 58: Austronesian : Iroquois <-> High.polygyny

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	71.032	0.676	0.637	1.171	0.889	0.598	1.141	1.101	1.156	69.358	0.867	0.868	0.867	0.869
2	71.246	0.735	0.703	1.036	0.874	0.665	1.015	0.951	0.967	69.249	0.863	0.864	0.863	0.864
3	70.397	0.756	0.733	0.981	0.866	0.71	0.966	0.888	0.891	69.33	0.866	0.867	0.866	0.867
Mean	70.892	0.722	0.691	1.063	0.876	0.658	1.041	0.98	1.005	69.312	0.865	0.866	0.865	0.867

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
BF	-3.347													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
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```

Table 59: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

```
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```

Table 60: Austronesian : Iroquois <-> Matri.anvunclocalresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	84.634	1.384	1.136	1.38	1.324	1.327	0	1.023	0	84.295	1.217	1.226	1.219	1.228
2	84.71	1.38	1.124	1.375	1.321	1.325	0	0.995	0	84.284	1.219	1.228	1.222	1.23
3	84.928	1.377	1.137	1.375	1.312	1.327	0	1.004	0	84.29	1.222	1.231	1.224	1.233
Mean	84.757	1.38	1.132	1.377	1.319	1.326	0	1.007	0	84.29	1.219	1.228	1.222	1.23
BF	-0.678													

```
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```

Table 61: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

```
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```

Table 62: Austronesian : Iroquois <-> Polygyny

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	75.66	0.967	0	1.136	1.136	0.74	1.028	1.014	1.126	75.768	1.063	1.064	1.063	1.064
2	76.132	0.959	0	1.131	1.131	0.771	1.03	1.018	1.124	75.775	1.063	1.064	1.063	1.064
3	75.959	0.952	0	1.136	1.136	0.728	1.028	1.02	1.126	75.771	1.061	1.062	1.061	1.063
Mean	75.917	0.959	0	1.134	1.134	0.746	1.029	1.017	1.125	75.771	1.062	1.063	1.062	1.064
BF	0.217													

```
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```

Table 63: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.000	1.000
Independent	1.001	1.003

```
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```
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```

Table 64: Austronesian : Iroquois <-> Uni.linealdescent

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	90.088	2.408	0	2.904	2.92	1.93	2.667	2.711	2.914	91.098	1.453	1.484	1.456	1.491
2	89.454	2.375	0	2.907	2.91	2.014	2.673	2.732	2.898	91.07	1.451	1.486	1.456	1.492
3	90.644	2.367	0	2.897	2.924	2.023	2.688	2.731	2.901	91.105	1.449	1.479	1.452	1.484
Mean	90.062	2.383	0	2.903	2.918	1.989	2.676	2.725	2.904	91.091	1.451	1.483	1.455	1.489
BF	2.022													

```
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```

Table 65: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.000	1.001
Independent	1.001	1.002

```
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```
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```

Table 66: Austronesian : Iroquois <-> Uni.localresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	91.308	2.888	0	2.887	2.879	2.345	2.731	2.803	2.875	93.127	1.318	2.2	2.265	2.269
2	90.397	2.869	0	2.868	2.859	2.371	2.738	2.794	2.859	93.345	1.311	2.204	2.302	2.297
3	90.488	2.872	0	2.874	2.859	2.336	2.723	2.79	2.858	92.745	1.336	2.169	2.24	2.239
Mean	90.731	2.876	0	2.876	2.866	2.351	2.731	2.796	2.864	93.072	1.322	2.191	2.269	2.268
BF	3.637													

```
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```

Table 67: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

```
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```
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```

Table 68: Bantu : Crow <-> Matri.anvunclocalresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	67.638	2.344	0	2.355	2.314	0	1.873	2.23	2.389	68.086	1.38	15.445	2.653	2.941
2	68.188	2.342	0	2.359	2.31	0	1.891	2.239	2.395	68.711	1.388	15.456	2.65	2.945
3	67.908	2.343	0	2.355	2.304	0	1.855	2.224	2.389	67.8	1.399	15.65	2.608	2.913
Mean	67.911	2.343	0	2.356	2.309	0	1.873	2.231	2.391	68.199	1.389	15.517	2.637	2.933
BF	0.897													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
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```

Table 69: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.001

```
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```
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.

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```

Table 70: Bantu : Crow <-> Matrilineal

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	66.04	2.246	0	2.448	2.264	2.153	2.23	2.335	2.469	66.264	1.207	9.153	2.022	2.253
2	66.204	2.254	0	2.455	2.283	2.144	2.224	2.356	2.479	66.316	1.158	6.649	2	2.223
3	66.366	2.263	0	2.443	2.292	2.147	2.216	2.325	2.465	65.72	1.252	10.048	2.029	2.24
Mean	66.203	2.254	0	2.449	2.28	2.148	2.223	2.339	2.471	66.1	1.206	8.617	2.017	2.239
BF	0.447													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
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```

