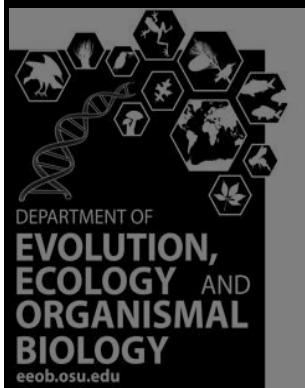
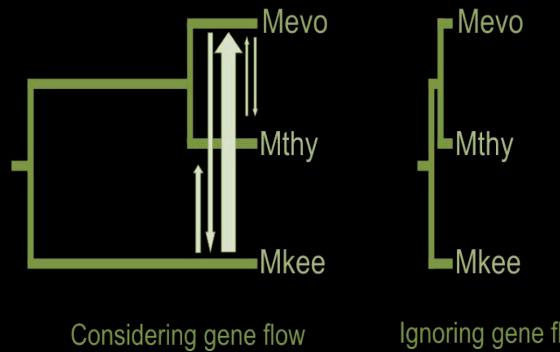


Speciation with gene flow in *Myotis* bats



Divergence time estimates

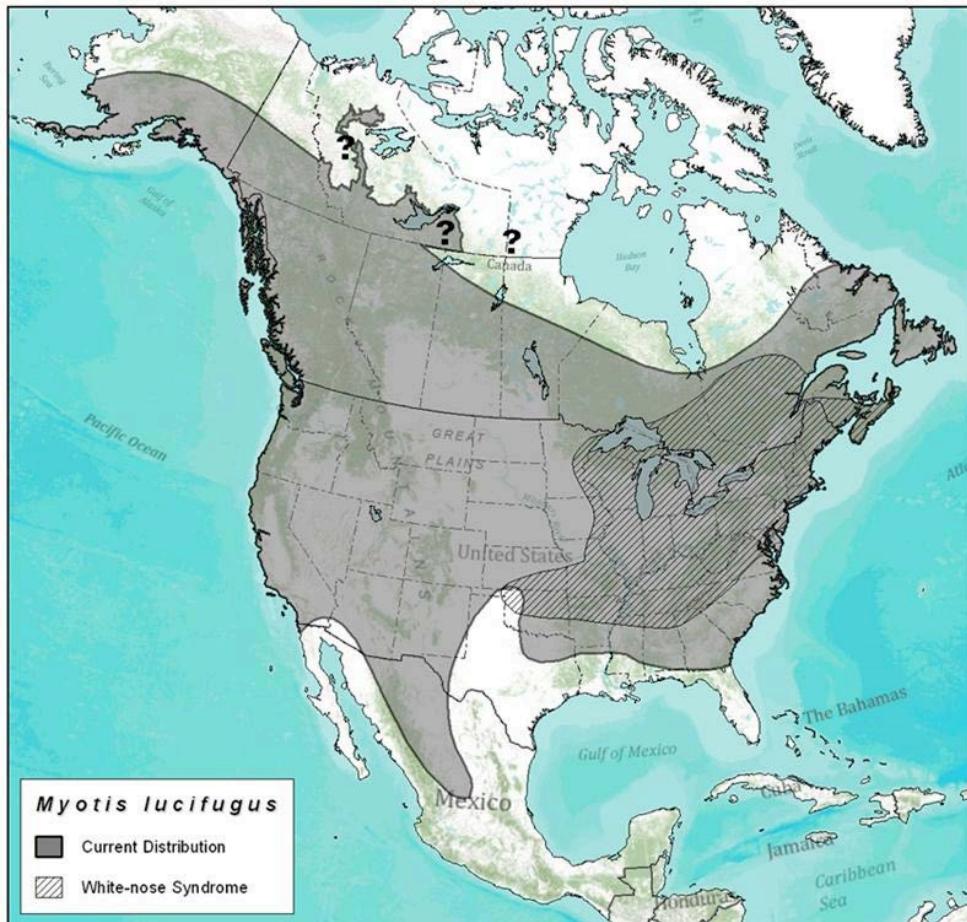


@bryancarstens
carstens.12@osu.edu

<http://carstenslab.org.ohio-state.edu>



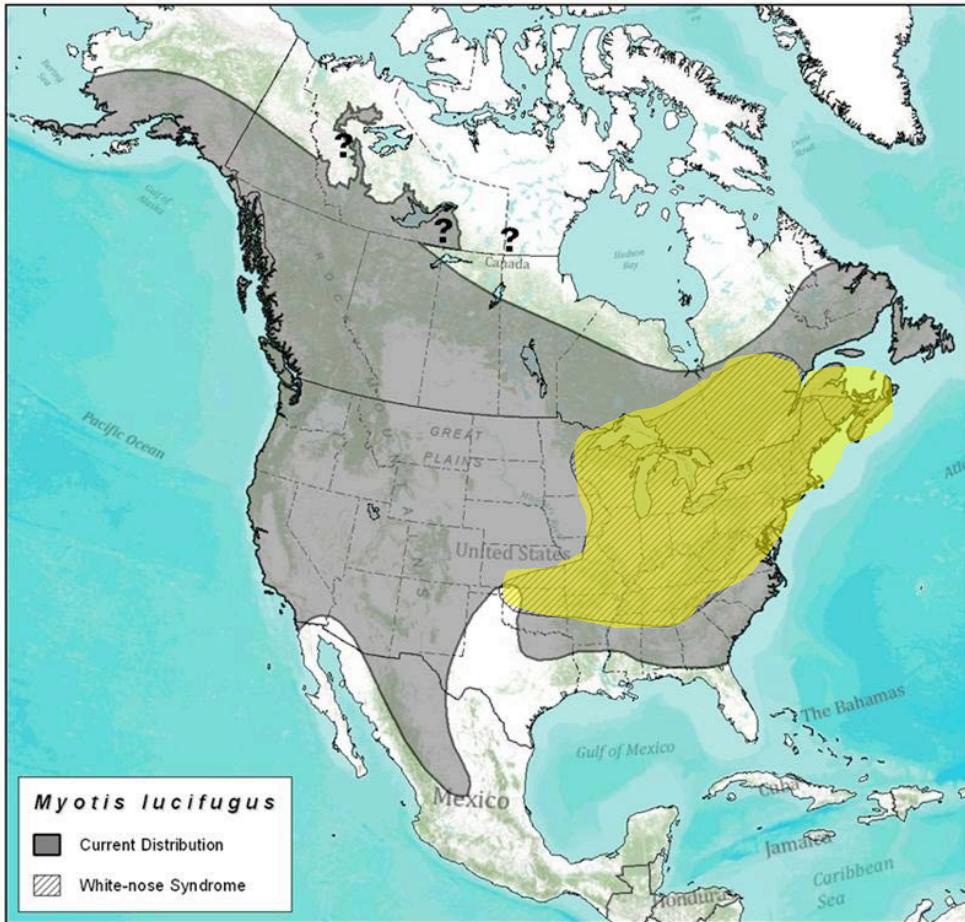
Little brown bat (*Myotis lucifugus*)



ESD©2003



Little brown bat (*Myotis lucifugus*)



M.l.alacensis

M.l.carissima

M.l.relictus

M.l.lucifugus

Myotis lucifugus (*alascensis*, *carissima*, *lucifugus*, *relictus*)

Myotis evotis (*evotis*, *pacificus*, *jonesorum*, *chryonotus*)

Myotis thysanodes (*aztecus*, *thysanodes*, *pahasapensis*, *vespertinus*)

Myotis keenii

Syst. Biol. 59(4):400–414, 2010

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DOI:10.1093/sysbio/syq024

Advance Access publication on May 24, 2010

Species Delimitation Using a Combined Coalescent and Information-Theoretic Approach: An Example from North American *Myotis* Bats

BRYAN C. CARSTENS^{1,*} AND TANYA A. DEWEY²

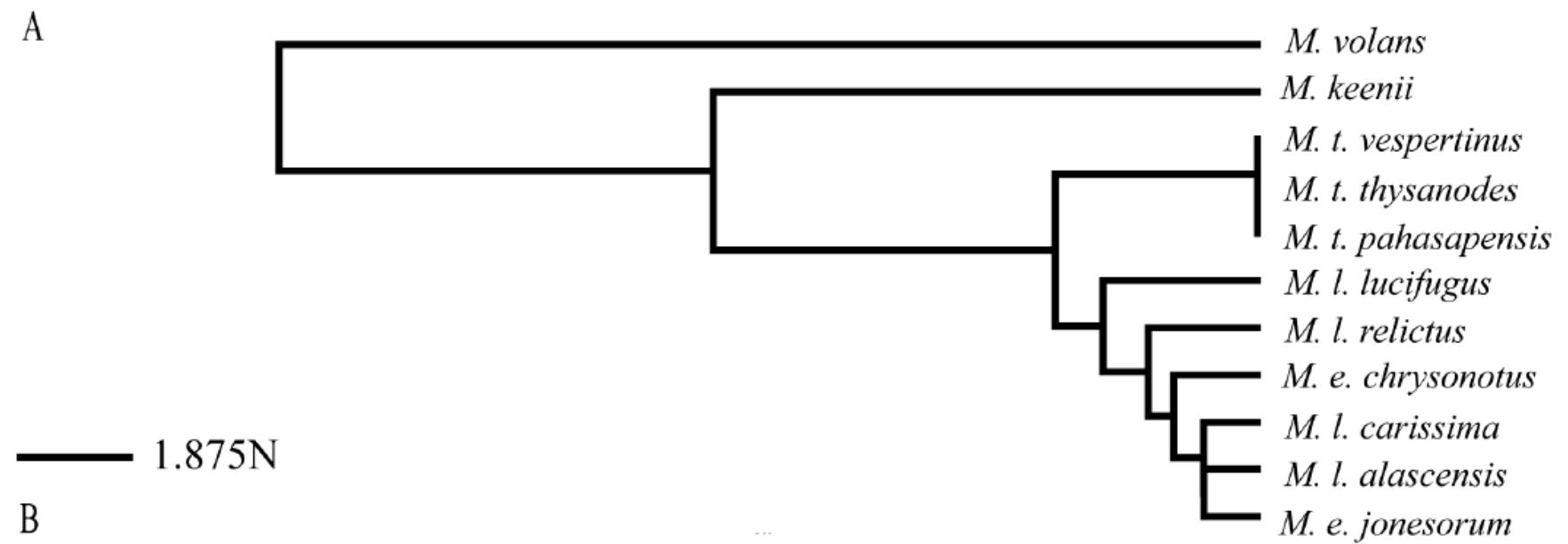
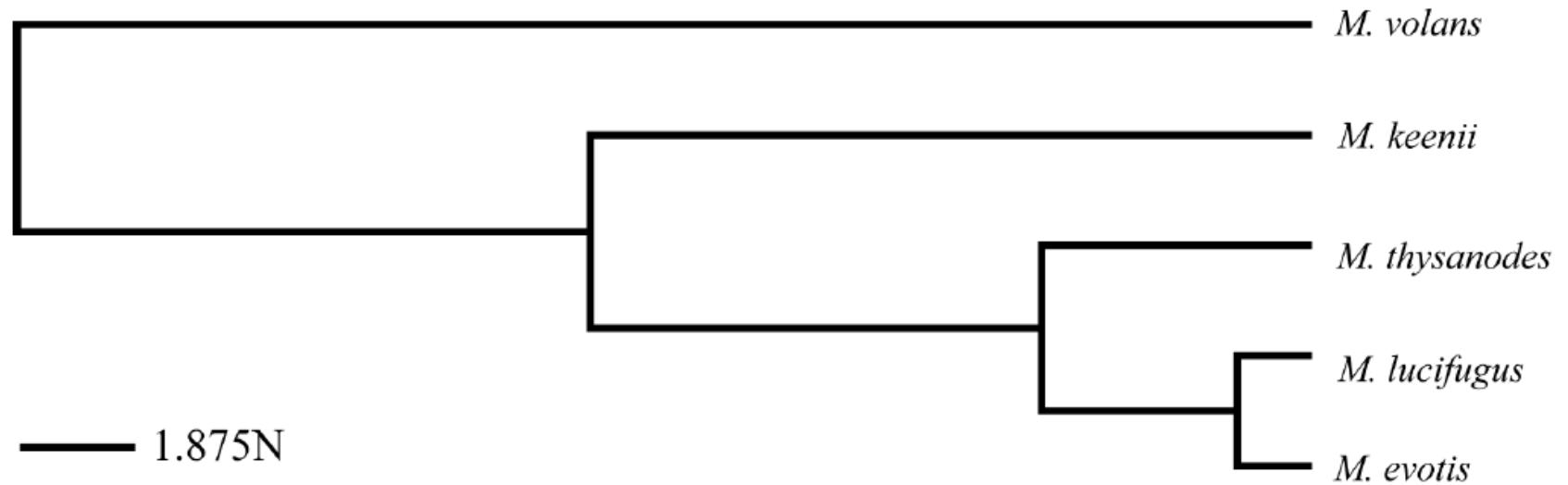
¹Department of Biological Sciences, Louisiana State University, 202 Life Sciences Building, Baton Rouge, LA 70808, USA; and ²Department of Ecology and Evolutionary Biology, Museum of Zoology, University of Michigan, 1109 Geddes Avenue, Ann Arbor, MI 48109-1079, USA;

*Correspondence to be sent to: Department of Biological Sciences, Louisiana State University, 202 Life Sciences Building, Baton Rouge, LA 70808, USA;
E-mail: carstens@lsu.edu.

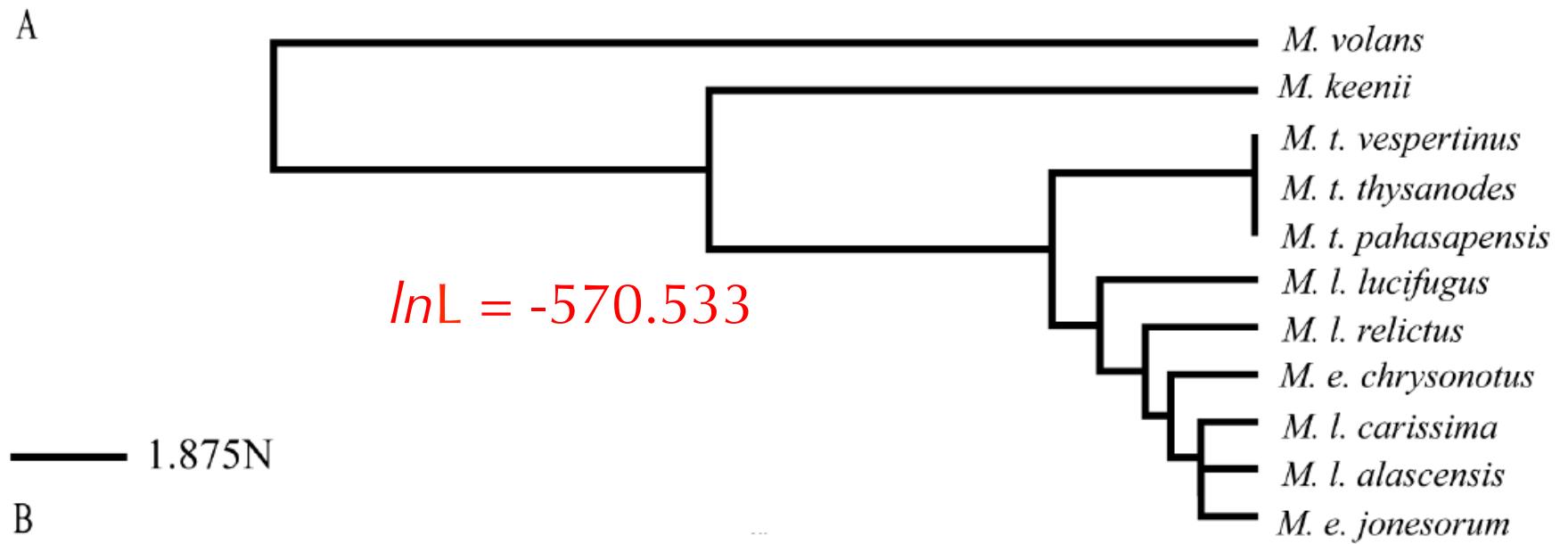
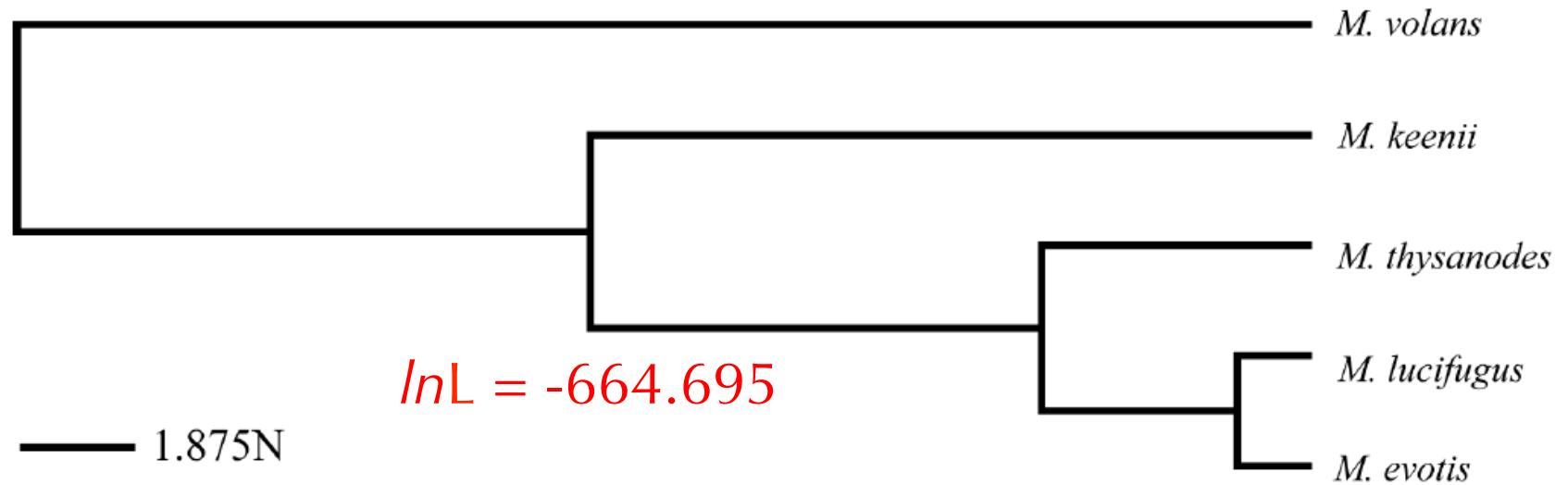
Received 20 May 2009; reviews returned 18 August 2009; accepted 11 December 2009

Associate Editor: Marshal Hedin





Carstens & Dewey, 2010



Carstens & Dewey, 2010

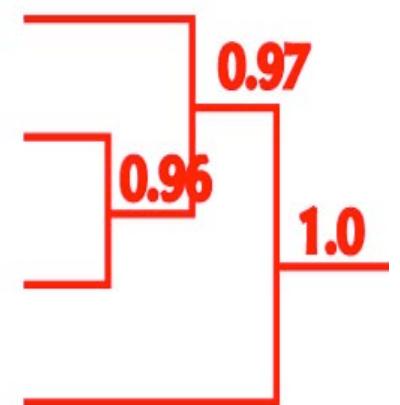
Lineage composition	-lnL	k	AIC	Δi	L (Model data)	w_i
<i>Clock-like loci</i>						
Mtp_Mtt_Mtv, Mla, Mlc, Mll, Mlr, Mej, Mec	-570.533	8	1157.065	0.000	1.000	0.685
Mtp_Mtv, Mtt, Mla, Mlc, Mll, Mlr, Mej, Mec	-570.533	9	1159.065	2.000	0.135	0.093
Mtt_Mtp, Mtv, Mla, Mlc, Mll, Mlr, Mej, Mec	-570.533	9	1159.065	2.000	0.135	0.093
Mtt_Mtv, Mtp, Mla, Mlc, Mll, Mlr, Mej, Mec	-570.533	9	1159.065	2.000	0.135	0.093
Mtp_Mtt_Mtv, Mla_Mlc, Mll, Mlr, Mej, Mec	-573.375	7	1160.751	3.686	0.025	0.017
Mtp, Mtt, Mtv, Mla, Mlc, Mll, Mlr, Mej, Mec	-570.533	10	1161.065	4.000	0.018	0.013
Mtp_Mtv, Mtt, Mla_Mlc, Mll, Mlr, Mej, Mec	-573.375	8	1162.751	5.686	0.003	0.002
Mtt_Mtp, Mtv, Mla_Mlc, Mll, Mlr, Mej, Mec	-573.375	8	1162.751	5.686	0.003	0.002
Mtt_Mtv, Mtp, Mla_Mlc, Mll, Mlr, Mej, Mec	-573.375	8	1162.751	5.686	0.003	0.002
Mtp, Mtt, Mtv, Mla_Mlc, Mll, Mlr, Mej, Mec	-573.375	9	1164.751	7.686	0.000	0.000

Information theory metrics for 10 best models...