Table 71: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.000	1.001
Independent	1.001	1.002

```
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## Please specify format in kable. kableExtra can customize either HTML or
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```

Table 72: Bantu : Crow <-> Matrilocal

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	39.476	0.345	0.347	0.321	0.335	0.325	0.323	0.31	0.309	38.169	0.405	0.411	0.405	0.412
2	39.103	0.355	0.354	0.313	0.321	0.315	0.314	0.292	0.294	36.892	0.407	0.412	0.407	0.413
3	40.354	0.355	0.354	0.321	0.332	0.325	0.32	0.303	0.304	37.782	0.395	0.4	0.395	0.401
Mean	39.644	0.352	0.352	0.318	0.329	0.322	0.319	0.302	0.302	37.614	0.402	0.408	0.402	0.409
BF	-2.613													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
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```

Table 73: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.002	1.004
Independent	1.001	1.002

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
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```

Table 74: Bantu : Crow <-> Uni.localresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	48.038	0.462	0.412	0.567	0.567	0.438	0.462	0.502	0.517	47.094	0.572	0.574	0.572	0.573
2	48.377	0.458	0.413	0.571	0.572	0.442	0.468	0.507	0.522	47.099	0.571	0.573	0.571	0.573
3	48.105	0.459	0.417	0.569	0.569	0.442	0.473	0.505	0.524	47.003	0.57	0.572	0.57	0.571
Mean	48.173	0.46	0.414	0.569	0.569	0.441	0.468	0.505	0.521	47.065	0.571	0.573	0.571	0.572
BF	-1.888													

```
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```

Table 75: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.001	1.002
Independent	1.000	1.001

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
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## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 76: Bantu : Hawaiian <-> Absenceofcousinmarriage.permitted

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	56.076	0.726	0.611	0.796	0.795	0.525	0.599	0.675	0.757	54.82	0.788	0.788	0.788	0.788
2	56.289	0.725	0.597	0.797	0.797	0.51	0.606	0.683	0.758	54.767	0.791	0.791	0.79	0.791
3	56.211	0.726	0.612	0.796	0.796	0.507	0.588	0.67	0.757	54.841	0.789	0.789	0.789	0.789
Mean	56.192	0.726	0.607	0.796	0.796	0.514	0.598	0.676	0.757	54.809	0.789	0.789	0.789	0.789
BF	-2.511													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
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```

Table 77: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
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## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 78: Bantu : Hawaiian <-> Absenceofcousinmarriage.preference

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	54.678	0.769	0.769	0.675	0	0.384	0	0.667	0.634	55.109	0.742	0.742	0.742	0.744
2	55.43	0.772	0.772	0.675	0	0.425	0	0.672	0.646	55.16	0.74	0.74	0.74	0.741
3	54.583	0.77	0.77	0.671	0	0.372	0	0.673	0.644	55.186	0.743	0.743	0.743	0.744
Mean	54.897	0.77	0.77	0.674	0	0.394	0	0.671	0.641	55.152	0.742	0.742	0.742	0.743
BF	0.862													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
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```

Table 79: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
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## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 80: Bantu : Hawaiian <-> Bi.linealdescent

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	61.391	0.842	0.841	0.783	0.776	0.793	0.712	0.605	0.544	59.655	0.846	0.846	0.846	0.846
2	61.68	0.846	0.841	0.783	0.775	0.792	0.701	0.587	0.559	59.648	0.843	0.844	0.843	0.844
3	60.881	0.852	0.844	0.788	0.782	0.792	0.715	0.603	0.553	59.747	0.849	0.85	0.849	0.851
Mean	61.317	0.847	0.842	0.785	0.778	0.792	0.709	0.598	0.552	59.683	0.846	0.847	0.846	0.847
BF	-3.473													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 81: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
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## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 82: Bantu : Hawaiian <-> Bi.localextendedfamily

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	75.898	1.707	1.211	1.764	1.337	1.36	1.513	1.259	1.489	74.228	1.404	1.419	1.425	1.428
2	75.305	1.921	1.14	2.069	1.46	1.355	1.563	1.331	1.677	74.508	1.402	1.418	1.423	1.425
3	75.599	2.329	1.038	3.055	1.663	1.377	1.616	1.47	2.173	74.55	1.395	1.408	1.415	1.417
Mean	75.601	1.986	1.13	2.296	1.487	1.364	1.564	1.353	1.78	74.429	1.4	1.415	1.421	1.423
BF	-3.341													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
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```