- four models account for 96.4% of the total model probability
- all treat subspecies within *M. lucifugus* as independent evolutionary lineages

BPP (Yang & Rannala 2010)

I. relictus
I. lucifugus
I. alascensis
I. carriSIMA



doi:10.1111/j.1558-5646.2012.01640.x

SPECIES DELIMITATION WITH ABC AND OTHER COALESCENT-BASED METHODS: A TEST OF ACCURACY WITH SIMULATIONS AND AN EMPIRICAL EXAMPLE WITH LIZARDS OF THE *LIOLAEMUS DARWINII* COMPLEX (SQUAMATA: LIOLAEMIDAE)

Arley Camargo,^{1,2} Mariana Morando,³ Luciano J. Avila,³ and Jack W. Sites, Jr.¹

¹Department of Biology & Monte L. Bean Museum, Brigham Young University, Provo, Utah 84602

²E-mail: arley.camargo@gmail.com

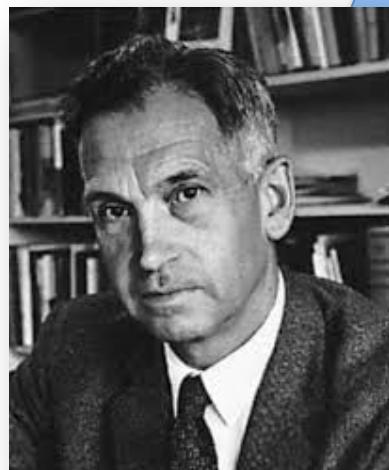
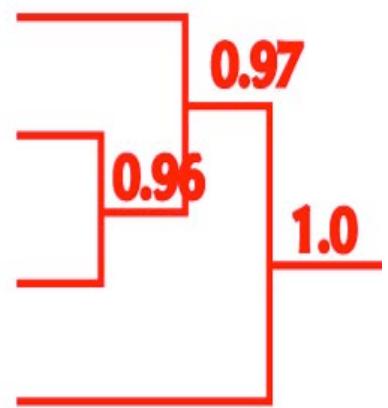
³CONICET-CENPAT, Boulevard Almirante Brown 2915, U9120ACD, Puerto Madryn, Chubut, Argentina

Species delimitation...
ABC, BPP > spedeSTEM

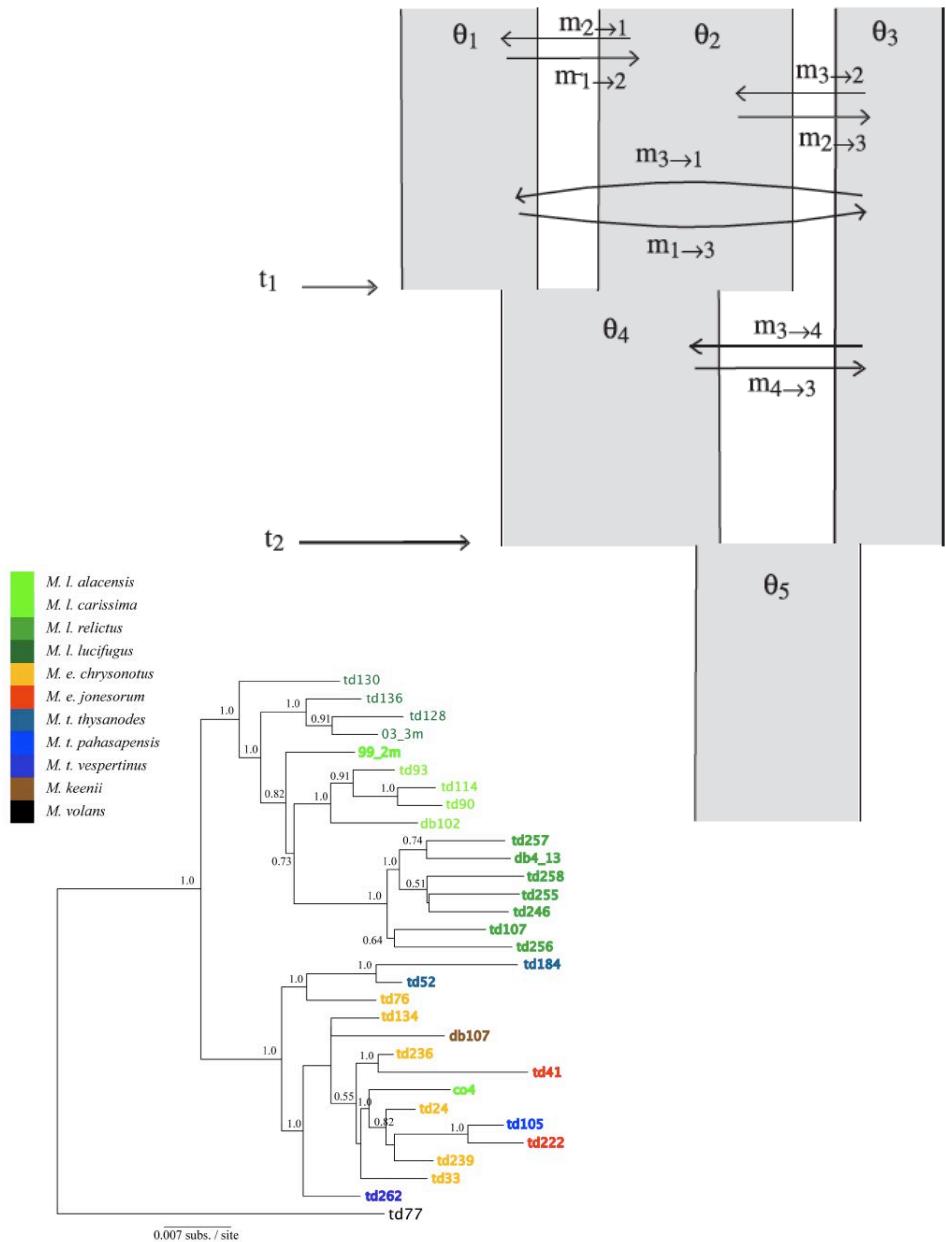


BPP (Yang & Rannala 2010)

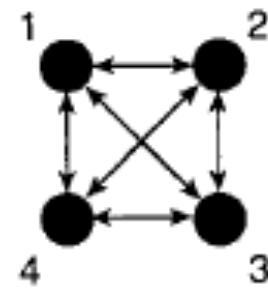
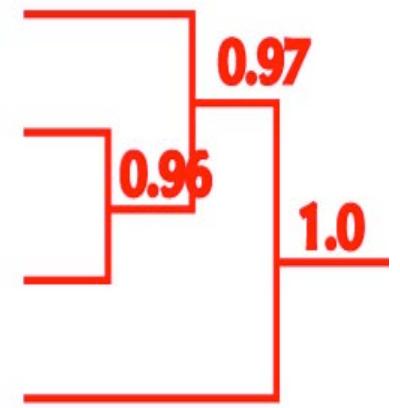
I. relictus
I. lucifugus
I. alascensis
I. carrisima



"species are groups of interbreeding natural populations that are reproductively isolated from other such groups."



l. relictus
l. lucifugus
l. alascensis
l. carissima



Why do we choose certain models to analyze our data?

Phylogenetics

STEM: species tree estimation using maximum likelihood for gene trees under coalescence

Laura S. Kubatko^{1,*}, Bryan C. Carstens² and L. Lacey Knowles³

¹Departments of Statistics and Evolution, Ecology, and Organismal Biology, The Ohio State University, Columbus, OH 43210, ²Department of Biological Sciences, Louisiana State University, Baton Rouge, LA 70803 and

³Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, MI 48109, USA

Received on November 28, 2008; revised and accepted February 04, 2009

Associate Editor: Martin Bishop

$$L(S, \tau) = \prod_{j=1}^N f(g_j | S, \tau)$$

STEM: Assumptions of model.

- θ is constant
 - the sequences are evolving under the molecular clock
 - shared polymorphism results from incomplete lineage sorting
-
- Species tree methods ignore gene flow...



Contents lists available at ScienceDirect

Molecular Phylogenetics and Evolution

journal homepage: www.elsevier.com/locate/ympev



Does gene flow destroy phylogenetic signal? The performance of three methods for estimating species phylogenies in the presence of gene flow

Andrew J. Eckert^a, Bryan C. Carstens^{b,*}

^aSection of Evolution and Ecology, University of California at Davis, One Shields Avenue, Davis, CA 95616, USA

^bDepartment of Biological Sciences, 202 Life Sciences Building, Louisiana State University, Baton Rouge, LA 70803, USA

Syst. Biol. 63(1):17–30, 2014

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DOI:10.1093/sysbio/syt049

Advance Access publication August 13, 2013

The Influence of Gene Flow on Species Tree Estimation: A Simulation Study

ADAM D. LEACHE^{1,*}, REBECCA B. HARRIS¹, BRUCE RANNALA^{2,3}, AND ZIHENG YANG^{3,4}

¹Department of Biology and Burke Museum of Natural History and Culture, University of Washington, Seattle, WA 98195 USA;

²Genome Center and Department of Evolution & Ecology, University of California, Davis, CA 95616, USA;

³Center for Computational Genomics, Beijing Institute of Genomics, Chinese Academy of Sciences, Beijing 100101, China; and

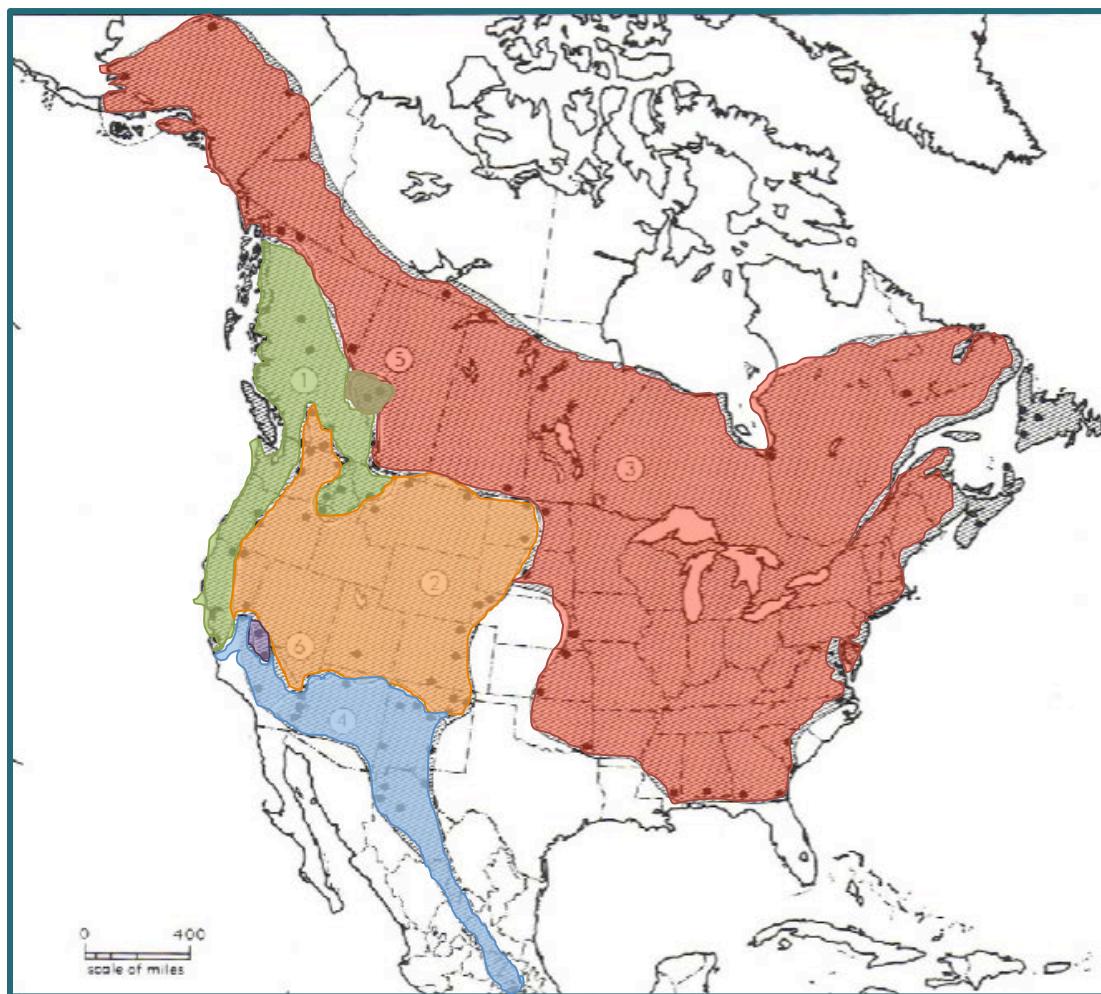
⁴Department of Biology, University College London, Gower Street, London WC1E 6BT, UK

*Correspondence to be sent to: Department of Biology, University of Washington, Seattle, WA 98195, USA;
E-mail: leache@uw.edu.

Received 15 February 2013; reviews returned 10 May 2013; accepted 2 August 2013

Associate Editor: Laura Kubatko

Little brown bat subspecies (*Myotis lucifugus*)



M.I.alascensis

M.I.carissima

M.I.relictus

M.I.lucifugus

(Hall 1981)

M.I.pernox

M.I.occultus



Ariadna
Morales-García

How do we detect gene flow? Use a program such as Migrate-*n* to estimate it . . .

**Maximum likelihood estimation of a migration matrix
and effective population sizes in *n* subpopulations
by using a coalescent approach**

Peter Beerli* and Joseph Felsenstein

PNAS | April 10, 2001 | vol. 98 | no. 8 | 4563–4568

Department of Genetics, University of Washington, Box 357360, Seattle, WA 98195-7360

Contributed by Joseph Felsenstein, February 9, 2001

Estimates $\theta = 4Ne\mu$ and $M = m / \mu$ using an *n*-island model.

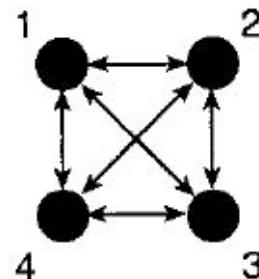
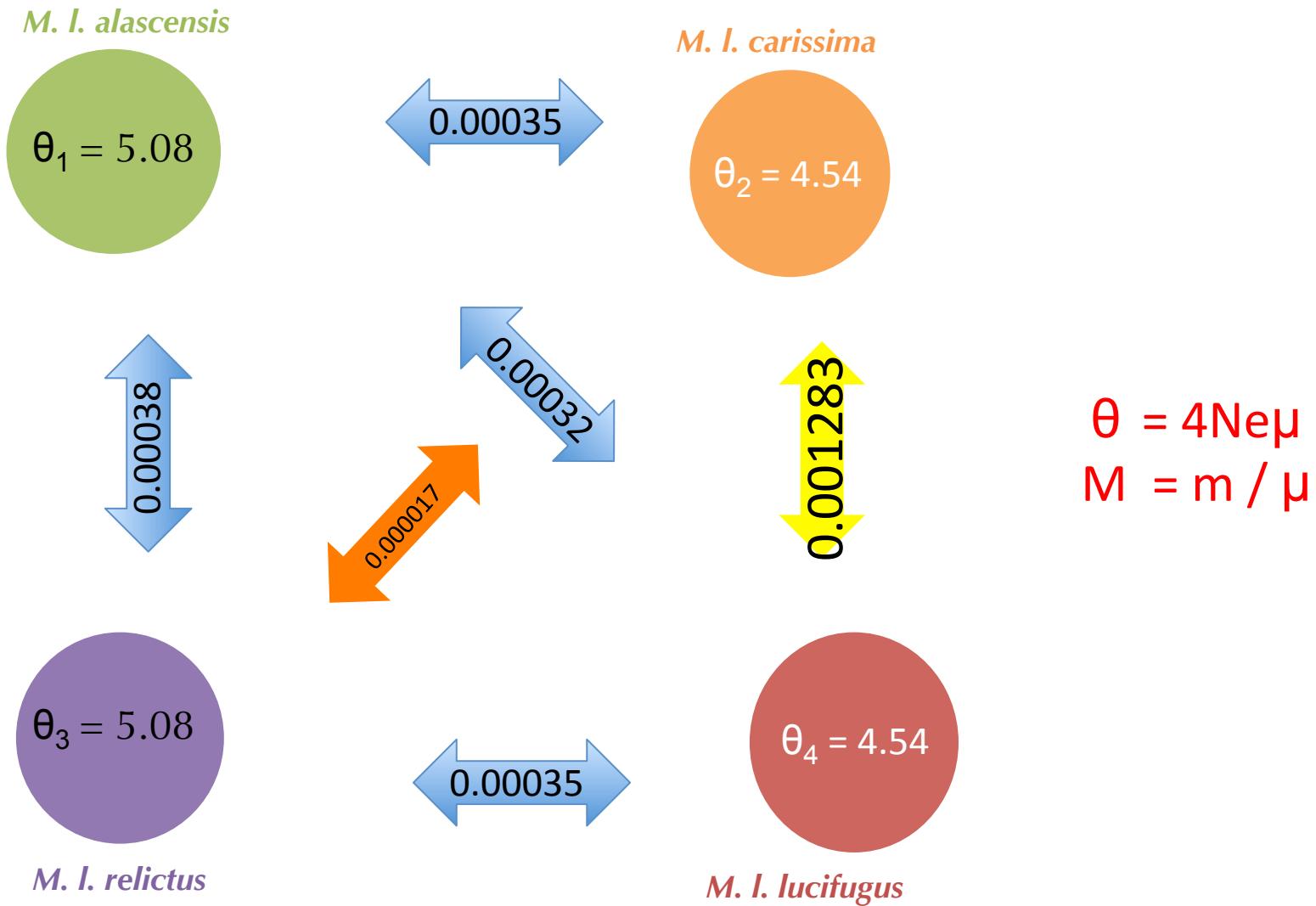


Fig. 1. *n*-island model with four populations of equal size, exchanging migrants with equal rates.