Table 83: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.003	1.011
Independent	1.000	1.002

```
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```

Table 84: Bantu : Hawaiian <-> Bi.localresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	51.207	0.697	0.697	0.488	0	0.598	0	0.589	0.588	51.27	0.664	0.664	0.664	0.664
2	51.062	0.699	0.699	0.469	0	0.611	0	0.592	0.592	51.271	0.661	0.661	0.66	0.661
3	51.283	0.699	0.7	0.494	0	0.608	0	0.591	0.589	51.235	0.665	0.665	0.664	0.665

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
Mean	51.184	0.698	0.699	0.484	0	0.606	0	0.591	0.59	51.259	0.663	0.663	0.663	0.663
BF	0.127													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
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```

Table 85: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
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```
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## Please specify format in kable. kableExtra can customize either HTML or
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```

Table 86: Bantu : Iroquois <-> Cross.cousinmarriage.permitted

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	73.224	0	1.513	0	1.456	1.66	1.656	1.65	1.58	75.395	1.404	1.413	1.395	1.413
2	73.879	0	1.514	0	1.449	1.658	1.655	1.649	1.582	74.917	1.396	1.406	1.386	1.406
3	73.213	0	1.515	0	1.457	1.657	1.653	1.65	1.579	74.844	1.397	1.408	1.386	1.407
Mean	73.439	0	1.514	0	1.454	1.658	1.655	1.65	1.58	75.052	1.399	1.409	1.389	1.409
BF	4.342													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
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```

Table 87: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.001

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
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```

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 88: Bantu : Iroquois <-> Cross.cousinmarriage.preferred

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	83.128	0	0	3.977	3.217	2.808	3.574	2.623	2.276	84.598	2.388	2.392	2.392	2.393
2	83.355	0	0	3.518	3.084	2.795	3.31	2.585	2.338	84.593	2.398	2.403	2.402	2.402
3	83.315	0	0	3.568	3.077	2.824	3.353	2.567	2.327	84.627	2.389	2.392	2.392	2.393
Mean	83.266	0	0	3.688	3.126	2.809	3.412	2.592	2.314	84.606	2.392	2.396	2.395	2.396
BF	2.94													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
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```

Table 89: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.001

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
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## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
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```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 90: Bantu : Iroquois <-> Exogamy.unilineal.descent

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	71.982	1.458	1.182	1.423	1.243	1.478	1.426	0	1.377	71.213	1.486	1.499	1.48	1.499
2	72.769	1.472	1.202	1.438	1.276	1.495	1.424	0	1.374	70.627	1.494	1.504	1.483	1.505
3	71.796	1.474	1.183	1.437	1.26	1.495	1.421	0	1.382	70.834	1.483	1.496	1.476	1.498
Mean	72.182	1.468	1.189	1.433	1.26	1.489	1.424	0	1.378	70.891	1.488	1.5	1.48	1.501
BF	-1.539													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
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```

Table 91: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.001	1.003
Independent	1.000	1.000

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
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```

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
```

```
## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 92: Bantu : Iroquois <-> Matri.anvunclocalresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	87.586	0	2.68	3.012	2.996	3.016	3.046	2.705	2.71	89.436	2.355	2.356	2.354	2.36
2	87.682	0	2.699	3.009	3.01	3.01	3.049	2.731	2.706	89.464	2.358	2.36	2.357	2.362
3	87.416	0	2.666	2.982	2.983	2.998	3.037	2.7	2.658	89.397	2.345	2.347	2.345	2.352
Mean	87.561	0	2.682	3.001	2.996	3.008	3.044	2.712	2.691	89.432	2.353	2.354	2.352	2.358
BF	3.7													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 93: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.001

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
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```

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 94: Bantu : Iroquois <-> Uni.linealdescent

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	81.009	1.207	0	1.373	1.419	1.365	1.412	1.463	1.441	78.803	1.469	1.476	1.473	1.461
2	80.949	1.221	0	1.381	1.431	1.373	1.424	1.473	1.454	78.83	1.464	1.47	1.468	1.456
3	81.043	1.208	0	1.364	1.409	1.357	1.402	1.456	1.438	78.834	1.472	1.477	1.476	1.464
Mean	81	1.212	0	1.373	1.42	1.365	1.413	1.464	1.444	78.822	1.468	1.474	1.472	1.46
BF	-4.413													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 95: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
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## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.

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## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 96: Bantu : Iroquois <-> Uni.localresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	73.838	0	0	1.113	1.356	1.312	1.319	1.421	1.38	72.652	1.286	1.293	1.287	1.277
2	74.152	0	0	1.119	1.363	1.317	1.317	1.429	1.38	72.636	1.289	1.298	1.292	1.276
3	74.48	0	0	1.118	1.354	1.309	1.313	1.418	1.37	72.634	1.289	1.296	1.291	1.276
Mean	74.157	0	0	1.117	1.358	1.313	1.316	1.423	1.377	72.641	1.288	1.296	1.29	1.276
BF	-2.372													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 97: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
## Please specify format in kable. kableExtra can customize either HTML or
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## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 98: Bantu : Omaha <-> Matri.anvunclocalresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	71.612	0	2.931	3.025	0	3.016	0	1.457	2.948	76.23	1.196	3.196	2.052	2.754
2	71.629	0	2.934	3.045	0	3.043	0	1.508	2.957	76.055	1.162	3.033	1.974	2.713
3	71.979	0	2.95	3.076	0	3.07	0	1.478	2.986	76.018	1.175	3.095	2.022	2.696
Mean	71.74	0	2.938	3.049	0	3.043	0	1.481	2.964	76.101	1.178	3.108	2.016	2.721
BF	9.234													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 99: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
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## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 100: Bantu : Omaha <-> Patrilineal

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	73.797	2.514	0	2.492	2.511	0	2.215	2.393	2.512	76.938	1.252	5.49	4.586	4.632
2	73.435	2.523	0	2.512	2.518	0	2.239	2.396	2.519	76.993	1.283	5.675	4.688	4.712
3	73.136	2.523	0	2.502	2.522	0	2.222	2.39	2.52	77.002	1.262	5.64	4.694	4.733
Mean	73.456	2.52	0	2.502	2.517	0	2.225	2.393	2.517	76.978	1.266	5.602	4.656	4.692
BF	6.282													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
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```

Table 101: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.000

```
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## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 102: Bantu : Omaha <-> Patrilocal

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	71.037	2.777	0	2.791	2.767	2.613	2.682	2.612	0	77.163	1.367	8.372	7.076	7.072
2	70.765	2.777	0	2.797	2.766	2.602	2.688	2.598	0	77.113	1.382	8.418	7.292	7.293
3	70.961	2.762	0	2.782	2.753	2.579	2.669	2.573	0	77.213	1.364	8.281	7.047	7.047
Mean	70.921	2.772	0	2.79	2.762	2.598	2.68	2.594	0	77.163	1.371	8.357	7.138	7.137
BF	12.251													

```
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## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 103: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1

	Point est.	Upper C.I.
Independent	1	1

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 104: Bantu : Omaha <-> Uni.localresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	54.633	0.572	0	0.744	0.744	0.608	0.669	0.649	0	54.368	0.721	0.722	0.72	0.721
2	54.805	0.575	0	0.742	0.742	0.592	0.665	0.651	0	54.412	0.722	0.723	0.722	0.722
3	54.668	0.579	0	0.747	0.747	0.59	0.665	0.654	0	54.475	0.722	0.723	0.721	0.722
Mean	54.702	0.575	0	0.744	0.744	0.597	0.666	0.651	0	54.418	0.722	0.723	0.721	0.722
BF	-0.531													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 105: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.001

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
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```

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 106: Uto : Hawaiian <-> Absenceofcousinmarriage.permitted

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	bet
1	15.093	14.869	15.637	0	11.593	0	14.018	21.913	22.039	14.521	19.959	20.281	20.09	20.
2	14.98	14.952	15.927	0	11.063	0	14.775	22.152	22.327	14.529	20.096	20.455	20.305	20.
3	14.78	14.576	15.316	0	11.857	0	14.895	22.11	22.225	14.51	20.568	20.852	20.683	20.
Mean	14.951	14.799	15.627	0	11.504	0	14.563	22.058	22.197	14.52	20.208	20.529	20.359	20.
BF	-1.144													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 107: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

```
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## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 108: Uto : Hawaiian <-> Absenceofcousinmarriage.preference

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	be
1	15.238	0	9.712	10.438	12.386	16.553	16.508	6.83	10.043	14.662	15.591	15.943	15.821	15
2	15.285	0	9.826	10.642	12.564	16.72	16.771	6.214	9.768	14.792	15.543	15.806	15.709	15
3	15.394	0	9.982	10.637	12.679	16.902	16.944	5.905	9.974	15.238	15.516	15.874	15.751	15
Mean	15.306	0	9.84	10.572	12.543	16.725	16.741	6.316	9.928	14.897	15.55	15.874	15.76	15
BF	-1.153													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 109: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 110: Uto : Hawaiian <-> Bi.linealdescent

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	b
1	15.411	0	11.127	12.971	15.298	19.351	19.099	5.282	10.702	15.433	17.426	17.941	17.633	1
2	15.416	0	11.12	12.71	15.363	19.327	19.035	5.969	11.009	15.283	17.171	17.596	17.395	1
3	15.275	0	11.118	12.807	15.126	19.232	18.963	4.64	10.631	15.341	17.098	17.569	17.297	1
Mean	15.367	0	11.122	12.829	15.262	19.303	19.032	5.297	10.781	15.352	17.232	17.702	17.442	1
BF	0.045													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
```

```
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 111: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.000
Independent	1	1.001

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.

## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 112: Uto : Hawaiian <-> Bi.localextendedfamily

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2
1	34.559	52.583	41.66	51.186	37.662	50.851	56.078	42.442	48.643	33.044	50.637	51.38	51.478
2	35.039	49.834	39.701	48.203	37.668	48.893	52.187	40.1	44.924	33.098	51.13	51.583	51.631
3	34.405	50.272	39.951	48.622	38.774	49.331	52.432	40.387	44.895	33.121	50.982	51.64	51.735
Mean	34.668	50.896	40.437	49.337	38.035	49.692	53.566	40.976	46.154	33.088	50.916	51.534	51.615
BF	-3.029												

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 113: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.026	1.087
Independent	1.000	1.000

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.