How do we detect gene flow? Use a program such as Migrate-*n* to estimate it . . .



Unified Framework to Evaluate Panmixia and Migration Direction Among Multiple Sampling Locations

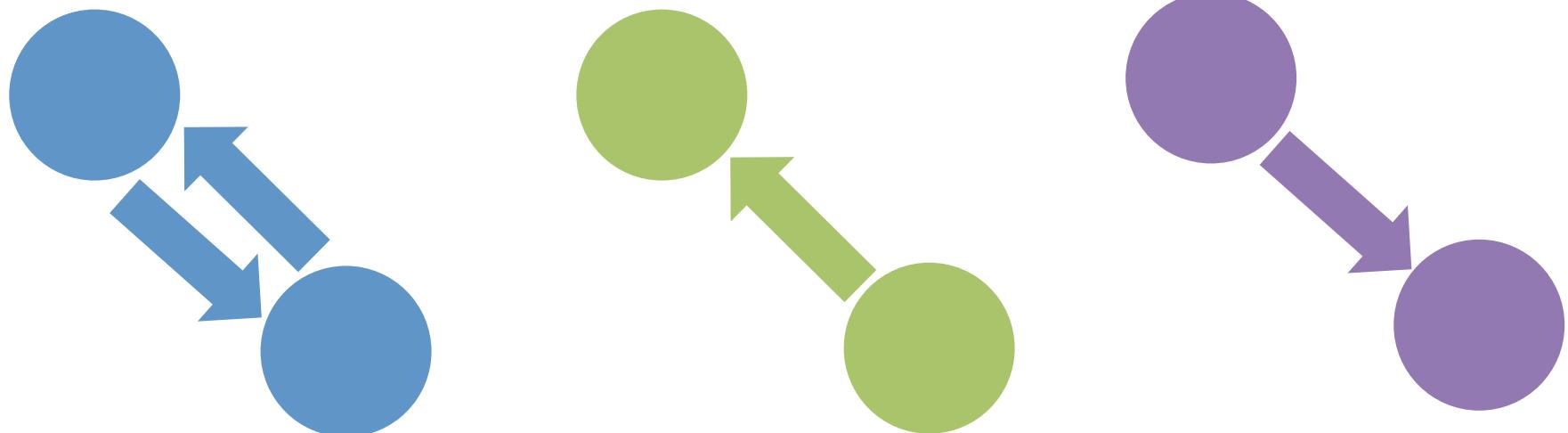
Peter Beerli¹ and Michal Palczewski

Department of Scientific Computing, Florida State University, Tallahassee, Florida 32306

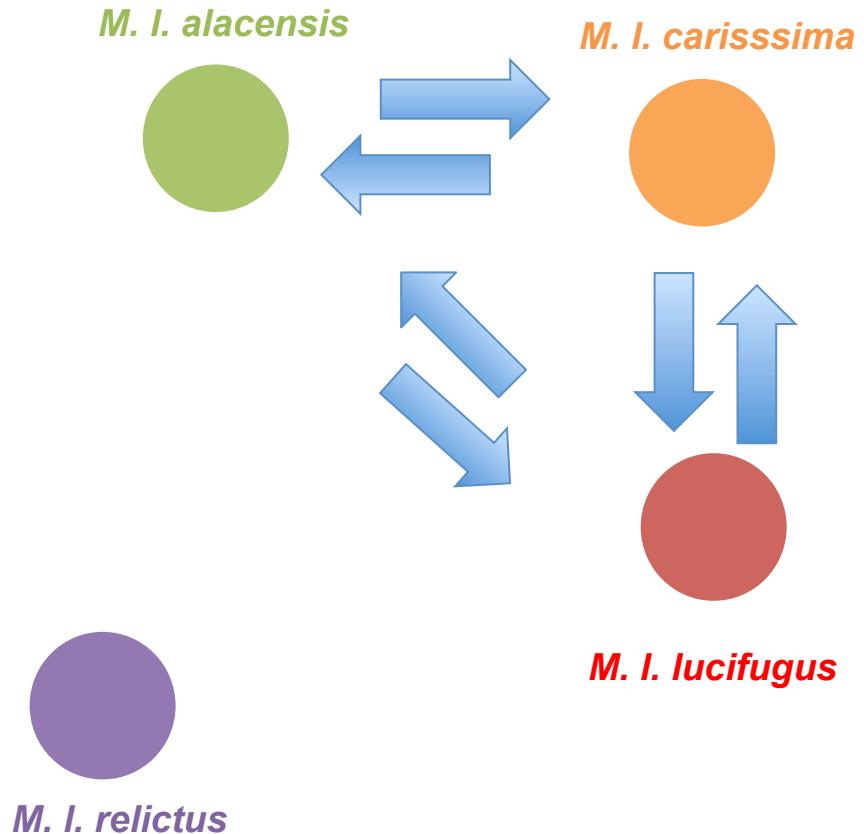
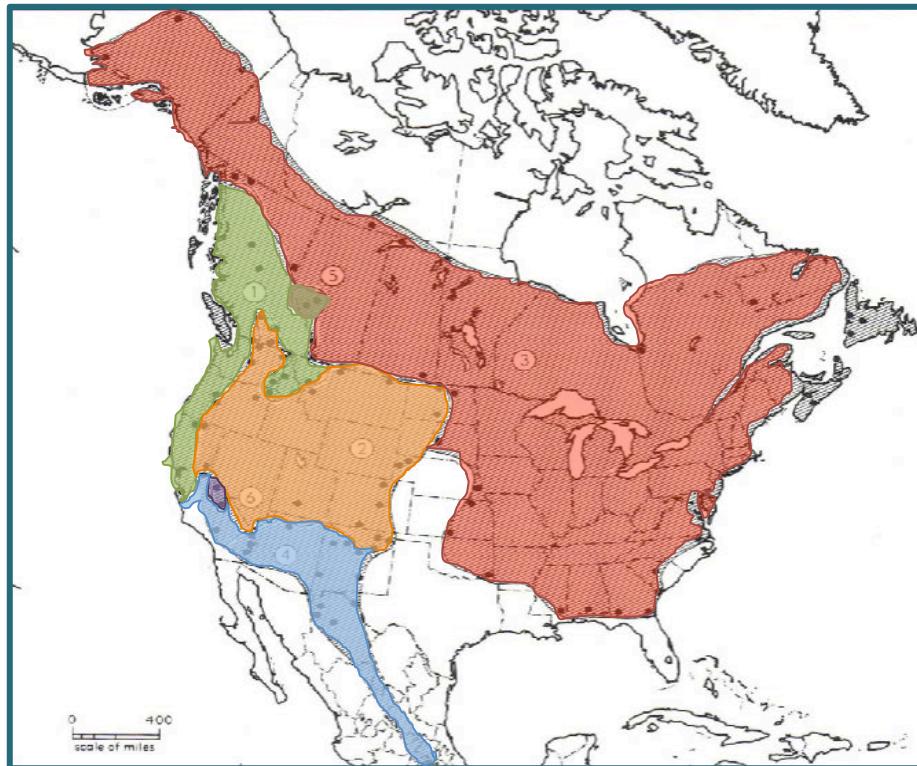
Manuscript received November 27, 2009

Accepted for publication February 17, 2010

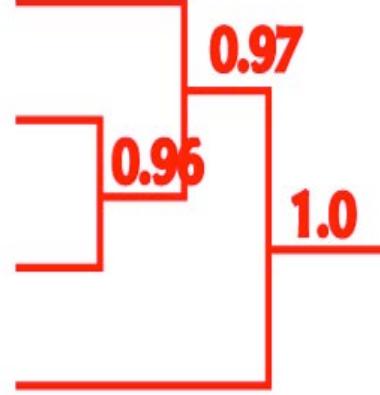
Migrate-*n* 3.6 has the ability to calculate marginal likelihoods, so migration models can be evaluated using information theory.



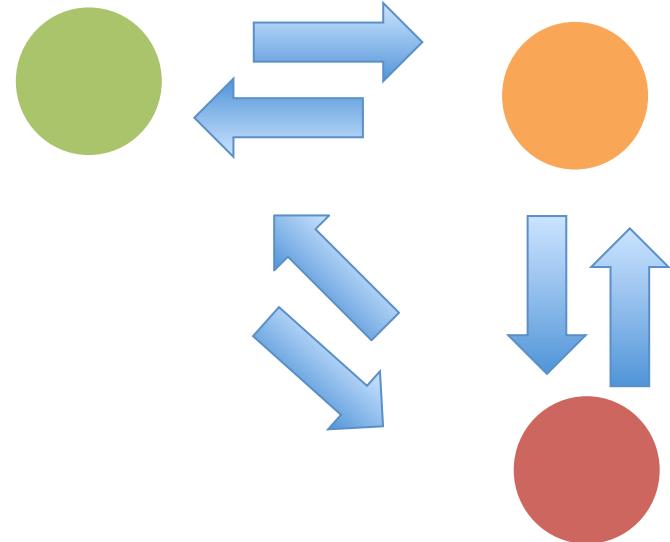
Optimal model finds that *M. I. relictus* is not connected via gene flow...



I. relictus
I. lucifugus
I. alascensis
I. carissima



M. I. alacensis *M. I. carissima*



M. I. relictus

- If we choose a species tree / delimitation approach, we infer that each subspecies within *M. lucifugus* is an independent evolutionary lineage (and probably assume that these lineages do not exchange alleles).
- If we choose an *n*-island migration model, we infer that three of the four subspecies exchange alleles at a substantial rate (and thus infer that they are not independent).

How do we justify our choices we analyze our data?

- we can **assess the fit** of the models that we choose
- we can **choose** the best model among a bunch of choices



posterior
probability

likelihood

prior

$$\Pr[\text{Tree} \mid \text{Data}] = \frac{\Pr[\text{Data} \mid \text{Tree}] \times \Pr[\text{Tree}]}{\Pr[\text{Data}]}$$



```
#NEXUS
[ID: 0852508174]
begin trees;
translate
  1 Anrm,
  2 Bnrm,
  3 Cnrm,
  4 Cnc,
  5 Dnc;
[
tree rep.1 = ((2:0.10000,(4:0.10000,5:0.10000):0.10000):0.10000,3:0.10000,1:0.10000);
tree rep.1000 = ((3:0.006993,(4:0.006555,5:0.007229):0.000554):0.014269,2:0.001265,1:0.007926);
tree rep.2000 = ((5:0.012335,(3:0.000672,4:0.000022):0.004186):0.016851,2:0.002214,1:0.005338);
tree rep.3000 = (((4:0.013396,3:0.001861):0.010962,5:0.000552):0.001771,2:0.000542,1:0.001639);
tree rep.4000 = ((4:0.002758,(3:0.005498,5:0.003617):0.005864):0.006643,2:0.005980,1:0.025120);
tree rep.5000 = ((4:0.001777,(3:0.000789,5:0.001393):0.006475):0.013680,2:0.004508,1:0.006280);
tree rep.6000 = ((5:0.002306,(4:0.002026,3:0.000966):0.003021):0.016065,2:0.008722,1:0.011203);
tree rep.7000 = (2:0.005251,((5:0.004186,4:0.003543):0.002246,3:0.001565):0.007210,1:0.002549);
tree rep.8000 = (2:0.003825,((3:0.000630,5:0.003034):0.001699,4:0.006023):0.022671,1:0.025138);
tree rep.9000 = (2:0.000986,((5:0.013872,4:0.005184):0.001416,3:0.003382):0.005159,1:0.003640);
tree rep.10000 = (2:0.004103,((3:0.000307,5:0.003384):0.000849,4:0.010198):0.002563,1:0.019618);
tree rep.11000 = ((3:0.001570,(5:0.009439,4:0.003157):0.008600):0.008988,2:0.020539,1:0.001156);
tree rep.12000 = (2:0.005935,(5:0.005158,(3:0.001101,4:0.003551):0.000527):0.012832,1:0.001782);
tree rep.13000 = (((3:0.000084,4:0.001978):0.001340,5:0.005619):0.021711,2:0.003141,1:0.004153);
tree rep.14000 = (((3:0.002721,5:0.003063):0.000965,4:0.002150):0.017916,2:0.002912,1:0.001911);
tree rep.15000 = (((5:0.003662,4:0.008229):0.001214,3:0.004921):0.003048,2:0.003570,1:0.005086);
tree rep.16000 = (2:0.001223,(4:0.009145,(5:0.002650,3:0.005159):0.000760):0.023695,1:0.005769);
```

posterior
probability

likelihood prior

$$\Pr[\text{Tree} \mid \text{Data}] = \frac{\Pr[\text{Data} \mid \text{Tree}] \times \Pr[\text{Tree}]}{\Pr[\text{Data}]}$$

```

NEXUS
[ID: 0825083174]
begin trees;
  translate
    1 AAG;
    2 ATG;
    3 CGG;
    4 CTC;
    5 GCG;
  [
tree rep.1 = ((2:0.100000,(4:0.100000,5:0.100000):0.100000):0.100000,3:0.100000,1:0.100000);
tree rep.1200 = ((3:0.00151),(0:0.00055,5:0.00723):0.00054);0.01429,2:0.001265,1:0.001265,0:0.001265;
tree rep.2000 = ((0:0.00133),(1:0.00055,4:0.00054):0.00054);0.01429,2:0.001265,1:0.001265,0:0.001265;
tree rep.3000 = (((0:0.023396,3:0.001651),(0:0.000542,5:0.000542):0.001771,2:0.000542,1:0.001651));
tree rep.4000 = ((4:0.002758,(3:0.005498,5:0.003617):0.005846):0.000643,2:0.005989,1:0.005120);
tree rep.5000 = ((4:0.001777,(3:0.000789,5:0.001395):0.000475):0.013680,2:0.004508,1:0.006280);
tree rep.6000 = ((5:0.002369,(1:0.002026,3:0.000962):0.003821):0.010655,2:0.008722,1:0.011203);
tree rep.7000 = ((0:0.000886),(2:0.000886,4:0.000886):0.000886);0.000886,2:0.000886,1:0.000886;
tree rep.8000 = ((2:0.000382),(0:0.000638,5:0.000380):0.001169,4:0.000623);0.02267,1:0.005348);
tree rep.9000 = ((2:0.000986,(0:0.01372,4:0.00516):0.003416,3:0.003382);0.005159,1:0.005640);
tree rep.10000 = ((2:0.001416),(3:0.000651,5:0.003345):0.000464,4:0.010194);0.002631,1:0.010184;
tree rep.11000 = (((0:0.000884,2:0.000884),(0:0.000884,4:0.000884):0.000884,3:0.000884);0.000884,1:0.000884);
tree rep.12000 = ((2:0.00595),(0:0.005154,(3:0.001814,4:0.000535):0.000527);0.012152,1:0.002152);
tree rep.13000 = (((0:0.000884,4:0.000884),(0:0.001349,5:0.000519):0.021711,2:0.003141,1:0.004535));
tree rep.14000 = (((0:0.002721,5:0.003082):0.000995,4:0.002150);0.017912,2:0.002912,1:0.001911);
tree rep.15000 = (((0:0.003662,4:0.000820),(0:0.001224,3:0.000492):0.003841,2:0.003570,1:0.009867);
tree rep.16000 = ((2:0.001223,(0:0.009145,(5:0.002059,3:0.005159):0.000768);0.003695,1:0.005769)

```

SCIENCE'S COMPASS

• REVIEW

REVIEW: EVOLUTION

Bayesian Inference of Phylogeny and Its Impact on Evolutionary Biology

John P. Huelsenbeck,^{1*} Fredrik Ronquist,² Rasmus Nielsen,³ Jonathan P. Bollback¹

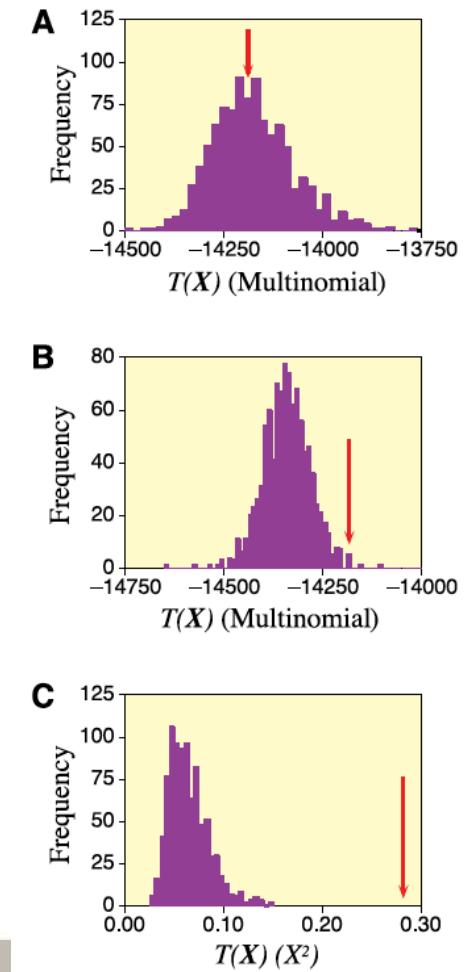


Fig. 3. The posterior predictive distributions for tests of (A) the adequacy of the GTR model, (B) of the adequacy of the Jukes-Cantor model, and (C) the hypothesis of constant nucleotide frequencies over time. The arrows above the distributions show the observed value of the test statistics.