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## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 114: Uto : Hawaiian <-> Bi.localresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2
1	22.208	0	13.928	16.594	19.974	24.309	24.341	11.166	16.268	22.114	22.116	22.533	22.487
2	22.345	0	14.339	16.174	19.31	24.112	24.114	10.637	15.945	22.057	22.107	22.512	22.47
3	22.004	0	14.236	16.347	19.738	24.558	24.566	10.926	15.765	22.314	22.25	22.662	22.65
Mean	22.186	0	14.168	16.372	19.674	24.326	24.34	10.91	15.993	22.162	22.158	22.569	22.536

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2
BF	-0.187												

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 115: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.001

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
## Please specify format in kable. kableExtra can customize either HTML or
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```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 116: Uto : Iroquois <-> Cross.cousinmarriage.permitted

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	12.543	12.018	11.985	7.339	1.484	6.011	0	7.55	7.089	12.258	11.576	11.503	11.585	11.527
2	12.461	11.974	11.92	7.294	0	5.545	0	7.499	7.001	12.188	11.424	11.392	11.442	11.377
3	12.575	12.116	12.135	7.327	1.368	5.775	0	7.255	7.043	12.096	11.416	11.352	11.422	11.355
Mean	12.526	12.036	12.013	7.32	0.951	5.777	0	7.435	7.044	12.181	11.472	11.416	11.483	11.42
BF	-0.569													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 117: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.000	1.001
Independent	1.001	1.002

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 118: Uto : Iroquois <-> Cross.cousinmarriage.preferred

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta
1	14.306	16.941	16.867	10.751	0	8.705	0	11.008	10.663	14.059	15.907	15.843	15.958	15.8
2	14.142	17.108	17.018	10.885	0	8.603	0	11.334	10.94	14.236	15.711	15.64	15.744	15.6
3	14.63	16.727	16.627	10.291	0	8.331	0	10.936	10.454	14.618	15.935	15.905	16.029	15.9
Mean	14.359	16.925	16.837	10.642	0	8.546	0	11.093	10.686	14.304	15.851	15.796	15.91	15.7
BF	-0.493													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 119: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1.001	1.002
Independent	1.000	1.001

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
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```

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 120: Uto : Iroquois <-> Exogamy.unilineal.descent

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	11.011	12.013	12.005	7.381	0	5.601	0	7.374	7.096	10.841	11.296	11.239	11.28	11.23
2	11.054	11.968	11.944	7.149	0	5.67	0	7.519	6.895	10.791	11.404	11.339	11.358	11.33
3	11.191	11.96	11.964	7.373	1.963	5.794	0	7.196	6.774	10.626	11.465	11.407	11.457	11.42
Mean	11.085	11.98	11.971	7.301	0.654	5.688	0	7.363	6.922	10.753	11.388	11.328	11.365	11.33
BF	-0.34													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 121: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
```

Table 122: Uto : Iroquois <-> High.polygyny

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2
1	20.347	23.579	18.678	18.538	15.161	13.345	21.069	14.811	20.542	19.029	22.009	21.985	22.211
2	20.105	23.566	18.831	18.445	15.814	13.385	21.023	14.834	20.748	19.185	21.918	21.888	22.1
3	19.767	23.662	18.618	18.32	15.748	13.047	21.041	14.709	20.721	19.029	22.093	22.07	22.238
Mean	20.073	23.602	18.709	18.434	15.574	13.259	21.044	14.785	20.67	19.081	22.007	21.981	22.183
BF	-2.635												

Table 123: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.001

Table 124: Uto : Iroquois <-> Matri.anvunclocalresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	25.058	34.072	33.32	34.233	0	0	0	23.573	22.949	25.177	29.398	29.434	29.666	29.69
2	25.346	33.887	33.138	34.059	0	0	0	23.04	22.525	25.272	29.375	29.374	29.595	29.599
3	25.621	33.73	33.136	33.88	0	0	0	22.68	21.85	25.243	29.415	29.423	29.645	29.66
Mean	25.342	33.896	33.198	34.057	0	0	0	23.098	22.441	25.231	29.396	29.41	29.635	29.65
BF	0.238													

Table 125: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.001

```
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.

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## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 126: Uto : Iroquois <-> Uni.linealdescent

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	12.711	17.175	0	14.585	16.051	8.291	11.331	0	0	12.497	13.552	13.514	13.644	13.475
2	12.928	16.927	0	14.431	15.775	8.509	11.239	0	0	12.259	13.742	13.725	13.826	13.635
3	12.532	17.093	0	14.633	15.905	8.819	11.075	0	0	12.364	13.514	13.467	13.547	13.429
Mean	12.724	17.065	0	14.55	15.91	8.54	11.215	0	0	12.373	13.603	13.569	13.672	13.513
BF	-0.428													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 127: Gelman-Rubin MCMC chain diagnostic test

	Point est.	Upper C.I.
Dependent	1	1.001
Independent	1	1.001

```
## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.

## Warning in kable_styling(., bootstrap_options = c("striped", "bordered")):
## Please specify format in kable. kableExtra can customize either HTML or
## LaTeX outputs. See https://haozhu233.github.io/kableExtra/ for details.
```

Table 128: Uto : Iroquois <-> Uni.localresidence

run	MLL	q12	q13	q21	q24	q31	q34	q42	q43	MLL	alpha1	beta1	alpha2	beta2
1	25.946	36.127	0	37.697	36.432	25.894	27.61	0	0	25.969	31.723	31.715	31.91	32.038
2	25.702	36.273	0	37.87	36.642	26.201	27.63	0	0	25.927	31.959	31.973	32.173	32.327
3	25.622	36.266	0	37.764	36.571	26.356	27.177	0	0	26.023	31.871	31.863	32.09	32.279
Mean	25.757	36.222	0	37.777	36.548	26.15	27.472	0	0	25.973	31.851	31.85	32.058	32.215
BF	0.046													

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 129: Gelman-Rubin MCMC chain diagnostic test

|	Point est.	Upper C.I.
Dependent	1	1
Independent	1	1

Bantu node 70 state inference

Here we re-construct node 70 within the Bantu tree, to confirm the hypotheses that the presence of both Iroquois terminologies and a preference for cross-cousin marriage existed at this point.

Table 1 in the main text shows that the dependent model is already preferred, so here we only look at the dependent model. The figure below shows the likelihood of each possibility. Top left: Absence of both Iroquois terminology & a preference for cross-cousin marriage. Top right: Absence of cross-cousin marriage and the presence of cross-cousin marriage preference. Bottom right: Both Iroquoian terminologies and cross-cousin marriage preferences are present. Bottom left: presence of an Iroquoian terminology, and absence of a cross-cousin marriage preference.

The graph clearly shows the presence of both traits being present here is the most likely option, with approximately 0.77 probability. This probability drops to around 0.5 on the ancestral node.

Bantu 70: Dependent model
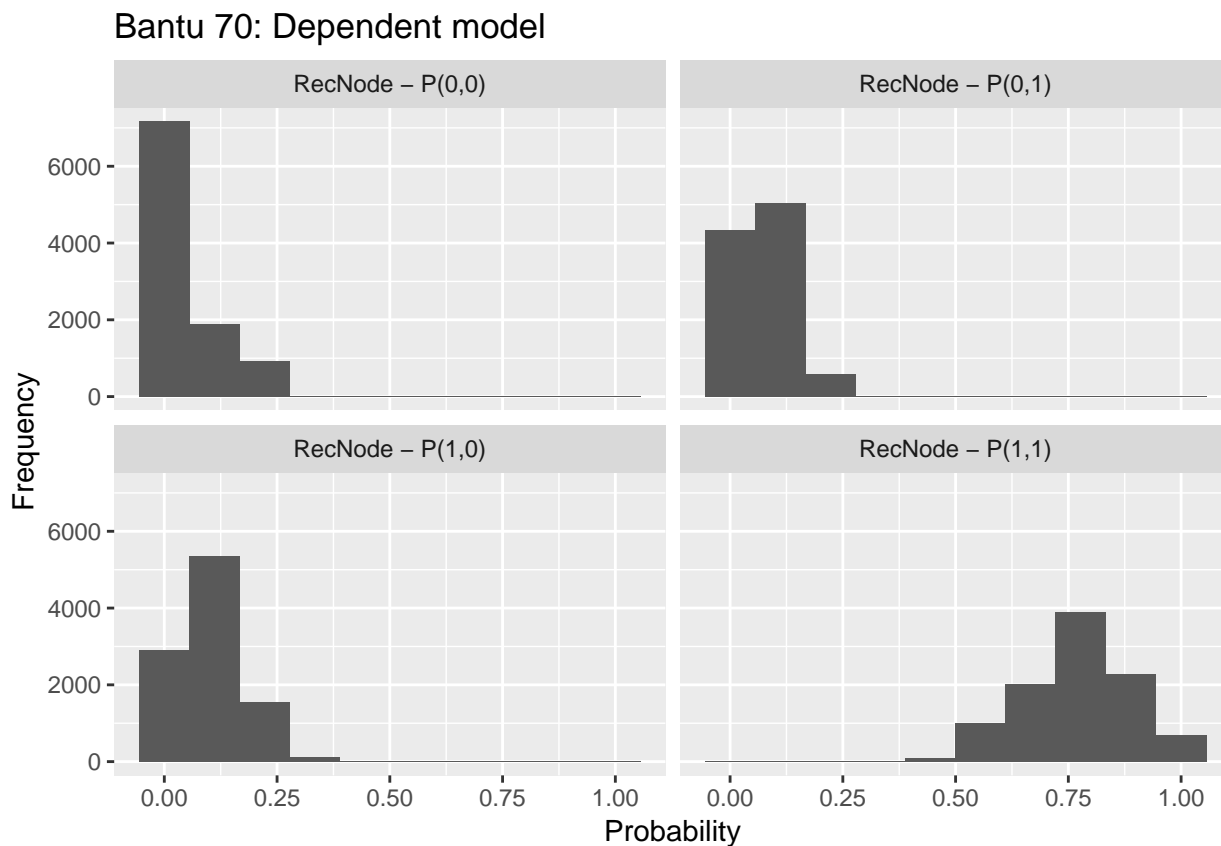
Multi-solution models