posterior
probability

likelihood prior

$$\Pr[\text{Tree} \mid \text{Data}] = \frac{\Pr[\text{Data} \mid \text{Tree}] \times \Pr[\text{Tree}]}{\Pr[\text{Data}]}$$



Multispecies Coalescent model (in
*Beast)

$L(g_i) = P(d_i|g_i)$. Likelihood of the data_i given genealogy_i

$L(u_i) = P(g_i|u_i)$. Likelihood of genealogy_i given the molecular clock_i

Likelihood of the molecular clock_i given the species tree*

$L(S) = P(u_i|S_i)$.

$$P(S|D) \propto \prod_{i=1}^n \int_{g_i} \int_{u_i} P(d_i|g_i) P(g_i|u_i) P(u_i|S) P(S) du_i dg_i.$$

P(S) is the joint prior probability distribution on the species tree*

Poor Fit to the Multispecies Coalescent is Widely Detectable in Empirical Data

NOAH M. REID^{1,*}, SARAH M. HIRD¹, JEREMY M. BROWN¹, TARA A. PELLETIER², JOHN D. MCVAY¹, JORDAN D. SATLER², AND BRYAN C. CARSTENS²

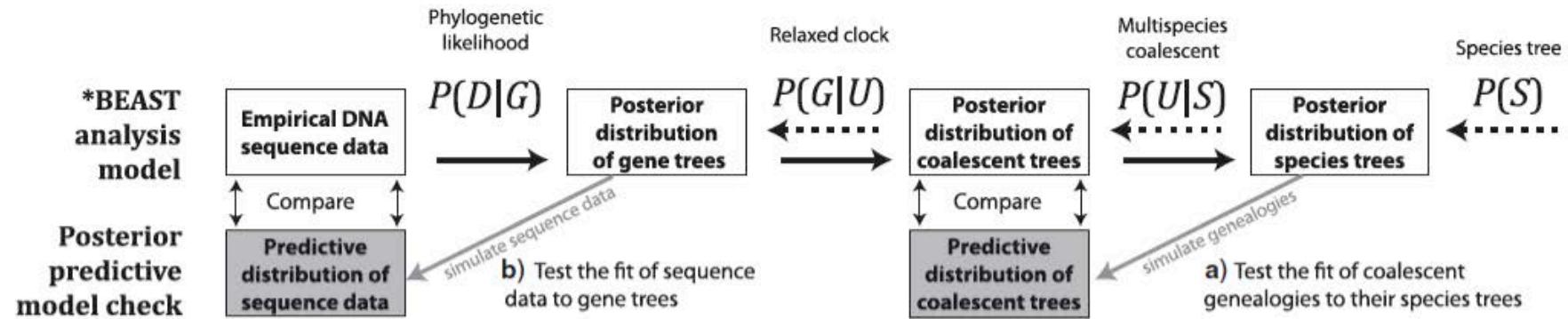
¹Department of Biological Sciences, Louisiana State University, Baton Rouge, LA 70803, USA; and

²Department of Evolution, Ecology & Organismal Biology, Ohio State University, Columbus, OH 43210, USA

*Correspondence to be sent to: 202 Life Sciences Building, Department of Biological Sciences, Louisiana State University, Baton Rouge, LA 70803, USA; E-mail: nreid1@tigers.lsu.edu.

Received 26 November 2012; reviews returned 2 March 2013; accepted 1 August 2013

Associate Editor: Laura Kubatko



4 / 25 data sets had poor fit on the species tree level
44 / 240 loci were outliers on the sequence data level

Poor Fit to the Multispecies Coalescent is Widely Detectable in Empirical Data

NOAH M. REID^{1,*}, SARAH M. HIRD¹, JEREMY M. BROWN¹, TARA A. PELLETIER², JOHN D. MCVAY¹, JORDAN D. SATLER²,
AND BRYAN C. CARSTENS²

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Received 26 November 2012; reviews returned 2 March 2013; accepted 1 August 2013
Associate Editor: Laura Kubatko

- analyzed data using *Beast (Heled & Drummond 2010)
- 50 million generations represented in posterior distribution
- posterior predictive simulations using P2C2M (Gruenstaeudl *et al.* 2015)

Poor Fit to the Multispecies Coalescent is Widely Detectable in Empirical Data

NOAH M. REID^{1,*}, SARAH M. HIRD¹, JEREMY M. BROWN¹, TARA A. PELLETIER², JOHN D. MCVAY¹, JORDAN D. SATLER²,
AND BRYAN C. CARSTENS²

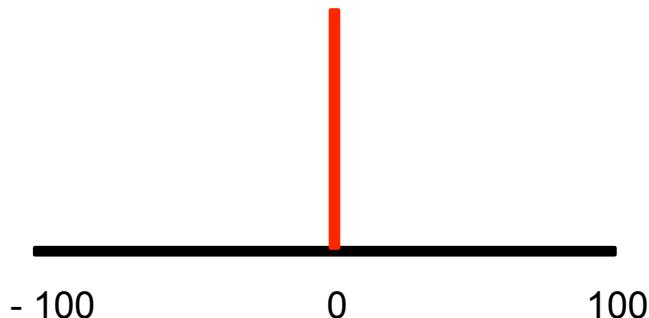
¹Department of Biological Sciences, Louisiana State University, Baton Rouge, LA 70803, USA; and

²Department of Evolution, Ecology & Organismal Biology, Ohio State University, Columbus, OH 43210, USA

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Received 26 November 2012; reviews returned 2 March 2013; accepted 1 August 2013
Associate Editor: Laura Kubatko

- analyzed data using *Beast (Heled & Drummond 2010)
- 50 million generations represented in posterior distribution
- posterior predictive simulations using P2C2M (Gruenstaeudl *et al.* 2015)



Difference (between posterior distribution and posterior predictive distribution) of some statistic or probability.

Poor Fit to the Multispecies Coalescent is Widely Detectable in Empirical Data

NOAH M. REID^{1,*}, SARAH M. HIRD¹, JEREMY M. BROWN¹, TARA A. PELLETIER², JOHN D. MCVAY¹, JORDAN D. SATLER²,
AND BRYAN C. CARSTENS²

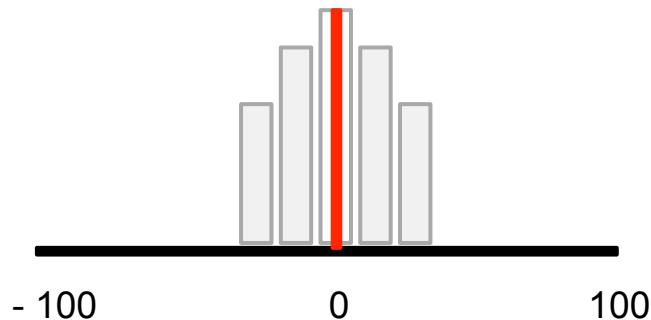
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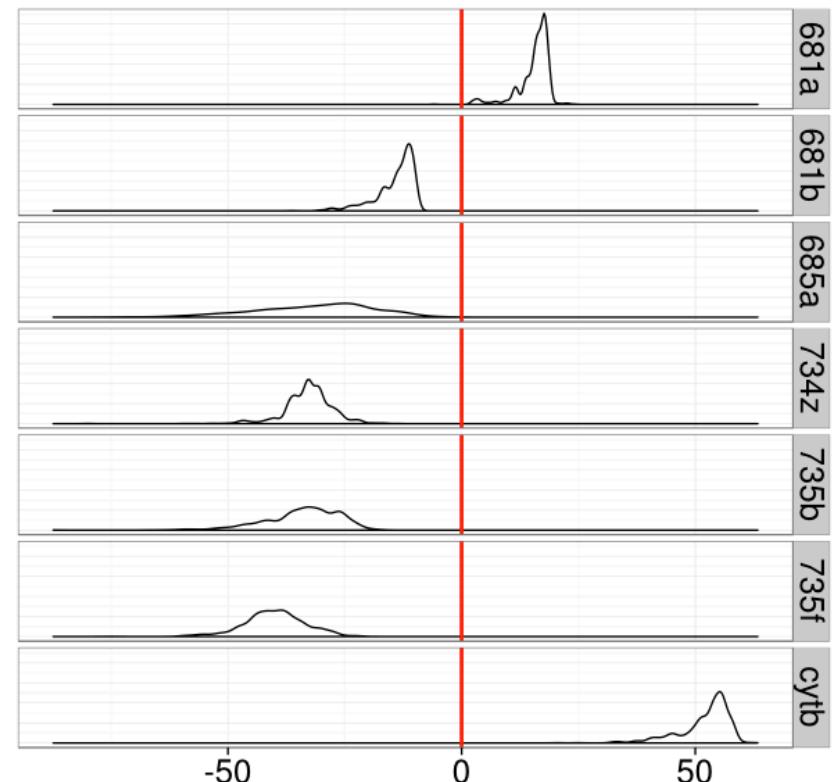
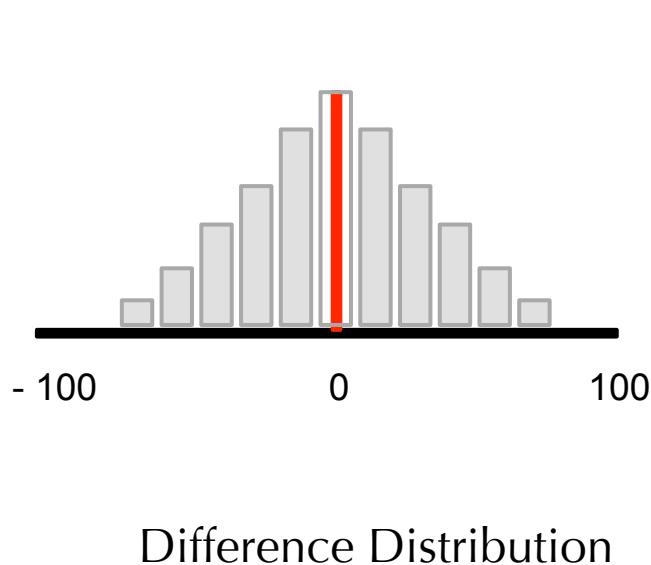
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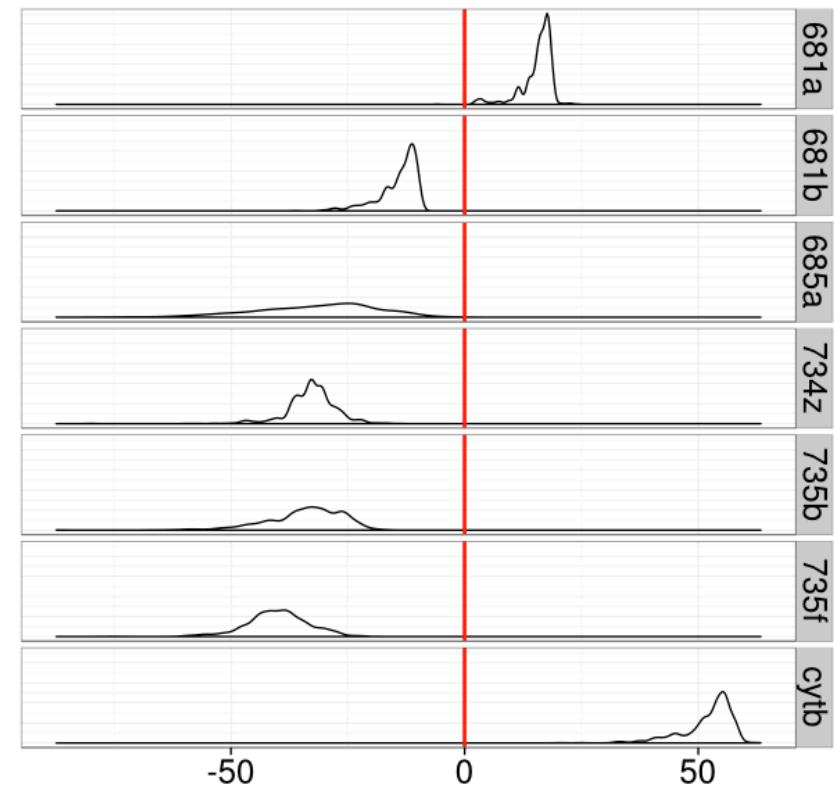
Received 26 November 2012; reviews returned 2 March 2013; accepted 1 August 2013

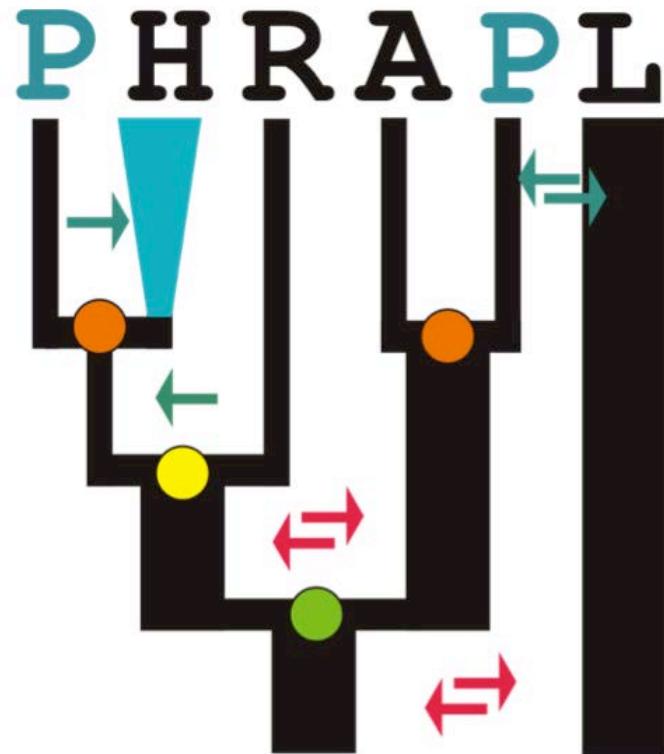
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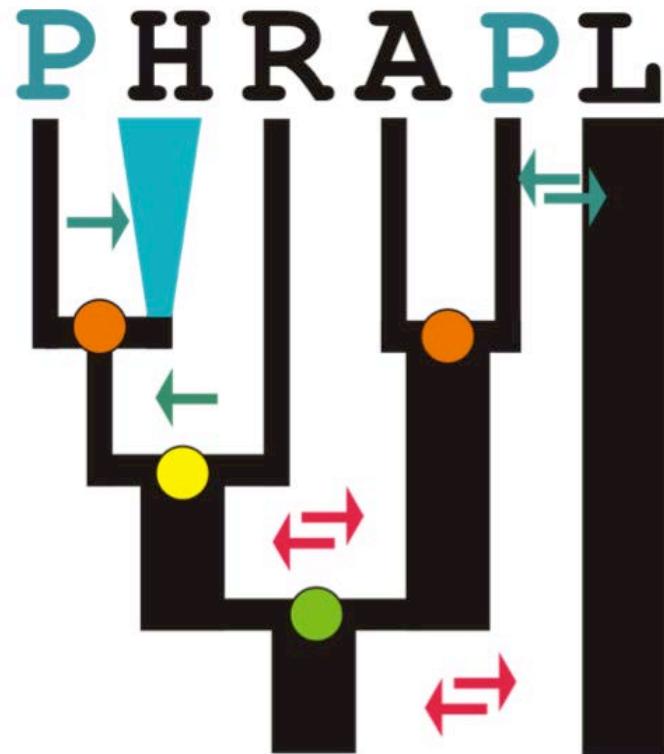
- A species tree model does not fit the *Myotis lucifugus* data...
- Rather than building machinery to test fit of model in Migrate-n, IMa2, or some other piece of software, we developed a general tool for phylogeographic model selection.



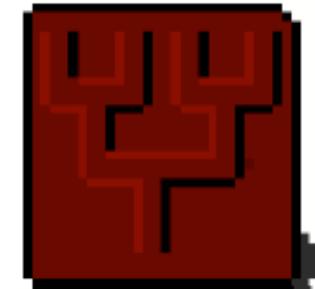


PHylogeographic
InfeRence
using
APproximated
Likelihood

w/ Brian O'Meara, Nathan Jackson, Ariadna Morales-García



\approx



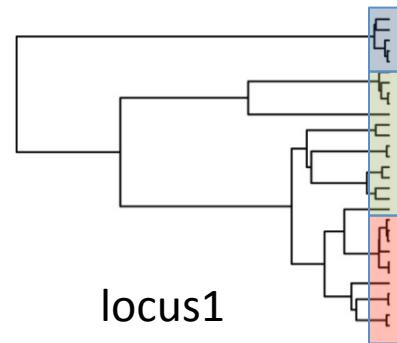
PHylogeographic InfeRence using APproximated Likelihoods

w/ Brian O'Meara, Nathan Jackson, Ariadna Morales-García

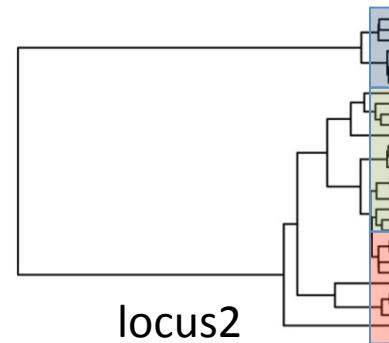
Input

1. Gene trees
2. Population assignments
3. Max K (max number of free parameters; t, m, N_e)

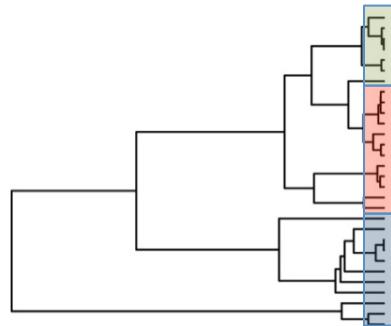
Pop A 
Pop B 
Pop C 



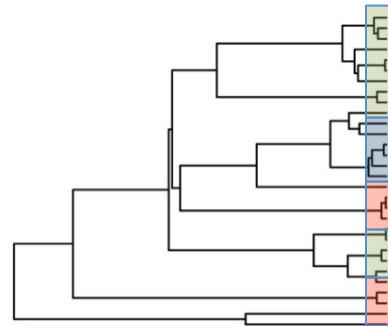
locus1



locus2

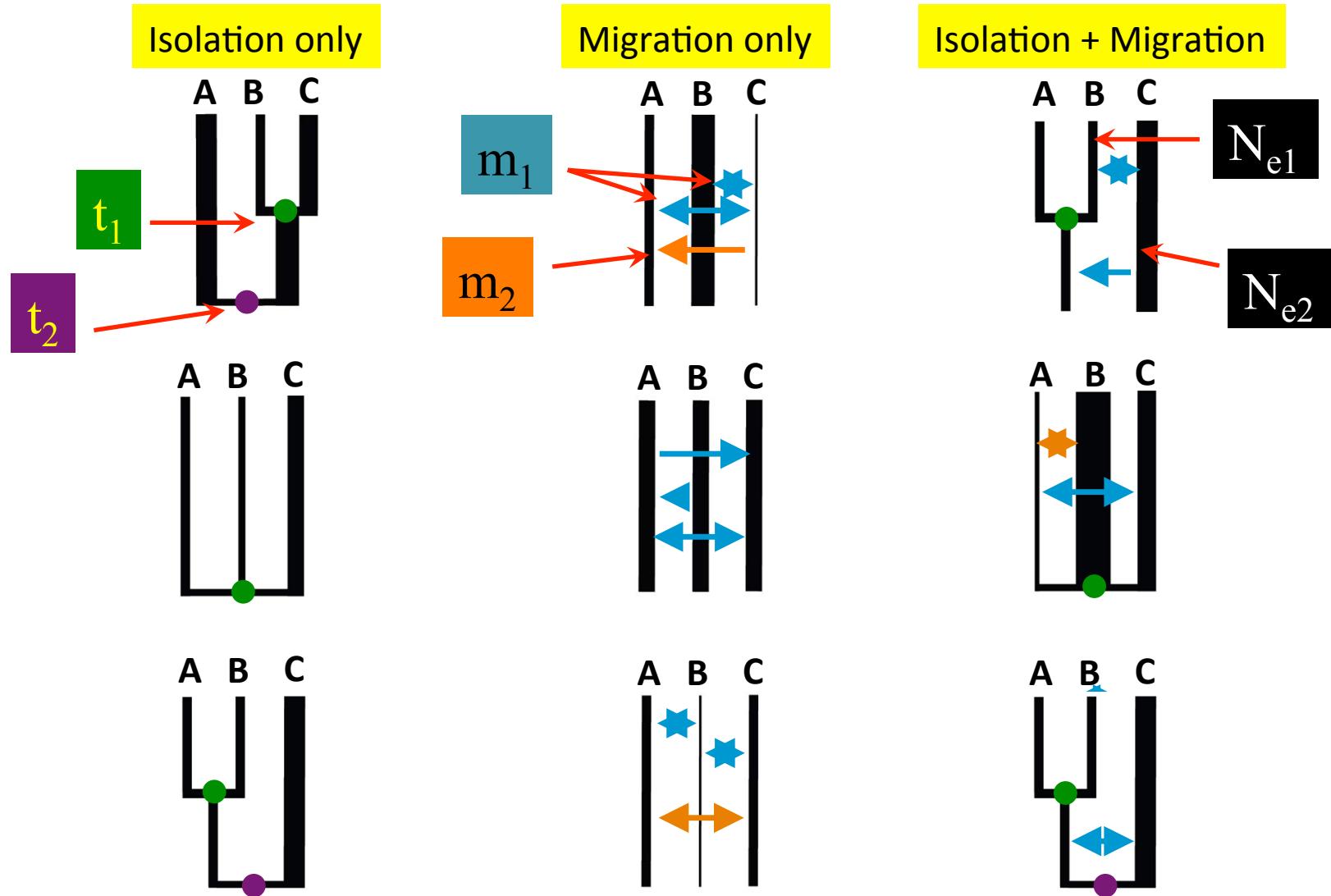


locus3



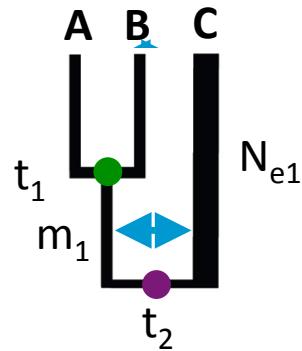
locus4

Phrapl functions: Define all possible models

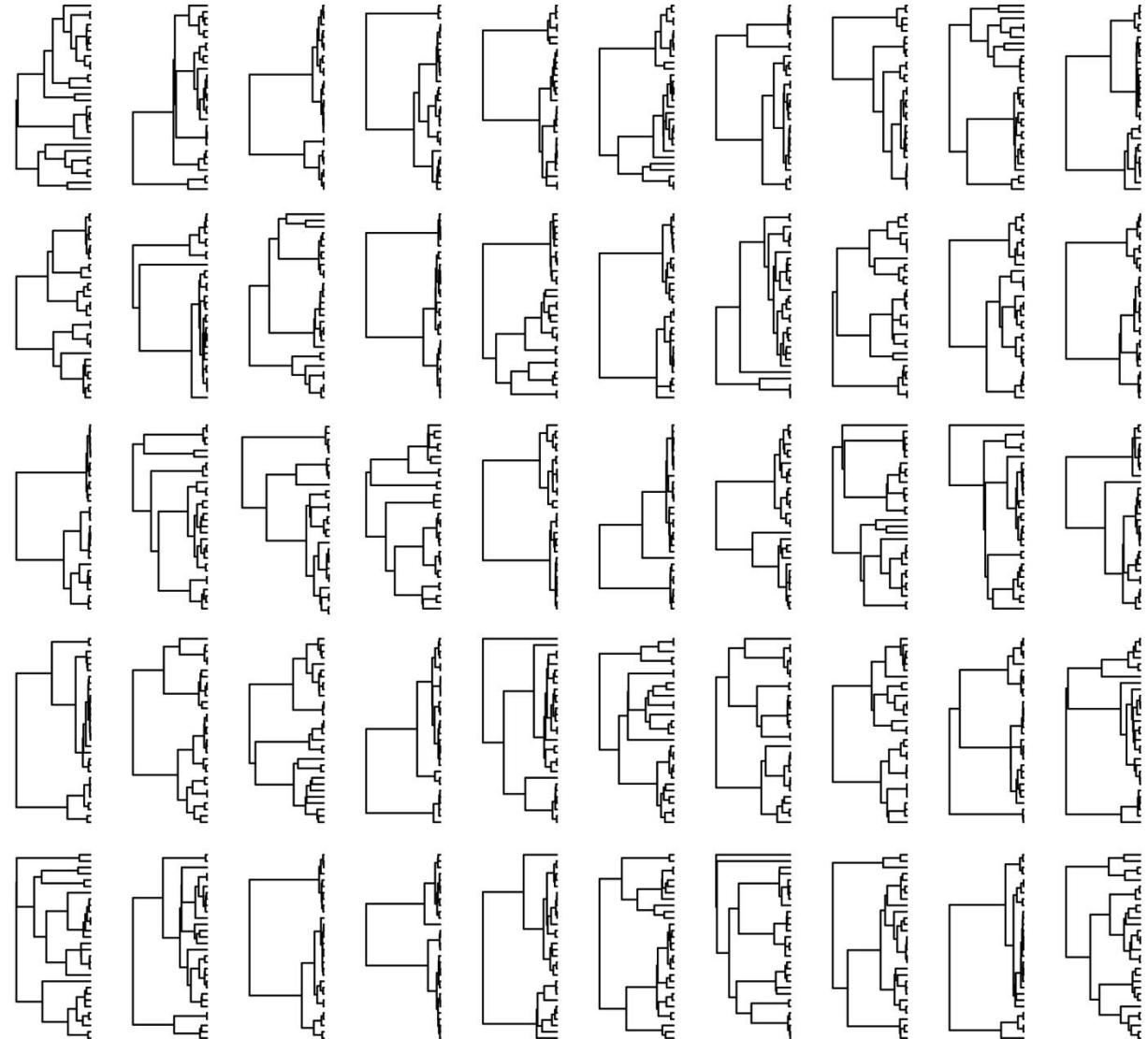


Phrapl functions: approximate likelihood

For each model...

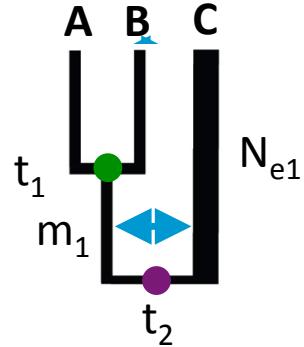


Simulate large number
of trees

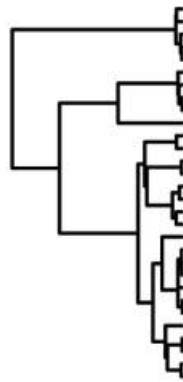


Phrapl functions: approximate likelihood

For each model...



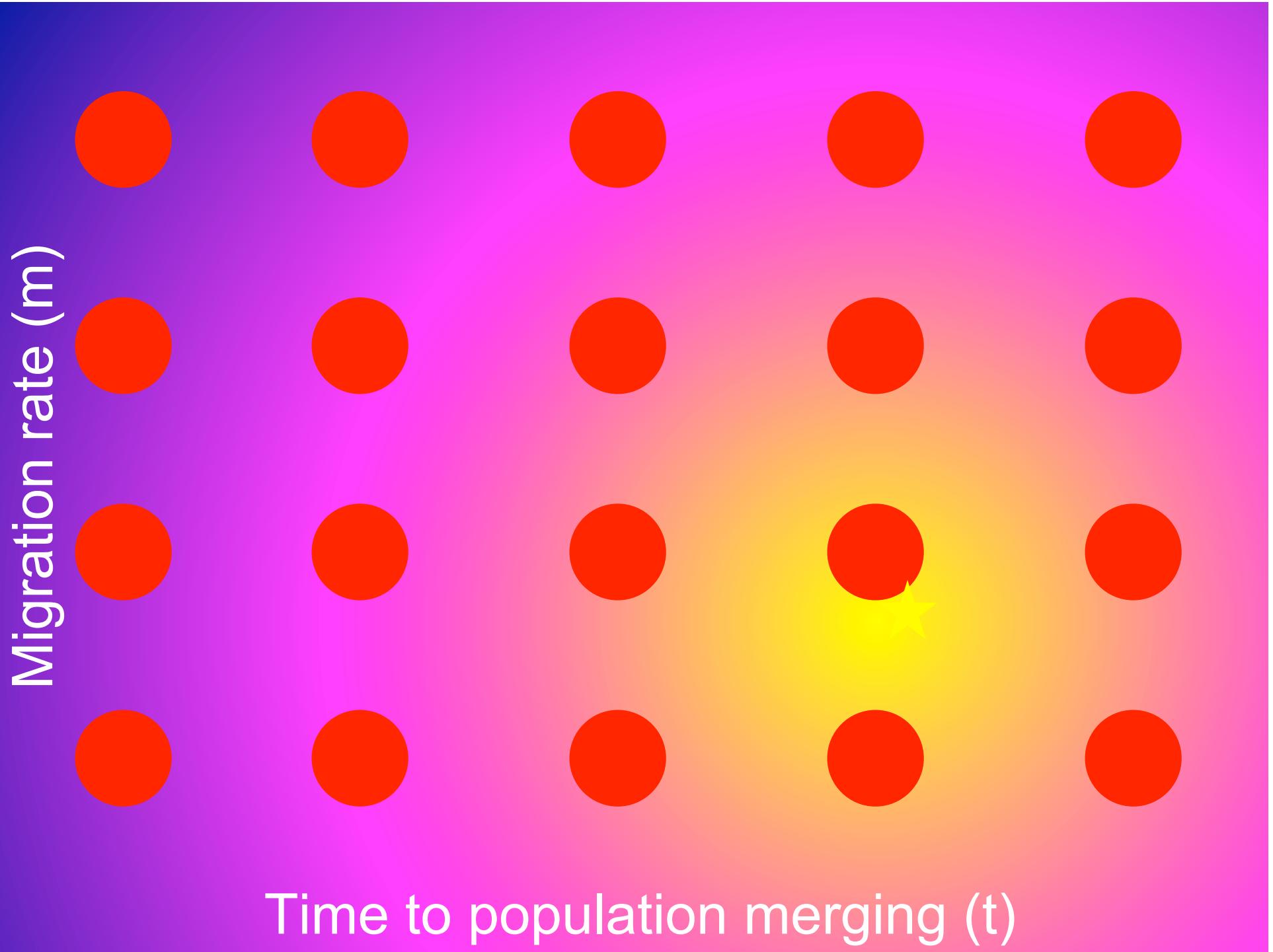
observed tree



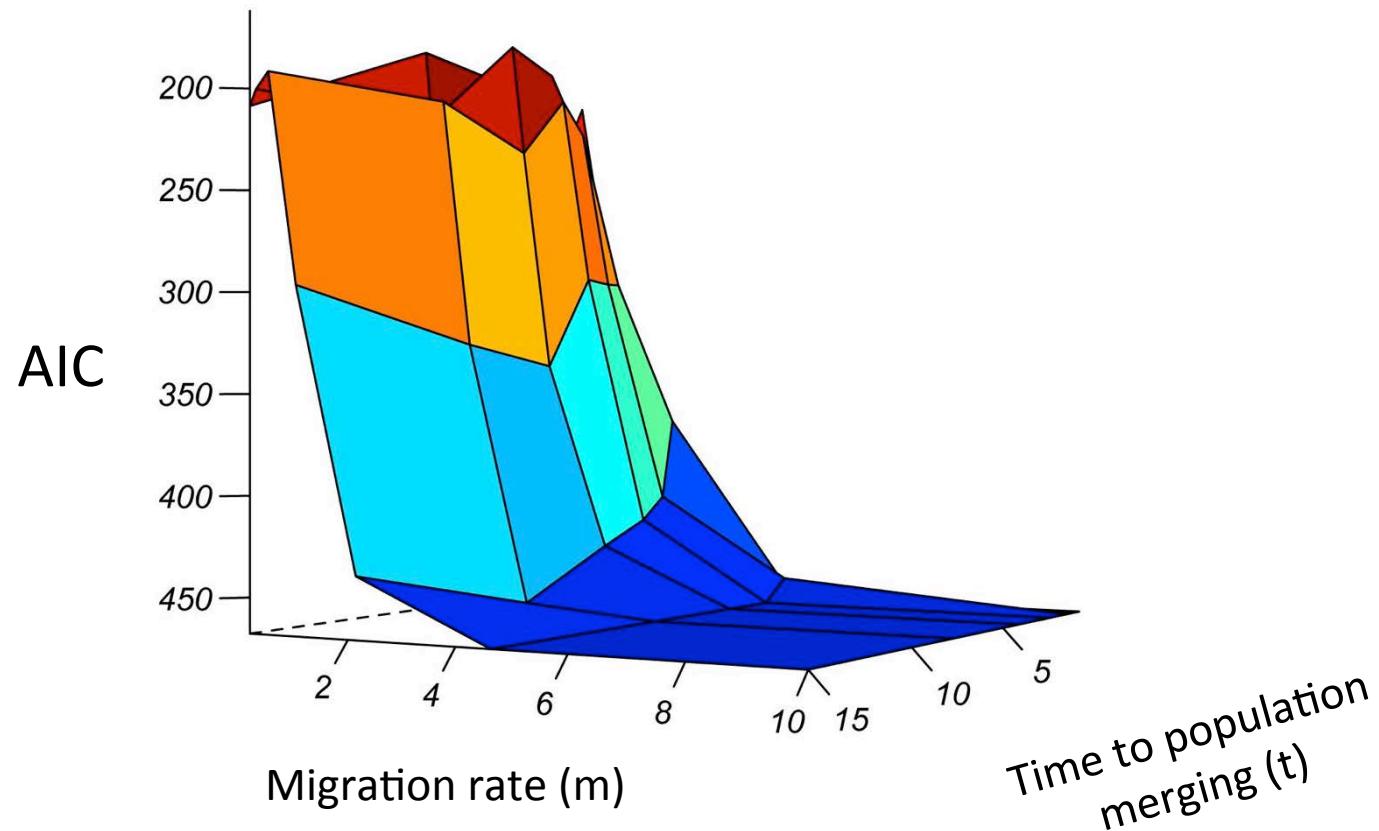
expected trees

Calculate # of topological
matches

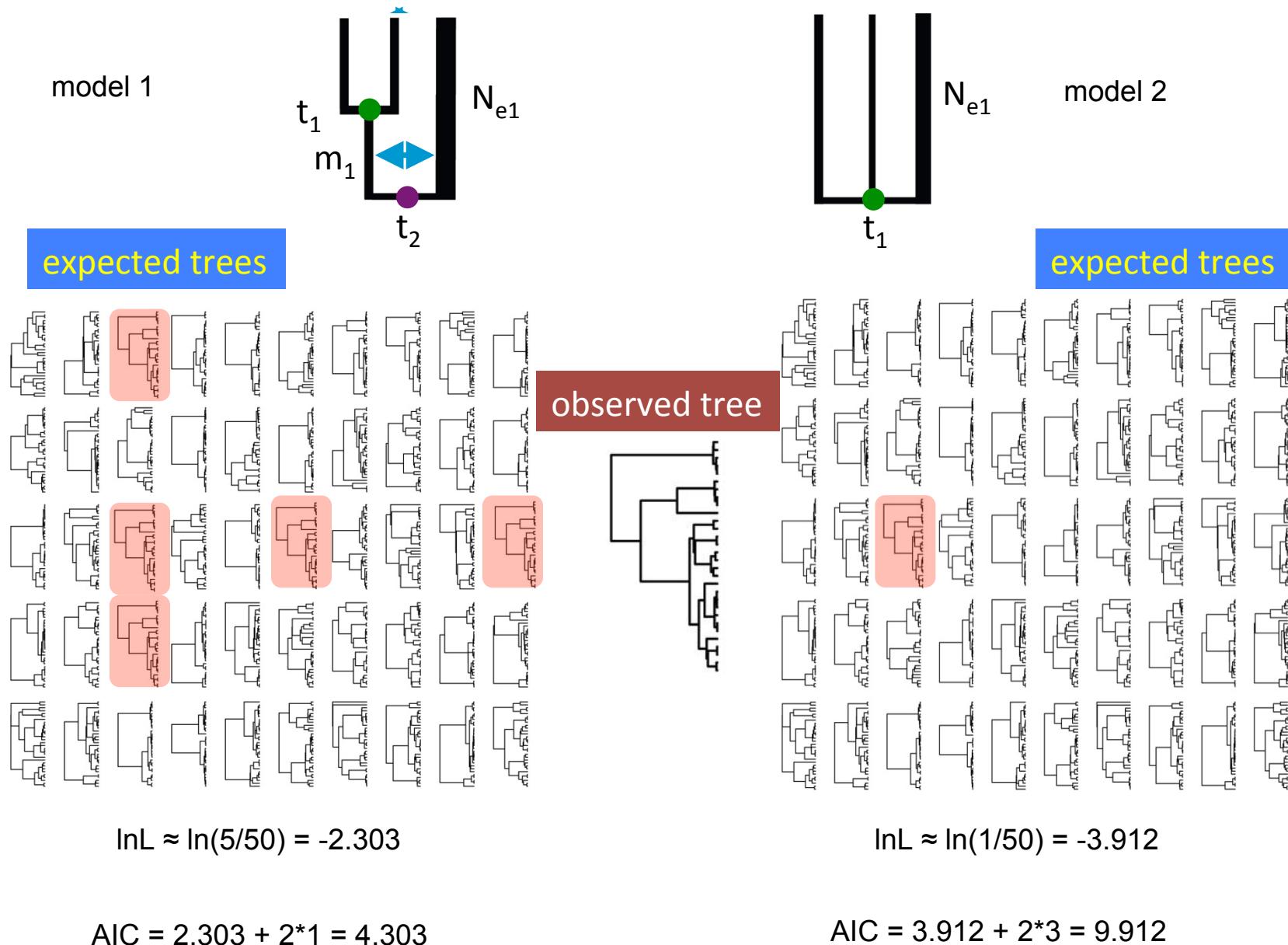
1 match / 50 simulated trees \approx
 $\text{prob}(\text{topology(observed)} | \tau_1, m_1, N_{e1}) =$
likelihood