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 (this is the longest run time allowed by server constraints). 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.
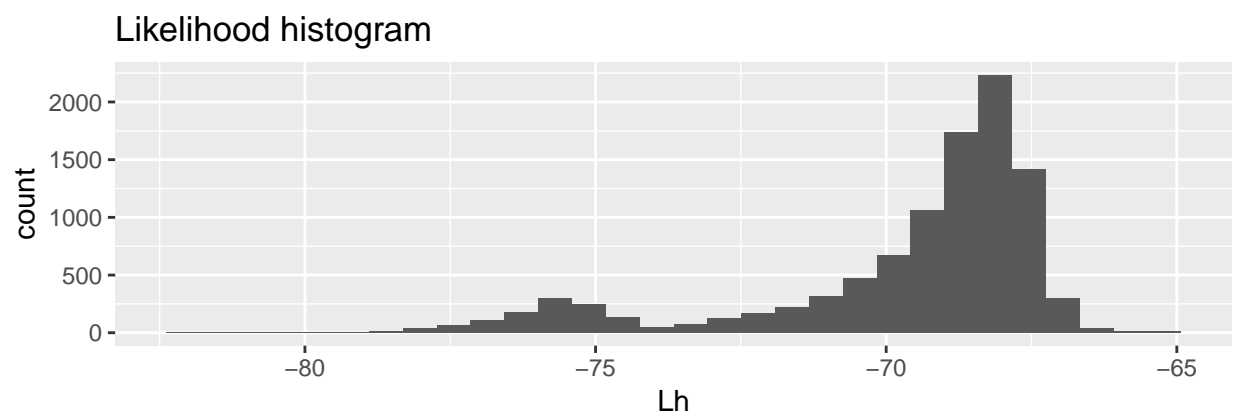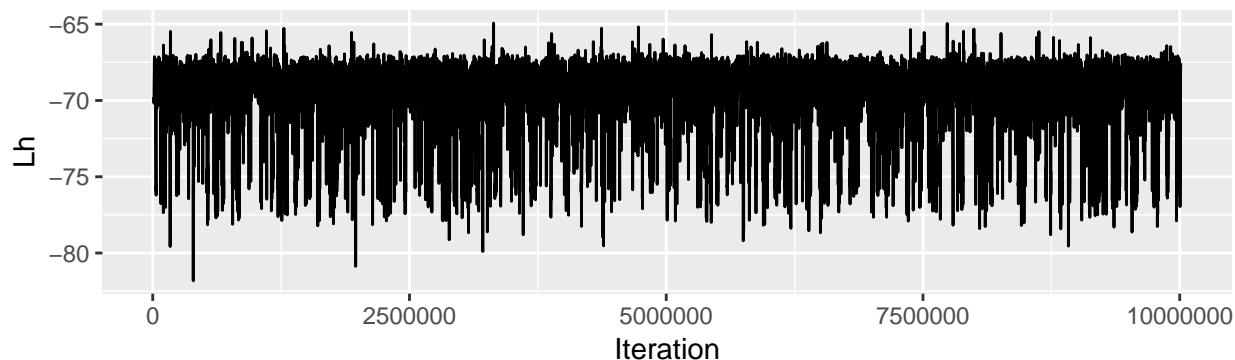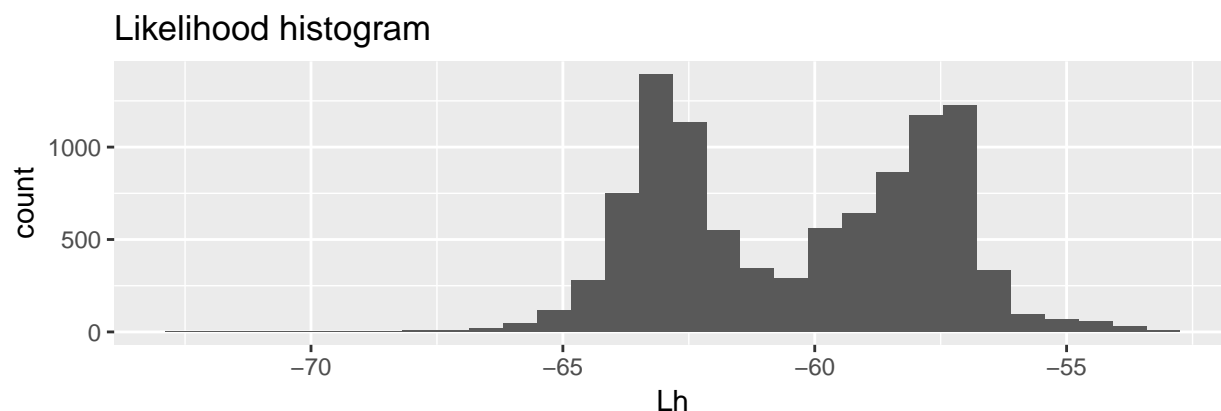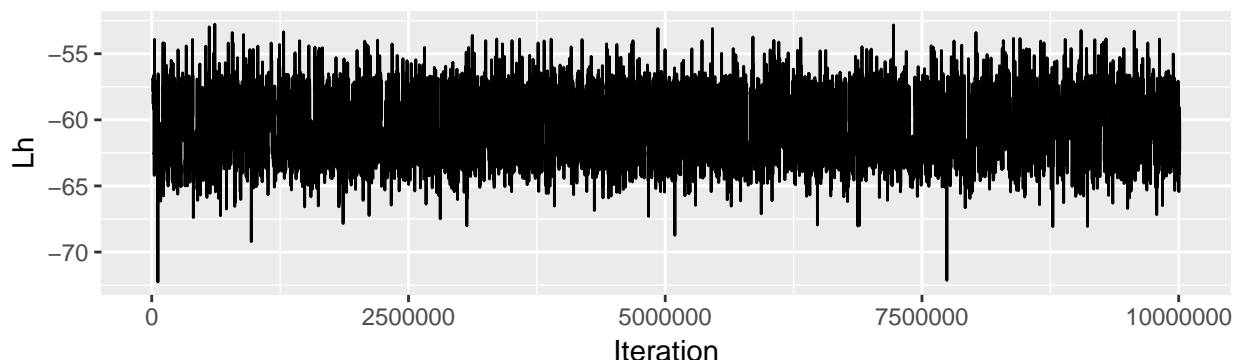