Phrapl functions: model parameters are optimized using a grid of values



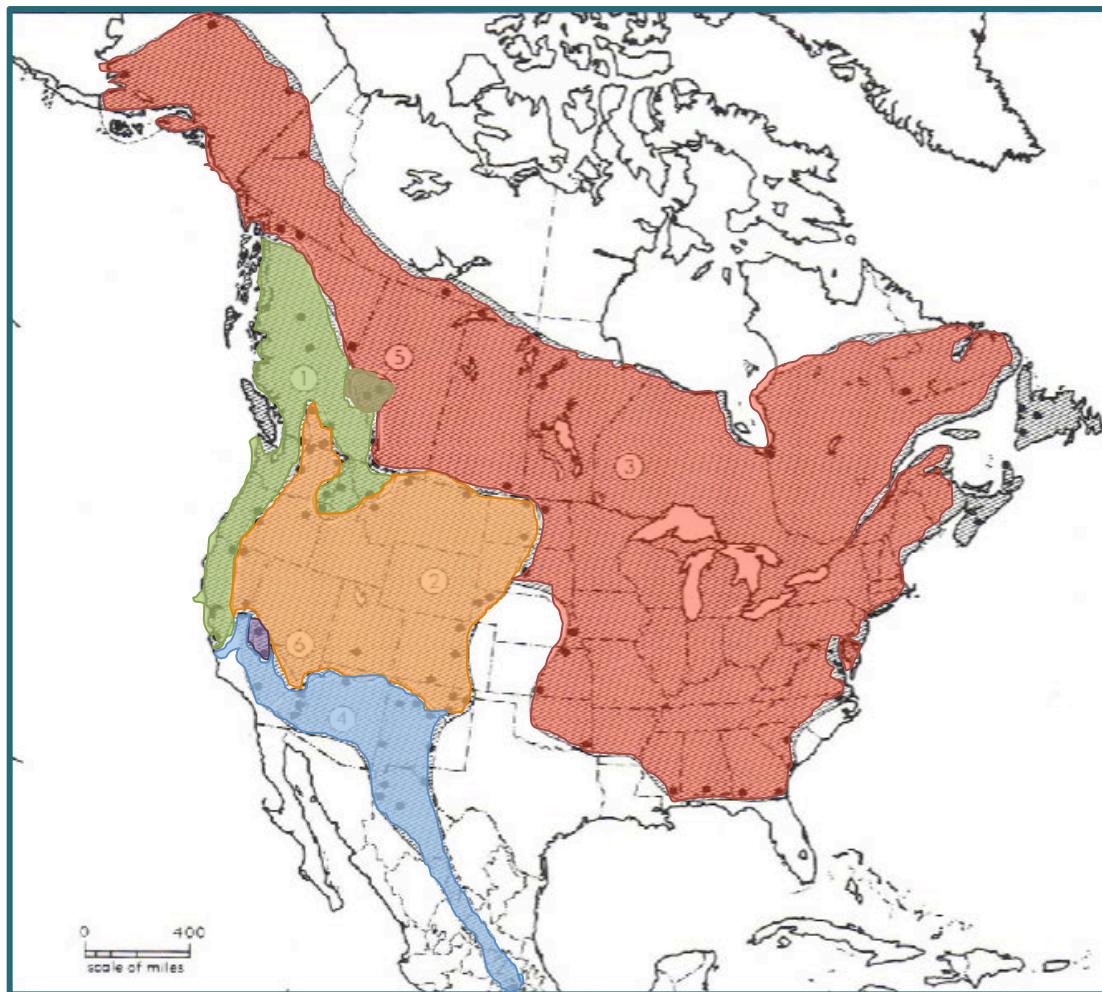
Phrapl functions: approximate likelihood



Phrapl output: comparing model fit using AIC

model	K	lnL	AIC	dAIC	AIC_weights	parameters
546	3	-52.79157	111.58314	0.00000	0.55011	tau1, tau2, Ne1
376	4	-53.23296	114.46593	2.88300	0.13014	tau1, Ne1, Ne2, m1
394	4	-54.81089	117.62177	6.03900	0.02686	tau1, tau2, Ne1, m1
330	4	-54.86685	117.73369	6.15100	0.02540	tau1, Ne1, Ne2, m1
288	4	-55.09833	118.19665	6.61400	0.02015	tau1, Ne1, m1, m2
91	3	-56.14528	118.29055	6.70700	0.01923	Ne1, Ne2, m1
399	4	-55.19640	118.39280	6.81000	0.01827	tau1, tau2, Ne1, Ne2
200	4	-55.49627	118.99254	7.40900	0.01354	tau1, Ne1, m1, m2
30	4	-55.52415	119.04829	7.46500	0.01317	Ne1, m1, m2, m3
69	3	-56.91221	119.82441	8.24100	0.00893	Ne1, m1, m2
25	3	-56.91288	119.82575	8.24300	0.00892	Ne1, m1, m2
615	4	-55.92477	119.84954	8.26600	0.00882	tau1, Ne1, m1, m2
291	4	-55.93903	119.87806	8.29500	0.00869	tau1, Ne1, m1, m2
322	4	-56.12679	120.25357	8.67000	0.00721	tau1, Ne1, Ne2, m1
549	4	-56.14120	120.28239	8.69900	0.00710	tau1, tau2, Ne1, m1
72	4	-56.15484	120.30967	8.72700	0.00700	Ne1, m1, m2, m3
632	4	-56.19445	120.38889	8.80600	0.00673	tau1, Ne1, m1, m2
635	4	-56.43589	120.87178	9.28900	0.00529	tau1, Ne1, m1, m2
97	4	-56.44301	120.88601	9.30300	0.00525	Ne1, Ne2, m1, m2
272	4	-56.49789	120.99579	9.41300	0.00497	tau1, Ne1, m1, m2
240	3	-57.50589	121.01177	9.42900	0.00493	tau1, Ne1, m1
415	4	-56.62749	121.25498	9.67200	0.00437	tau1, Ne1, m1, m2
560	4	-56.66308	121.32615	9.74300	0.00421	tau1, tau2, Ne1, m1

Little brown bat subspecies (*Myotis lucifugus*)



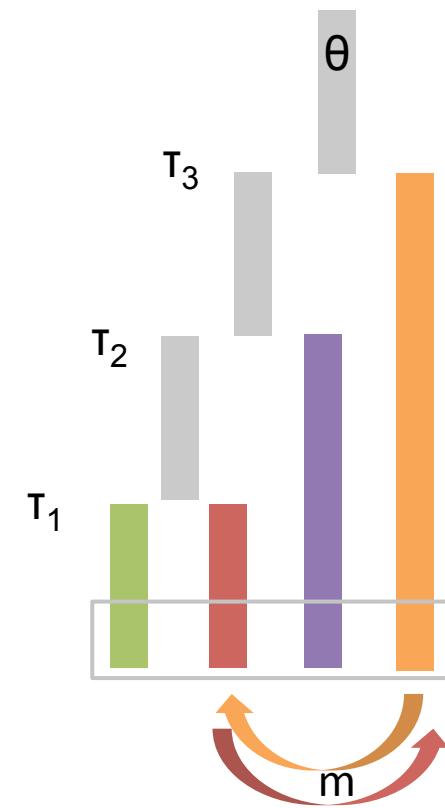
M.l.alascensis

M.l.carissima

M.l.relictus

M.l.lucifugus

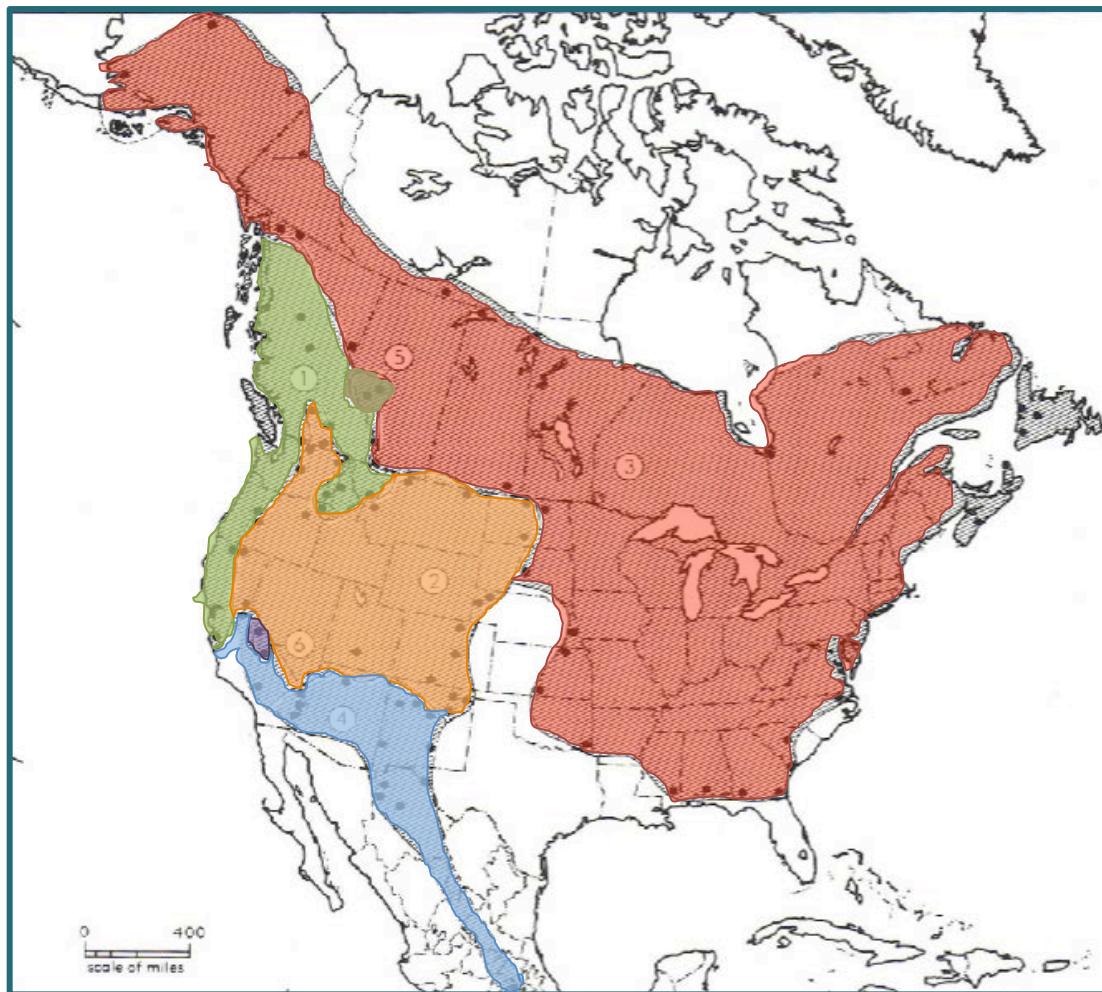
(Hall 1981)



$$w_{4101} = 0.405$$

Phrap w/ 7 loci from
Carstens & Dewey 2010

Little brown bat subspecies (*Myotis lucifugus*)



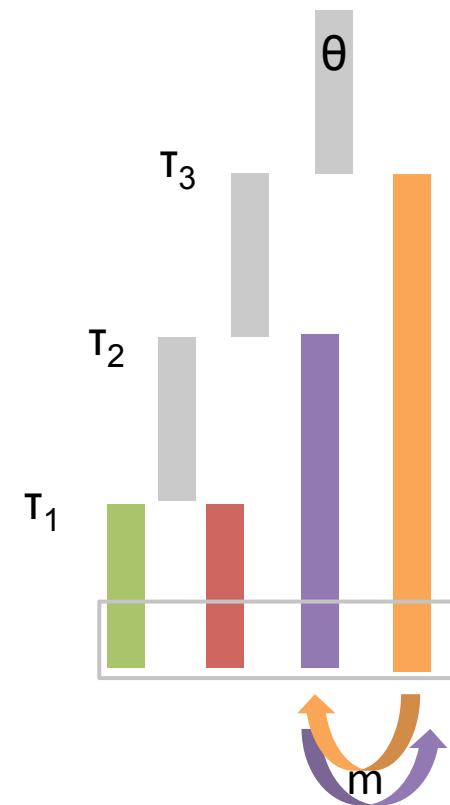
M.l.alascensis

M.l.carissima

M.l.relictus

M.l.lucifugus

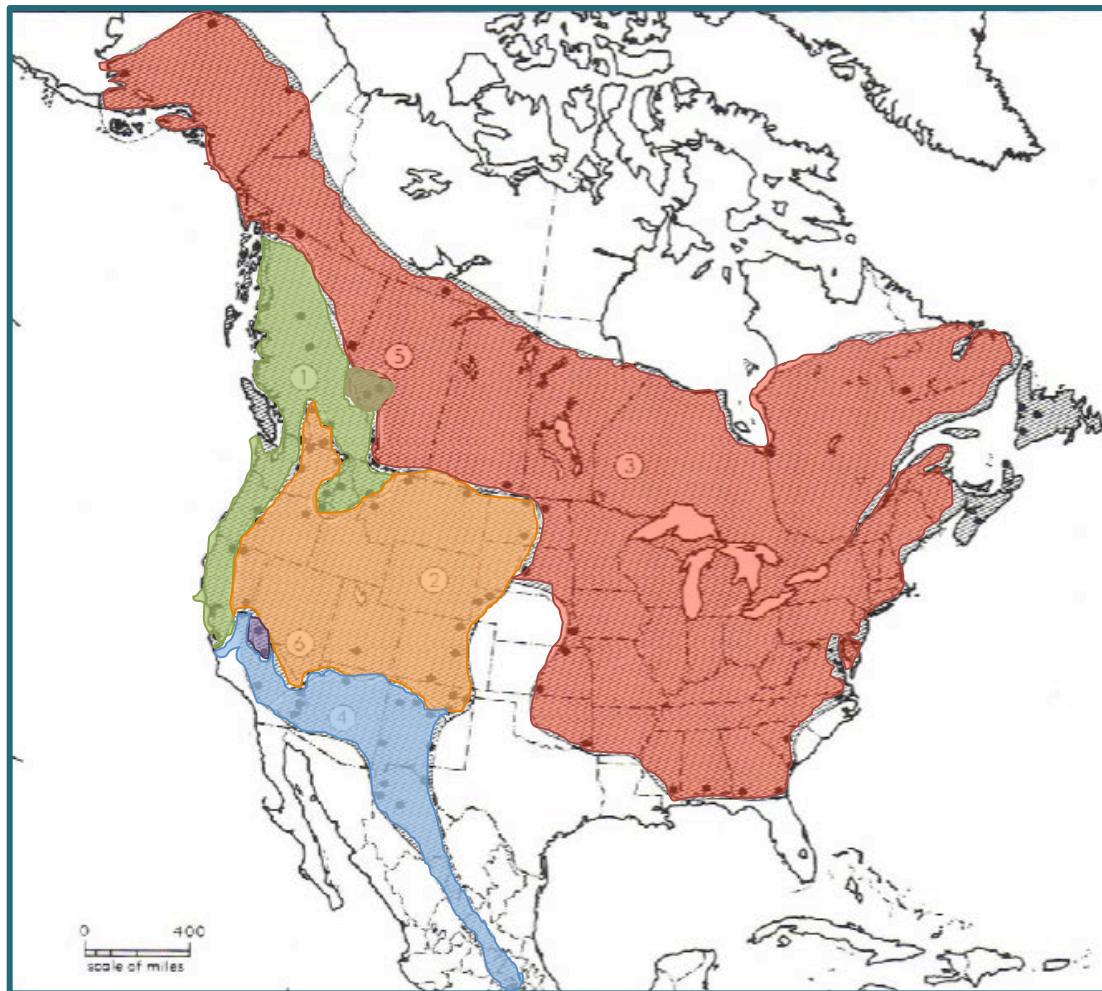
(Hall 1981)



$$w_{4113} = 0.352$$

Phrap w/ 7 loci from
Carstens & Dewey 2010

Little brown bat subspecies (*Myotis lucifugus*)



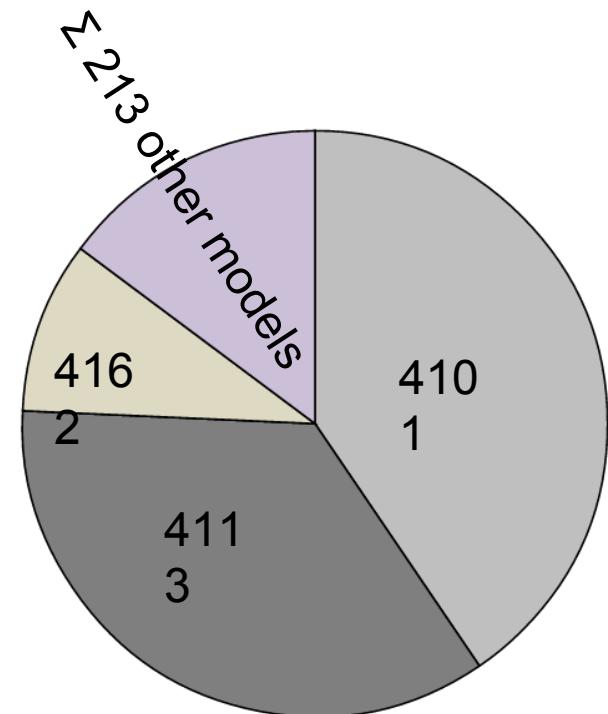
M.l.alascensis

(Hall 1981)

M.l.carissima

M.l.relictus

M.l.lucifugus

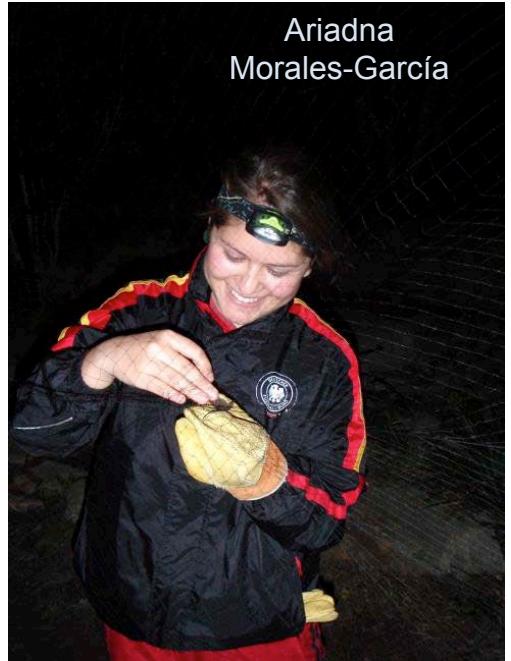


PhrapI w/ 7 loci from
Carstens & Dewey 2010

Custom sequence capture probes synthesized by MYcroarray



~1100 UCE loci
~2800 exons
~100 anonymous loci



The MYcroarray logo features a stylized icon composed of colored dots (red, green, yellow) arranged in a grid-like pattern. To the right of the icon, the word "MYcroarray" is written in a bold, sans-serif font. Below the logo, a large, semi-transparent blue banner contains the text "Custom molecular baits, probes and building blocks" in white, sans-serif font.

Consider 216 models using 100 UCE loci:

- island (4-population)
- divergence only
- divergence with gene flow
- secondary contact

Consider 216 models using 100 UCE loci:

- island (4-population)
- divergence only
- divergence with gene flow
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model (m)	topology	AIC	wAIC
Mlc-Mll migration	((l,r)a)c	2271.70235	0.99955678
Mlr-Mll migration	((c,l)(r,a))	2287.143951	0.00044322
Mlr-Mll migration	((c,r)(a,l))	2341.788941	6.03E-16
Mlc-Mll migration	(((c,r)a)l)	2366.068324	3.22E-21
Mlr isolated	((l,r)a)c	2433.450902	7.52E-36
Mlr-Mll migration	((a,r)(c,l))	2478.304448	1.37E-45
Mla isolated	((l,r)(a,c))	2481.319285	3.03E-46
full-symmetric	((l,r)a)c	2501.659771	1.16E-50
full-symmetric	((c,l)(r,a))	2517.717369	3.79E-54
full-symmetric	((a,l)(c,r))	2523.920644	1.70E-55
full-symmetric	((l,r)(a,c))	2524.057685	1.59E-55
full-symmetric	((a,r)(c,l))	2524.606804	1.21E-55
full-symmetric	((c,r)(a,l))	2524.606804	1.21E-55
full-symmetric	((a,c)(l,r))	2526.263385	5.28E-56
no migration	((l,r)c)a	2710.72578	4.65E-96
Mlc isolated	(((a,l)r)c)	2721.973848	1.68E-98
Mll isolated	((l,r)(a,c))	2743.6133	3.35E-103
no migration	(((a,r)l)c)	2744.941628	1.73E-103
Mll isolated	(((a,r)l)c)	2745.158291	1.55E-103
no migration	(((c,r)l)a)	2745.615323	1.23E-103
no migration	((c,l)(r,a))	2748.33777	3.16E-104
Mll isolated	(((c,r)l)a)	2748.744249	2.58E-104
no migration	(((a,l)r)c)	2750.409452	1.12E-104
Mll isolated	(((c,r)a)l)	2759.753459	1.05E-106

Consider 216 models using 100 UCE loci:

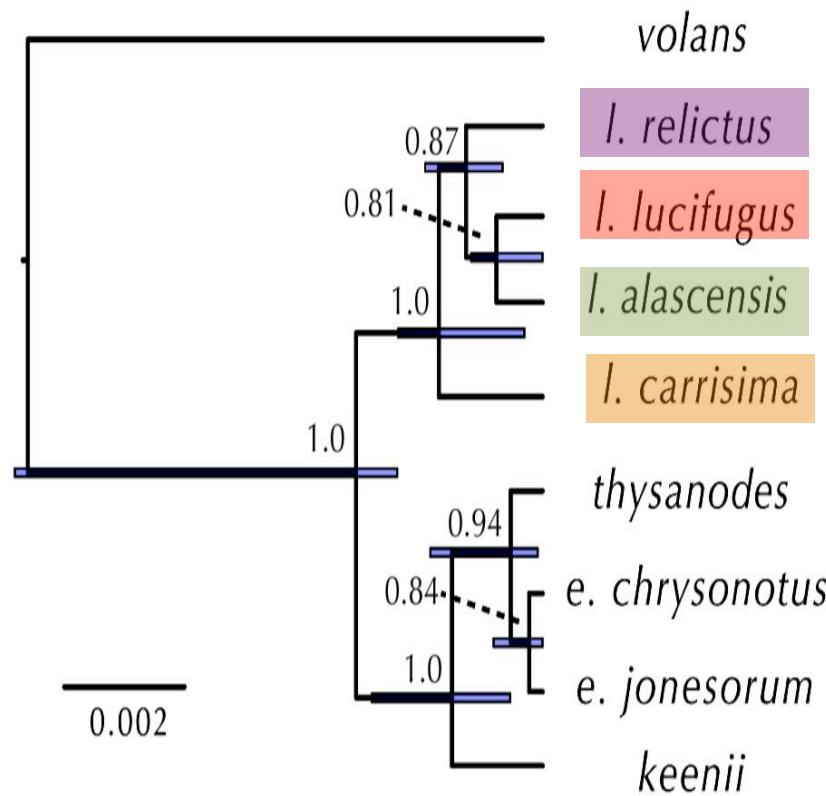
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Mlc-Mll migration	(((c,r)a)l)	2366.068324	3.22E-21
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Mla isolated	((l,r)(a,c))	2481.319285	3.03E-46
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metric	((c,l)(r,a))	2517.717369	3.79E-54
metric	((a,l)(c,r))	2523.920644	1.70E-55
metric	((l,r)(a,c))	2524.057685	1.59E-55
metric	((a,r)(c,l))	2524.606804	1.21E-55
metric	((c,r)(a,l))	2524.606804	1.21E-55
metric	((a,c)(l,r))	2526.263385	5.28E-56
ion	((l,r)c)a	2710.72578	4.65E-96
ated	(((a,l)r)c)	2721.973848	1.68E-98
ted	((l,r)(a,c))	2743.6133	3.35E-103
ion	(((a,r)l)c)	2744.941628	1.73E-103
ed	(((a,r)l)c)	2745.158291	1.55E-103
ion	(((c,r)l)a)	2745.615323	1.23E-103
ion	((c,l)(r,a))	2748.33777	3.16E-104
ed	(((c,r)l)a)	2748.744249	2.58E-104
no migration	(((a,l)r)c)	2750.409452	1.12E-104
Mll isolated	(((c,r)a)l)	2759.753459	1.05E-106

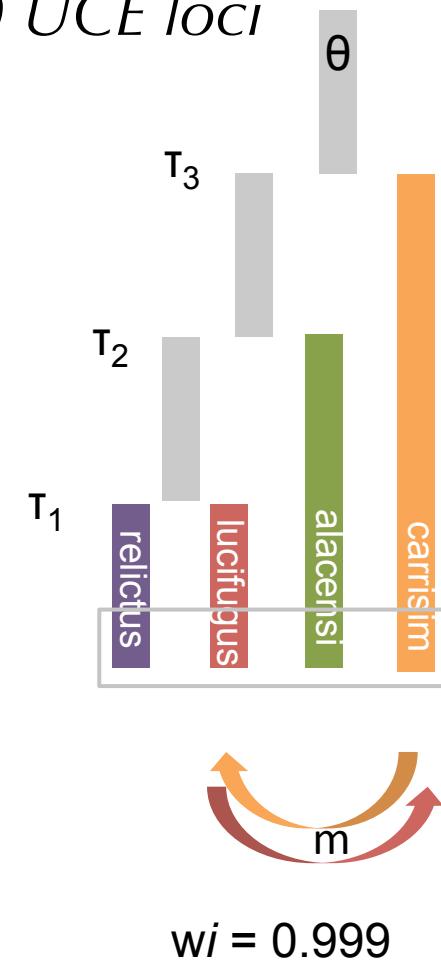
*species tree (*Beast)*

7 loci Carstens & Dewey
2010

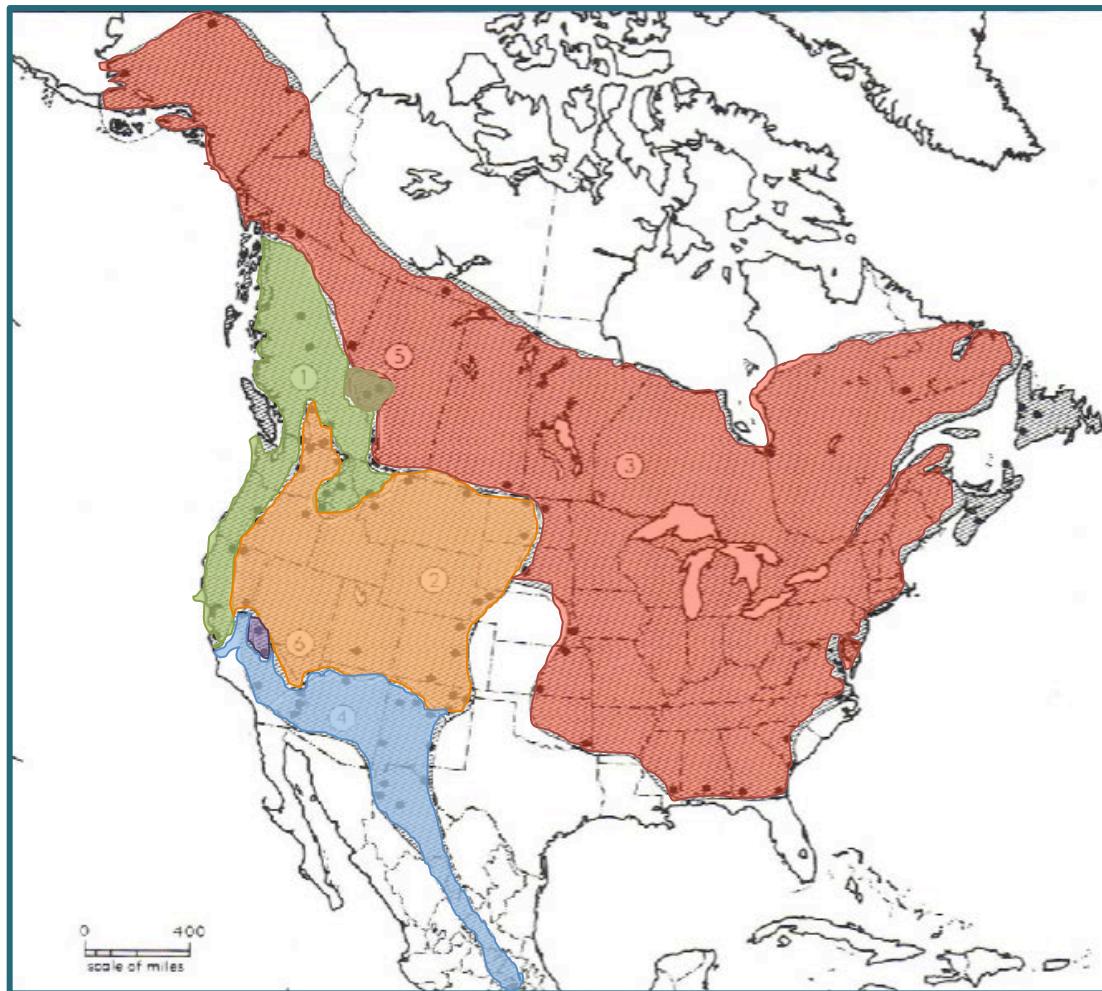


PhrapI's top model

100 UCE loci



Little brown bat subspecies (*Myotis lucifugus*) - more sampling in progress...



M.I.alascensis

M.I.carissima

M.I.relictus

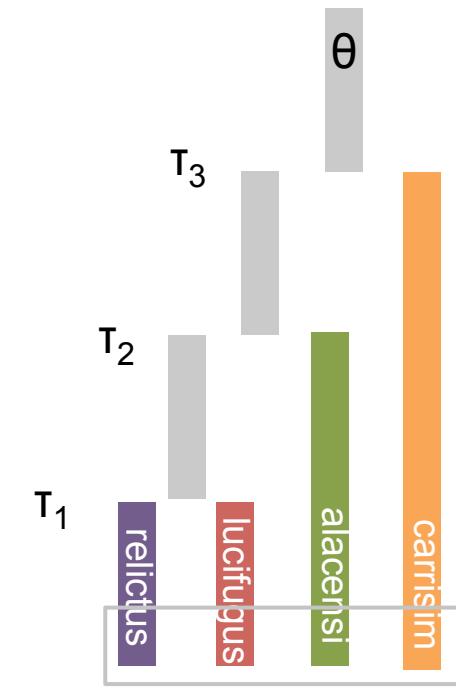
M.I.lucifugus

(Hall 1981)

M.I.pernox

M.I.occulthus

Phrapl w/ 100 UCE loci



$$wi = 0.999$$

Poor estimates of phylogeny ...

Speciation with gene flow may be common...

Divergence with Gene Flow:
Models and Data

Catarina Pinho¹ and Jody Hey²

¹CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Campus Agrário de Vairão, 4485-661 Vairão, Portugal; email: catarina@mail.icav.up.pt

²Department of Genetics, Rutgers University, Piscataway, New Jersey 08854; email: hey@biology.rutgers.edu

Annu. Rev. Ecol. Evol. Syst. 2010. 41:215–30

First published online as a Review in Advance on
August 19, 2010

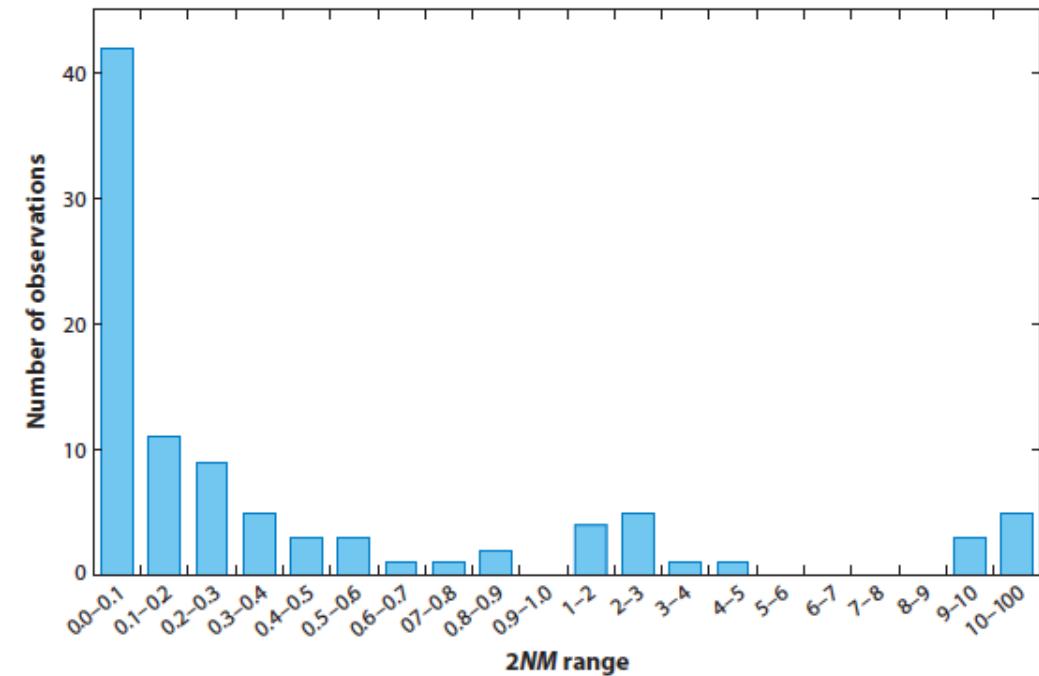


Figure 3

Counts of estimated mean $2NM$ values among studies. From those studies listed in **Supplemental Table 1** that reported $2NM$ values, or from which these values could be calculated, the mean of the values for each direction is given. Note the changing X-axis scale for larger values.

Speciation with gene flow may be common...