Likelihood histogram


```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 130: 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

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 131: 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.
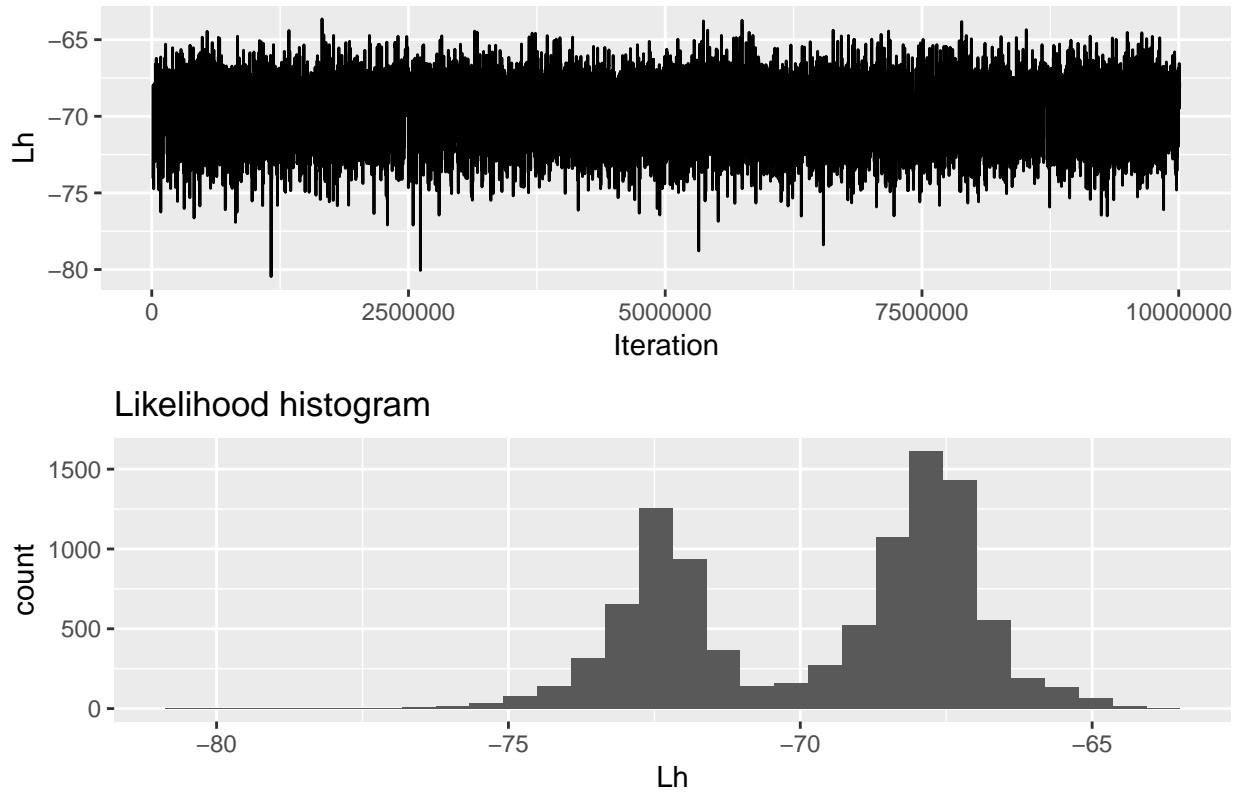


```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 132: 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

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 133: 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.

Likelihood histogram

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 134: 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

```
## Warning in kable_styling(.): Please specify format in kable. kableExtra can
## customize either HTML or LaTeX outputs. See https://haozhu233.github.io/
## kableExtra/ for details.
```

Table 135: 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

Multiple comparisons

Since this study has numerous hypothesis tests, it is important we address the statistical problem of multiple comparisons. The multiple comparison problem says that the more hypotheses tested simultaneously, the more likely an erroneous error is to occur. There is strong debate in the literature on whether this is a problem here, but we argue that it is not.

The primary reason for this not being a problem is that all our hypotheses were set out *a priori*. They are not the result of comparing all social variables against all binary kinship terminologies, and make a tiny portion of those that are possible. All hypotheses are established in theory and many had been previously tested.

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