Divergence with Gene Flow:
Models and Data

Catarina Pinho¹ and Jody Hey²

¹CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos, Universidade do Porto, Campus Agrário de Vairão, 4485-661 Vairão, Portugal; email: catarina@mail.icav.up.pt

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PERSPECTIVE

Speciation with gene flow could be common

PATRIK NOSIL

Zoology Department and Centre for Biodiversity Research,
University of British Columbia, 6270 University Boulevard,
Vancouver, British Columbia, Canada V6T 1Z4

Review



The genomics of speciation-with-gene-flow

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² Advanced Diagnostics and Therapeutics, University of Notre Dame, Notre Dame, IN 46556, USA

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DEB-0956069
DEB-1403034
OISE-1118408



Sarah Hird
Noah Reid
John McVay
Tara Pelletier
Jordan Satler
Ariadna Morales-García
Greg Wheeler
Sergei Soloneko



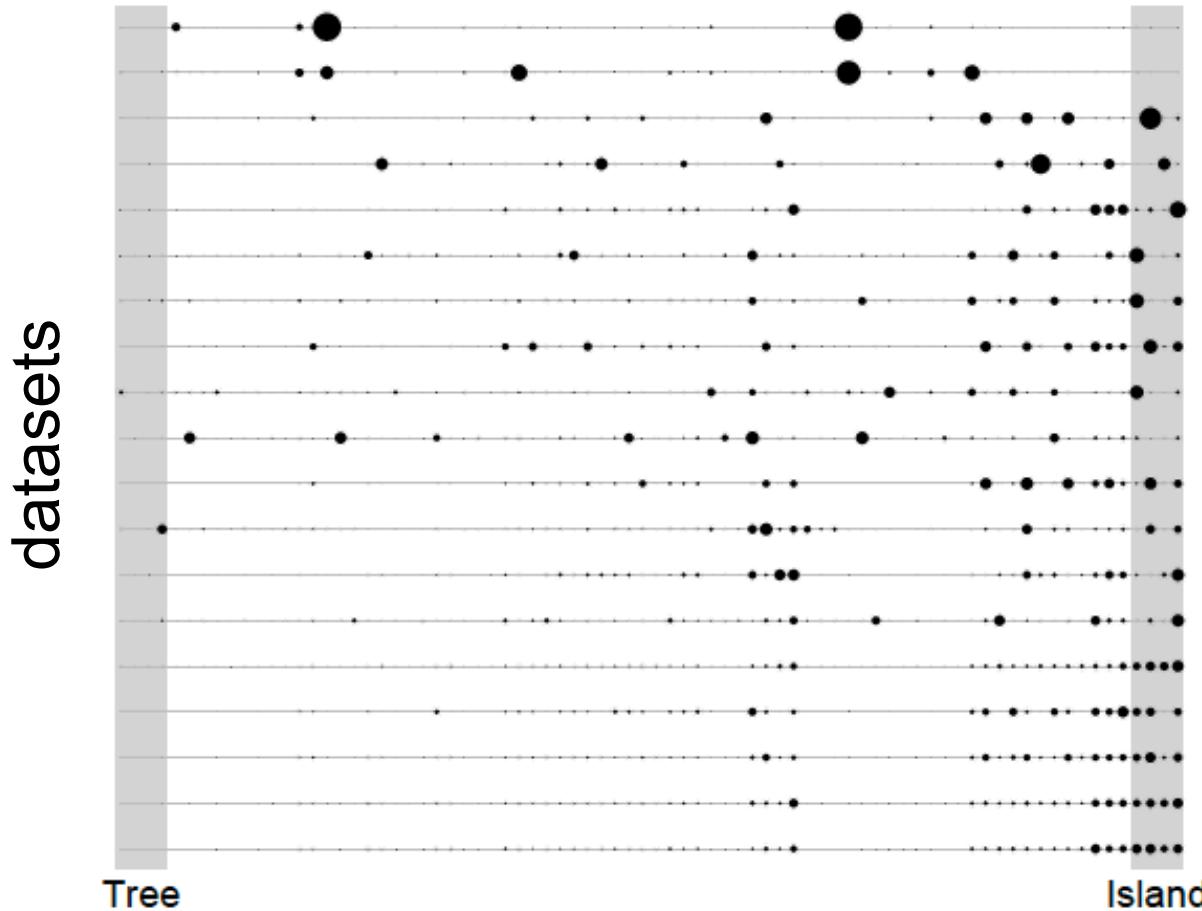
Louisiana Board Of Regents Research Competitiveness
Chancellors' Future Leaders in Research
Campus Federal Credit Union

Danielle Fuselier
Holly Stoute
Dan Ence
Matt Demarest
Maxim Kim
Edwin Rice



phylogeographic inference using approximated likelihoods

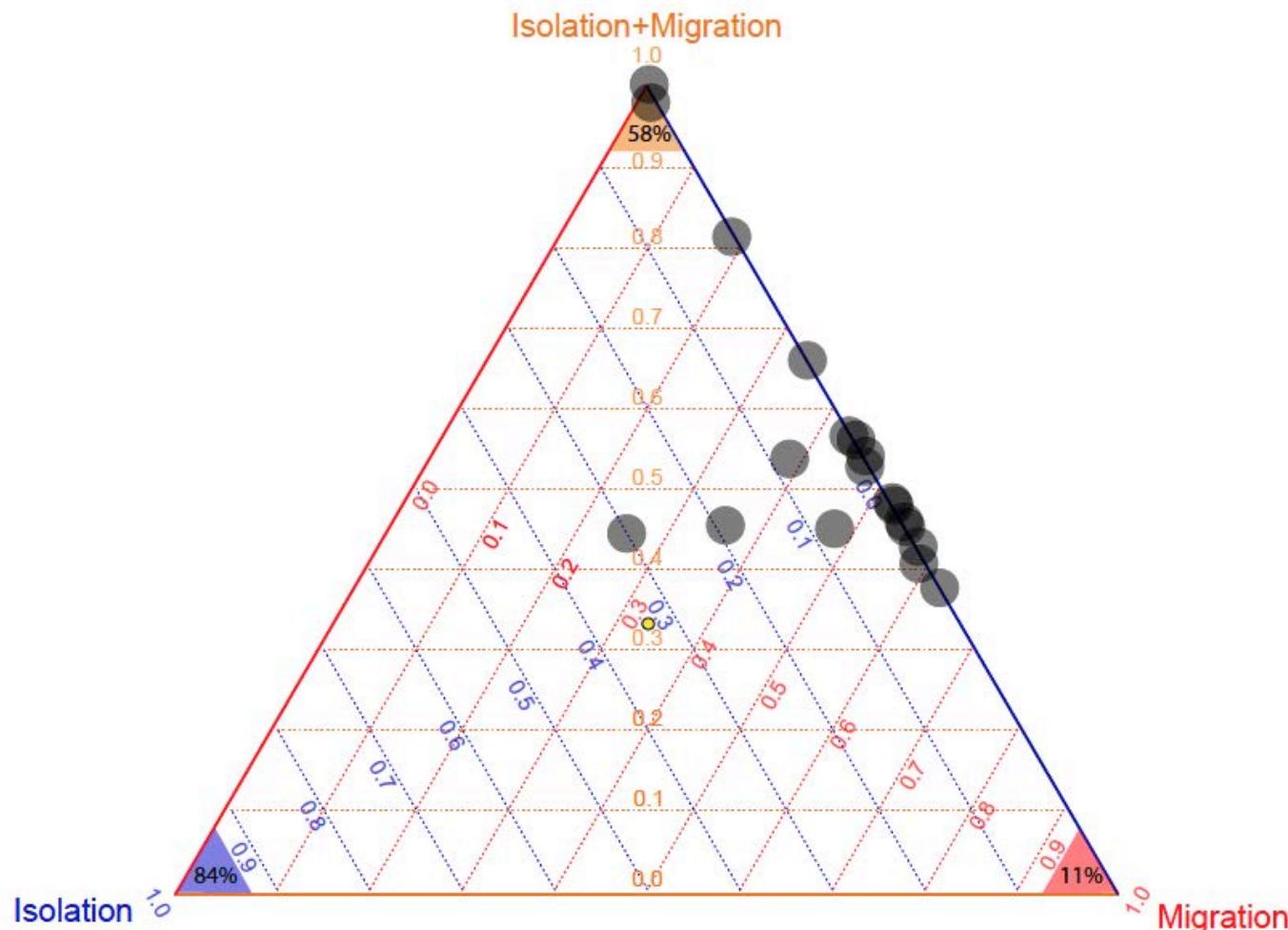
exploration using published phylogeographic data



model-averaging of
parameter values
accounts for model
uncertainty.

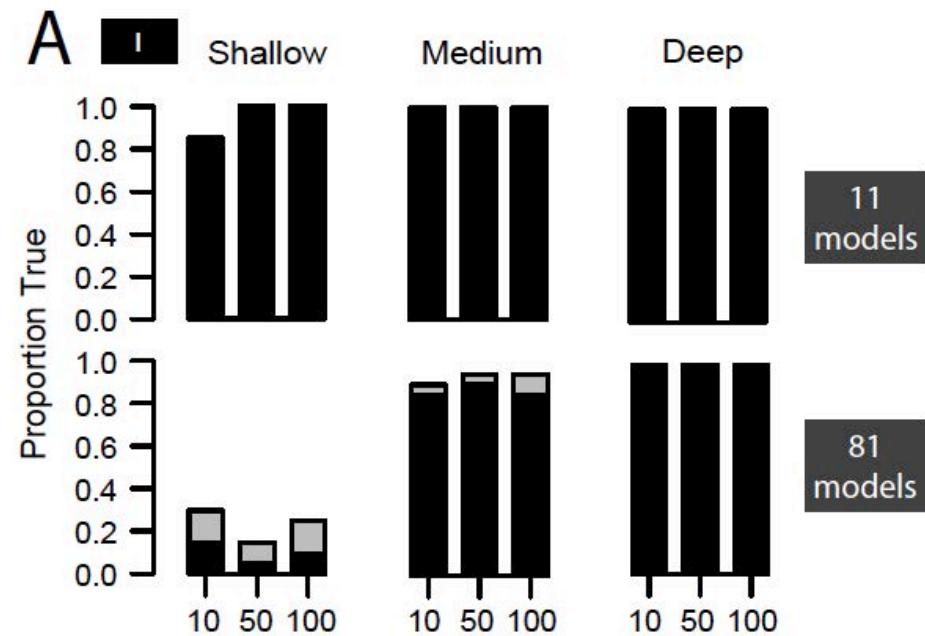
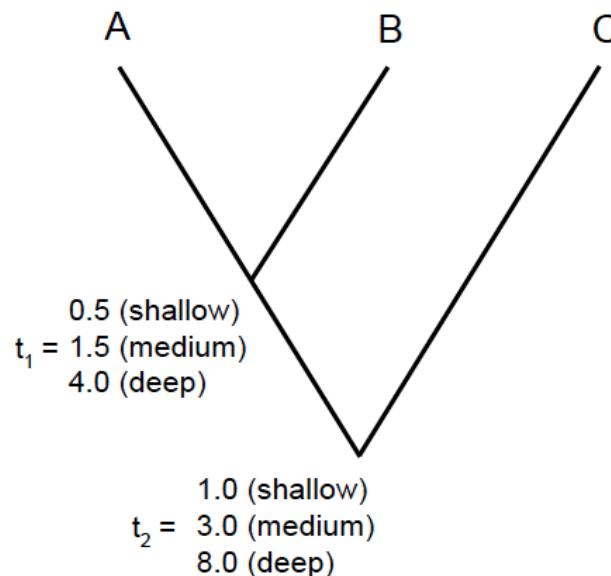
phylogeographic inference using approximated likelihoods

exploration using published phylogeographic data



phylogeographic inference using approximated likelihoods

Simulation testing: Isolation - only model

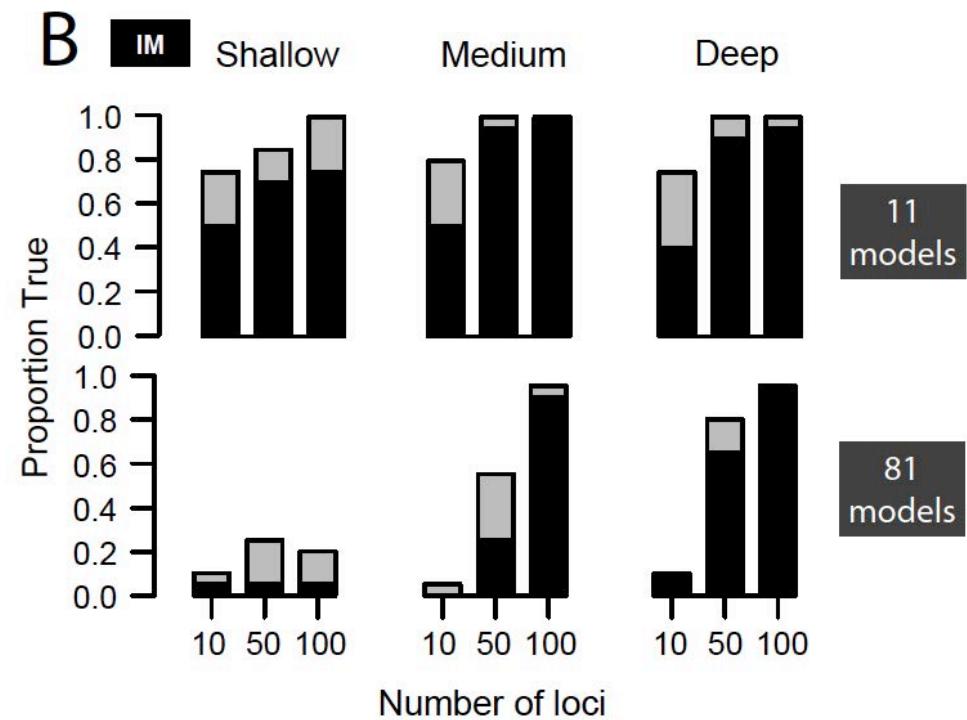
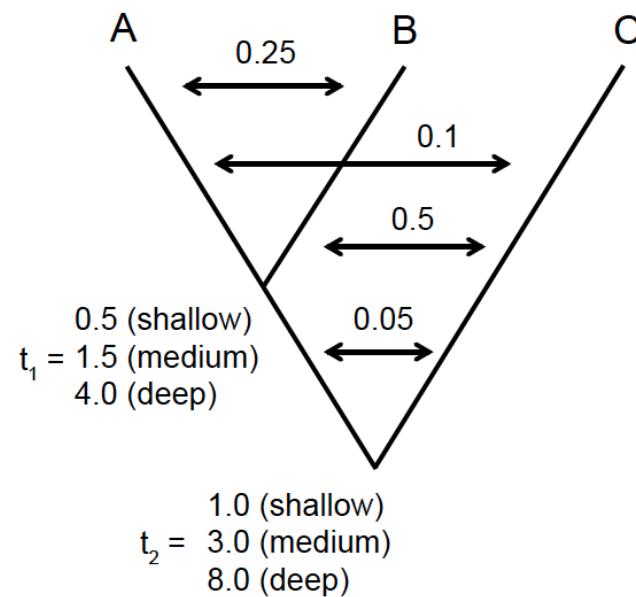


Black bar = proportion of replicates generating model had highest AIC score.

Grey bar = proportion of replicates generating model had second highest AIC score.

phylogeographic inference using approximated likelihoods

Simulation testing: Isolation-with-Migration model

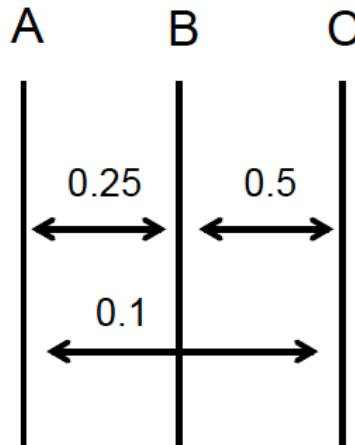


Black bar = proportion of replicates generating model had highest AIC score.
Grey bar = proportion of replicates generating model had second highest AIC score.

phylogeographic inference using approximated likelihoods

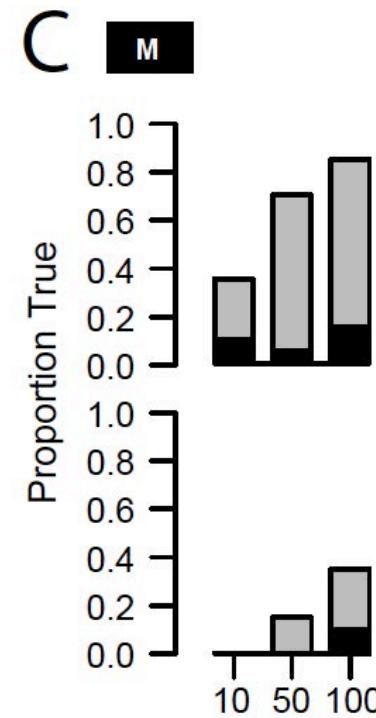
Simulation testing: Island Migration model

C migration only (MO)



11
models

81
models

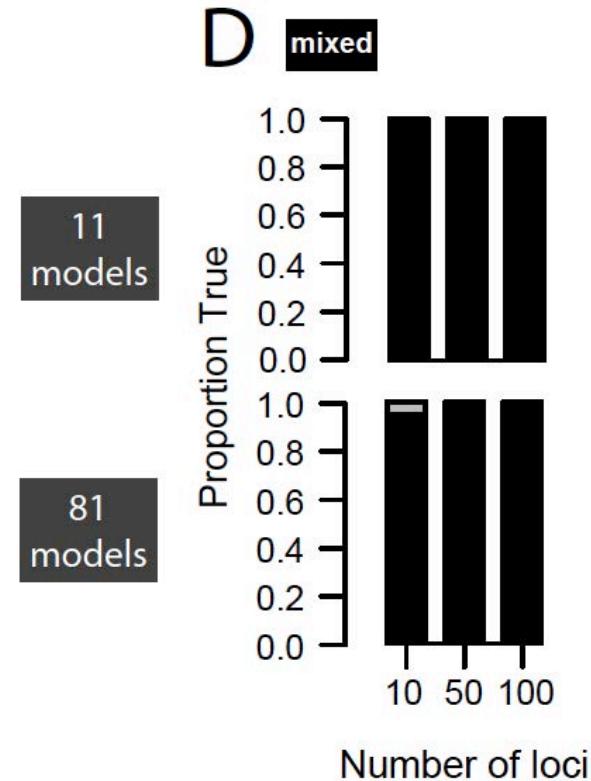
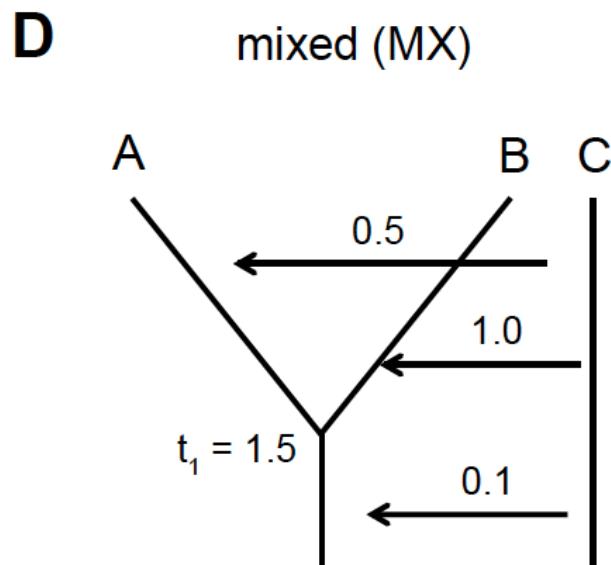


Black bar = proportion of replicates generating model had highest AIC score.

Grey bar = proportion of replicates generating model had second highest AIC score.

phylogeographic inference using approximated likelihoods

Simulation testing: Mixed model



Black bar = proportion of replicates generating model had highest AIC score.
Grey bar = proportion of replicates generating model had second highest AIC score.